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Adaptation, Diversification, and Desert Ecology of the Most Diverse Order of Mammals (Mammalia, Rodentia)

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ADAPTATION, DIVERSIFICATION, AND DESERT ECOLOGY OF THE MOST DIVERSE
ORDER OF MAMMALS (MAMMALIA, RODENTIA)

By

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This dissertation is dedicated to my parents.

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ABSTRACT

Globally, species diversity is regulated by speciation and extinction, and regionally it is regulated by competition, niche, colonization, emigration, and extinction, and more locally, by environmental tolerance and species interactions which filter out non-adapted species based on intrinsic characteristics, or their Hutchinsonian niche. In this dissertation, I examined some of the mechanisms that govern biodiversity patterns in order to determine the main causes of uneven diversity in muroid rodent clades, the most diverse superfamily of mammals, comprising 28% of all mammal species. This extensive diversity, in addition to the remarkable eco-morphological adaptability which facilitated their colonization of all terrestrial biomes make muroids an ideal system to study this fundamental question in evolutionary ecology. In addition, the use of robust phylogenies that have recently been developed in muroids and non-muroid rodents makes the order an especially attractive model system to understand the process of mammalian adaptation to arid environments and the ecological interactions that shaped patterns of coexistence within desert communities, the second main goal of the dissertation. The use of a combination of molecular phylogenetics and geometric morphometrics allows for a robust investigation of general patterns that shape the ecological evolution of this group within and without desert habitats, warranting a reinterpretation of classical studies in evolutionary biology, desert ecology, and the traditional systematics of desert rodent clades.

CHAPTER ONE

INTRODUCTION

Diversity of Rodents

One of the main themes of this dissertation is accounting for the diversity of rodents. Despite originating 10-30 million years after most orders (Flynn et al. 1985; Bininda- Emonds et al. 2007), they are the most diverse order of mammals, with 2,277 extant species in 481 genera currently described in Musser and Carleton (2005), and more genera described each year (e.g. *Paucidontomys*, Esselstyn et al. 2012; *Halmaheramys*, Fabre et al. 2013). Rodents constitute nearly half of extant mammal diversity, exceeding all orders in diversity at both the species and the genus level, and include a variety of forms including mice, rats, gophers, beavers, guinea pigs, porcupines, and squirrels (Wilson and Reeder 2005). Rodents are found on all continents, most islands, and all major landmasses except for Antarctica and New Zealand (Fabre et al. 2012) where they inhabit all terrestrial ecosystems ranging from hyper-arid deserts to rainforests (Kay and Hoekstra 2008). Rodents are defined by their continuously growing incisors (Nowak 1999) and are extremely diverse in terms of ecology and morphology, with adult body masses ranging from 7 grams in pygmy jerboas (Gromov and Eszhanov 2004) to 50 kilograms in capybaras (Barbella 1987) and even up to 1,000 kilograms in the extinct *Josephoartigasia monesi* (Rinderknecht and Ernesto 2008). An example of the great variation in the ecologies of rodents include their various locomotory modes which include quadrupedality, bipedality, arboriality, as well as the ability to swim, glide, and burrow (Nowak 1999). Most rodents are small generalists with short life cycles, prolific breeders, and opportunistic feeders, with diets that include seeds, grasses, bark, insects, fish, and scorpions (Kay and Hoekstra 2008).

Rodents are commonly divided into five suborders that vary greatly in diversity (Musser and Carleton 2005): Myodonta (Muroidea and Dipodoidea) with 1,569 species; Sciuroomorpha with 307 species; Hystricomorpha with 290 species; Castorimorpha with 102 species; Anomaluroomorpha with 9 species (Fabre et al. 2012). Over a half of rodents belong to the superfamily Muroidea (1,518-1,613 species, depending on the inclusion of newly described species), which is the most diverse superfamily of mammals, comprising nearly a third of extant mammal diversity (Musser and Carleton 2005). The relatively recent basal radiation of Muroidea

(40-45 mya, Schenk et al. 2013) and their wide geographic distribution that includes all terrestrial habitats (Macdonald 1984; Nowak 1999) make this group particularly amenable to the study adaptive radiation.

Adaptive Radiation and Other Ecological Correlates of Diversity

Adaptation is the degree to which an organism is able to survive and reproduce in a given habitat (Dobzhansky 1970), commonly inferred by correlation to abiotic and biotic factors. Adaptive radiation is the evolution of ecological diversity in a rapidly diversifying lineage (Schluter 2000; Rundell and Price 2009) or the simultaneous divergence of ancestral populations from one adaptive “type” into many due to adaptation to different adaptive zones (Simpson 1953). The study of adaptive radiation increasingly relies on phylogenetic comparative methods that test the association between diversification rates and other extrinsic and intrinsic factors that may explain differences in diversity between clades. Theoretically, the main causes of adaptive radiation include the evolution of key innovations, biogeographic transitions (movement into new regions), and mass extinction of competitors or predators all of which provide “ecological opportunities” for diversification (Simpson 1953; Schluter 2000).

Key innovations, such as the evolution of flight in the ancestor of birds (Feduccia 1999), are traits that allow a clade to expand its niche, and therefore facilitate diversification by reducing competition in the newly evolved niche. Similarly, biogeographic transition, if it leads to the colonization of a region the lacks close competitors and predators, and has sufficient resources, also facilitates diversification by reducing competition. A common example of an adaptive radiation, brought about by the ecological opportunity presented by biogeographic transition, is Darwin’s finches colonization of the Galápagos which lacked close relatives making the niche space relatively “empty” and spurring diversification (Grant 1999). However, in order for a biogeographic transition to lead to an adaptive radiation, three opportunities need to be present: (1) geographic opportunity is brought about by geological events that facilitate range expansion (e.g. the formation of the Isthmus of Panama), (2) physiological opportunity (the ability to tolerate abiotic conditions of a new area), and (3) ecological opportunity due to large unoccupied niche space as a consequence of the area lacking close relatives (Pruitt et al. 2000). Ecological opportunity can also be a consequence of mass extinctions of competitors or

predators, such as the Cretaceous–Tertiary extinction event that lead to the replacement of non-avian dinosaurs with mammals (Ocampo et al. 2006).

Other approaches to study of adaptive radiation focus on intrinsic characteristics of clades that may explain their exception diversity. These generally focus on such attributes as morphology and ecology and how they may enhance or hinder diversity. Differences in clade diversity in various taxa have been explained in terms of ecological disparity (e.g. Isaac et al. 2005; Phillipmore et al. 2006; Ricklefs 2006, 2007; Langerhans 2010; Gómez and Verdú 2012; Rojas et al. 2012) using various methods (e.g. Mitter et al. 1988; Nee et al. 1992; Slowinski and Guyer 1993; Mooers and Heard 1997; Heilbuth 2000; Isaac et al. 2003; Paradis 2005; Maddison 2006; Vamosi and Vamosi 2005; Maddison et al. 2007; FitzJohn et al. 2009; FitzJohn 2010) where ecological attributes are thought to affect diversification rates by directly influencing the rates of speciation and extinction (FitzJohn 2010). In the past, most tests of ecological diversification consist of sister-group comparisons, where diverse clades are compared to less diverse sister clades in terms of ecological attributes. This is done by various methods but generally consist of comparing observed rates of trait evolution in focal clades to null models of trait evolution such as the Brownian motion (Felsenstein 1988; O’Meara et al. 2006) or the Ornstein-Uhlenbeck (Hansen and Martins 1996) process.

Trait-dependent diversification methods, however, are becoming increasingly sophisticated incorporating model comparison frameworks as well as maximum likelihood and Bayesian inference to test the association between diversification rates and ecological traits for various data types (binary, Maddison et al. 2007, FitzJohn et al. 2009; multistate, FitzJohn 2010; continuous, FitzJohn 2010; geographic, Goldberg et al. 2011). This class of diversification methods work by maximizing the likelihood of the tree and the character states for the tips based on a combination of parameter values for speciation, extinction, and transition rates for each character state (FitzJohn 2010). They also compare the fit of various intermediate trait-dependent diversification models (where various combinations of speciation, extinction, and transition rates are constrained to be equal for some or all of the states) to the fully constrained (character-state independent) null model (FitzJohn 2010) and can accommodate incompletely sampled and/or incompletely resolved trees (FitzJohn et al. 2009).

Why are Muroid Rodents so Diverse?

There are many factors that contribute to the extreme, and uneven, diversity of muroids. These include variations in extrinsic factors experienced by subclades such as climate, vegetation and resource diversity, the geographical location of the clades, and the presence or absence of competitors (e.g. mass extinctions events) all of which may provide an ‘opportunity for diversification’ (Simpson 1953; Schluter 2000) for some clades and not others. Although most muroids share similar characteristics that lead them to diversify greatly, such as small size and elevated fecundity, phylogenetic patterns of species richness also depend on intrinsic species characteristics such as body size, behavior, diet, and other ecological traits (which may include key innovations) which may enhance or hinder the diversification process (e.g. FitzJohn 2010).

In the first part of the dissertation (chapters 3-5), I address the question of what drives uneven muroid rodent clade diversity using both a 297 (chapters 3-4) and a 317 (chapter 5) species chronograms estimated by Schenk et al. (2013) and Steppan et al. (in prep). This is done by first (chapter 3) testing the fit of the *phenotypic* predictions of the ecological opportunity model of adaptive radiation brought about by primary continental colonization. This study follows a similar study of the *taxonomic* predictions of the ecological opportunity model of adaptive radiation by Schenk et al. (2013) where they detected multiple accelerations in taxonomic diversification, most of which do not coincide with biogeographic transition. I use the same phylogeny (the most thoroughly sampled muroid phylogeny to date; Schenk et al. 2013) and biogeographic analyses to test the phenotypic predictions of ecological opportunity. Tested phenotypic predictions of the ecological opportunity model include an acceleration in ecomorphological evolution rate, early ecomorphological disparity, and a gradual slowdown in the rate of ecomorphological evolution through time as niches fill up following primary continental colonization (e.g. Baldwin and Sanderson 1998; Schluter 2000; Lovette et al. 2002; Harmon et al. 2008).

Next (chapter 4), I examine the role of intrinsic factors (ecological traits and ecomorphology) in driving the pattern of diversification in muroids. I tested the correlation between ecology/eco-morphology (including such traits as body mass, body proportions, and diet) with diversification rates using “trait-dependent diversification methods,” extensions of “BiSSE” (Binary State Speciation and Extinction, Maddison et al. 2007) in the Diversitree library (FitzJohn 2012) in R (R Development Core Team 2013). I collected ecological and

ecomorphological data from the literature from online data repositories (e.g. IUCN and GBIF (Global Biodiversity Information Facility), field guides, and other sources (e.g. Nowak 1999). This investigation was conducted to assess the relative importance of extrinsic (chapter 3) vs. intrinsic (chapter 4) factors in explaining the pattern of muroid rodent diversity.

In chapter 5, I address the question of whether the diversity of muroids is explained by the pattern of morphological evolution/disparity, or more specifically, whether diversity/diversification rates are correlated with disparity/morphological evolution rates, which is predicted by both the punctuated equilibrium hypothesis (Gould and Eldredge 1977) and the theory of ecological adaptive radiation (Schluter 2000). The morphological dataset is based on the cranium, which is an important measure of niche since it houses most of the sensory organs and masticatory muscles which impact the morphology of the underlying bone. I quantified cranial morphology using both traditional distance based morphometrics, and the three dimensional geometric morphometric approach. Geometric morphometrics is a Cartesian coordinate based method for shape quantification that removes the effects of translation, rotation, and scale (sequestering shape and size variables into different datasets) through the use of a generalized procrustes analysis (Rohlf and Slice 1990), retaining the geometry of the throughout the analyses and therefore facilitating visualization of shape differences using thin-plate spline deformation grids (Zelditch et al. 2004). I also used the geometric morphometric approach in two of the three subsequent desert ecology chapters.

While in the first part of the dissertation I focused on one clade, muroids, and some of the ecological and evolutionary explanations of their uneven diversity and adaptive radiation. In the second part of the dissertation, I focused on one habitat, deserts, and some of the ecological and evolutionary patterns of taxonomic and morphological diversity of rodents within this habitat, as well as patterns of morphological adaptation, community structure, and systematics of desert rodent clades; all topics that fall within the realm of ‘Desert Ecology.’

Desert Ecology

A desert is a region of extreme aridity that can vary greatly in temperature and includes cold regions like Antarctica (Sowell 2001; Ward 2009). However, heat increases aridity through increased evapotranspiration, which increases daytime heating as a consequence of increased

solar radiation penetration (Sowell 2001). Deserts are formed through extended periods of low rainfall that generally does not exceed an annual average of 25 centimeters (Lomolino et al. 2005). However, unpredictable (rather than low) precipitation is the main cause of aridity (Ward 2009), since some deserts receive more rainfall annually than mesic regions through a few unpredictable cloudbursts that erode the soil and render it unusable to plants and animals (Louw and Seely 1982; Sowell 2001). The consequence of this rainfall pattern is a landscape that is a dry and unproductive with <10% perennial cover (Sowell 2001). Deserts are found on all continents and cover one-fifth of dry land, constituting the largest terrestrial biome (Hickman et al. 2004).

Desert ecology is the study of the interaction between organisms and arid environments. This includes such topics as the interactions of organisms in desert communities, systematics of desert clades, as well as (convergent) morphological and physiological adaptations to aridity. Adaptation to aridity is achieved through water and energy conservation which is attained through lowered metabolic rate (e.g. lizards, Snyder 1971, Mautz 1979, Putnam and Murphy 1982, Kamel and Gatten 1983, Fusari 1984, Peterson 1990, Dial and Grismer 1992, Mautz and Nagy 2000; insectivores, Lindstedt 1980; marsupials, Hulbert and Dawson 1974; ungulates, Shkolnik et al. 1972; rodents, Hart 1971), lowered body mass (Hickman et al. 2004), and bipedal/asymmetrical gaits (Berman 1985; Rocha 1995; Rocha et al. 2007) that are more energy efficient than quadrupedal gaits in long distance travel and conserve energy in long distance travel at the expense of dexterity (McHenry and Rodman 1980). Bipedality, fleshy footpads, and scaly fingers reduce the transfer of heat from the warm surface to the body (Ezcurra et al. 2006) and hence conserve water through the reduced need for evaporative cooling. Other common mammalian adaptations to aridity include the evolution of short, hard, and compact fur coats with increased ventilation that allow sweat to evaporate directly from the skin (Ezcurra et al. 2006). Many small desert mammals avoid heat and aridity by being nocturnal and living in mesic micro-habitats such as burrows or oases (Sowell 2001; Ward 2009). Other common desert adaptations are to the environmental manifestation of aridity, which include low vegetative cover and unique soil structure, leading to widely dispersed food and water resources, increased airborne predation risk, and the need for distinct locomotory style, and fossoriality (Sowell 2001; Ward 2009). Many traits that are characteristic of rodents such as prolific breeding during periods of abundance and generalized feeding are pre-adaptations to desert environments.

The International Union for Conservation of Nature Red List classifies 11% of rodents (243 species) as living in desert habitats, most of which are myodont, castorimorph, and sciromorph (IUCN 2013). These rodents have undergone numerous convergent adaptations to aridity leading to ecological equivalence in families inhabiting different deserts around the world; such as the independent evolution of bipedality in North American heteromyids, Palearctic jerboas, and Australian hopping mice (Mares 1975, 1976, 1980, 1993a, b; Nevo 1979; Randall 1994; Ojeda et al. 1999). Desert rodents also frequently converge on increased nasal passage complexity to assist water conservation during exhalation (Schmidt-Nielsen and Schmidt-Nielsen 1951; Cortes et al. 1988, 1990), leaf shaving feeding behavior to remove salt deposits on the epidermis (Mares et al. 1997; Ojeda et al. 1999), as well as inflated tympanic bulla to assist in sound detection in open habitats (Ojeda et al. 1999). Other frequent convergent adaptations exhibited by desert rodents include more complex kidneys and increased digestive tract complexity for efficient urine concentration and fecal dehydration, burrowing behavior, reduction in basal metabolic rate, and lowered thermal conductance (Ma and Foster 1986; Merkt and Taylor 1994; Tirado et al. 2007) which occur in various rodent groups in South America: southern viscacha, red vizcacha rat, mountain cavies, vesper mice, silky desert mice, and salt flat mice; North American heteromyids; and in Palearctic desert groups: dipodoids, gerbils, and spiny mice (Bozinovic and Gallardo 2005; Bozinovic et al. 2007; Diaz 2001; Diaz and Ojeda 1999; Diaz et al. 2001; Sassi et al. 2007).

Seminal studies in desert ecology/adaptation have been conducted before the development of the field of molecular phylogenetics and consequently did not use phylogenetic comparative methods that account for the non-independence of compared taxa as a consequence of their shared evolutionary histories (e.g. Harvey and Pagel 1991; Purvis et al. 1995; Schluter et al. 1997; Cunningham et al. 1998; Freckleton and Harvey 2006). The recent growth of the field of molecular phylogenetics in all taxa and especially in rodents (muroids, Steppan et al. 2003, 2004a, 2005, Jansa and Weksler 2004, Rowe et al. 2008, Schenk et al. 2013; dipodoids, Fan et al. 2009, Lebedev et al. 2013; sciromorphs, Mercer and Roth 2003, Steppan et al. 2004; castorimorphs, Alexander and Riddle 2005; anomaluromorphs, Matthee and Robinson 1997; hystricomorphs, Rowe and Honeycutt 2002; heteromyids, Alexander and Riddle 2005, Light and Hafner 2008; as well as the whole rodent order using the supermatrix approach, Montgelard et al. 2008, Fabre et al. 2012) warrant the re-examination of fundamental questions in desert

ecology/adaptation with a phylogenetic perspective. Moreover, the fundamental question in ecology of whether neutral or deterministic processes limit local assemblages to subsets of regional species pools (Elton 1946; Cardillo 2011), have been traditionally conducted on granivorous desert rodents of North America (e.g. Bowers and Brown 1982; Kotler and Brown 1988; Brown 1989) without a detailed understanding of the phylogenetic relationships of the compared taxa. The development of phylogenetic community ecology methods (Webb 2000; Webb et al. 2002) facilitates the use of molecular phylogenies to address fundamental questions in community ecology, while using phylogenetic distance as an index of ecological similarity, and has recently been used to explore patterns of community organization in rodents of the Mojave Desert (Steven et al. 2012).

General and Specific Trends in Cranial and Mandibular Adaptation to Aridity in Rodents

Understanding how organisms adapt to aridity is a central theme in traditional desert ecology research. In chapter 6, I use a composite chronogram of rodents (based on a combination of Fabre et al.'s (2012) 1,265 species supermatrix molecular phylogeny of rodents and Steppan et al.'s (in prep) 913 species phylogeny of muroid rodents based on multiple nuclear and mitochondrial markers) to apply phylogenetic correction (e.g. Felsenstein 1985) and test the correlation between cranial, mandibular, and dental characters with measures of habitat aridity in 591 desert and mesic species sampled throughout this composite phylogeny. I estimated aridity indices using species range data from IUCN combined with WorldClim bioclimatic variables (Hijmans et al. 2005) extracted using GIS. I tested the association between skull morphology and aridity to identify the adaptive value of morphological changes and to determine if there are general trends in desert adaptation shared by members of the order, while focusing on traits that earlier studies have found to be desert adaptive at more limited scales including tympanic bulla inflation (considered to be an adaptation to increased auditory sensitivity in open habitats; e.g. Lay 1972), nasal passage elongation (considered as an adaptation for water conservation; e.g. Schmidt-Nielsen and Schmidt-Nielsen 1951), and increased lower incisor index (indicating a squarer shape, associated with leaf shaving feeding behavior in open habitats; e.g. Ojeda et al. 1999). I also use habitat information collected for 2,414 OTUs along with the composite chronogram (with all missing desert and mesic species grafted onto the closest relatives that

appear in the tree), representing all rodent species available in IUCN (2013) to investigate the general pattern rodent transition between desert and mesic ecosystems.

In a subsequent study (chapter 8), I combine all DNA sequence data available from GenBank, in addition to newly collected, and unpublished sequences of gerbils and deomyines, which together amount to the largest molecular dataset for gerbils and deomyines (both in terms of taxa sampled and characters examined; which with the addition of outgroups amount to 95 species, representing ~52% of gerbil species and ~44% of deomyine species) in order to estimate the phylogenetic relationships within the group. I estimated the phylogeny for the proposed taxonomic revisions in this group, where especially gerbils are plagued by discordance between morphological and molecular phylogenies (e.g. Pavlinov et al. 1990 vs. of Chevret and Dobigny 2005) as well as frequent paraphyly at taxonomic levels ranging from tribes to subgenera which is commonly attributed to widespread convergent adaptations to aridity in this predominantly desert clade (Chevret and Dobigny 2005). In addition, I use a chronogram estimated using the aforementioned sequence data along with multiple fossil calibrations in order to re-examine the pattern bullar adaptation to aridity (i.e. do desert gerbils/deomyines have more inflated tympanic bulla, as an adaptation to increased auditory sensitivity in open habitats? e.g. Lay 1972) in a more focused scale that includes gerbils and deomyines and using a more detailed geometric morphometric approach based on sliding semi-landmarks. The use of this approach allows for isolating size from shape when testing the correlation between bullar morphology with aridity, which was not examined in the broader taxonomic scale investigated in chapter 6.

Community Structure in Ecological Assemblages of Desert Rodents

The main objective of community ecology is to understand the mechanisms that facilitate coexistence in local assemblages. Classical studies of coexistence in desert rodent communities have typically explained community structure in terms of competition theory as a consequence of the observed pattern of over-dispersion in body size (e.g. Bowers and Brown 1982; Kotler and Brown 1988; Brown 1989). In chapter 7, I use the community phylogenetic approach (Webb 2000; Webb et al. 2002) to test the prediction that desert rodent assemblages around the world are non-randomly assembled from species pools of desert regions, which in turn are non-randomly assembled from the larger biogeographic regions. I test this prediction using the aforementioned composite phylogeny of rodents (from chapter 6) and also test the prediction that

desert rodent assemblages exhibit morphological structure (i.e. are non-randomly assembled relative to their morphology) using a newly collected two dimensional cranial and mandibular geometric morphometric dataset for 234 desert rodent species and body mass data for 1,411 desert and mesic species (collected from PanTHERIA database; Jones et al. 2009). The two possible patterns of community structure are significantly clumping or over-dispersion, two patterns that are generally attributed to environmental filtering and competitive exclusion respectively (Webb 2000; Webb et al. 2002) and are generally contrasted with random or neutral assembly (e.g. Hubbell 2001).

Significance

This dissertation contributes to the understanding of the mechanisms that promote biodiversity in muroid rodents as well as the desert ecology of rodents. The main novelty of this work is its large order-level scale as well as the relatively large sample of species used in comparative analyses which range from 95 to 591 species in each chapter (with several analyses conducted on all 2,414 rodent species). Analyses conducted at this large scale and using a phylogenetic perspective are important to put results obtained from analyses conducted on more limited taxonomic scope into broader context to test the generality ecological and evolutionary patterns. In addition, studying the ecology and evolution of relatively uncharismatic taxa such as desert rodents is becoming increasingly urgent since habitat loss caused by human development is leading to increased extinction rates in these taxa (e.g. Valone et al. 1995; Prakash 1997; Waser and Ayers 2003) which are persecuted more than others.

CHAPTER TWO

OVERVIEW OF CRANIAL AND MANDIBULAR MORPHOLOGICAL DATA COLLECTION AND PROCESSING

Cranial and Mandibular Morphological Sample

Most of the morphological data that I collected come from crania and jaws housed at the Field Museum of Natural History, the Museum of Vertebrate Zoology, the Smithsonian Institution National Museum of Natural History, the American Museum of Natural History, the Florida Museum of Natural History, Laboratorio de Citogenetica Mamiferos, Facultad de Medicina, Universidad de Chile, and the Oklahoma Museum of Natural History. When possible, I digitized at least two adult male and two female skulls per species using a Microscribe MX5 3D stylus digitizer (accurate to 0.002 mm; Immersion Corporation, San Jose, CA, USA) and a Nikon D3200 digital SLR camera (Nikon, Tokyo, Japan) using a Nikon 40mm f/2.8G AF-S DX Micro-Nikkor Lens (Nikon, Tokyo, Japan) at 24 megapixels (resolution = 6,016 x 4,000; JPEG) in a standardized manner (see photography section below). I only digitized wild caught, adult individuals as determined by basioccipital – basisphenoid epiphyseal fusion (as in Robertson and Shadle 1954; Samuels 2009) and a completely erupted 3rd molar that has reached the occlusal surface (Steppan 1997). I confirmed adult status by examining the associated skin and choosing average body sized specimens and excluding juvenile body sizes and extremely large outliers as to not skew the results from the species average, or the typical condition.

I used the three-dimensional dataset for the first part of the dissertation that dealt with the correlates of diversity in muroid rodents, and therefore only muroids and their closest relatives, the dipodoids, were digitized. Complete taxonomic sampling was not possible for several reasons. (1) Not all species are available in the visited museums (e.g. rare species). (2) Not all specimens that were available are suitable for microscribe digitization. Some species have extremely small and delicate crania where mounting them on clay for three-dimensional digitization (see below) would risk breaking them and therefore were not included. (3) Crania represented by one or a few specimens that are in bad condition were avoided. I based taxonomic sampling of muroid rodents on the following criteria. (1) Subclades were sampled as broadly as possible, making sure to include most basal splits. (2) Species included in Schenk et al.'s (2013)

muroid phylogeny were prioritized. (3) Species with unusual morphology were prioritized to include a good representation of the extent of disparity in the group. For example, only 1 specimen of Delacour's marmoset rat (*Hapalomys delacouri*) was found in all the museums that I visited, and therefore was prioritized because it is unique in having a fully opposable hind toe (wide hallux), which bears a flattened nail instead of the usual claw thought to be an extreme adaptation to arboriality (Musser 1972). Other rare and unique specimens (that are in good condition) were also prioritized such as the long-tongued arboreal mouse (*Rhagomys longilingua*).

Following Schenk et al. (2013), I sampled species in a way that is both random and proportionate to the diversity of each subclade, making sure not to oversample one group at the expense of another. The three-dimensional dataset include representatives from all 6 families and all subfamilies of muroids and a sample of dipodoids (Table 2.1). The morphological dataset consists of 1,125 crania digitized in three-dimensions using the microscribe digitizer (Appendix Table A.1) in addition to 2,075 skulls photographed and subsequently digitized in two dimensions (Appendix Table A.3). Crania were photographed dorsally, ventrally, and laterally, at multiple magnifications in each orientation while including a scale bar in each photograph (more details in the photography section). Jaws were photographed in the same manner as the crania in the lateral and occlusal orientations. A total of 312 OTUs (309 species) are included in the three-dimensional dataset and 602 OTUs (542 species) are included in the two dimensional dataset. Different data are extracted from different subsets of this list of species for each chapter (Appendix Tables A.1, A.3, A.4, and A.6).

Table 2.1. Taxonomic sampling for muroid and dipodoid subfamilies in the 3D dataset. Total species is based on Musser and Carlton (2005). Most genera in the focal group are sampled.

	# species	Total species	Proportion
Muroidea			
Calomyscidae			
Calomyscinae	1	8	0.13
Cricetidae			
Arvicolinae	22	151	0.15
Cricetinae	6	18	0.33
Neotominae	29	124	0.23
Sigmodontinae	83	377	0.22

Table 2.1—continued.

	# species	Total species	Proportion
Tylomyinae	3	10	0.30
Muridae			
Deomyinae	9	42	0.21
Gerbillinae	20	103	0.19
Lophiomyinae	1	1	1.00
Murinae	101	566	0.18
Nesomyidae			
Cricetomyinae	3	8	0.38
Delanomyinae	1	1	1.00
Dendromurinae	6	24	0.25
Petromyscinae	1	4	0.25
Mystromyinae	1	1	1.00
Nesomyinae	10	23	0.43
Platacanthomyidae			
Platacanthomyinae	1	2	0.50
Spalacidae			
Myospalacinae	2	6	0.33
Spalacinae	1	13	0.08
Rhizomyinae	2	4	0.50
Tachyoryctinae	1	13	0.08
Total focal group	304	1499	0.20
<u>Dipodoidea</u>			
Allactaginae	1	16	0.06
Cardiocrainiinae	0	7	0
Dipodinae	1	8	0.13
Euchoreutinae	0	1	0
Sicista	1	13	0.08
Zapodinae	1	5	0.20
Total outgroup	4	50	0.08
<u>Other</u>			
Abrocomidae	1	10	0.10

Microscribe Data Processing

Choosing crania to digitize for each species consisted of eliminating the following suboptimal choices. (1) Disarticulated crania. (2) Crania where most landmarks are not identifiable. Since three common landmarks were digitized on both the anterior and posterior orientations and are used to combine the dataset (see below), if all three of these landmarks were

not visible in a specimen, they were avoided. (3) Specimens with observable damage or non-visible suture lines. (4) Captive and/or specimens without locality information, because phenotypic plasticity may alter cranial morphology. I relaxed criteria for important groups (e.g. rare subclades, or species with distinct morphology) with few available specimens, which was only necessary for few specimens.

Overview of Three-dimensional Landmarks

Thirty four landmarks were digitized on each cranium, comprising 16 dorsal and 18 ventral landmarks (Table 2.2). Preliminary analyses on data collected following the first two museum visits showed no significant lateral asymmetry. Therefore, to increase sample size, I collected data only on the left side of the cranium on subsequent museum visits. Furthermore, analyses using both sides of the cranium in bilaterally symmetric organisms places more weight on lateral landmarks than on landmarks along the midline and also constitutes pseudoreplication. Restricting analyses to one side of the cranium is common practice in geometric morphometric studies of rodents (e.g. Elewa 2004; Samuels 2009; Yazdi et al. 2012). Because I did not detect significant sexual dimorphism in most species in the preliminary dataset, in rare specimens with few usable skulls, the criteria of balanced sampling of males and females was relaxed.

Landmarks are two or three-dimensional coordinates of homologous points like junctions of suture lines (Zelditch et al. 2004) with only evolutionary or developmental structures such as organs or tissues considered to be homologous biological structures (Zelditch et al. 1995). D'Arcy Thompson's generalized concept of biological homology includes discrete geometric structures such as points, curves, and partial warp scores (see below) of points and curves (Mitteroecker and Gunz 2009). Therefore, homologous points in geometric morphometrics refer to points with the same name in different species or within a species/specimen (e.g. Bregma) that are treated as biologically homologous landmarks. Linear distances were extracted from three-dimensional point coordinates prior to any geometric morphometric processing for comparison with studies that use traditional morphometrics (Table 2.3).

Chosen landmarks are present (homologous) in most muroid species and are evenly distributed throughout the cranium. Most landmarks follow Cheverud (1995) and Marroig and Cheverud (2001) in addition to end points of caliper measurements described in Steppan (1997). Due to the broad taxonomic scope of the study, I chose landmarks that are present in almost all

muroid skulls which were the ones most clearly defined in mammals. Very few species lacked any of these landmarks, and if they did, these landmarks were treated as missing data in the raw dataset. I digitized Type I, II, and III landmarks (Table 2.2). Type I landmarks are defined based on the discrete union of tissues such as triple-point suture intersections; Type II landmarks, or semilandmarks, are points with consistent operational definition such as maxima of curves and are not necessarily homologous; Type III landmarks are endpoints of maximum length or depth, or extreme points on a structure, and are not homologous (Bookstein 1991). Although Type I landmarks are biologically preferable over Type II and Type III landmarks due to being more consistently defined (Gunz et al. 2004), fewer landmarks of this sort are available in muroid crania than the other two types. Moreover Type I landmarks do not cover all the regions of the cranium, and inclusion of Type II and III landmarks were necessary to digitized those regions. This is especially true in functionally important regions of the cranium (e.g. bulla, auditory meatus, and teeth). These landmarks were consistently found in most taxa. I used equal numbers of Type I and Type III landmarks and only two Type II landmarks.

Table 2.2. List of three-dimensional landmark type. Numbers and acronyms match the full description below and the numbering in Figure 2.1.

Landmark	Acronym	Type
1. Bregma	BR	I
2. Pterion	PT	I
3. Anterior petrous region of the temporal bone	APT	I
4. Dorsal zygomatic point	DZ	III
5. Anterior nasal suture	ANS	I
6. Nasion	NA	I
7. Lateral frontomaxillary suture	LFM	III
8. Interorbital region	IR	III
9. Anterior naso-premaxillary suture	ANP	III
10. Anterior zygomatic plate	AZ	II
11. Ventral infraorbital foramen	VIF	II
12. Squamosal-parietal-frontal-sphenoid suture	SPF	I
13. Ventral zygomatic point	VZ	III
14. Ventral temporo-zygomatic suture	VTZ	III
15. Lateral incisor socket	LIS	III
16. Medial premaxilla-maxilla suture	MPM	I
17. Anterior edge of the first molar	AFM	I
18. Posterior edge of the third molar	PTM	III
19. Maxillary tuberosity	MT	III
20. Alisosphenoid-parapteregoid-temporal junction	APT	I

Table 2.2—continued.

Landmark	Acronym	Type
21. Medial edge of the bulla spine	MBS	III
22. Posterior tip of the hamular process	PH	III
23. Interdental region	IDR	I
24. Anterior edge of the incisive foramen	AIF	I
25. Posterior edge of the incisive foramen	PIF	I
26. Posterior edge of the interpalatine suture	PIP	I
27. Basion	BA	III
28. Opisthion	OP	III
29. Posterior edge of the jugular process	PJ	III
30. Lambda	LD	I
31. Medial parietal-interparietal suture	MPI	I
32. Asterion	AS	I
33. Dorsal-external edge of the auditory meatus	DM	III
34. Ventral-external edge of the auditory meatus	VM	III

Table 2.3. List of linear distances between three-dimensional landmark coordinates. Descriptions follow the included references, and acronyms match Table 2.2.

Distance	Description	Reference
BR-PT	Cranial	Marroig and Cheverud (2001)
BR-APT	Cranial	Marroig and Cheverud (2001)
PT-APT	Cranial	Marroig and Cheverud (2001)
PT-BA	Cranial	Marroig and Cheverud (2001)
PT-DM	Cranial	Marroig and Cheverud (2001)
PIP-APT	Cranial	Marroig and Cheverud (2001)
LD-AS	Cranial	Marroig and Cheverud (2001)
BR-LD	Cranial	Marroig and Cheverud (2001)
OP-LD	Cranial	Marroig and Cheverud (2001)
PT-AS	Cranial	Marroig and Cheverud (2001)
PJ-AS	Cranial	Marroig and Cheverud (2001)
BA-OP	Cranial	Marroig and Cheverud (2001)
BA-DM	Cranial	Marroig and Cheverud (2001)
IDR-ANS	Nasal	Marroig and Cheverud (2001)
NA-PIP	Nasal	Marroig and Cheverud (2001)
ANS-DZ	Nasal	Marroig and Cheverud (2001)
IDR-MPM	Oral	Marroig and Cheverud (2001)
MPM-DZ	Oral	Marroig and Cheverud (2001)
MPM-VZ	Oral	Marroig and Cheverud (2001)
MPM-MT	Oral	Marroig and Cheverud (2001)
DZ-VZ	Oral	Marroig and Cheverud (2001)
VZ-MT	Oral	Marroig and Cheverud (2001)
MT-PIP	Oral	Marroig and Cheverud (2001)
DM-VTZ	Zygomatic	Marroig and Cheverud (2001)
VTZ-SPF	Zygomatic	Marroig and Cheverud (2001)

Table 2.3—continued.

Distance	Description	Reference
VZ-VTZ	Zygomatic	Marroig and Cheverud (2001)
VZ-SPF	Zygomatic	Marroig and Cheverud (2001)
PT-VTZ	Zygomatic	Marroig and Cheverud (2001)
PT-SPF	Cranial , Zygomatic	Marroig and Cheverud (2001)
IDR-PIP	Oral , Nasal	Marroig and Cheverud (2001)
ANS-VZ	Oral , Nasal	Marroig and Cheverud (2001)
APT-BA	Basioccipital length	Marroig and Cheverud (2001); Steppan (1997)
NA-BR	Frontal length	Marroig and Cheverud (2001); Steppan (1997)
ANS-NA	Nasal length	Marroig and Cheverud (2001); Steppan (1997)
MPI-BR	Parietal length	Steppan (1997)
MPI-LD	Interparietal length	Steppan (1997)
AFM- LIS	Diastema length	Steppan (1997)
AFM-PTM	Molar tooth row	Steppan (1997)
APT- PTM	Pterygoid region	Steppan (1997)

Description of Three-dimensional Landmarks

Landmark descriptions are mostly based on Marroig and Cheverud (2001). Numbers and acronyms of landmarks are as in Figure 2.1 and Tables 2.2, and 2.3.

1. (BR) Bregma. Located at the intersection between the coronal suture and the sagittal suture perpendicularly. It is found on the superior mid-portion of the skull cap and the point of junction between the frontal and parietal bones. The landmark is digitized on the dorsal surface of the skull at the medial-most region of the suture at the junction between the frontal and parietal. Although the landmark is easy to measure and is found in all muroid rodents, the suture lines do tend to differ between species in the direction of the small invaginations where the anterior-most point of the suture is on the frontal in some cases and between the parietals in others. Because this landmark easy to find and unambiguously measure in all muroid rodents, it is one of the three landmarks that are used in the primary procrustes superimposition to merge together data from the two orientations of the cranium (see below).

2. (PT) Pterion. Located at the posterior end of the sphenoparietal suture and is the point of junction between the sutures of the parietal, frontal, and temporal bones. This landmark is also easy to find and unambiguously measure in all muroid rodents and therefore used in the primary procrustes superimposition to merge data from the two orientations of the cranium (see below).

3. (APT) Anterior petrous region of the temporal bone. Wedged in at the base of the skull between the sphenoid and occipital bones, digitized at the lateral-most region of the suture

that demarcates the basisphenoid and the basioccipital. This suture is also easy to find and is often used to determine the age of various muroid rodent groups, and is the third landmark used to merge data collected from the two orientations of the cranium (see below).

4. (DZ) Dorsal zygomaxillary point. The zygomatic arch is composed of the maxilla, jugal, and squamosal bones. The landmark is located at the most dorsal extent of the suture that delimits the zygomatic process of the maxilla and the jugal.

5. (ANS) Anterior nasal suture. The nasals are rectangular and cover the dorsal surface of the rostrum and their junction forms the bridge of the nose. The rostral margin of the nasals is joined in preparations of some species and in others, they are joined more posteriorly. The nasals join in the median plane forming the internasal suture and the landmark is the anterior-most point of the internasal suture. In individuals with disarticulated nasals, the lateral surface of the nasal bone is traced to the most anterior point and the landmark is digitized on the lateral side of the left nasal bone.

6. (NA) Nasion. The posterior regions of the nasal bones make contact with the anterior region of the frontal bone at the frontonasal suture. The landmark is the junction between the frontal (frontonasal suture) and two nasals (internasal suture) which usually occurs between the orbits, superior to the bridge of the nose.

7. (LFM) Lateral frontomaxillary suture. The landmark is the point of junction between the nasal process of the frontal bone and the frontal process of the maxilla at the top of the bridge of the nose. This serrated suture contacts the frontonasal suture in the anterior-medial margin and the landmark is digitized on the lateral most point of the suture, on the dorsal surface of the cranium. There is great variation in this suture in muroid rodents and sometimes it divides into two sutures laterally near the lacrimal bone, and in those instances the landmark is digitized on the median point between these two suture divisions before the split.

8. (IR) Interorbital region. The landmark is located between the orbits and exhibits great variation in muroids. In some groups (e.g. cricetids and gerbils), the frontal bone exhibits two faint ‘suture’ lines along the sagittal and horizontal planes that sub-divide the bone into four roughly equally sized bones, two anterior which join the nasals, and two posterior which join the parietal. The landmark is digitized on the lateral-most of the horizontal faint ‘suture’ on the dorsal surface of the skull, which separates the two anterior regions of the frontal bone from the two posterior regions. When this suture is not clearly visible, the landmark is digitized on the the

median of the frontal bone, which is the region where the suture is found in individuals with a clear demarcation. This landmark coincides with the endpoints of calipers when measuring interorbital width.

9. (ANP) Anterior naso-premaxillary suture. This landmark is the point of contact between the nasal and the premaxilla, digitized on the anterior-most point of the suture, or the first point of contact between the bones. There is great variation in the region of first contact (anterior intersection) between the bones. This landmark coincides with the endpoints of calipers when measuring nasal breadth.

10. (AZ) Anterior zygomatic plate. This bony plate is composed of the flattened anterior region of the zygomatic arch (cheekbone) that is expanded along the sagittal plane (Voss 1988) and is unique to rodents. The posterior region of this structure connects to the front of the maxillary root of the zygomatic arch (Steppan 1995) and the anterior-dorsal point connects to the rest of the skull through the antorbital bridge (Wood 1935). It is the part of the maxilla where the upper molars attach, and is among the most variable structures in the examined species and in rodents in general. The range of variation includes nearly horizontal zygomatic plate in some groups, to different degrees of elongation towards the frontal and sagittal planes in others, with differences believed to be associated with specializations in zygomatico-masseteric structures (Wood 1935). The function of the zygomatic plate is to resist muscular tension through the contraction of the incisors by the anterior deep masseter muscle which allows certain rodents, with broad zygomatic plates, to pulverize hard food with the incisors (Voss 1988). Rodents that do not use their incisors to process food and rely exclusively on their molars tend to have narrower zygomatic plates (Wood 1935).

In muroid rodents, this structure is usually broad and tilted upwards (Ellerman et al. 1941), however, there is great variation in this structure in this group. The plate may extend to the anterior region of the maxillary root of the zygomatic arch, which creates a zygomatic notch (Steppan 1995), or it could extend at the anterior region into a spinous process, the zygomatic spine (Weksler et al. 2006). Platacanthomyids tend to have a narrow zygomatic plate (Miller and Gidley 1918), whereas in calomyscids, the anterior margin tends to be straight (Ellerman et al. 1941). There are two main variations in the fossorial spalacids. *Tachyoryctes* and Rhizomyinae tend to have a zygomatic plate that is tilted upward and is fused to the sides of the rostrum (Miller and Gidley 1918). This is contrasted to the condition in Spalacinae and Myospalacinae,

where the plate is tilted downward and tends to be more horizontal in position (Miller and Gidley 1918). The remaining three families: Nesomyidae, Cricetidae, and Muridae have such great variation in the morphology of this structure that few generalizations can be made. Except for deomyines, some hydromyines, and a few other groups, most murids tend to have broad and high zygomatic plates (Ellerman et al. 1941). Nesomyids and cricetids exhibit possibly the greatest extent of variation in the zygomatic plate in terms of width, curvature, and height (Ellerman et al. 1941; Voss 1988; Steppan 1995). The landmark is digitized on the dorsal region of the zygomatic plate, on the anterior-dorsal most extreme of the Antorbital Bridge.

11. (VIF) Ventral infraorbital foramen. This structure is a ventral opening in the maxilla, below the lower margin of the orbits through which several maxillary and other cranial nerve branches and blood vessels pass (Ellerman et al. 1941). The size of this structure varies greatly in rodents, sometimes projecting beyond the dorsal and ventral margins of the zygomatic plate and in other instances it is enclosed in a very small region within it (Ellerman et al. 1941). The landmark is digitized on the ventral-most extreme of the infraorbital foramen, which coincides with the region of maximum curvature. In some groups, it coincides with the anterior-ventral-most region of the zygomatic plate.

12. (SPF) Squamosal-parietal-frontal-sphenoid suture. This landmark, located on the lateral side of the cranium, is the point of intersection between five bones: temporal, parietal, frontal, orbitosphenoid, and alisphenoid. There is variation in the order of contact between these bones, in some groups the bones all connect onto a single point (through 5 sutures) and in other groups the temporal, frontal, and alisphenoid join at one point and the orbitosphenoid, frontal and alisphenoid join at a different point with a suture line joining these two triple junctions; in these groups, the landmark is digitized on the median of the suture that connects these two triple junctions, which demarcates the alisphenoid from the temporal and frontal. Other groups were variations on these two arrangements and were treated the same way.

13. (VZ) Ventral zygomaxillary point. The zygomatic arch is composed of the maxilla, jugal, and squamosal. The landmark is located at the lowest extent of the zygomatico-maxillary suture, digitized at the ventral extent of the suture that delimits the zygomatic process of the maxilla and the jugal and also delimits the ventral extreme of DZ.

14. (VTZ) Ventral temporo-zygomatic suture. The zygomatic arch forms the cheekbone and is composed of the jugal, the zygomatic process of the maxilla, and the

protruding bone that joins posteriorly with the zygomatic process of the squamosal. The landmark is digitized on the ventral extreme of the suture that separates the squamosal from the jugal. In species with broad zygomatic arches, the landmark is digitized on the medial point of the ventral surface of this suture.

15. (LIS) Lateral incisor socket. This landmark is digitized on the lateral most edge of the alveolus of the point of contact between the incisors and the premaxilla. For larger skulls and associated deep incisors, the landmark is digitized on the medial point between the anterior and the posterior extremes of the incisors. This landmark also coincides with endpoints of calipers when measuring width of the incisors or the length of the diastema.

16. (MPM) Medial premaxilla-maxilla suture. This landmark is digitized on the medial-most edge of the suture that separates the premaxilla from the maxilla and usually demarcates the lateral-medial edge of the incisive foramen although there are exceptions in several groups. The position of this landmark facilitates measuring the width of the incisive foramen, an important measure in the diagnoses of many rodent species.

17. (AFM) Anterior edge of the first molar. This landmark is digitized on the anterior margin of the alveolus of the first molar. In larger skulls with wide molars, the measurement is taken in the medial most region of the molar and coincides with the endpoints of calipers when measuring the length of the molar row or the length of the diastema.

18. (PTM) Posterior edge of the third molar. This landmark is digitized on the posterior margin of the alveolus of the third molar, and as in AFM, is digitized on the medial most of the region in larger skulls with wide molars and coincides with the endpoints of calipers when measuring the length of the molar row or the pterygoid region size (e.g. Steppan 1997).

19. (MT) Maxillary tuberosity. This landmark is located very close to PTM and in small specimens is almost at the exact same position due to the limitation of the microscribe probe size. It is located slightly posterior to PTM and designates the convex-shaped porous bone immediately following the molar row and posterior most edge of the ventral region of the maxilla and functions as the point of attachment of various masticatory muscles (Ellerman et al. 1941). In some species, this region is demarcated with a suture that marks the point of contact between the maxilla, temporal, palatine, and the parapterygoid bones.

20. (APT) Alisphenoid-parapteregoid-temporal junction. This landmark is digitized on the lateral edge of the suture that separates the alisphenoid from the parapteregoid and contacts the lateral border of the temporal bone.

21. (MBS) Medial edge of the bulla spine. The tympanic bulla is a structure that houses the middle ear bones and exhibits a great range of variation in size and shape. Many desert species exhibit a hypertrophied condition (e.g. Lay 1972). The bulla spine is a small protruding structure found on the anterior surface of the tympanic bulla. This landmark is digitized on the medio-posterior edge at the base of the bulla spine. In larger skulls with wide bullar spines, the measurement is taken on the most medial region of the bulla spine. This landmark is important because although the bulla is functionally important, it exhibits very few homologous structures.

22. (PH) Posterior tip of the hamular process. The hamular process of sphenoid bone, or the pterygoid hamulus, refers to the protruding hook-like process that is medial to the pterygoid plate of the sphenoid. It curves laterally at its posterior extremity and serves as an attachment site of palatine tendons (Ellerman et al. 1941). The landmark is digitized on the posterior-ventral tip of this process.

23. (IDR) Interdental region. This landmark is digitized on the ventral-anterior most edge of the premaxilla, between the alveoli of the upper incisors and the gnathic process.

24. (AIF) Anterior edge of the incisive foramen. This landmark is digitized on the anterior edge of the incisive foramen and in larger skulls where the two cavities of the incisive foramen are widely separated, is digitized between the cavities at the anterior extreme (i.e. between the two antero-medial edges of the incisive foramen).

25. (PIF) Posterior edge of the incisive foramen. This landmark is the posterior equivalent of AIF and along with it can be used to measure the length of the incisive foramen.

26. (PIP) Posterior edge of the interpalatine suture. This landmark is on the posterior edge of the mid-sagittal suture that demarcates the left and the right halves of the palatine. In some species, a spine protrudes posteriorly from this suture (i.e. post-palatal spine) and consequently, the landmark is digitized on the posterior extreme of the interpalatine suture.

27. (BA) Basion. This landmark is digitized on the antero-medial edge of the foramen magnum along the sagittal plane, coinciding with the midline of the basioccipital bone.

28. (OP) Opisthion. This landmark is the posterior equivalent of BA along with it was digitized in such a way that they lie on the same sagittal plane, and consequently can be used to measure the length of the foramen magnum.

29. (PJ) Posterior edge of the jugular process. The jugular process is a triangular plate of bone that protrudes from the lateral edge of the occipital bone and extends laterally from the posterior edge of the occipital condyle. The landmark is digitized just posterior to the jugular foramen and at the edge of the occipital condyle. The jugular foramen serves as a passage for nerves and blood vessels (Voss 1988).

30. (LD) Lambda. This landmark is located on the medial edge of the suture that separates the interparietal from the supraoccipital bone along the mid-sagittal plane. The location of this landmark in rodents differs from other mammals. In other mammals, where the interparietal is absent, it is the meeting point between the parietal and the supraoccipital.

31. (MPI) Medial parietal-interparietal suture. This landmark is digitized on the medial-most of the suture that separates the interparietal from parietal along the mid-sagittal plane. MPI along with LD can be used to measure the length of the interparietal bone.

32. (AS) Asterion. This landmark is located on the posterior end of the parietomastoid suture and in many rodent species, the suture also coincides with a bump or a lateral process at the parietal on the suture that joins the parietal with the squamosal near the edge of the occipital suture. This suture joins the occipitoparietal suture, the point of connection between the supraoccipital and the parietal bones. In some species, these two sutures join at a single point that joins the parietal, interparietal, supraoccipital, and temporal bones together, while in others, a small gap exists between the occipitoparietal and the temporo-parietal and occipitotemporal sutures. In the latter case, the landmark is digitized on the median of this suture, which is relatively variable along the ventro-dorsal and antero-posterior axes in muroids.

33. (DM) Dorsal-external edge of the auditory meatus. This landmark is located on the external surface of the auditory meatus at the antero-dorsal edge that also coincides with the anterior edge of the ethmoid bone in most species.

34. (VM) Ventral-external edge of the auditory meatus. This landmark is the posterio-ventral equivalent of DM and along with it can be used to measure the height of the external auditory meatus.

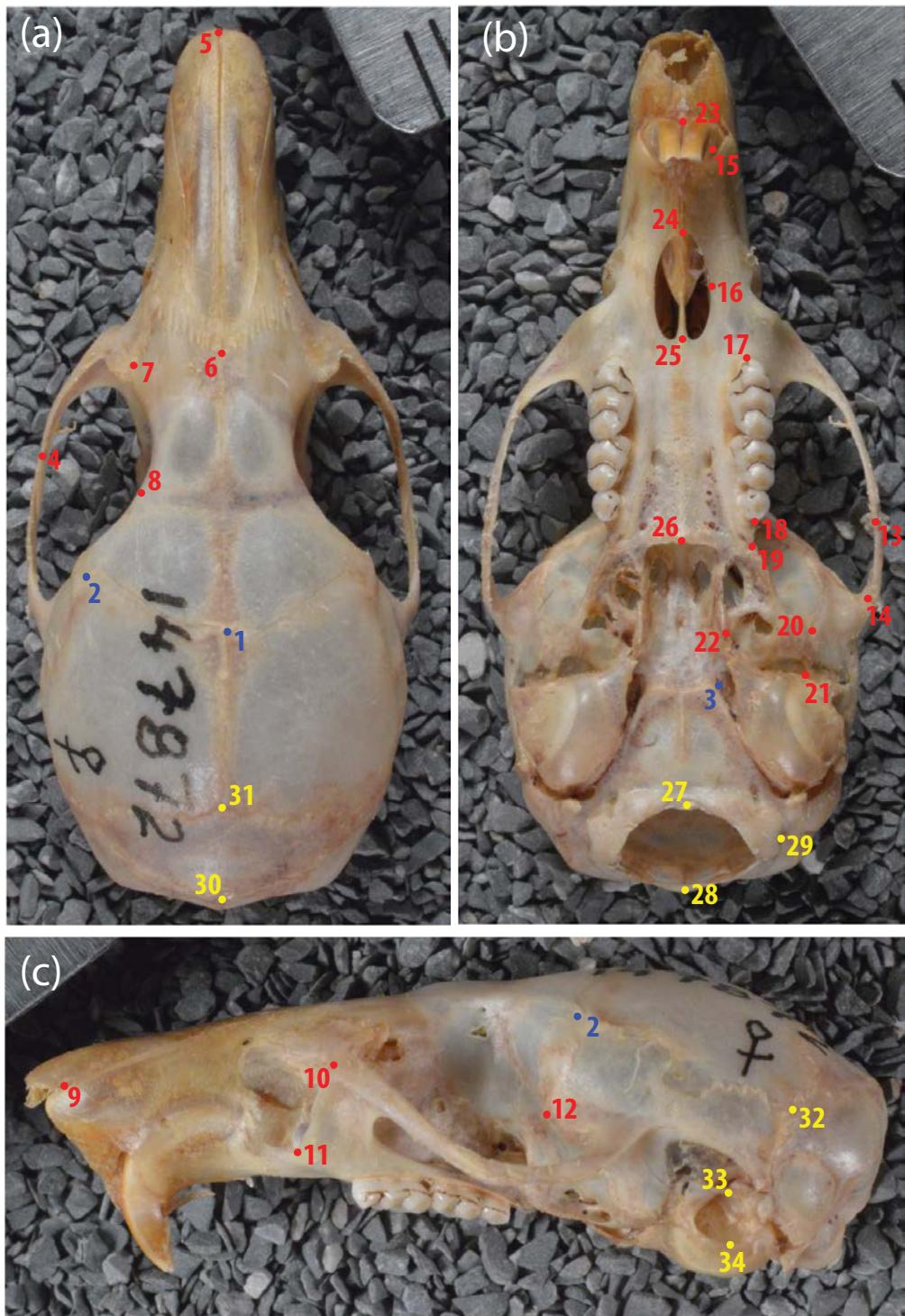


Figure 2.1. Positions of three-dimensional cranial landmarks. Landmarks are shown on the (a) dorsal, (b) ventral, and (c) lateral views of the Mount Apo Forest Mouse (*Apomys hylocoetes*; FMNH 147872) with numbers corresponding with the descriptions above and Table 2.2. Landmarks in red are digitized in the anterior orientation, those in yellow are digitized in the posterior orientation, and those in blue are digitized in both orientations and used to merge the data from the two orientations. The jugular process is missing in this specimen and landmark 29 is positioned where it is commonly present.

Microscribe Data Collection Procedure

I used the microscribe digitizer along with its utility software (Immersion Corporation, San Jose, CA, USA) to capture the three-dimensional coordinates of each landmark. The x, y, and z coordinate values of each landmark were exported to a spreadsheet. Landmarks on the anterior surface of the skull (rostral end of the skull projecting upwards) were digitized separately from landmarks on the posterior surface of the skull (rostral end of the skull projecting downwards). This was necessary as all landmarks could not be reached from either orientation as part of the skull needs to be in contact with clay to stabilize it. These two landmark datasets were later merged (see below). Because most of the sampled muroids were very small, landmarks were located and digitized with the assistance of a 10x SE 10X, 21mm Triplet Professional Loupe. I used two direct light sources to illuminate the crania at all times. In order to free one hand for the microscribe probe and the other for the magnifying loupe, a double digital foot pedal (Immersion Corporation, San Jose, CA, USA) was used to record landmark positions. The landmarks were digitized in sequence in the anterior orientation, and then the exact same landmarks were re-digitized in the same sequence in a second group of columns in the spreadsheet. The Euclidean distance between the two positions of each landmark was calculated and if the distance was greater than 0.3 millimeters (i.e. the repeatability was less than 0.3 mm) then the landmarks were re-digitized until a repeatability of 0.3 mm was achieved. In addition, a number of crucial distance measures (i.e. Table 2.3) were also calculated from these landmarks and a same repeatability threshold of 0.3 mm was maintained. Most landmarks had a repeatability score that is far less than 0.3 mm. The same procedure was repeated for the posterior orientation of the cranium. Klean Klay Natural Firm modeling clay (Art Chemical Products Inc., Huntington, IN, USA) was used to stabilize crania at all times.

Prior to each day of landmark digitization, the calibration of the microscribe is checked using graph paper by measuring a sequence of five points that are 1.0 centimeter apart then re-measuring the exact same sequence of five points and calculating the Euclidean distance between the two positions each of these five points as well as the distance between each of the five points next to each other. If there was a deviation of more than 0.1 mm then the microscribe was recalibrated prior to data collection following the directions of the manufacturer. After each day of digitization, the coordinates were transferred to a text file and saved in NTSYS format. These files were used to confirm the validity of the data by running the following checks. (1) NTSYS

files for both anterior and posterior datasets were visualized using M_vis (Slice 2007) and rotated in three-dimensions looking for points that are out of place, which are due to measurement error. (2) A Euclidean distance based dendrogram was generated using all the distance measures in Table 2.3 digitized from both orientations in R (R Developmental Core Team 2007). Newly digitized specimens were sequentially added to the dataset and clustering of conspecifics was the main criterion used to assess the quality of the data. If an error was detected in any of the aforementioned two checks then two actions are taken. Offending landmarks were treated as a missing, and the microscribe was recalibrated in the next day of digitization.

Each digitized specimen was also photographed along with the mandible and the associated skin; all photographs include a scale bar for separate two dimensional morphometric analyses (see below). Specimen tags and vial labels were also photographed and manually transcribed following each museum trip. Skins are useful for future reference in order to determine if there are any differences in appearance of conspecifics that do not cluster together (skin characters are used to delimit some species). Most tags include locality information, age class, and sex; some include the standard measurements: total head-body length, tail length, hindfoot length, and ear length.

Dataset Merging and Estimation of Missing Data

Three landmarks (BR, PT, and APT) were included in both the anterior and the posterior datasets and were used to merge them together. These landmarks were chosen because they are the most identifiable points available and were found in all examined specimens and were also relatively far apart in both the dorsal, lateral, and the ventral sides of the skull which minimize error when “stitching” the two datasets together, which was done following a modified version of Watanabe and Slice’s (2014) procedure that uses the batch function in Morpheus et al. (Slice 2011). The output of this process is a single (separate) file that contains all 32 raw landmark positions for each of the 1,125 digitized specimens.

The “stitching” procedure of the modified version of Watanabe and Slice’s (2014) procedure takes the following steps. The NTSYS files of the anterior and the posterior coordinate are first imported into Morpheus et al. and converted into MDT format, the native format of the program, and then 8 additional ‘posterior’ landmarks were added to the end of the anterior landmark dataset and coded as missing data. 23 additional ‘anterior’ landmarks were added to

the beginning of the posterior landmark dataset, after the 3 common landmarks, but before the rest of the posterior landmarks and also coded as missing data. This process leads both datasets to have 34 landmarks that are in the same order (i.e. 3 common landmarks, followed by the 23 anterior landmarks, followed by the 8 posterior landmarks). The ‘posterior’ landmarks in the anterior dataset and the ‘anterior’ landmarks in the posterior dataset were demoted and coded as secondary points (which are ignored from the analyses) and the three common landmarks in each dataset were coded as primary points. A Generalized Procrustes superimposition, which minimizes the sum of squares distance between the three common landmarks by removing the effect of size, orientation, and translation (Rohlf and Slice 1990), was conducted on the three common landmarks in both datasets, while preventing reflections. The positions of the secondary landmarks in each orientation is not considered in the superimposition but is moved in relative to the position of the primary points. Scale is restored following the analyses to retain size in the combined dataset. The secondary points are then promoted to primary status and the average shape of the two superimposed datasets is calculated. Missing values do not contribute to the calculation of mean shape and the process simply realigns the data (Watanabe and Slice 2014).

The final dataset was visually inspected in M_vis to confirm the quality of the data. Errors caused by the merging procedure were fixed by either dropping the out of place point if that is the only visible error, or were fixed by using alternative points to merge the two datasets (2 additional landmarks were digitized on both orientations to give a total of 5 common, two of which were not described above). Estimating missing data is essential because geometric morphometric analysis requires equal numbers of landmarks for each row in the dataset. The positions of missing landmarks that were the result of either damage, absence in a particular species, or that were dropped due to measurement or merging error, were estimated in the Geomorph library (Adams and Castillo 2013) in R (R Development Core Team 2013). This was done individually for each specimen that contains at least one missing landmark based on the locations of corresponding landmarks in a reference specimen with complete data, by aligning the complete reference specimen with the target specimen (missing one or more landmarks) using landmarks common to both specimens and then using thin-plate spline interpolation to estimate the locations of the missing landmarks (Adams and Castillo 2013). The reference specimens were chosen on a case-by-case basis as follows. (1) The average shape of all complete conspecifics was chosen as the reference specimen whenever possible. If there was no single

complete conspecific specimen available (which is the case for rare species), then (2) the average shape of all complete congeners was chosen as the reference specimen. If there was no single complete congeneric available (which is the case for rare and monotypic genera) then (3) the average shape of the next higher taxonomic level was chosen as the reference specimen. A list of all target specimens (with at least 1 missing landmark) and the reference specimens used to estimate their missing landmarks is found in Appendix Tables A.2 and A.5. The complete datasets (with all missing data estimated) for all 1,125 specimens were then visually inspected for errors in M_vis as in above.

In order to obtain shape variables in a geometric morphometric framework, the first step is to conduct a generalized procrustes analysis (GPA) on the complete dataset (Rohlf and Slice 1990). Generalized procrustes superimposition translates the coordinate configurations to a common centroid by scaling them to unit centroid size and rotating them in order to minimize the sum of squared distances between the corresponding landmarks as well as account for the effects of translation (Zelditch et al. 2004). The output of this procedure is a new set of procrustes coordinates that describe size-independent shape differences within the sample as well as centroid-size, which is sequestered in a separate variable.

First, GPA was conducted in order to align specimens prior to estimating species averages. This GPA generated both shape (procrustes coordinates) and size (centroid size) variables for each specimen. The centroid sizes of the specimens were averaged to yield species average size (average centroid size) and the average procrustes coordinates (i.e. consensus shape) for each species were calculated using the Geomorph library in R with the method described in Claude (2008), which calculates the average coordinate positions of aligned specimens. A second GPA was conducted on these procrustes coordinates in order to re-align the data. The output of the second procrustes superimposition is a new set of procrustes coordinates that describe interspecific size-independent shape differences within the sample (311 OTUs) and along with the average centroid size were used for all subsequent statistical analyses.

Photographic Data Collection Procedure

A total of 2,075 skulls (crania + jaws) were photographed (Appendix Table A.3) in a standardized manner (described below). Most of the landmarks digitized in three-dimensions

using the microscribe were also digitized on photographs in two dimensions. Several different landmarks and distance measures were extracted from the photographs and are described in their respective method sections (chapters 6-8). The choice of specimens with clear suture lines was especially important in the two dimensional dataset to facilitate the digitization of landmarks on photographs. Lateral photographs were taken on the left side of the skull to facilitate comparison with the three-dimensional dataset. In cases where the left side of the skull was damaged or had unclear suture lines, the right side of the skull was photographed instead and subsequently reflected. When equal sampling of males and females was not possible (see above), at least 4 specimens of either sex were photographed. The occlusal and labial views of the upper and lower left molar tooth rows were also photographed.

The photography procedure was modified from Samuels (2009) and Yazdi et al. (2012). Photographs were taken by placing the camera with the macro lens attached on a mobile Albinar High Load 28" Copy Macro Stand with 15.75"x19" base and a quick release mount as well as other photography stands when available at the various visited museums. Photography stands ensured that the photography plane is parallel to the ground plane. The skulls were cleaned and mounted on a box that was filled with Crabworx Extra Fine Crab Gravel. Standardization of the position of the skulls in the photographs was achieved by adjusting their orientation while viewing them through the eyepiece of the camera using the following criteria: (1) in ventral and dorsal photographs of the crania, the position of the specimens was adjusted in such a way that there is perfect symmetry in the left and the right sides of the cranium. Essentially the cranium was rotated in the medio-lateral direction in such a way that it was resting on its zygomatic arch and when viewed through the eyepiece, the left and the right sides of the cranium look symmetrical and hence the palate is parallel to the photographic plane. Adjustment in the antero-posterior direction was less of an issue and followed the same procedure with the palate or the frontal bones ensured to be parallel to the photographic plane. The use of the gravel allowed parts of the skull to be buried in order to achieve this symmetry. (2) In the lateral photographs of the crania, the position of the specimens was adjusted in such a way that there is perfect overlap of the bulla, molar row, optic canal, and incisors. However, due to the large taxonomic scale, slight taxa specific adjustments had to be made. Essentially, parts of the right side of the cranium were submerged in the gravel and the left side of rotated in the medio-lateral and antero-posterior direction so that the mid-sagittal plane becomes parallel to the photographic plane

which is ensured by the overlap of the aforementioned structures which cover the antero-posterior extent of the skull. (3) Being a flat structure, the jaw is much easier to adjust prior to photography. The gravel allowed the photography of lateral sides of jaws that retain the fusion at the mandibular symphyses by sinking the jaw into the gravel and only exposing the left side of the jaw above the surface of the gravel. The same criteria for photographing the crania described above were used to ensure the photographs of the lateral and the occlusal views of the jaws were taken at a standardized manner (i.e. overlap of molar rows and incisors in the lateral images; left-right symmetry of the molars and incisors of the occlusal images).

The specimens were magnified (zoomed in) maximally to cover most of the photograph which was near 6,016 pixels wide and 4,000 pixels high. This means that it was essential to magnify smaller taxa much more than larger taxa. Based on the standardization process and preliminary analyses conducted at different magnification levels on graph paper, the effects of flattening a three-dimensional structure to a two dimensional image as well as the effect of parallax was assumed to be similar for all the photographed specimens. The same scale bar was included in all the images near the mid-depth of the specimen (e.g. near the mid-sagittal plane in the lateral images, and near the mid-coronal plane in ventral and dorsal images) to allow for the acquisition of a scale factor and assess the linearity of specimens in subsequent analyses.

All data will be deposited in online repositories after the publication of dissertation chapters in journals. Sequences will be deposited in GenBank and morphological data will be included in the supplemental data or Dryad.

CHAPTER THREE

ECOMORPHOLOGICAL DIVERSIFICATION FOLLOWING CONTINENTAL COLONIZATION IN MUROIDIA: A TEST OF THE ECOLOGICAL OPPORTUNITY MODEL OF ADAPTIVE RADIATION

Summary

Biogeographic transitions, mass extinctions of antagonists, and key innovations may provide an ecological opportunity for lineages to diversify due to newly available underutilized adaptive zones, leading to rapid radiations. The exceptional diversity in the most diverse level taxon of mammals, muroid rodents has been explained in terms of multiple independent adaptive radiations. However, a recent diversification analysis only finds strong support for ecological opportunity (burst in diversification followed by density dependent slowdown in rate of diversification through time) following the primary colonization of South America, but no or weak patterns following the primary colonization of the other investigated continents (Madagascar, North America, Africa, Sahul, and Southeast Asia). Here, I test the phenotypic predictions of the ecological opportunity model (an early burst in the rate of ecomorphological evolution followed by a density dependent decline in the rate of ecomorphological evolution through time) using data on body size, appendage proportions, and elevation using the same time-calibrated molecular phylogeny of extant muroids and biogeographic analyses conducted in the aforementioned study. Similarly, I find the strongest evidence in support of the phenotypic predictions of ecological opportunity occurring after the primary colonization of South America, and weaker evidence following the primary colonization of Sahul and Southeast Asia. There was little to no support following the primary colonization of other continents. The results also indicate that not all traits showed similar patterns of consistency with ecological opportunity, which may indicate that they have different importance in niche utilization in different continents. I also found support for the predictions of the ecological opportunity model coincident with lineages that have undergone significant increases in phylogenetic diversification rates that were not associated with biogeographic transition, which may indicate that other

biogeographically-independent factors could have precipitated ecological opportunity-mediated adaptive radiation in these lineages, or the features were not good indicators of niche occupation.

Introduction

Muroid rodents belong to the most diverse superfamily of mammals, with over 1,600 species, representing 28% of mammal species diversity (Musser and Carleton 2005). Due to the relatively recent basal radiation of Muroidea (40-45 mya, Schenk et al. 2013), the exceptional diversity of the group has been described in terms of multiple independent bursts of adaptive radiation (Patterson and Pascual 1968) and recent diversification analyses using molecular phylogenies do find some support for this characterization considering the widely differing diversification rates among equal aged lineages (e.g. Fabre et al. 2012; Schenk et al. 2013). These radiations followed their gradual expansion out of Eurasia into most terrestrial habitats in all continents and every major landmass except New Zealand and Antarctica (Flynn et al. 1985; Fabre et al. 2012; Schenk et al. 2013). For instance, the South American colonization of sigmodontines from North America has been described as an adaptive radiation spurred by the lack of muroid and other small rodent competitors from the region, which at the time only contained relatively larger caviomorphs and a few marsupials (Hooper 1949; Simpson 1950; Patterson and Pascual 1968; Baskin 1978; Schenk et al. 2013).

Exceptional diversification rates in clades is often explained in terms of the emergence of ecological opportunities (EO) for diversification, precipitated by biogeographic transitions, mass extinctions of protagonists, and/or the evolution of key innovations; all of which lead lineages to exploit new and underutilized adaptive zones (Simpson 1953; Schluter 2000a; Grant and Grant 2008). The two main predictions of EO are: (1) an early increase in the rate of phylogenetic and phenotypic diversification (indicating that lineages are taking advantage of relatively empty niche space as a consequence of underutilized adaptive zones); (2) a gradual density dependent decline in the rate of phylogenetic and phenotypic diversification consistent with increased competition due to niche crowding (Walker and Valentine 1984; Futuyma 1986; Baldwin and Sanderson 1998; Schluter 2000a; Lovette et al. 2002; Harmon et al. 2003, 2008a, 2010; McCormack and Smith 2008; Yoder et al. 2010). High extinction and/or oscillation in diversification rates can erase the first signature of EO, an early burst in diversification, but

evidence for EO may still be detected by examining the pattern of phenotypic evolution (e.g. Harmon et al. 2003; Slater et al. 2010; Martin and Wainwright 2011).

Most tests of EO are conducted in small clades in narrow geographic distributions (e.g. Caribbean *Anolis* lizards, Mahler et al. 2010). Recently, Schenk et al. (2013) showed that EO, brought about by biogeographic transition, does not explain the uneven diversity patterns in muroid clades well, considering the fact that out of the six primary continental colonizations (and the 22 secondary colonizations), only the primary colonization of South America fits all the *phylogenetic* predictions of the EO model (significant burst in *early* phylogenetic diversification rate followed by a significant slowdown in the rate of phylogenetic diversification through time). The primary colonizations of Sahul (Australia, New Guinean and neighboring islands) and Southeast Asia showed weaker support for EO; in Sahul, there was an increase in early diversification rate (however, occurring shortly after the transition took place and in only 1 out of 3 diversification shift methods employed) followed by a significant slowing in the rate of diversification through time (Schenk et al. 2013). Whereas in Southeast Asia all diversification methods showed a significant increase in diversification rate (however, this occurred shortly after the transition took place and was concentrated later in the diversification process) which was *not* followed by a significant slowing of diversification through time; all other biogeographic transitions (primary colonization of North America, Africa, Madagascar, and all other secondary transitions) were not associated with an early burst in diversification rate (Schenk et al. 2013). Schenk et al. (2013) also detected increased diversification rates at lineages not associated with biogeographic transitions.

In the present study, I expand on Schenk et al. (2013) and test the phenotypic predictions of EO: an early burst in phenotypic evolution followed by a gradual slowdown in the rate of evolution (Simpson 1953; Schluter 2000a); following primary continental colonization using the same phylogeny and the biogeographic analyses documented in that study. I also test whether lineages that have experienced biogeographically-independent increase in diversification rates show support for the phenotypic predictions of EO. I test the phenotypic predictions of EO in a suite of ecomorphological traits that were chosen as indices of niche. The first is size, which is estimated using body mass and is a strong predictor of diet in various taxa (Schluter 2000b; Kozak et al. 2005; Clabaut et al. 2007). The second examined trait was the relative length of the tail (RTL), which is a strong predictor of climbing ability in *Peromyscus* (Lemen 1980) and other

mammals (Fooden and Albrecht 1999). I also tested the phenotypic predictions of EO in elevation (geographic altitude), which is among the first traits that sister species diverge in (Endler 1982; Porter et al. 2002; Navas 2003; Hall 2005; Altshuler and Dudley 2006; Cadena 2007). I also examine the phenotypic predictions of EO in an index of external appendage proportions based on body length, tail length, hindfoot length, and ear length, which is expected to correlate with habitat use. The phenotypic predictions of EO are only expected to be reflected in the patterns of evolution of these traits if they are correlated with niche (Schlüter 2000b).

Materials and Methods

Phylogenetic Diversification and Biogeographic Framework

The chronogram used in this study, which includes a total of 297 muroid species sampled proportional to the total diversity of the clades, was obtained from Schenk et al. (2013), which was estimated using multiple nuclear genes and calibrated using several fossils. Schenk et al. (2013) detected multiple shifts in diversification rates based three methods: Δ parameters (Chan and Moore 2002, 2005), relative cladogenesis tests (Purvis et al. 1995; Harmon et al. 2008b), and the stepwise AIC model selection approach (Medusa; Alfaro et al. 2009); fourteen nodes were identified by one method, four were identified by two methods, and none were identified by all three methods, but generally all shifts were concentrated in three regions of the tree. In the present study, I sampled nine nodes to test the phenotypic predictions of EO: all four nodes that were identified by two methods, and five additional nodes that received the highest AIC scores in Medusa (diversification nodes 1-9; Figure 3.1). In addition, Schenk et al. (2013) detected multiple biogeographic transitions out of Eurasia, the ancestral biogeographic location of Muroidea, based on three methods: S-Diva and Bayesian binary MCMC analyses (BBM; Yu et al. 2010) as implemented in RASP v2.0 (Ali et al. 2012), and maximum likelihood ancestral-state-estimation function as implemented in the Ape library (Paradis et al. 2004) in R (R Development Core Team 2005); all of which converged on nearly identical reconstructions for the primary continental colonizations, and all of which I use to test the phenotypic predictions of EO (Figure 3.1; Appendix Figure B.1). In nodes that correspond with primary continental colonization, I pruned species that subsequently dispersed out of the biogeographic region from the clades prior to ecomorphological diversification analyses.

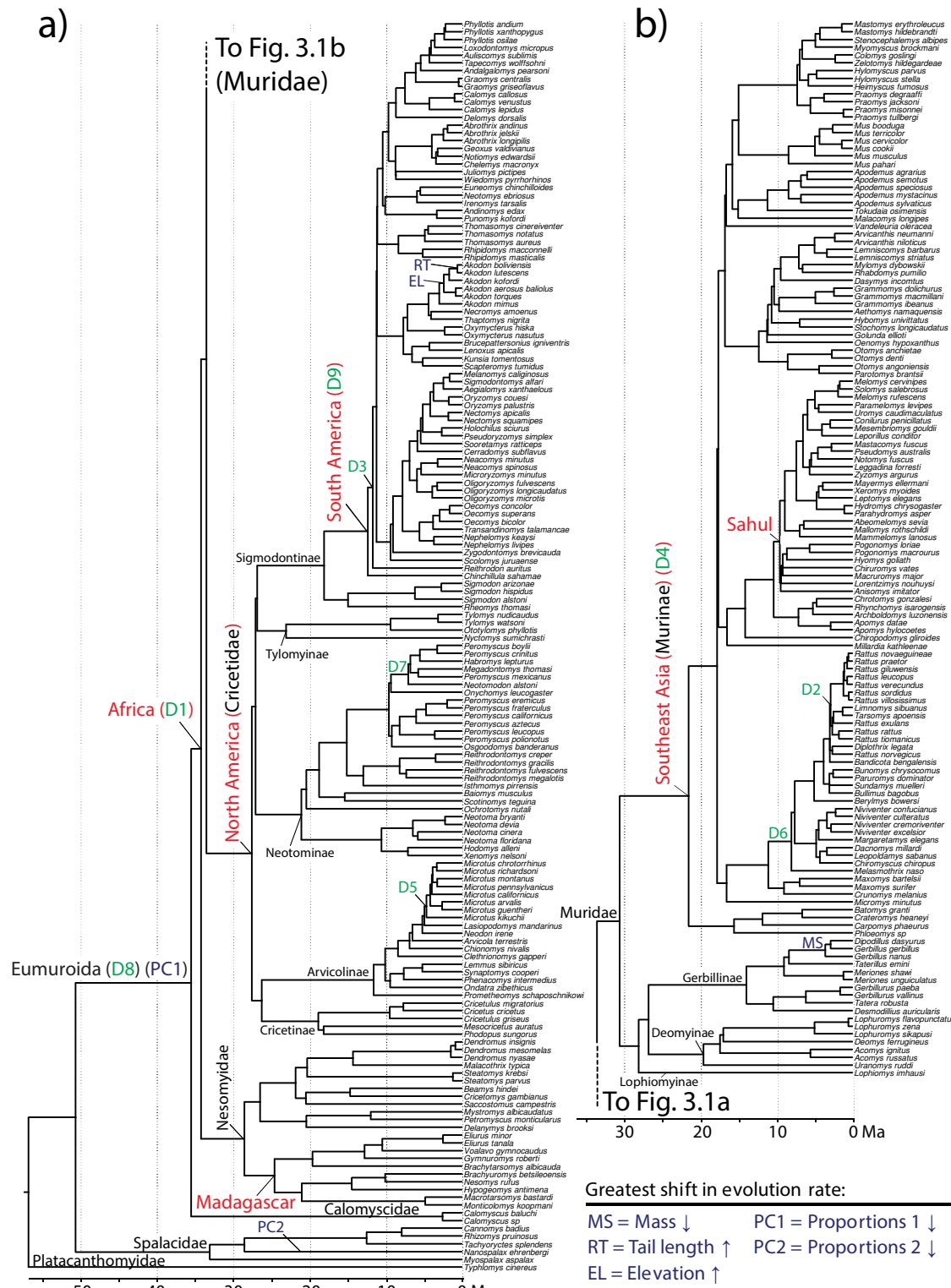


Figure 3.1. Muroid rodent chronogram from Schenk et al. (2013). Significant increases in phylogenetic diversification (D1-D9), primary continental colonizations (both as detected by Schenk et al. 2013), and greatest shifts in ecomorphological evolution rates are indicated in green, red, and blue respectively. Taxonomic groups are shown. Tail length= relative tail length; Proportions= relative appendage proportions based on PPCA.

Data Collection

For each species, I compiled data for body mass of adults in grams; head-body length, tail length, hind foot length, and ear length of adults in millimeters; as well as elevation in meters above sea level (Appendix Table B.1). Sexual dimorphism is uncommon in muroids, however, when possible, data were averaged from equal numbers of males and females. Average data were used; however, when not available, averages of the ranges or averages of individual accounts were used instead. Species averages were calculated based on multiple data from different sources to minimize the effects of outliers and misreported data. Body mass, head-body length, and hind foot length were log transformed to meet the assumptions of normality of subsequent analyses; ear length and tail length were also log transformed, but only after a value of 1 mm was added to each species in order to account for the fact that *Nannospalax ehrenbergi* has no visible ear or tail (= 0 mm). Elevation data were gathered from Musser and Carleton (2005) and GPS coordinates of voucher specimens from Arctos (2011) using Google Earth v6.0 (2010).

An index of overall appendage proportions (head-body length, tail length, hind foot length, and ear length) was estimated using a phylogenetically correct principal component analysis (PPCA; Revell 2009) after phylogenetic size correction (Revell 2009) following the published code using the Ape library in R. PPCA reduces type I error rate by accounting for phylogenetic relationships making it more conservative than traditional principal component analysis in comparative analyses (Revell 2009). The first axis is strongly correlated with all measurements except for body length; the second axis is most strongly correlated with ear length and moderately correlated, inversely, with tail length (Table 3.1). I use principal component scores for the first two axes, that together account for 80.5% of total variance (Table 3.1) as indices of overall appendage proportions.

Table 3.1. Loadings of the principal component analysis on appendage proportions.

Variable	PC1	PC2	PC3	PC4
Body length	-0.274	-0.055	0.883	0.378
Tail length	-0.922	-0.354	-0.141	0.067
Hindfoot length	-0.550	-0.192	0.507	-0.635
Ear length	-0.562	0.827	-0.018	-0.003
Eigenvalues	0.517	0.288	0.131	0.064

Shift in Evolution Rates

I test the EO prediction of a significant increase in the rate of ecomorphological evolution (Schluter 2000a) using the censored rate test (CRT) under Brownian motion as implemented in Brownie v2.1 (O'Meara et al. 2006). CRT compares the fit of two nested models evolution; the first is a one rate model where the rate of evolution of the whole tree is constrained to be the same and estimated using ML, and the second is a two rate model, where the rate of evolution of the foreground clade (focal clade; e.g. node coincident with biogeographic transition and/or increase in phylogenetic diversification) and a background clade (the rest of the phylogeny excluding the foreground clade) are optimized separately using ML (O'Meara et al. 2006). The two rate model was preferred over the one rate model if the improvement in the Akaike information criterion (AIC; Akaike 1974) score exceeded 4 units (Burnham and Anderson 2002) after applying a more conservative correction for finite sample sizes (AICc; Hurvich and Tsai 1989). EO is supported if evolution rate is significantly greater in the foreground clade.

I also determined the phylogenetic location of the greatest shift in evolution rate (node with the greatest posterior probability of rate shift) of all examined traits using the Bayesian Markov chain Monte Carlo (MCMC) approach following Revell et al. (2012a) as implemented in the Phytools library (Revell 2012b) in R (R Development Core Team 2012). This was done to determine if primary continental colonizations and/or nodes with increased phylogenetic diversification occur prior (and close to) the nodes with the greatest increase in the rate of evolution, as predicted by EO (Schluter 2000a). The default of 10,000 generations (sampling every 100 steps) was used. Most parameters reached converge in all traits except for mass where several parameters did not converge after 100,000 generations. Adequate sampling, convergence, and burn-in were determined by inspecting the posterior sample in the Coda library (Plummer et al. 2012) in R.

Disparity through Time

The EO prediction of disproportionately greater early phenotypic disparification as a consequence of relatively empty niche space (Schluter 2000a) was tested by the use disparity through time (DTT) plots using the Geiger library (Harmon et al. 2008b) in R. In DTT plots, average sub-clade disparity (average squared pair-wise Euclidean distances between all species in morphospace, Foote 1997) is plotted against relative time and is subsequently used to

calculate the morphological disparity index (MDI; Harmon et al. 2003) to determine if disparity is greater than expected by chance by comparing an average of 1,000 plots generated by Brownian motion simulations of trait evolution to the observed plots and then calculating the area between the two curves (Harmon et al. 2003, 2008b). Because EO predicts disproportionately greater *early* disparity, I modified the calculation of the MDI score to only include the first third of the DTT plot; a negative MDI score indicates that early sub-clade disparity is lower than expected under Brownian motion, as predicted by EO (Harmon et al. 2003; Slater et al. 2010). Significance testing is uncommon in DTT plots and I use a threshold value of $MDI < -0.01$ to indicate substantial early ecomorphological disparity. I also assess significance by calculating the probability of obtaining a negative MDI score when the evolutionary process follows a Brownian motion model by calculating the MDI between each of the 1,000 simulated datasets and the observed dataset and then calculating the proportion of cases where the MDI score is positive.

I test the EO prediction of a significant slowdown in the rate of ecomorphological evolution through time (Schluter 2000a) using node-height tests (NHT; Freckleton and Harvey 2006) as implemented in the Ape library in R. NHT tests for a relationship between the absolute values of standardized independent contrasts (IC; Felsenstein 1985) of the ecomorphological traits with the height of the node which they subtend. Since ICs are Brownian rate parameters, a significant negative correlation indicates that rates of evolution have slowed down through time (McPeek 1995), indicative of species subdividing and filling niche space more finely through time as expected by EO (Freckleton and Harvey 2006; Derryberry et al. 2011).

Results

Ecomorphological Evolution/Disparity Following Primary Continental Colonizations

Out of the ten significant shifts in evolution rates detected by the CRT coincident with primary continental colonizations; seven were slowdowns and four were speedups (Table 3.2; Appendix Table B.2). The rate of evolution of relative tail length (Table 3.2) and elevation (Table 3.2) both doubled following the colonization of South America; whereas the rate of evolution of body mass (Table 3.2) and PC2 of appendage proportions (Table 3.2) were elevated 3-4 fold following the colonization of Sahul (Table 3.2; Appendix Table B.2). Primary colonizations of Africa, Madagascar, North America, and Southeast Asia were not associated

with significant speedups in the rate of evolution of any of the traits; either the 1-rate model was preferred, or the evolution rate of the colonizing lineage was not significantly different or slower than the rest of the tree.

Out of the 80 DTT analyses (5 traits in 16 clades/grades) only one (node D7 for PC1 of appendage proportions; see below) showed a significant result for the MDI score, where the proportion in which the MDI score is positive is 0.019 (p-value); for all 79 other analyses this proportion is greater than 0.05 indicating non-significance. This pattern may indicate that the test of significance of MDI scores considered in this study was prohibitively conservative. Substantially negative MDI scores ($MDI < -0.01$) were associated with the primary colonization of: South America for PC2 of appendage proportions (Figure 3.2; $p= 0.292$); Sahul for PC2 of appendage proportions (Figure 3.2; $p= 0.243$) and elevation (Figure 3.2; $p= 0.095$); and Southeast Asia for relative tail length (Figure 3.2; $p= 0.405$). The primary colonization of Madagascar, Africa, and North America were not associated with substantially negative MDI scores in any of the examined traits. A substantially negative MDI score was also associated with the whole tree for elevation (Figure 3.2; $p= 0.34$).

The NHT indicates a significant negative relationship between node height and the absolute standardized contrasts following the primary colonization of: Africa for relative tail length (Figure 3.3; Coef = -0.014, $R^2 = 0.156$) and elevation (Figure 3.3; Coef = -0.053, $R^2 = 0.273$); Madagascar for relative tail length (Figure 3.3; Coef = -0.020, $R^2 = 0.434$); North America for elevation (Figure 3.3; Coef = -0.030, $R^2 = 0.215$); South America for body mass (Figure 3.3; Coef = -0.041, $R^2 = 0.236$), relative tail length (Figure 3.3; Coef = -0.034, $R^2 = 0.062$), and elevation (Figure 3.3; Coef = -0.075, $R^2 = 0.050$); and Southeast Asia for PC2 of appendage proportions (Figure 3.3; Coef = -0.002, $R^2 = 0.206$) and elevation (Figure 3.3; Coef = -0.024, $R^2 = 0.123$). The primary colonization of Sahul was not associated with a significant slowdown in evolution rate of any of the traits. A significant negative relationship between node height and the absolute standardized contrasts was associated with the whole tree for body mass (Figure 3.3; Coef = -0.007, $R^2 = 0.067$), PC2 of appendage proportions (Figure 3.3; Coef = -0.001, $R^2 = 0.012$), relative tail length (Figure 3.3; Coef = -0.005, $R^2 = 0.045$), and elevation (Figure 3.3; Coef = -0.024, $R^2 = 0.097$).

Table 3.2. Model parameters of the censored rate test for primary continental colonizations. Significant fit of the 2-rate parameter model over the 1-rate parameter model is based on a Δ AICc > 4 units. σ^2 = evolution rate. Full output is in Appendix Table B.2.

	σ^2						
	2-rate						
	1-rate	Foreground	Background	Δ (F-B)	Δ AICc	Preferred Model	Rate Shift
Africa							
Mass	0.02345	0.02005	0.02373	-0.00368	-1.77	1-rate	n.s.
Proportions 1	0.00375	0.00267	0.00385	-0.00118	-0.84	1-rate	n.s.
Proportions 2	0.00213	0.00086	0.00224	-0.00138	5.11	2-rate	slowdown
Tail length	0.01263	0.01131	0.01274	-0.00143	-1.91	1-rate	n.s.
Elevation	0.20158	0.26239	0.19647	0.06592	-1.09	1-rate	n.s.
Madagascar							
Mass	0.02346	0.02510	0.02340	0.00170	-2.03	1-rate	n.s.
Proportions 1	0.00374	0.00084	0.00384	-0.00300	4.48	2-rate	slowdown
Proportions 2	0.00213	0.00134	0.00215	-0.00081	-1.22	1-rate	n.s.
Tail length	0.01262	0.00371	0.01293	-0.00922	3.21	2-rate	n.s.
Elevation	0.20182	0.04972	0.20712	-0.15740	4.52	2-rate	slowdown
North America							
Mass	0.02350	0.01755	0.02422	-0.00667	-0.69	1-rate	n.s.
Proportions 1	0.00372	0.00235	0.00388	-0.00153	0.60	2-rate	n.s.
Proportions 2	0.00213	0.00035	0.00233	-0.00198	25.43	2-rate	slowdown
Tail length	0.01260	0.00888	0.01305	-0.00417	-0.14	1-rate	n.s.
Elevation	0.20181	0.16258	0.20655	-0.04397	-1.29	1-rate	n.s.
South America							
Mass	0.02345	0.01503	0.02605	-0.01102	5.25	2-rate	slowdown
Proportions 1	0.00374	0.00441	0.00353	0.00088	-0.81	1-rate	n.s.
Proportions 2	0.00212	0.00229	0.00207	0.00023	-1.79	1-rate	n.s.
Tail length	0.01266	0.02023	0.01033	0.00990	11.40	2-rate	speedup
Elevation	0.20160	0.32326	0.16408	0.15918	11.64	2-rate	speedup
Sahul							
Mass	0.02339	0.06787	0.01876	0.04911	27.45	2-rate	speedup
Proportions 1	0.00374	0.00142	0.00399	-0.00256	7.09	2-rate	slowdown
Proportions 2	0.00212	0.00632	0.00168	0.00464	26.20	2-rate	speedup
Tail length	0.01257	0.01018	0.01282	-0.00264	-1.42	1-rate	n.s.
Elevation	0.20185	0.15732	0.20649	-0.04917	-1.18	1-rate	n.s.
Southeast Asia							
Mass	0.02322	0.02374	0.02317	0.00057	-2.05	1-rate	n.s.
Proportions 1	0.00367	0.00336	0.00370	-0.00034	-1.97	1-rate	n.s.
Proportions 2	0.00213	0.00076	0.00226	-0.00150	7.33	2-rate	slowdown
Tail length	0.01253	0.01084	0.01270	-0.00187	-1.75	1-rate	n.s.
Elevation	0.20156	0.10761	0.21134	-0.10373	2.77	2-rate	n.s.

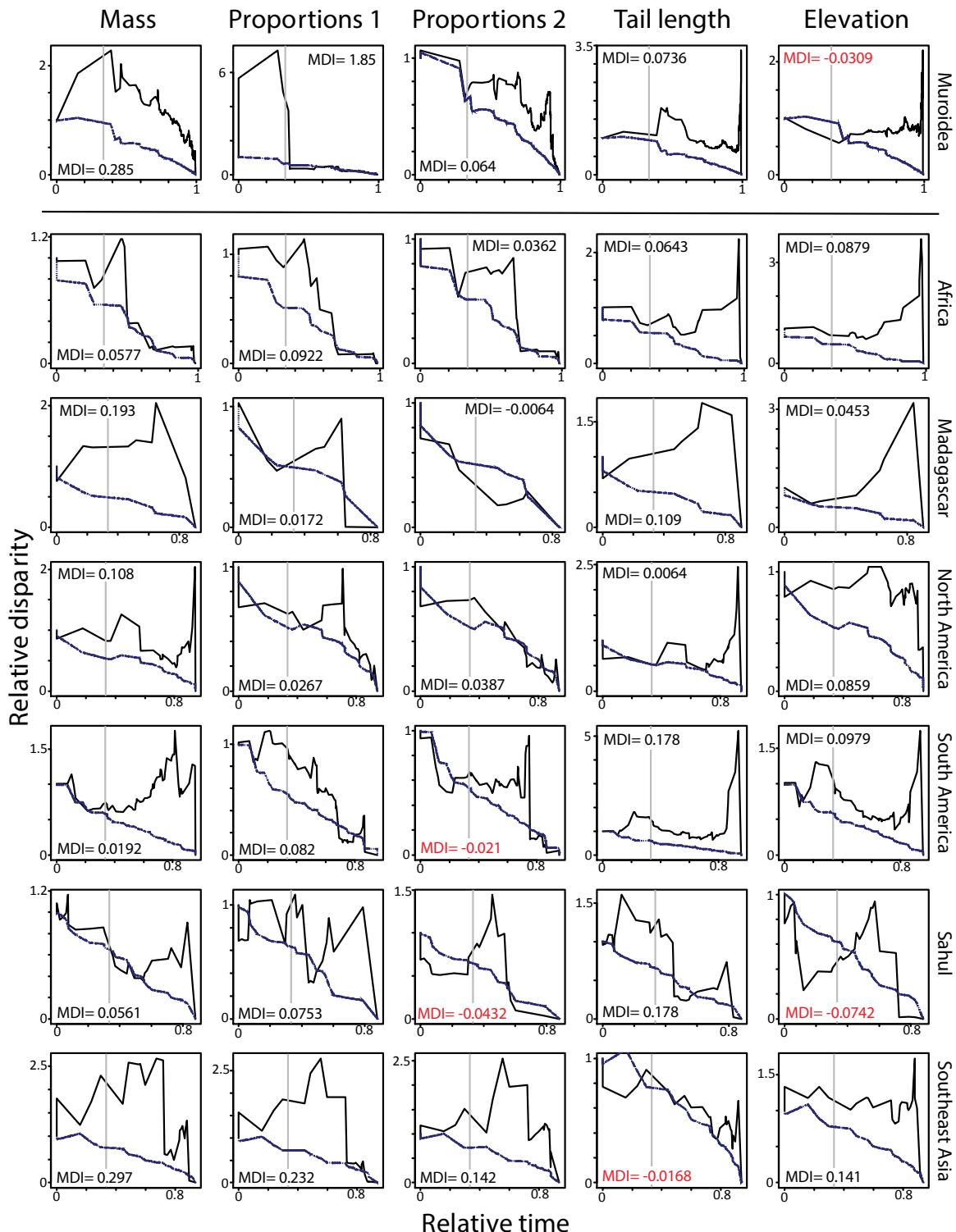


Figure 3.2. DTT plots for primary continental colonizations. Black lines are observed disparity and blue lines are the average 1,000 simulations on the muroid phylogeny under Brownian motion. MDI scores for the first 1/3 of the curve, left of the gray line, are indicated with substantially negative scores (< -0.01) highlighted in red. X and y axes have different scales.

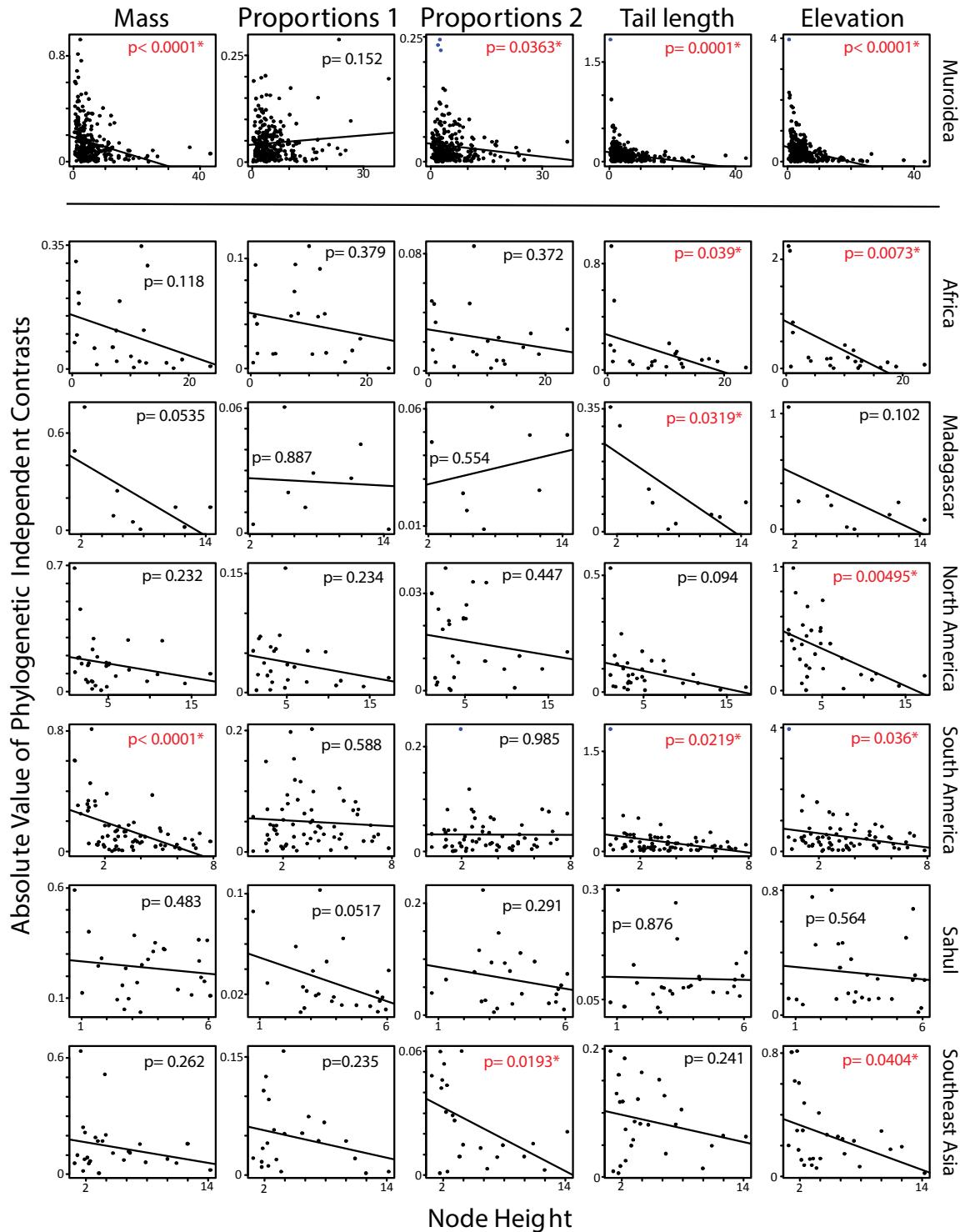


Figure 3.3. NHT plots for primary continental colonizations. Best fit regression lines are indicated with significantly negative correlations highlighted in red. X and y axes have different scales. Outliers (in blue) represent contrasts of shallow nodes and are associated with short branches which lead to high rates (e.g. for relative tail length of Muroidea and South America the outlier is the contrast between *Akodon lutescens* and *Akodon boliviensis*).

Ecomorphological Evolution/Disparity Following Increased Phylogenetic Diversification

An increase in the rate of evolution was found following the increased phylogenetic diversification at node: D3 (shortly after the colonization of South America) for relative tail length (Table 3.3) and elevation (Table 3.3); D4 (Southeast Asia including emigrations) for body mass (Table 3.3) and PC2 of appendage proportions (Table 3.3); D8 (Eumuroidea) for elevation (Table 3.3); and D9 (Oryzomyalia) for relative tail length (Table 3.3) and elevation (Table 3.3). The increased phylogenetic diversifications at nodes D1, D2 (partial *Rattus* sensu lato), D5 (*Microtus*), D6 (Murines), and D7 (recent North American radiation) were not associated with significant speedups in the rate of evolution of any of the traits.

Substantially negative MDI scores were associated with the increased phylogenetic diversification at node: D2 for body mass (Figure 3.4; $p= 0.295$) and relative tail length (Figure 3.4; $p= 0.401$); D5 for PC1 of appendage proportions (Figure 3.4; $p= 0.218$) and elevation (Figure 3.4; $p= 0.279$); D6 for PC1 of appendage proportions (Figure 3.4; $p= 0.179$), relative tail length (Figure 3.4; $p= 0.224$), and elevation (Figure 3.4; $p= 0.44$); D7 for body mass (Figure 3.4; $p= 0.333$), PC1 (Figure 3.4; $p= 0.019$) and PC2 (Figure 3.4; $p= 0.143$) of appendage proportions, and elevation (Figure 3.4; $p= 0.229$); and D9 for PC2 of appendage proportions (Figure 3.4; $p= 0.26$). The increased phylogenetic diversification at nodes D1, D3, D4, and D8 were not associated with an increase in early ecomorphological sub-clade disparity.

The NHT indicates a significant negative relationship between node height and the absolute standardized contrasts following the increased phylogenetic diversification at node: D1 for body mass (Figure 3.5; Coef = -0.010, $R^2 = 0.091$), PC2 of appendage proportions (Figure 3.5; Coef = -0.001, $R^2 = 0.016$), relative tail length (Figure 3.5; Coef = -0.008, $R^2 = 0.057$), and elevation (Figure 3.5; Coef = -0.034, $R^2 = 0.115$); D3 for body mass (Figure 3.5; Coef = -0.041, $R^2 = 0.222$) and relative tail length (Figure 3.5; Coef = -0.035, $R^2 = 0.063$); D4 for body mass (Figure 3.5; Coef = -0.014, $R^2 = 0.093$), PC1 (Figure 3.5; Coef = -0.003, $R^2 = 0.051$) and PC2 (Figure 3.5; Coef = -0.003, $R^2 = 0.053$) of appendage proportions, relative tail length (Figure 3.5; Coef = -0.006, $R^2 = 0.058$), and elevation (Figure 3.5; Coef = -0.035, $R^2 = 0.119$); D6 for PC2 of appendage proportions (Figure 3.5; Coef = -0.007, $R^2 = 0.191$) and elevation (Figure 3.5; Coef = -0.120, $R^2 = 0.126$); D8 for body mass (Figure 3.5; Coef = -0.010, $R^2 = 0.086$) PC2 of appendage proportions (Figure 3.5; Coef = -0.001, $R^2 = 0.017$), relative tail length (Figure 3.5; Coef = -0.008, $R^2 = 0.059$), and elevation (Figure 3.5; Coef = -0.033, $R^2 = 0.115$); and D9 for body mass

(Figure 3.5; Coef = -0.039, R^2 = 0.217), relative tail length (Figure 3.5; Coef = -0.033, R^2 = 0.060), and elevation (Figure 3.5; Coef = -0.070, R^2 = 0.042). The increased phylogenetic diversification at nodes D2, D5, and D7 (all three nodes close to the tips of the tree) were not associated with a significant slowdown in the rate of evolution of any of the examined traits.

Table 3.3. Model parameters of the censored rate test for nodes with increased phylogenetic diversification. See Table 3.3 for more information; full output is in Appendix Table B.3.

	σ^2						
	2-rate						
	1-rate	Foreground	Background	Δ (F-B)	Δ AICc	Preferred Model	Rate Shift
Node D1							
Mass	0.02350	0.02375	0.01437	0.00938	-1.21	1-rate	n.s.
Proportions 1	0.00372	0.00333	0.01817	-0.01484	15.59	2-rate	slowdown
Proportions 2	0.00213	0.00215	0.00104	0.00111	-0.62	1-rate	n.s.
Tail length	0.01263	0.01246	0.01854	-0.00608	-1.36	1-rate	n.s.
Elevation	0.20188	0.20618	0.04657	0.15961	3.59	2-rate	n.s.
Node D2							
Mass	0.02287	0.03792	0.02223	0.01569	-0.11	1-rate	n.s.
Proportions 1	0.00375	0.00395	0.00374	0.00021	-2.05	1-rate	n.s.
Proportions 2	0.00213	0.00106	0.00216	-0.00111	-0.26	1-rate	n.s.
Tail length	0.01262	0.01342	0.01258	0.00084	-2.03	1-rate	n.s.
Elevation	0.20162	0.68926	0.18109	0.50817	13.80	2-rate	n.s.
Node D3							
Mass	0.02345	0.01470	0.02620	-0.01150	6.05	2-rate	slowdown
Proportions 1	0.00375	0.00440	0.00354	0.00086	-0.85	1-rate	n.s.
Proportions 2	0.00212	0.00219	0.00210	0.00010	-2.01	1-rate	n.s.
Tail length	0.01262	0.02090	0.01002	0.01088	14.30	2-rate	speedup
Elevation	0.20124	0.31515	0.16545	0.14970	10.35	2-rate	speedup
Node D4							
Mass	0.02350	0.03254	0.01754	0.01500	11.89	2-rate	speedup
Proportions 1	0.00374	0.00294	0.00426	-0.00131	2.09	2-rate	n.s.
Proportions 2	0.00213	0.00302	0.00155	0.00148	12.55	2-rate	speedup
Tail length	0.01263	0.01067	0.01391	-0.00324	0.40	2-rate	n.s.
Elevation	0.20188	0.16195	0.22820	-0.06625	2.01	2-rate	n.s.
Node D5							
Mass	0.02349	0.00532	0.02399	-0.01867	3.70	2-rate	n.s.
Proportions 1	0.00375	0.00182	0.00381	-0.00199	-0.57	1-rate	n.s.
Proportions 2	0.00213	0.00063	0.00217	-0.00153	1.54	2-rate	n.s.
Tail length	0.01263	0.00343	0.01288	-0.00945	2.60	2-rate	n.s.
Elevation	0.20168	0.27232	0.19972	0.07260	-1.64	1-rate	n.s.

Table 3.3-continued.

σ^2							
	1-rate	2-rate			Δ AICc	Preferred Model	Rate Shift
		Foreground	Background	Δ (F-B)			
Node D6							
Mass	0.02345	0.04012	0.02165	0.01847	3.82	2-rate	n.s.
Proportions 1	0.00374	0.00417	0.00370	0.00047	-1.91	1-rate	n.s.
Proportions 2	0.00213	0.00110	0.00222	-0.00112	2.07	2-rate	n.s.
Tail length	0.01263	0.01390	0.01249	0.00141	-1.90	1-rate	n.s.
Elevation	0.20181	0.32409	0.18857	0.13551	2.38	2-rate	n.s.
Node D7							
Mass	0.02347	0.02459	0.02345	0.00114	-2.05	1-rate	n.s.
Proportions 1	0.00373	0.00073	0.00377	-0.00305	1.28	2-rate	n.s.
Proportions 2	0.00213	0.00003	0.00216	-0.00213	10.83	2-rate	slowdown
Tail length	0.01262	0.00818	0.01271	-0.00453	-1.56	1-rate	n.s.
Elevation	0.20059	0.15485	0.20153	-0.04668	-1.87	1-rate	n.s.
Node D8							
Mass	0.02348	0.02362	0.01659	0.00703	-1.73	1-rate	n.s.
Proportions 1	0.00361	0.00330	0.01943	-0.01613	12.42	2-rate	slowdown
Proportions 2	0.00212	0.00214	0.00115	0.00099	-1.28	1-rate	n.s.
Tail length	0.01262	0.01282	0.00311	0.00970	1.86	2-rate	n.s.
Elevation	0.20188	0.20581	0.01130	0.19451	9.63	2-rate	speedup
Node D9							
Mass	0.02350	0.01482	0.02628	-0.01145	5.99	2-rate	slowdown
Proportions 1	0.00375	0.00434	0.00356	0.00078	-1.06	1-rate	n.s.
Proportions 2	0.00212	0.00224	0.00208	0.00016	-1.93	1-rate	n.s.
Tail length	0.01263	0.02071	0.01005	0.01066	13.86	2-rate	speedup
Elevation	0.20157	0.32099	0.16336	0.15763	11.74	2-rate	speedup

Phylogenetic Locations of Greatest Shifts in Ecomorphological Evolution

The greatest shift in body mass evolution rate occurred in the most recent common ancestor of *Gerbillus*+*Dipodillus* (Figure 3.1; MS, PP = 0.38) with the evolutionary rate prior this node ($\sigma_1 = 0.147$) being faster than after the node ($\sigma_2 = 0.058$) indicating a slowdown in the rate of evolution. The greatest shift in relative tail length evolution occurred in the terminal node that includes *Akodon boliviensis*+*Akodon lutescens* (Figure 3.1; RT, PP = 0.71) with the evolutionary rate before this node ($\sigma_1 = 0.022$) being slower than after the node ($\sigma_2 = 0.328$) indicating a speedup in the rate of evolution. For elevational evolution rate, the greatest shift occurred in the clade that includes *Akodon boliviensis*+*Akodon lutescens*+*Akodon kofordi* (Figure 3.1; EL, PP = 0.38) with the evolutionary rate before this node ($\sigma_1 = 0.234$) being slower

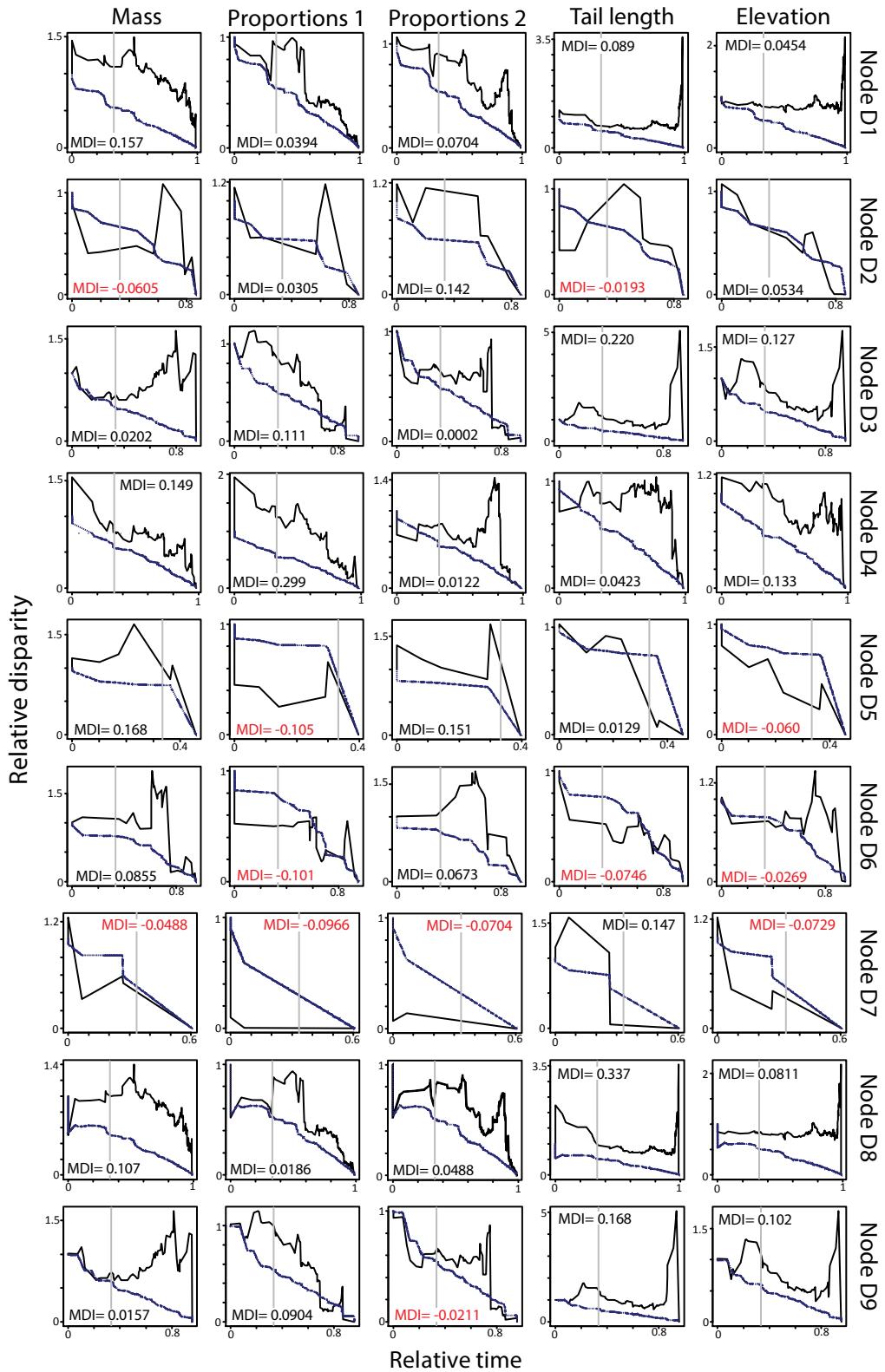


Figure 3.4. DTT plots for nodes with increased phylogenetic diversification. See Figure 3.2 legend for more information.

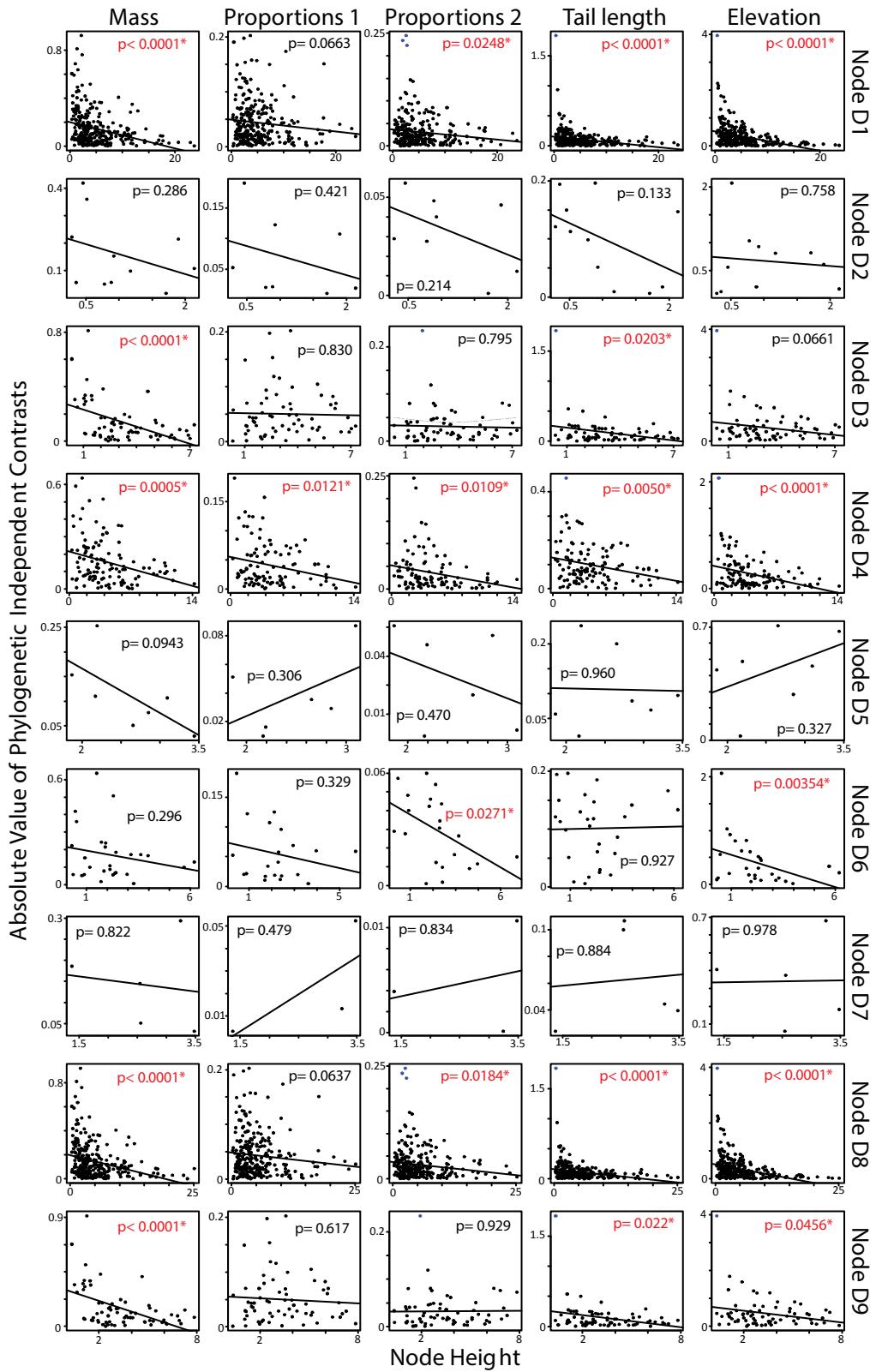


Figure 3.5. NHT plots for nodes with increased phylogenetic diversification. See Figure 3.3 legend for more information.

than after the node ($\sigma_2 = 1.313$) indicating a speedup in the rate of evolution. The greatest shift in PC1 of appendage proportions evolution rate occurred in Eumuroidea (Figure 3.1; PC1, PP = 0.21) with the evolutionary rate before this node ($\sigma_1 = 0.0935$) being faster than after the node ($\sigma_2 = 0.0068$) indicating a slowdown in the rate of evolution. For PC2 of appendage proportions, the greatest shift occurred at the *Nanospalax ehrenbergi* branch (Figure 3.1; PC2, PP = 0.63) with the evolutionary rate before this branch ($\sigma_1 = 0.0936$) being faster than after the branch ($\sigma_2 = 0.0061$) which indicates a slowdown in the rate of evolution.

Discussion

Support for Ecological Opportunity Triggered by Primary Continental Colonizations

Schenk et al. (2013) tested the *phylogenetic* predictions of EO following biogeographic transition in muroids and found that only the primary colonization South America fits all the predictions of the model which was associated with both an increase in the rate of *phylogenetic* diversification based by all three employed methods (with the lineage through time plots indicating that the diversification was concentrated early following the transition) as well as a significant slowdown in the rate of diversification through time. Similarly, in the present study, only the primary colonization of South America fit all the *phenotypic* predictions of EO (for some of the traits), where this biogeographic transition was associated with both a significant increase in the rate of evolution of two (relative tail length and elevation) out of the five examined ecomorphological traits (with the DTT plots indicating that disparification occurred early for PC2 of appendage proportions) as well as a significant slowdown in the rate of evolution of body size, relative tail length, and elevation. The colonization of South America by sigmodontines from the north has been described as an EO/adaptive radiation event in the past (Patterson and Pascual 1968) that is probably precipitated by the lack of potential competitors at the time of the muroid colonization; the present mammalian fauna at the time of this colonization included only relatively larger caviomorphs and marsupials (Hooper 1949; Simpson 1950; Patterson and Pascual 1968; Baskin 1978; Schenk et al. 2013).

The primary colonization of Sahul fits most of the *phenotypic* predictions of EO (for some of the traits) where there was a significant increase in the rate of evolution for both body size and PC2 of appendage proportions (with the DTT plots indicating that disparification

occurred early for PC2 of appendage proportions and elevation). However, none of the ecomorphological traits showed a significant slowdown in the rate of evolution through time, as predicted by niche-filling. Schenk et al. (2013), on the other hand, detected an increase in the rate of *phylogenetic* diversification based on one of the three employed methods (with the lineage through time plots indicating that the diversification was concentrated early following the transition) along with a significant slowdown in the rate of diversification through time. Similar to the primary colonization of South America, by the time that muroids first colonized Sahul, it lacked close mammalian competitors, with the mammal fauna at the time of the muroid colonization being composed of only bats, monotremes, and relatively larger marsupials (Schenk et al. 2013).

Similarly, the primary colonization of Southeast Asia fits most of the *phenotypic* predictions of EO (for some traits) where although there was no significant increase in the rate of evolution for any trait, the DTT plots indicate that disparification occurred early for relative tail length; this was followed by a significant slowdown in the rate of evolution of both PC2 of appendage proportions and elevation. Similarly, this continent was one of the only three (including South America and Sahul) where Schenk et al. (2013) found support for the *phylogenetic* predictions of EO, an increase in the rate of *phylogenetic* diversification based by all three employed methods (however, the lineage through time plots indicate that diversification was *not* concentrated early following the transition) but no significant slowdown in the rate of diversification through time. Unlike the primary colonizations of South America and Sahul which were “virgin” and did not contain ecologically similar rodent or non-rodent incumbents prior to muroid colonization, this was not the case for Southeast Asia, that did contain ecologically similar rodent competitors, including possibly early muroids that may have competed with the colonizing muroids (Schenk et al. 2013).

There was no significant increase in the rate of *phenotypic* evolution of any of the examined traits following the primary colonizations of North America, Madagascar, and Africa, and hence they do not fit the EO model. This was the same pattern detected by Schenk et al. (2013) where the primary colonization of these continents was not associated with an increase in the rate of *phylogenetic* diversification. This pattern was unsurprising for North America and Africa which (along with Southeast Asia) contained diverse early non-muroid and muroid rodent incumbents by the time of these colonizations. Consequently, competitive exclusion could

explain the lack of utilization of the ecological opportunity. This was not the case for Madagascar which (along with South America and Sahul) lacked ecologically similar potential rodent competitors prior to these muroid colonizations (Schenk et al. 2013).

Although prior studies have shown that extinction and fluctuations in speciation rates can erase the *phylogenetic* diversification signal of EO (increase in the rate of *phylogenetic* diversification) from molecular phylogenies while retaining the pattern of *phenotypic evolution* (Harmon et al. 2003; Slater et al. 2010; Martin and Wainwright 2011); I did not find such support in the study. Instead, by analyzing the pattern of phenotypic evolution following primary continental colonization I found almost identical patterns to those found previously when Schenk et al. (2013) examined the phylogenetic predictions of EO: South America showing the strongest support followed by Sahul and Southeast Asia which both show some support and all other continents showing no support. Nevertheless, the results indicate that EO, which is usually tested within the context of island colonizations in less diverse taxa (Losos et al. 1994; Grant 1998, 1999; Herrel et al. 2008) can be extended to larger spatial scales and more diverse taxa (e.g. Drummond et al. 2012; Schenk et al. 2013; this study).

Ecological Opportunity Patterns at Nodes with Increased Phylogenetic Diversification

EO may also be triggered by the mass extinction of competitors, the evolution of key innovation, as well as more localized biogeographic transition (Simpson 1953, Schluter 2000a; Grant and Grant 2008); all of which are much harder to trace on a molecular phylogeny since muroids leave equivocal evidence in the fossil record (Schenk et al. 2013). Here I find evidence consistent with the *phenotypic* prediction of EO at four of the nine sampled nodes where Schenk et al. (2013) found significant increases in the rate of *phylogenetic* diversification, with the trigger of these events being yet to be determined.

Node D3, which is a few nodes downstream of the primary colonization of South America, showed both a significant increase in the rate of evolution of relative tail length and elevation (however, the DTT plots indicate that disparification does not occur early in any of the examined traits) as well as a significant slowdown in the rate of evolution of body mass and relative tail length. Similarly, node D4, which occurs at the same node as the primary colonization of Southeast Asia without the removal of emigrating species, showed both a significant increase in the rate of evolution of body mass and PC2 of appendage proportions

(however, the DTT plots indicate that disparification does not occur early in any of the examined traits) as well as a significant slowdown in the rate of evolution of all examined traits. Node D8 (Eumuroidea) showed both a significant increase in the rate of evolution of elevation (however, the DTT plots indicate that disparification does not occur early in any of the examined traits) as well as a significant slowdown in the rate of evolution of body mass, PC2 of appendage proportions, relative tail length, and elevation. Lastly, node D9 (Oryzomyalia) showed both a significant increase in the rate of evolution of relative tail length and elevation (with the DTT plots indicating that disparification occurs early in PC2 of appendage proportions) as well as a significant slowdown in the rate of evolution of body mass, relative tail length, and elevation.

Since D3 is a few nodes downstream of the primary colonization of South America and D9 occurs at the same node as the colonization event (without the removal of emigrants) they are both expected to be influenced by the colonization event, which is evident by the similar observed phenotypic diversification patterns. Similarly, since node D4 occurs at the same node as the dispersal into Southeast Asia (without the removal of emigrants) it is also expected to be influenced by the colonization event. However, node D8 does not occur at or closely after a colonization event, (although it occurs one node upstream of the colonization of Africa), but is rather associated with the evolution of Eumuroidea and consequently may be explained by biogeographically independent mechanisms as a consequence of the divergence of most of the diverse muroid clades from spalacids and placanthomysids.

Interestingly, when groups are not defined *a priori* (i.e. in the MCMC approach), the greatest shifts in the rate of ecomorphological evolution for 4 out of the 5 examined traits did not coincide with (or are even close to) nodes that experienced increased *phylogenetic* diversification and/or primary continental colonizations. With the exception of the slowdown in the rate of evolution of PC1 of appendage proportions which coincided with D8 (Eumuroidea), these shifts occurred mostly near the tips of the tree. This general trend of discordance between morphological evolution rates and diversification rates may indicate either that ecomorphological evolution analyses is detecting signatures of EO not detected by *phylogenetic* diversification analyses, that these two indices of diversity (i.e. phylogenetic and phenotypic) are not tightly linked (e.g. Derrberry et al. 2011), non-ecological speciation (Schluter 2000; Rundell and Price 2009), or simply that the examined traits do not capture niche well for the focal clades. I explore some of these alternatives in chapter 5.

Variation in Ecological Opportunity Support among Traits

Although the primary colonization of South America, Sahul, and Southeast Asia all showed support for some of the *phenotypic* predictions of EO, these patterns were not exhibited by the same traits. In other words, the traits that underwent the significant increase in evolution rate (CRT) were not always the same as the traits with the disproportionately greater early disparity (DTT) which in turn were not always the same traits that underwent the significant deceleration in evolution rates (NHT). For example, in South America, relative tail length and elevation underwent a rapid increase in evolution rate, but only PC2 of appendage proportions underwent disproportionately greater early disparity. However, body mass, relative tail length, and elevation underwent a significant decline in evolution rate through time. Moreover, support for EO differed widely between traits for different continents. Some variation between patterns among traits is expected since they capture different aspects of niche and may have different degrees of importance in niche utilization in different continents, and therefore not all five traits are expected to show patterns consistent with the *phenotypic* predictions of EO, even if this process did take place. For example, elevational variation may be more important in South America than Sahul. Only the traits with the strongest association with niche in a particular biogeographic region (at the time of the colonization) are expected to show detectable patterns consistent with EO; which may or may not have been sampled in this study. Furthermore, a trait that is of crucial importance in the first stages of the diversification process following the primary continental colonization (e.g. traits associated with surviving the abiotic conditions and for maintaining relatively high populations) may not continue to be of importance later in the diversification process and other traits may show opposite pattern (e.g. traits associated with predator avoidance and mediating interspecific competition may be of more importance at late and not early stages of the diversification process following biogeographic transitions).

Conclusions

In this study, by testing the *phenotypic* predictions of EO, I show that ecological opportunity is not the inevitable consequence of continental colonizations; a result previously shown by Schenk et al. (2013) in their test of the *phylogenetic* predictions of EO. Moreover, my results are very similar to the results of Schenk et al. (2013), with only the primary colonization

of South America showing support for all the *phenotypic* predictions of EO; whereas Sahul and Southeast Asia show support for some but not all the predictions, and no support detected for the other primary continental colonizations. Both South America and Sahul lacked ecologically similar sized rodent or other mammalian incumbents prior to these muroid colonizations, which may account for the detected pattern of support for EO. However, this was not the case for Southeast Asia which did contain ecologically similar potential competitors by the time of muroid colonization. However, competition or lack thereof does not fully account for EO since Madagascar lacked close competitors by the time of first muroid colonization, but this did not translate into either *phylogenetic* or *phenotypic* diversification. This may either reflect the lower power of the analyses in Madagascar as a consequence of its smaller size, or that other unaccounted extrinsic factors such as stochasticity may have had an effect on whether or not colonizing lineages exploit EO (Schenk et al. 2013).

CHAPTER FOUR

THE ROLE OF ECOLOGY AND ECOMORPHOLOGY IN THE DIVERSIFICATION OF MUROIDS

Summary

Understanding the causes of uneven clade richness is a fundamental theme in ecology and evolutionary biology. A recent study in muroid rodents has shown that this group has experienced frequent speedups in diversification rates. Extrinsic factors, specifically ecological opportunity driven by biogeographic transition, has been shown to be a poor predictor of the diversity patterns in this group, as most biogeographic transitions were not associated with an increase in phylogenetic or phenotypic diversity. In the present study, I test the role of intrinsic factors in the diversification of muroid rodents, using a recently published molecular phylogeny of the group along with ecological and ecomorphological data from the literature. I test whether directional changes in continuous ecomorphological attributes are associated with increased diversification rates and whether different multistate ecological attributes are associated with differences in diversification rates, using recently developed “trait-dependent diversification” methods. I find that all examined traits are correlated with diversification rates in muroids, most of which are consistent with diversity and diversification rate patterns previously published in other mammals. This result indicates that intrinsic factors may play a larger role than extrinsic factors in driving the diversification process in muroid rodents.

Introduction

Muroid rodents are the most diverse superfamily of mammals, representing over a quarter of mammal species (Musser and Carleton 2005) distributed among highly uneven subclades that vary greatly in origination time and extant diversity (Steppan et al. 2004; Schenk et al. 2013). Muroids are also highly variable in ecological attributes including diet, locomotory mode, morphology, physiology, and behavior (Nowak 1999) as well as in habitat tolerance, with species adapted to most terrestrial habitats on all continents and most islands including rainforests, hyper-arid deserts, arctic tundra, and even some aquatic habitats (Fabre et al. 2012).

Schenk et al. (2013) and a subsequent study (chapter 3) found that biogeographic transitions do not sufficiently explain the uneven pattern of phylogenetic and phenotypic diversity in muroid rodents well (out of six primary continental colonizations only one, South America, fit all the predictions of the model), and that frequent increases in diversification rates cannot be sufficiently explained by ecological opportunity mediated by the primary colonization of continental landmasses (Schenk et al. 2013). This result suggests that other factors may better explain this uneven pattern of clade richness.

Causes of uneven clade richness is a topic that has been extensively studied in various taxa including mammals (Isaac et al. 2005), birds (Ricklefs 2006), and fish (Langerhans 2010). Despite the variation in the focal taxa, mechanistic explanations for uneven clade richness are generally divided into two main categories: (1) extrinsic abiotic factors that are clade-specific attributes including biogeography and habitat, and (2) intrinsic ecological factors which are species specific attributes including morphology and physiology (Rojas et al. 2012). Regardless of the proximate cause of uneven diversity, the ultimate cause is variation in diversification rates brought about by differences in the rates of speciation and extinction (FitzJohn et al. 2009; FitzJohn 2010). Speciation and extinction rates have been shown to be influenced by various intrinsic ecological attributes including body size (e.g. primates, FitzJohn 2010, Matthews et al. 2011; frogs, Wollenberg et al. 2011), life history (e.g. mammals, Isaac et al. 2005), sexual dichromatism (e.g. birds, Owens et al. 1999; lizards, Stuart-Fox and Owens 2003), dispersal ability and range (birds, Owens et al. 1999, Phillimore et al. 2006; frogs, Wollenberg et al. 2011), and diet (birds, Owens et al. 1999, Phillimore et al. 2006; primates, Gómez and Verdú 2012; bats, Rojas et al. 2012).

It has long been assumed that body size is inversely correlated with diversity (Hutchinson and MacArthur 1959; May 1986); a pattern that is sometimes attributed to the ability of small species to subdivide the environment more finely, permitting them to speciate and/or avoid extinction more readily (Dial and Marzluff 1988). While some empirical evidence has shown support for this correlation in carnivores (Gittleman and Purvis 1998) this is not the case in other mammals as well as in birds, fish, reptiles, amphibians, insects, and marine invertebrates (Dial and Marzluff 1988; Gardezi and da Silva 1999; Owens et al. 1999), where medium body sized groups are the most diverse (Dial and Marzluff 1988). Moreover, the inverse relationship has been documented in passerine birds (Kochmer and Wagner 1988) and North American mammals

(Martin 1992). More recent studies that use phylogenetic methods have found a correlation between small body size and increased diversification rate in mammals as a consequence of higher speciation rates and/or lower extinction rates (Gardezi and Silva 1999; Cardillo et al. 2005; Clauset and Erwin 2008); while in primates, averaged sized lineages have the highest speciation rates (FitzJohn 2010).

The correlation between elevation and diversity/diversification rate is well known (i.e. elevational diversity gradient; EDG); diversity tends to increase with increasing elevation, maximizing at mid-elevations and therefore, early colonization of mid-elevational habitats tends to be associated with increased diversification rates (e.g. tree frogs, Smith et al. 2007; salamanders, Wiens et al. 2007; nonvolant small mammals, McCain 2005, McCain and Grytnes 2010). EDG is commonly explained in terms of increasing habitat productivity with increasing altitude that maximizes at mid-elevations, as a consequence of increased precipitation, temperature, net primary productivity and resource abundance, increased habitat heterogeneity and diversity, and increased biotic interactions including competition (McCain 2005).

Shifts in life history traits (e.g. diet) are expected to enhance diversification rates through the utilization of new adaptive zones (Hunter 1998) and specialization in various ecological attributes has been shown to be correlated with increased diversification rates (e.g. habitat specialization in Coyotes, Sacks et al. 2008; specialization to frugivory in bats, Rojas 2012; frugivory in primates, Gómez and Verdú 2012; specialization to host plants in fungi, Walker et al. 2014). Adaptive specialization through ecological fitting or niche specialization can lead specialists to diversify greatly by competing better for narrower niche space, with the consequent ecological divergence promoting reproductive isolation (Schluter 2000, 2001).

In the present study, I use a recently published molecular phylogeny of muroid rodents (Schenk et al. 2013) along with widely reported ecological and ecomorphological data from literature to test the correlation between diversification rates and: (1) body size, a frequently used proxy for ecological role being highly correlated with physiology(e.g. Peters 1983; Gardezi and Silva 1999; Isaac et al. 2005); (2) elevation, a trait that is among the first to diverge in sister taxa (Endler 1982; Hall 2005); (3) life history traits (diet, nesting site, and activity period), where shifts and specializations are associated with increased diversification (e.g. Schluter 2000, 2001); (4) appendage proportions (index based on body length, tail length, hindfoot length, and ear length) including relative tail length, an important predictor of climbing ability in *Peromyscus*

(Lemen 1980) and in squirrels (Hayssen 2008) with longer tails being associated with higher elevations and greater scansoriality.

I predict that, similar to other mammals, increased diversification rates in muroids are associated with: (1) small to average body sizes; (2) average elevations; and (3) specialized life history traits. The association between appendage proportions and diversification have not been studied before. However, assuming that appendages evolve according to Allen's rule (Allen 1877), where increased appendage proportions in endotherms are associated with warmer climates, I expect that (4) lineages with long to average appendages will experience the greatest diversification rates because they are expected to occur at mid to low latitudes and at altitudes (which are associated with mid-temperatures).

Materials and Methods

Phylogenetic Framework

The chronogram used in this study (Figure 4.1), which includes a total of 297 muroid species sampled proportional to total clade diversity, comes from a Bayesian phylogenetic and divergence-times analysis conducted in Beast v.1.6.1 (Drummond and Rambaut 2007) by Schenk et al. (2013). In addition, some of the analyses conducted in the present study also rely on the diversification rate shift analyses (Figure 4.1) conducted by Schenk et al. (2013) using three approaches: Δ parameters (Chan and Moore 2005), relative cladogenesis tests (Purvis et al. 1995), and the stepwise AIC model selection approach (Medusa; Alfaro et al. 2009) as implemented in R (R Development Core Team 2005).

Data Collection

For each species, I used previously compiled data (chapter 3) for body mass of adults in grams; head-body length, tail length, hind foot length, and ear length of adults in millimeters; as well as elevation in meters above sea level (Appendix Table B.1, chapter 3). Details on the collection of this ecomorphological dataset are discussed elsewhere (chapter 3); body mass of the sampled muroid adults ranged from 5 to 2,225 grams (mean= 126 grams), the head body length ranged from 55 to 446 millimeters, and elevation ranged from sea level to 4,450 meters above sea level (Figure 4.2; Appendix Table B.1, chapter 3). Unlike in the previous chapter,

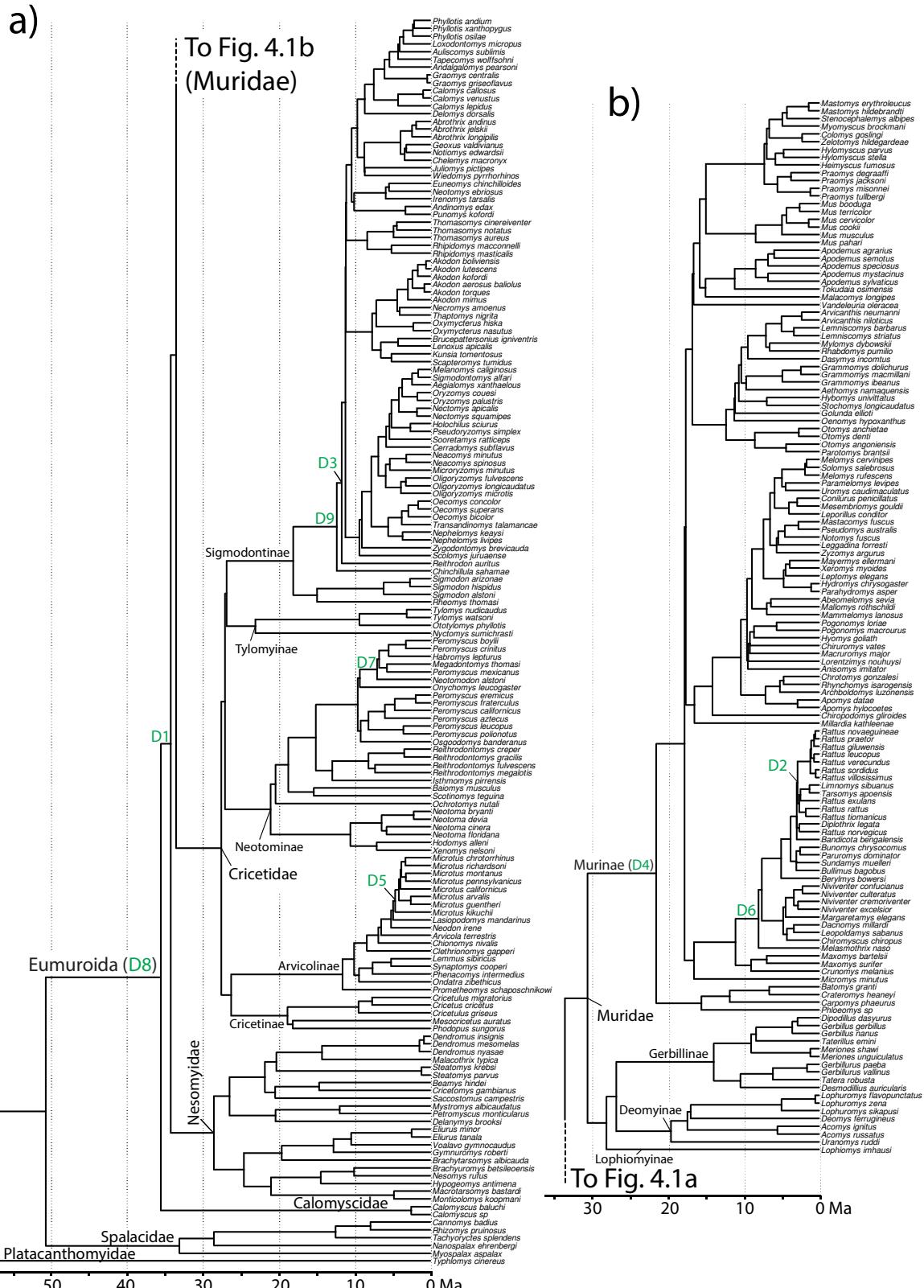


Figure 4.1. Muroid rodent chronogram and diversification analyses from Schenk et al. (2013). Nodes with significantly increased diversification rates are indicated in green (D1-D9). Some of the major taxonomic groups are indicated.

phylogenetically corrected principle component analysis (PPCA; Revell 2009) was performed on the appendage proportions (head-body length, tail length, hind foot length, and ear length) following the published code using the Ape library (Paradis et al. 2004) in R, without size correction. Consequently, the first principal component axis was highly correlated with body size (Table 4.1) and was discarded; only PC2, which accounts for 15.4% of the total variance (49% of remaining variance; Table 4.1) was used as the sole index of appendage proportions.

Ecological data for all species were collected from Nowak (1999) and supplemented by monographic sources from the literature and other field guides (Appendix Table C.1). Species were assigned to a multistate dietary classification based on the primary food items consumed; dietary categories were similar to Williams and Kay (2001), Samuels (2009), and Martin (2010) (Table 4.2; Table 4.3; Appendix Table C.1). Two dietary classification schemes were devised, the first (general diet) is the broadest, where species are classified as either faunivorous, omnivorous, or herbivorous. In the second scheme (specific diet) faunivorous species are partitioned into carnivores that consume vertebrates and large invertebrates, and insectivores; herbivores are partitioned into generalists that consume soft vegetable matter, and specialists that consume more abrasive vegetable matter. Placement of species into dietary categories was based on strongest evidence, with stomach content prioritized unless the number of field observations were much greater than the number of stomachs examined, however, field observations from multiple localities were prioritized over stomach contents from a single location.

Nesting site (arboreal, fossorial, or terrestrial) and activity period (diurnal, nocturnal, or other) were also obtained from the literature (Table 4.3; Appendix Table C.1). Species that are most often cited as sheltering in trees are included in the arboreal category, whereas species that spend a significant amount of time sheltering underground were included in the fossorial category; these species are not necessarily strictly fossorial (e.g. naked mole rats or spalacids) but include species that dig burrows and forage above ground. Species that do not fit these two categories are included in the terrestrial category, and includes species capable of limited climbing and/or burrowing but spend most of their time in the surface. Activity period refers to the dominant (i.e. although not exclusive) time of activity; species with no dominant period of activity and are active in both the day and the night and/or are crepuscular are placed in the ‘other’ category.

Table 4.1. Loadings of the PPCA on non-size corrected appendage proportions.

Variable	PC1	PC2	PC3	PC4
Body length	-0.830	-0.077	-0.507	0.218
Tail length	-0.896	-0.227	0.379	0.048
Hindfoot length	-0.883	-0.138	-0.286	-0.346
Ear length	-0.646	0.757	0.092	-0.005
Eigenvalues	0.686	0.154	0.127	0.033

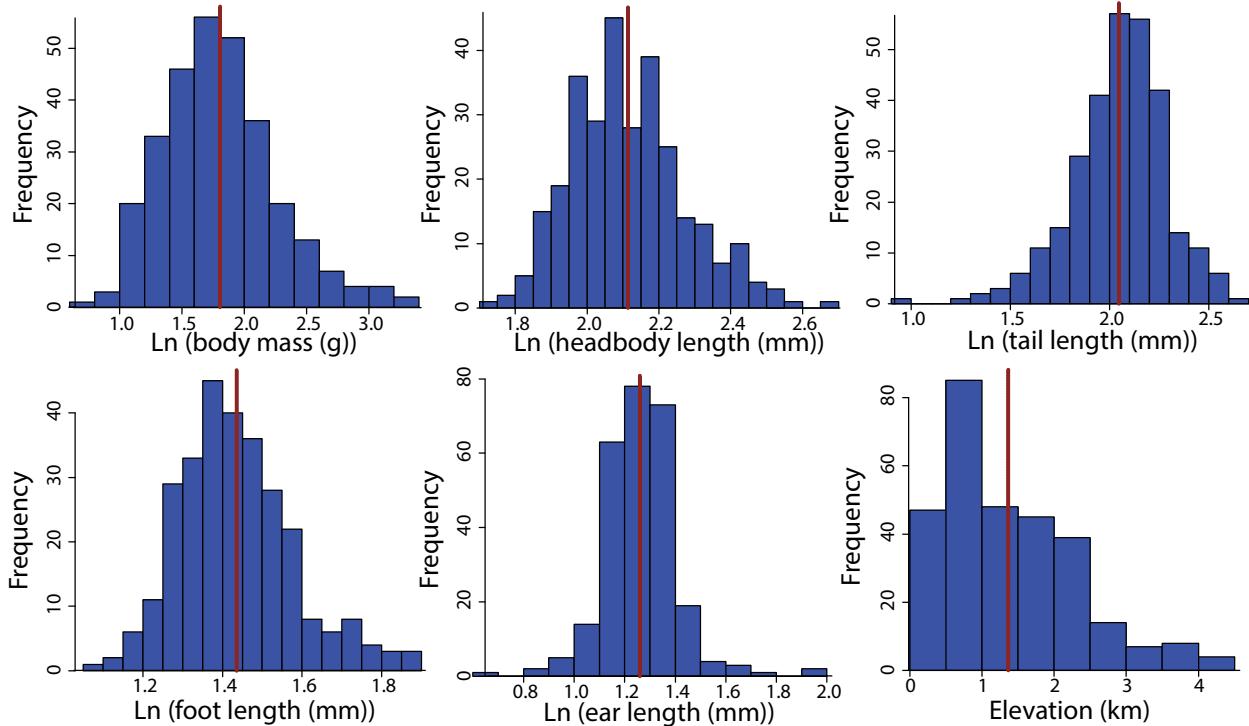


Figure 4.2. Range of ecomorphological data for sampled muroid rodents. Red lines indicate mean values of each variable.

Trait Dependent Diversification

I used “trait-dependent diversification” methods to test the association between diversification rates and ecomorphological/ecological evolution; these methods test this association by modeling trait evolution with speciation and extinction rates being dependent on character states of lineages (FitzJohn 2010; FitzJohn 2012). Continuous ecomorphological traits were analyzed with the quantitative state speciation and extinction (QuaSSE; FitzJohn 2010) model and the discrete traits were analyzed using the multistate speciation and extinction (MuSSE; FitzJohn 2012) model, both of which are generalizations of the binary state speciation

Table 4.2. Dietary classifications for muroids. See Appendix Table C.1 for more information.

General diet	Specific diet	Description
Faunivore	Carnivore	Diet composed mostly of vertebrates and large invertebrates
Faunivore	Insectivore	Diet composed mostly of arthropods and small invertebrates
Omnivore	Omnivore	Plant and animal material consumed at roughly equal amounts
Herbivore	Generalist herbivore	Diet composed mostly of seeds, leaves, and fruit
Herbivore	Specialist herbivore	Diet composed mostly of grass, wood, and roots

Table 4.3. Muroid species sampled from each dietary, nesting site, and activity period category.

	# sampled	Proportion
General diet		
Faunivore	29	0.10
Omnivore	126	0.42
Herbivore	111	0.37
No data	31	0.10
Specific diet		
Carnivore	7	0.02
Insectivore	22	0.07
Omnivore	126	0.42
Generalist herbivore	71	0.24
Specialist herbivore	34	0.11
No data	37	0.12
Nesting site		
Arboreal	57	0.19
Fossorial	96	0.32
Terrestrial	100	0.34
No data	44	0.15
Activity period		
Diurnal	28	0.09
Nocturnal	176	0.59
Other	28	0.09
No data	65	0.22

and extinction (BiSSE; Maddison et al. 2007) model. I correct for incomplete phylogenetic information in both these methods under the assumption that sampled muroid species are a random representation of extant species diversity (FitzJohn et al. 2009). Because diversification models tend to be poorly behaved when character states are missing (FitzJohn et al. 2010), I pruned species with missing data from the tree prior to the analysis. The tree included three polytomous nodes which were randomly resolved prior to trait diversification analyses using the Ape library in R.

Using QuaSSE, I fit flat, linear, sigmoidal, and modal likelihood models for speciation and extinction rates to the ecomorphological data (FitzJohn 2010). I constrained extinction rates to be the same because estimated extinction rates are not reliable in molecular phylogenies with ML estimates of extinction rates frequently being zero despite fossil evidence for nonzero extinction (FitzJohn 2010). Moreover, preliminary analyses indicate no significant correlation between extinction rates and ecomorphological evolution (i.e. no significant improvement over the flat function; data not shown). A drift parameter significantly improved fit and is included in all models. I compared the fit of the linear, sigmoidal, and modal models of speciation relative to the fit of the flat (null, where speciation rates are constant, or character-independent) model.

Shifts in diversification rate may bias the results if lineages that are rapidly diversifying share similar traits, which would be overrepresented, and therefore spuriously appear to be directly linked to the increase in speciation rate (FitzJohn 2010). To control for this possibility, in one set of analyses, I used the diversification rate shift analyses from Schenk et al. (2013), to partition the tree into “foreground” groups that consist of lineages that have undergone significant increases in diversification rate and “background” groups that consist of the rest of the tree excluding the “foreground” group; each with an independent set of parameters for the speciation and extinction functions, while sharing a common diffusion coefficient and a zero directional term (FitzJohn 2010). However, because of computational complexity and the large number of parameters not all partitioned analyses reached convergence after several weeks of analyses. This problem is common and some authors address it by discretizing continuous variables (e.g. Bergmann and Irschick 2011). Therefore, I focus on the unpartitioned analyses (see results).

I used MuSSE to test whether diversification rates significantly differ between states of ecological traits by comparing the fit of: (1) the fully constrained, character-independent (null)

model, where speciation (λ_i), extinction (μ_i), and transition (q_{ij}) rates for and between all character state of a specific trait are constrained to be the same; (2) an intermediate model where μ_i and q_{ij} are constrained and λ_i is allowed to vary; (3) an intermediate model where λ_i and q_{ij} are constrained and μ_i is allowed to vary; (4) an intermediate model where q_{ij} is constrained and λ_i and μ_i are allowed to vary; (5) a fully unconstrained, MuSSE model, where all parameters (λ_i , μ_i , and q_{ij}) are unconstrained and optimized for each state (FitzJohn 2010). I used the character-independent birth-death fit to make a heuristic estimate of starting points for each parameter, a method that is reasonably successful in reaching the ML point (FitzJohn 2012). I used the Akaike information criterion (AIC; Akaike 1974; Burnham and Anderson 2002) to assess the fit in these nested models of diversification. The ML values for the parameters of the models were further optimized and confidence intervals were calculated under a Bayesian framework by computing the posterior probability of parameters in a Markov chain Monte Carlo (MCMC) simulation with a 10,000 steps using an exponential prior with a mean equal to 2 times the diversification rate for the parameters (FitzJohn et al. 2009). QuaSSE, MuSSE, and MCMC analyses were conducted in the Diversitree library (FitzJohn 2012) in R (R Development Core Team 2013).

Results

Ecomorphological-Dependent Diversification

The 2-rate, partitioned models (i.e. partitioning based on diversification nodes), fit the data better than the unpartitioned, 1-rate (linear) models in 15 out of the 20 analyses that reached convergence (Appendix Tables C.2, C.3, C.4, C.5, and C.6). However, the linear foreground, flat background model fit the data best in only 3 out of the 20 analyses (Appendix Tables C.2, C.3, C.4, C.5, and C.6), which indicates that lineages that have undergone shifts in diversification rates (Figure 4.1) do not exhibit significantly different diversification patterns from the rest of the tree, and therefore, results and interpretation are based on the unpartitioned, 1-rate models.

The linear, sigmoidal, and modal models of speciation fit the data significantly better than the flat function (Table 4.4; Table 4.5). Out of these three models, the modal model fit the data best for body mass (Table 4.4; $\Delta\text{AIC} = 35.30$) which indicates that lineages with average values (mean = 1.79, around 125.73g; Appendix Table B.1, chapter 3) have the highest speciation rates. The drift parameter (μ_d), an estimate of the directional tendency of BM

evolution, was negative (Table 4.5; $\mu_d = -0.02$) indicating a trend of decreasing body mass through time. The linear model fit the data best for the PC2 of appendage proportions (Table 4.4; $\Delta AIC = 8.71$). Both the slope (Table 4.5; $\lambda_m = 0.42$) and the drift (Table 4.5; $\mu_d = 0.008$) parameters were positive, indicating a positive linear association between speciation rate and PC2 of appendage proportions and that there is a general tendency for values of the trait to increase through time, generally associated with the evolution of longer ears (Table 4.1). The modal function fits the data best for relative tail length (Table 4.4; $\Delta AIC = 36.46$), which indicates that lineages with average relative tail lengths ($= 0.929$ units; Appendix Table B.1, chapter 3) have the highest speciation rates. The drift parameter for the modal function was also negative (Table 4.5; $\mu_d = 0.05$), which indicates a trend of increasing relative tail length through time. The linear function fit the data best for elevation (Table 4.4; $\Delta AIC = 45.70$), with a positive slope parameter (Table 4.5; $\lambda_m = 0.0001$) indicating that increased elevation is associated with increased speciation rate. The drift parameter, however, was negative ($\mu_d = -26.76$) indicating a tendency of decreased elevation through time.

Table 4.4. Fit of the four models of correlation between diversification rates and continuous ecomorphological data. ΔAIC indicates the fit of the best model (italicized) relative to the null (flat) model. Complete parameters are indicated in Table 4.5.

	AIC					ΔAIC
	Flat	Linear	Sigmoidal	Modal		
Mass	1216.00	1205.20	1192.80	<i>1180.70</i>	35.30	
Proportions 2	474.37	465.66	473.14	<i>472.56</i>	8.71	
Tail length	1031.65	1003.25	1006.96	<i>995.19</i>	36.46	
Elevation	5969.30	5923.60	5930.70	<i>5974.50</i>	45.70	

Table 4.5. ML parameter estimates for the four models for correlation between diversification rates and continuous ecomorphological data. λ = speciation rate; λ_m = slope of speciation function; λ_{y0} = speciation rate approaching negative infinity; λ_{y1} = speciation rate approaching infinity; λ_i = speciation rate at the inflection or midpoint; λ_d = rate of exponential decay, or steepness of speciation function; λ_v = variance of speciation function; μ = constant (flat) extinction rate; σ_2 = diffusion coefficient, or BM evolution rate; μ_d = drift parameter, or rate of the directional tendency of trait evolution. The best fit model parameters for each trait are italicized. Parameters not applicable for a given model are indicated with (-).

	λ	λ_m	λ_{y0}	λ_{y1}	λ_i	λ_d	λ_v	μ	σ_2	μ_d
Flat										
Mass	0.40585	-	-	-	-	-	-	0.25956	0.014370	-
Proportions 2	0.36695	-	-	-	-	-	-	0.21487	0.001386	-

Table 4.5-continued.

	λ	λ_m	λ_{y0}	λ_{y1}	λ_i	λ_d	λ_v	μ	σ_2	μ_d
Tail length	0.40460	-	-	-	-	-	-	0.25844	0.008040	-
Elevation	0.40657	-	-	-	-	-	-	0.26056	136150.1	-
Linear										
Mass	0.58813	-0.12666	-	-	-	-	-	0.17383	0.015133	-0.03885
Proportions 2	0.28627	0.42098	-	-	-	-	-	0.14836	0.001439	0.00798
Tail length	0.14181	0.20009	-	-	-	-	-	0.11720	0.008393	0.01585
Elevation	0.14450	0.00010	-	-	-	-	-	0.00000	141922.2	-26.7613
Sigmoidal										
Mass	-	-	0.35228	0.16800	2.29854	27445.1	-	0.14199	0.016134	-0.00733
Proportions 2	-	-	-0.05534	0.84469	0.18013	1.03310	-	0.22092	0.001406	0.03202
Tail length	-	-	-0.00066	0.52203	0.11960	1.49024	-	0.21457	0.008369	0.06007
Elevation	-	-	0.36046	0.15108	2371.76	287.516	-	0.13541	149406.1	274.341
Modal										
Mass	-	-	0.14510	0.38948	1.74787	-	0.19790	0.13732	0.017457	-0.02045
Proportions 2	-	-	-0.01076	0.37617	0.21283	-	0.99137	0.21905	0.001422	0.00310
Tail length	-	-	0.11653	0.36954	1.07001	-	0.18207	0.10614	0.009185	0.05443
Elevation	-	-	0.40829	-0.00308	2249.74	-	3.70270	0.26084	133493.5	29.1847

Diversification Rates in Different Ecological States

When species were divided into three dietary states, although the fully unconstrained model fit the data best (Table 4.6; $\Delta\text{AIC} = 0.7$), this model did not show a significant improvement over the 7 parameter model (Table 4.6; $\chi^2 = 10.742$, $p = 0.057$), which was used instead. When species were divided into five dietary categories, the 11 parameter model fit the data best (Table 4.6; $\Delta\text{AIC} = 14.7$, $\chi^2 = 22.7$, $p = 0.00015^*$). The fully unconstrained model fit the data best for both nesting site (Table 4.6; $\Delta\text{AIC} = 6.4$, $\chi^2 = 16.408$, $p = 0.0058^*$) and activity period (Table 4.6; $\Delta\text{AIC} = 4.8$, $\chi^2 = 14.789$, $p = 0.0113^*$).

The extinction rates were highly similar and overlapping for all examined traits (Figure 4.3a, b, c, d; Table 4.7). For general diet, faunivores showed the highest speciation (Figure 4.4a) and net diversification (Figure 4.5a) rates in 99-100% of the posterior sample (Table 4.7); omnivores had the second highest speciation and net diversification rates in 85-96% of the posterior sample (Table 4.7), however, these parameters were highly overlapping with herbivores (Figure 4.4a; Figure 4.5a). For specific diet, the states were much more overlapping in both speciation (Figure 4.4b) and net diversification rates (Figure 4.5b), however, insectivores had the highest speciation and net diversification rates in 63% of the posterior sample (Table 4.7).

The arboreal group had the highest speciation (Figure 4.4c) and net diversification rates (Figure 4.5c) among nesting sites in 96-99% of the posterior sample (Table 4.7); fossorial and

terrestrial groups had highly similar and overlapping speciation (Figure 4.4c) and net diversification rates (Figure 4.5c). For activity period, the ‘Other’ group had the highest speciation (Figure 4.4d) and net diversification rates (Figure 4.5d) in 90-92% of the posterior sample (Table 4.7); the diurnal group had the second highest speciation (Figure 4.4d) and net diversification rates (Figure 4.5d) in 96-97% of the posterior sample (Table 4.7), however, these parameters were highly overlapping with the nocturnal group.

Table 4.6. Fit of four models of association between multistate ecological traits and diversification rates. n = number of estimated parameters; lnL = log likelihood score; ΔAIC = fit relative to the model with the lowest AIC score (italicized); p = significance of improvement in fit based on the chi-square (χ^2) test.

	n	lnL	AIC	ΔAIC	χ^2	p
General diet						
Fully constrained	3	-1062.80	2131.5	32.2	50.215	9.81E-08
λ unconstrained	5	-1053.50	2116.9	17.6	31.604	4.81E-05
μ unconstrained	5	1057.00	2124	24.7	38.695	2.24E-06
λ and μ unconstrained	7	-1043.00	2100	0.7	10.742	0.057
<i>Fully unconstrained</i>	12	<i>-1037.70</i>	<i>2099.3</i>	<i>0</i>	-	-
Specific diet						
Fully constrained	3	-1113.5	2233	38.5	54.46	5.62E-09
λ unconstrained	7	-1092.90	2199.9	5.4	13.342	0.0097
μ unconstrained	7	-1097.60	2209.2	14.7	22.7	0.00015
λ and μ unconstrained	11	<i>-1086.30</i>	<i>2194.5</i>	<i>0</i>	-	-
Fully unconstrained	30	-1069.20	2198.4	3.9	34.081	0.01798
Nesting site						
Fully constrained	3	-1060.60	2127.2	35.8	53.782	2.08E-08
λ unconstrained	5	-1051.70	2113.4	22	35.973	7.33E-06
μ unconstrained	5	-1055.30	2120.5	29.1	43.109	3.18E-07
λ and μ unconstrained	7	-1041.90	2097.8	6.4	16.408	0.0058
<i>Fully unconstrained</i>	12	<i>-1033.70</i>	<i>2091.4</i>	<i>0</i>	-	-
Activity period						
Fully constrained	3	-912.49	1831	37.2	55.219	1.11E-08
λ unconstrained	5	-905.04	1820.1	26.3	40.302	1.10E-06
μ unconstrained	5	-901.48	1813	19.2	33.183	2.45E-05
λ and μ unconstrained	7	-892.28	1798.6	4.8	14.789	0.0113
<i>Fully unconstrained</i>	12	<i>-884.88</i>	<i>1793.8</i>	<i>0</i>	-	-

Table 4.7. Effect of ecological traits on muroid diversification. The values in the cells indicate the proportion of 10,000 MCMC simulations in which the rates of speciation (λ), extinction (μ), or diversification (r) followed the trend specified in each line.

	λ	μ	r
General diet			
Herbivore > omnivore	0.035	0.177	0.148
Herbivore > faunivore	0	0.405	0.001
Omnivore > faunivore	0.001	0.675	0.002
Specific diet			
Specialist herbivore > generalist herbivore	0.905	0.693	0.806
Specialist herbivore > omnivore	0.431	0.3	0.734
Specialist herbivore > insectivore	0.07	0.548	0.064
Specialist herbivore > carnivore	0.528	0.338	0.574
Generalist herbivore > omnivore	0.045	0.115	0.342
Generalist herbivore > insectivore	0.03	0.367	0.044
Generalist herbivore > carnivore	0.417	0.185	0.542
Omnivore > insectivore	0.071	0.735	0.049
Omnivore > carnivore	0.54	0.462	0.555
Insectivore > carnivore	0.635	0.306	0.639
Nesting site			
Fossorial > terrestrial	0.584	0.543	0.511
Fossorial > arboreal	0.004	0.484	0.006
Terrestrial > arboreal	0.032	0.449	0.03
Activity period			
Nocturnal > other	0.074	0.482	0.071
Nocturnal > diurnal	0.032	0.562	0.026
Other > diurnal	0.909	0.569	0.909

Discussion

Body Size Variation and Diversification

I found a modal relationship between body mass and diversification rates in muroids, indicating that average sized lineages have the highest diversification rates. By using the same method, FitzJohn (2010) found the same relationship in primates, where lineages with average body mass had the highest diversification rates. Similarly, Dial and Marzluff (1988) found that medium sized mammals from various assemblages were the most diverse. However, both Cardillo et al. (2005) and Clauset and Erwin (2008) found that smaller mammals are associated

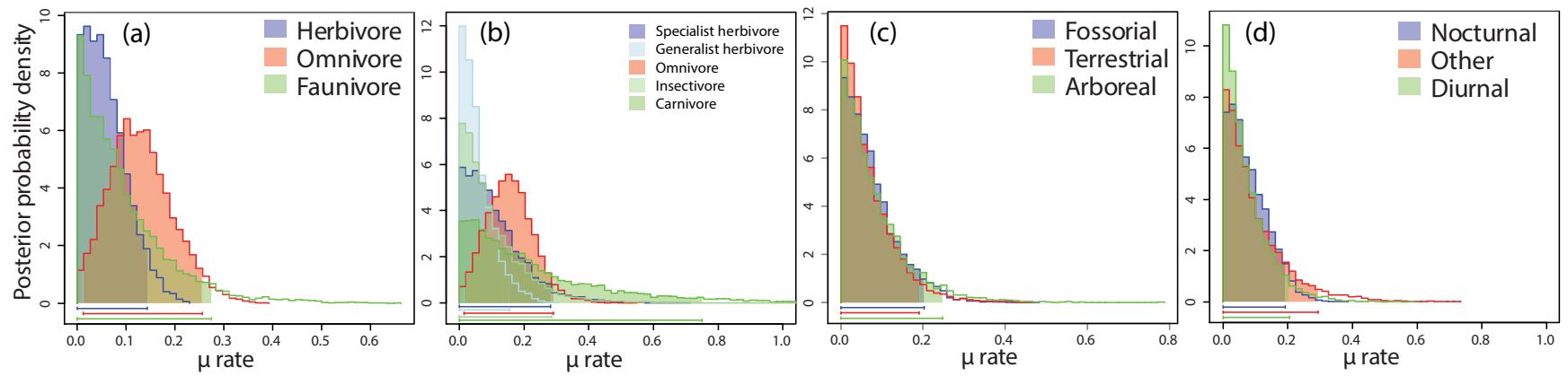


Figure 4.3. Posterior probability distributions of extinction rates for (a) general diet, (b), specific diet, (c) nesting site, and (d) activity period. Distributions based on a 10,000 step MCMC simulation. Bars below the distributions indicate the 95% credibility intervals.

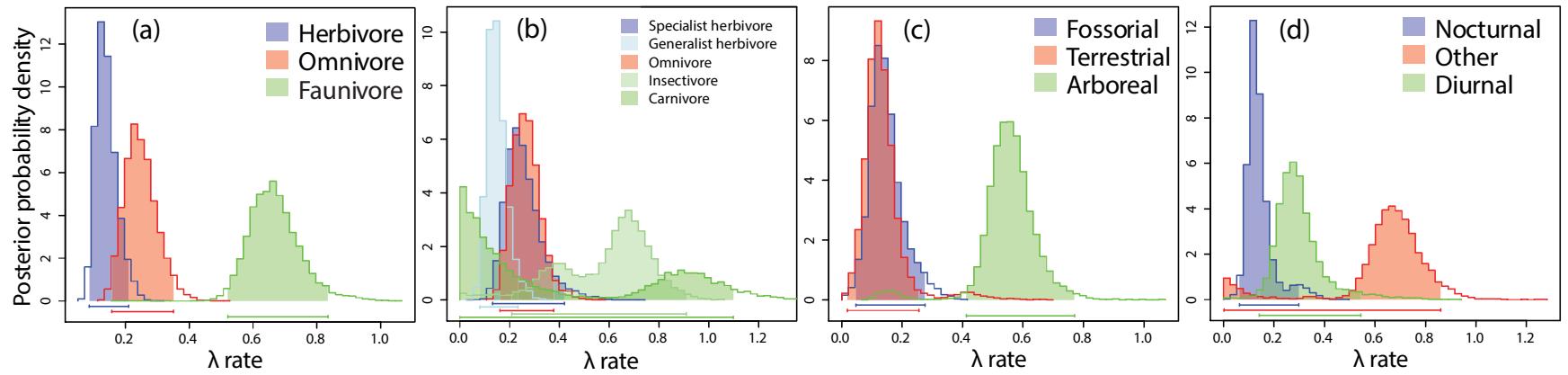


Figure 4.4. Posterior probability distributions of speciation rates for (a) general diet, (b), specific diet, (c) nesting site, and (d) activity period. See Figure 4.3 legend for more information.

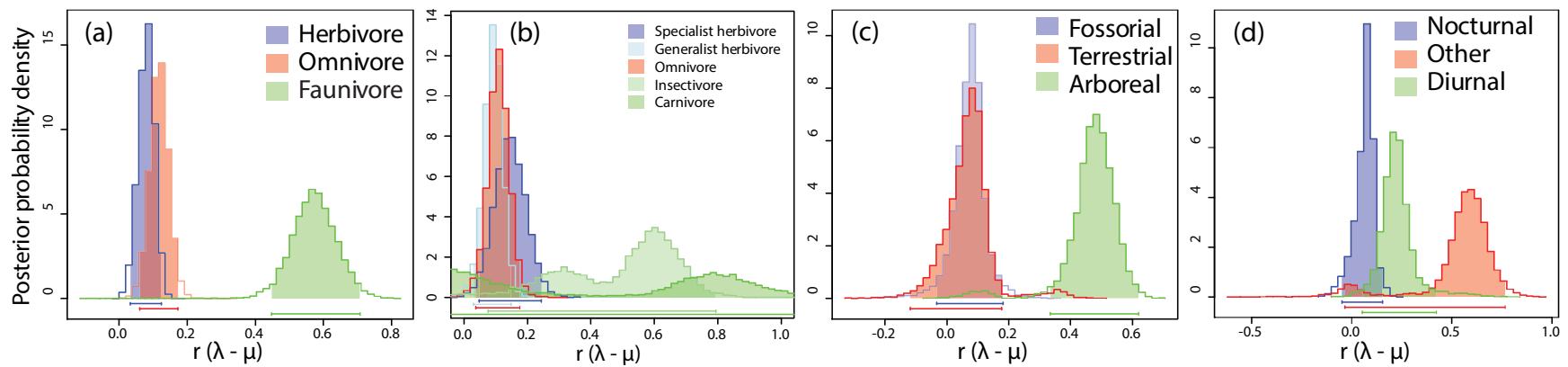


Figure 4.5. Posterior probability distributions of net diversification rates for (a) general diet, (b), specific diet, (c) nesting site, and (d) activity period. See Figure 4.3 legend for more information.

with the highest diversification rates and Martin (1992) found larger body sizes are associated with higher diversity in American mammals.

The discrepancy between the results from the different studies may indicate real differences between the sampled taxa or an artifact of the methods employed. For instance even though the modal speciation function fit the data best in FitzJohn (2010), he also found support for a positive linear relationship between body size and speciation rate, a result that is in accord with most studies conducted in primates whereby the fit of a modal function was not tested (e.g. Gittleman and Purvis 1998; Paradis 2005; Freckleton et al. 2008). Similarly, although the modal speciation function fit the data best, I also found support (Table 4.4; $\Delta AIC = 10.8$) for a negative linear relationship between the speciation rate and body size (Table 4.5; $\lambda_m = -0.12666$), which is in accord with empirical studies conducted in mammals where the modal function was not investigated (e.g. Cardillo et al. 2005; Clauset and Erwin 2008). These results indicate that by not considering alternative non-linear associations between diversity/diversification and body size, a modal relationship could be misdiagnosed as linear.

The association between decreased body size and increased diversification rates can be explained by its association with various ecological attributes including decreased generation time and increased population size (Peters 1983; Gardezi and Silva 1999; Isaac et al. 2005) as well as the increased ability to more finely subdivide the environment (Dial and Marzluff 1988). I also found a general tendency of a decrease in body size in muroid rodents over time, which is in disagreement with Cope's rule (Cope 1885) where larger body size is shown to enhance survival, mating success, and fecundity (Hone and Benton 2005). Moreover, this result also conflicts with empirical studies (North American fossil mammals, Alroy 1998; primates, FitzJohn 2010).

Diversification at Different Elevations

EDG is a biogeographic pattern whereby diversity increases with increasing altitude, maximizing at mid-elevations due to increased environmental diversity as a consequence of increased precipitation, temperature, resource abundance, habitat complexity, and habitat diversity resulting in increased competition and diversification (Rosenzweig 1992; McCain 2005; McCain and Grytnes 2010). EDG has also been shown to be associated with diversification rates in empirical studies whereby early colonization of mid-elevational habitats

is correlated with increased diversification rates (tree frogs, Smith et al. 2007; salamanders, Wiens et al. 2007; nonvolant small mammals, McCain 2005, McCain and Grytnes 2010).

I found that muroids occurring at relatively high elevations had the highest diversification rates, however, I did not find that diversification rates maximize at mid-elevations. This discrepancy may either indicate a true difference or may be a sampling artifact as a consequence of not sampling muroid species at extremely high elevations (only 4 species, *Akodon boliviensis*, *Chinchillula sahamae*, *Akodon lutescens*, and *Auliscomys sublimis*, have been sampled at elevations > 4 km; Appendix Table B.1, chapter 3).

Association between Appendage Proportions and Diversification Rates

Diversification rates exhibited a modal relationship with relative tail length and a positive linear relationship with PC2 of appendage proportions (mostly associated with increased ear length) in muroids. The correlation between appendage proportions and diversification rates has not been investigated before in other taxa and consequently explanations for this pattern may be harder to decipher. However, if appendage proportions in muroids vary according to Allen's rule (Allen 1877), whereby appendage lengths are directly correlated with climate temperature, then this pattern may reflect the combined effect of EDG and the latitudinal diversity gradient. Similar to EDG, the latitudinal diversity gradient is a biogeographic pattern of increased species richness from the poles to the tropics, correlated with increased habitat productivity and temperature (Brown 2014) which is documented in various taxa (butterflies, Cardillo 1999; birds, Cardillo 1999, Ricklefs 2006b; amphibians, Wiens 2007; flowering plants; Jansson and Davies 2008; mammals, Rolland et al. 2014). Consequently, if the variation in appendage proportions are adaptive to climate, the pattern of association between appendage proportions and diversification rates in muroids may reflect the association between diversification rates and extrinsic abiotic factors. However, for relative tail length, the association seems to maximize at average relative tail lengths, which may either reflect selection against the deleterious effect of having extremely long or short tails, or may indicate that extreme elongation reflects a pattern that is independent of climatic adaptation, such as locomotory specialization to arboreality or bipedality, and hence do not fit the general pattern.

The Role of Ecological Specialization in the Diversification Process

It is commonly believed that the common ancestor of mammals was omnivorous, terrestrial, and nocturnal; this condition is also the most represented in the sampled muroids (47%, 40%, and 75% respectively; Appendix Table B.1, chapter 3). Therefore, the result of increased diversification in muroids being associated with faunivory, arboreality, and a non-nocturnal activity period may reflect a pattern of increased diversification being associated with increased ‘specialization’, or a transition to a derived state. This transition may either reflect a transition from a generalized ancestor to a specialized decedent (e.g. omnivorous and terrestrial to faunivorous and arboreal) or vice versa (e.g. nocturnal to generalized activity period). This pattern of increased specialization being associated with increased diversification may be a consequence of reduced competition with the more frequent species that retained the ancestral condition, which is precipitated by transitioning to relatively less crowded niche space. There is some support for this explanation considering that most of these transitions occurred relatively recently (Appendix Figures C.1, C.2, C.3, C.4).

The result of increased diversification being associated with faunivory is somewhat unexpected given that only 10% of the species are faunivores (Appendix Table C.1). However, a recent study by Rojas (2012) on phyllostomid bats that employed similar methods arrived at a similar result; whereby the group with the lowest diversity (the most specialized form, the strictly frugivorous genera; representing 15% of the total diversity) had the highest diversification rates. Similar to Rojas (2012), increased diversification rates in faunivorous muroids are associated with taxa that are clustered into clades with short branches (e.g. *Oxymycterus*, *Akodon*, and relatives) that diversify rapidly towards the present (Appendix Figure C.1). However, the pattern was diminished when faunivorous species were divided into carnivores and insectivores, however, there was some indication that the pattern exhibited by faunivores was a consequence of the pattern exhibited by insectivorous species that represent 76% of faunivores (Appendix Figure C.2).

Similarly, the result of increased diversification being associated with arboreality and with a generalized activity period (i.e. the ‘Other’ category) is counterintuitive insofar as being the least diverse states (23% and 12% of sampled diversity respectively; Appendix Table C.1). This may be explained by the fact that arboreal species are clustered in clades separated by short branches (Appendix Figure C.3); however, this was not the case for the generalized activity

period (Appendix Figure C.4). Moreover, for activity period, the diversification rates of diurnal species, which also constitute 12% of the sampled muroid diversity are significantly lower than those exhibited by the generalized state. These results indicate that factors including branch lengths, group clustering, and phylogenetic location of transitions may play a stronger role in determining trait-dependent diversification rates than extant diversity. Although the association between nesting site and activity period with diversification rate has not been investigated before, the general pattern observed of diversification being associated with specialization (i.e. transitioning to a derived condition) is a pattern that have been observed in multiple taxa (e.g. habitat specialization in coyotes, Sacks et al. 2008; specialization to frugivory in bats, Rojas 2012; specialization to host plants in fungi, Walker et al. 2014).

Through ecological fitting, adaptive niche specialization can lead to increased diversification by allowing specialists to escape competition with the more frequent generalists by outcompeting them at a select number of resources and/or habitats (e.g. Schlüter 2000, 2001). However, the results indicate that only one type of transition/specialization is associated with increased diversification; for diet only transitions to faunivory (and not herbivory), for nesting site only transitions to arboreality (and not fossoriality), and for activity periods only transitions to generalized activity (and not diurnality) are associated with increased diversification. This could indicate that these transitions only translate into increased diversification rates if there is an ecological opportunity for the species to exploit.

Other Factors that may Influence Diversification Patterns

The nodes that underwent shifts in diversification do not appear significantly alter the results of the trait-dependent diversification analyses. This may be explained by the results from recent studies which suggest that muroids exhibit very frequent diversification shifts (24 in the Myodonta, Fabre et al. 2012; 28 in Muroidea, Schenk et al. 2013) which are widely separated on the tree (Figure 4.1), and therefore may show unique patterns of association with ecology/ecomorphology. The frequency and the wide dispersion of these diversification shifts means that no one clade is likely to have a strong enough influence that overpowers the overall signal. This may not be the case for other mammals that have much less, and more localized diversification shifts which may benefit more from a partitioned approach (e.g. one diversification rate shift in primates, FitzJohn 2010). Furthermore, the partitioned approach is

also more useful for when examined traits show strong phylogenetic signal within the rapidly diversifying clades that share traits that differ from the rest of the tree (FitzJohn 2010); which was not the case for the examined traits in muroids.

Trait dependent diversification methods employed in the study seem to do a poor job at estimating extinction rates in muroids, which show considerable overlap and/or similar patterns to the null expectation of no association with ecology/ecomorphology. This pattern may be a consequence of the general unreliability of these methods in molecular phylogenies lacking fossil taxa, or may be due to the limited taxonomic sampling (i.e. only 20% of muroid rodent species have been sampled in this study). However, simulation studies indicate that with appropriate correction, trait-dependent diversification methods perform relatively well when 50% of the focal group diversity have been sampled (FitzJohn et al. 2009). The taxonomically proportional phylogenetic sampling scheme employed by Schenk et al. (2013) is expected to represent the true trait diversity only if traits are phylogenetically conserved. Therefore, limited taxonomic sampling is expected to impact discrete ecological traits more than continuous ecomorphological traits, because the former show less phylogenetic signal.

Conclusions

It appears that shifts in the rates of all sampled traits are associated with diversification rates, most match the predictions based on previous empirical and theoretical evidence. Increased diversification rates are associated with lineages with average body size, which along with small sizes, are the most diverse mammals in various assemblages. Similarly, increased diversification was associated with increasing elevation, which is generally in accord with the elevational diversity gradient; and with appendage proportions consistent with Allen's rule, and consequently, with the latitudinal diversity gradient. Increased specialization in diet, nesting site, and activity period seem to be associated with increased diversification, a pattern detected in other taxa based on similar methods, and is generally attributed to the reduced crowding in niche space encountered by more specialized lineages. Overall, the results of this study indicate that intrinsic ecological and ecomorphological factors may be important in explaining the diversity patterns in Muroidea.

CHAPTER FIVE

IS MUROID DIVERSITY CORRELATED WITH PHENOTYPIC VARIANCE? RESULTS FROM GEOMETRIC AND LINEAR MORPHOMETRICS

Summary

A positive correlation between diversity and phenotypic variance is predicted by multiple evolutionary theories. However, recent empirical studies conducted in various taxa, including mammals, indicate that these two variables are not always correlated. In this study, I test the correlation between these two variables based on cranial morphological and molecular phylogenetic data from 317 muroid rodent species and dipodoid outgroups analyzed using both three dimensional geometric morphometrics and linear morphometrics. Despite testing this relationship using both phylogenetic and non-phylogenetic approaches, size and shape datasets, and using alternate clade designations, I find no significant correlation between diversity and morphological variance. This result indicates that within clades, an increase in clade richness is not necessarily followed by an increase in morphological divergence and vice versa. Furthermore, the distribution of families in morphospace is highly overlapping suggesting greater cranial size and shape variation within than between clades. Taken together with the observation that families with the most distinctive cranial morphologies (nesomyids, dipodids, and spalacids) are the least diverse indicates the evolution of new cranial morphologies may not play an important role in the diversification of muroid rodents.

Introduction

Biological variation in clades is usually described in terms of taxonomic diversity (e.g. number of species or genera) and phenotypic disparity (how distinct clade members are from one another; Foote 1993) which is usually associated with ecological divergence. Muroid rodents are the most diverse superfamily of mammals comprising over 28% of all mammal species diversity (Musser and Carleton 2005) and are among the most variable in ecological attributes including

locomotion, diet, and behavior (Nowak 1999). This diversity is usually explained in terms of multiple independent adaptive radiations (Patterson and Pascual 1968) and recent work has shown that muroids have undergone frequent and recent diversification shifts in many widely separated clades (24 in the Myodonta, Fabre et al. 2012; 28 in Muroidea, Schenk et al. 2013) and consequently provide an adequate system to test the correlates of speciation. Previous studies indicate that muroid clade richness is not satisfactorily explained by extrinsic factors such as the ecological opportunity model of adaptive radiation mediated by continental colonization (Schenk et al. 2013; chapter 3), but is rather better explained by variation in intrinsic factors such as ecology and ecomorphology (chapter 4). In both these studies the association between diversity and phenotypic variance is implied but not directly tested. I explicitly examine this association in the present study by testing the correlation between diversity indices (log richness and diversification rate) and indices of phenotypic variance (disparity and evolution rate).

Gould and Eldredge's (1977) punctuated equilibrium hypothesis provided a model that predicted a positive relationship between diversity and phenotypic variance. This hypothesis postulates that most phenotypic divergence occurs at speciation events, which are followed by long periods of stasis until the next speciation event, and as a consequence clade diversification rates is expected to be correlated with phenotypic divergence (Ricklefs 2004, 2006a). This relationship is also predicted by the theory of ecological adaptive radiation (*sensu* Schlüter 2000) whereby lineages that exploit ecological opportunities undergo an early increase in both phylogenetic diversification and functional, adaptive, phenotypic divergence as recently diverged species occupy new ecological niches. This early increase in diversification is followed by a density dependent decline in both the rate of diversification and disparification associated with the crowding of adaptive zones (Simpson 1944; Freckleton and Harvey 2006). These theories assume that phenotypic and ecological divergence are positively correlated with reproductive isolation, a pattern that is supported in plant, invertebrate, and vertebrate taxa (Funk et al. 2006). However, diversification can occur without phenotypic/ecological divergence, at least initially, through geographic isolation and “non-adaptive radiation”, which leads to ecologically similar species that diverge in allopatry; a pattern that is associated with recent radiations, as subsequent divergence in old radiations renders their pattern indistinguishable from adaptive radiations (Rundell and Price 2009).

One of the earliest studies that test the correlation between phenotypic disparity and species diversity was conducted in clades of passerine birds and found a significant correlation (Ricklefs 2004). However, this correlation was later attributed to variation in clade age and not to the rates of diversification and phenotypic evolution (Purvis 2004; Ricklefs 2006a). Adams et al. (2009) did not find a significant correlation between diversification rates and phenotypic evolution rates of either body size or shape in 190 species of plethodontid salamanders, which they argued due to rapid diversification with little morphological change, or rapid morphological evolution with little speciation. Later, they tested the correlation between morphological and ecological variation (i.e. microhabitat use) and found that morphology is not a good index of ecology in their group as they are largely decoupled (Blankers et al. 2012). Interestingly, when they examined the correlation between the rates of morphological evolution (using the same body size and shape dataset) and log species richness (instead of species diversification rates) they did find a significant positive correlation, which is consistent with the hypothesis that increased morphological evolution rates promote diversification (Rabosky and Adams 2012). This discrepancy was interpreted as due to diversification not being modeled adequately as a simple time-dependent process in their system (Rabosky and Adams 2012).

Using phylogenetic generalized least squares (PGLS) multiple regression analyses (Martins and Hansen 1997), Gonzalez-Voyer et al. (2011) found that species richness and diversification rate were not significantly correlated with clade-age. Rather it was attributed to a combination of ecological and phenotypic traits (including skin attributes, altitude, and body size) that explain most of the variation in diversity of a clade of 80 Neotropical amphibian species (40% of the species diversity of Terrarana; Gonzalez-Voyer et al. 2011). This pattern suggests a positive correlation between diversity and phenotypic variance (Gonzalez-Voyer et al. 2011). In another study, Rabosky et al. (2013) sampled 7,822 out of the more than 30,000 extant species of ray-finned fishes (comprising the majority of vertebrate diversity) and found that rates of body size evolution are highly positively correlated with species diversification; a pattern that was used to support the phenotypic “evolvability” hypothesis, where speciation is driven by the capacity of organisms to evolve.

Although they did not directly test the correlation between diversity and phenotypic variance, Slater et al. (2010) tested the predictions of adaptive radiation in a clade of 84 neocete cetaceans using node height tests (Freckleton and Harvey 2006) and disparity through time plots

(Harmon et al. 2003). They found that this group has undergone a significant increase in body size disparity with little increase in diversity (Slater et al. 2010). This pattern is explained as due to high extinctions, or fluctuations in diversification rates leading to the decoupling of these two variables, or that diversification and ecomorphological disparity are uncorrelated in this group (Slater et al. 2010). Similarly, Rowe et al. (2011) found that the recent radiation of the most diverse rodent genus, *Rattus*, which consists of 66 species and exhibits among the highest reported rates of diversification in vertebrates, was not associated with a significant increase in phenotypic disparity (based on twenty morphological measurements and two ecological characters), an expected result given that this genus lacks overt ecomorphological variation. The decoupling of phylogenetic diversity and phenotypic disparity in adaptive radiations has also been observed in anomodont therapsids (Ruta et al. 2013) and the trilobite family Ptercephaliidae (Hopkins 2013). High diversity with low disparity (i.e. “non-adaptive radiation,” Rundell and Price 2009) is common in young clades, whereas the opposite pattern is more common in old clades and is precipitated by the cumulative effect of extinction at the late history of a clade, rather than increased rates of phenotypic evolution (Hopkins 2013).

The aforementioned two mammalian studies suggest that diversification is generally not correlated with morphological divergence in this group, in both old and new radiations. However, diversification was not explicitly measured in Slater et al. (2010) and was considered to be unexceptional *a priori*, whereas the group chosen by Rowe et al. (2011) did not show sufficient external ecomorphological variation to robustly test for phenotypic variance. This, together with the relatively small species sample sizes make these studies suboptimal for testing the correlation between diversity and phenotypic variance in mammals.

In the present study, the correlation between diversity and phenotypic variance indices are directly tested in muroid rodent clades. The present study has numerous advantages, including the use of the newly estimated molecular phylogeny of the group (Schenk et al. 2013; Steppan et al. in prep), the relatively large sample size of clades, the use of both size and shape morphological datasets to quantify morphological variance, the use of both phylogenetic and non-phylogenetic estimates of diversity and morphological variance, and the use of alternative clade designations. In addition, I quantify morphological variance in the cranium using three dimensional geometric morphometric (GM) approaches, which is not common in studies of association between diversity and phenotypic variance, where more common linear

morphometric (LM) approaches are used. Because results from different approaches to quantify skull morphology may differ (e.g. a study of the mandible morphology of caviomorph rodents by Álvarez and Perez (2013) lead to different results when they were quantified the mandibles in two dimensions vs. three dimensions) and because cranial morphology estimated using three dimensional landmark coordinate data is commonly converted into one dimensional distance measurements prior to analyses (e.g. Cheverud 1995; Marroig and Cheverud 2001; Wilson and Sánchez-Villagra 2010); I also quantify morphological variance using LM and compare the results with GM. Additional patterns examined in this study include the association between: (1) diversification rates and net diversity; (2) morphological evolution rates and net disparity; (3) clade age vs. net diversity and disparity; and (4) shape vs. size evolution and disparity.

Materials and Methods

Phylogenetic Sampling

Diversity indices were quantified from a 317 species chronogram extracted from Steppan et al.'s (in prep) 913 species tree of muroid rodents and dipodoid outgroups, that is based on multiple nuclear and mitochondrial markers, and multiple fossil calibrations. Nearly all species are found in the topographically congruent 297 species chronogram of Schenk et al. (2013). Species were sampled proportional to extant diversity and representative of the extent of morphological disparity; both species typical of clades and morphological outliers were chosen (subject to museum availability) to approximate dispersion of clades in morphospace. This resulted in the sampling of all extant subfamilies and 73% of muroid genera (Figure 5.1; Table 2.1, chapter 2). Four species lacking molecular data (*Lophuromys flavopunctatus*, *Gerbillus gleadowi*, *Gerbillus cheesmani*, and *Apodemus sylvaticus*) were grafted onto the tree as polytomies using the Ape library (Paradis et al. 2004) in R (R Development Core Team 2013) based on taxonomic information from Musser and Carleton (2005) and are indicated by asterisks.

Chronological Clade Sampling

Diversity and phenotypic variance indices were compared between non-nested clades. Clades were not based on taxonomic rank (e.g. subfamily, genus) because these ranks originate at different ages. Rather, clade comparisons were conducted on a sample of origination times, on

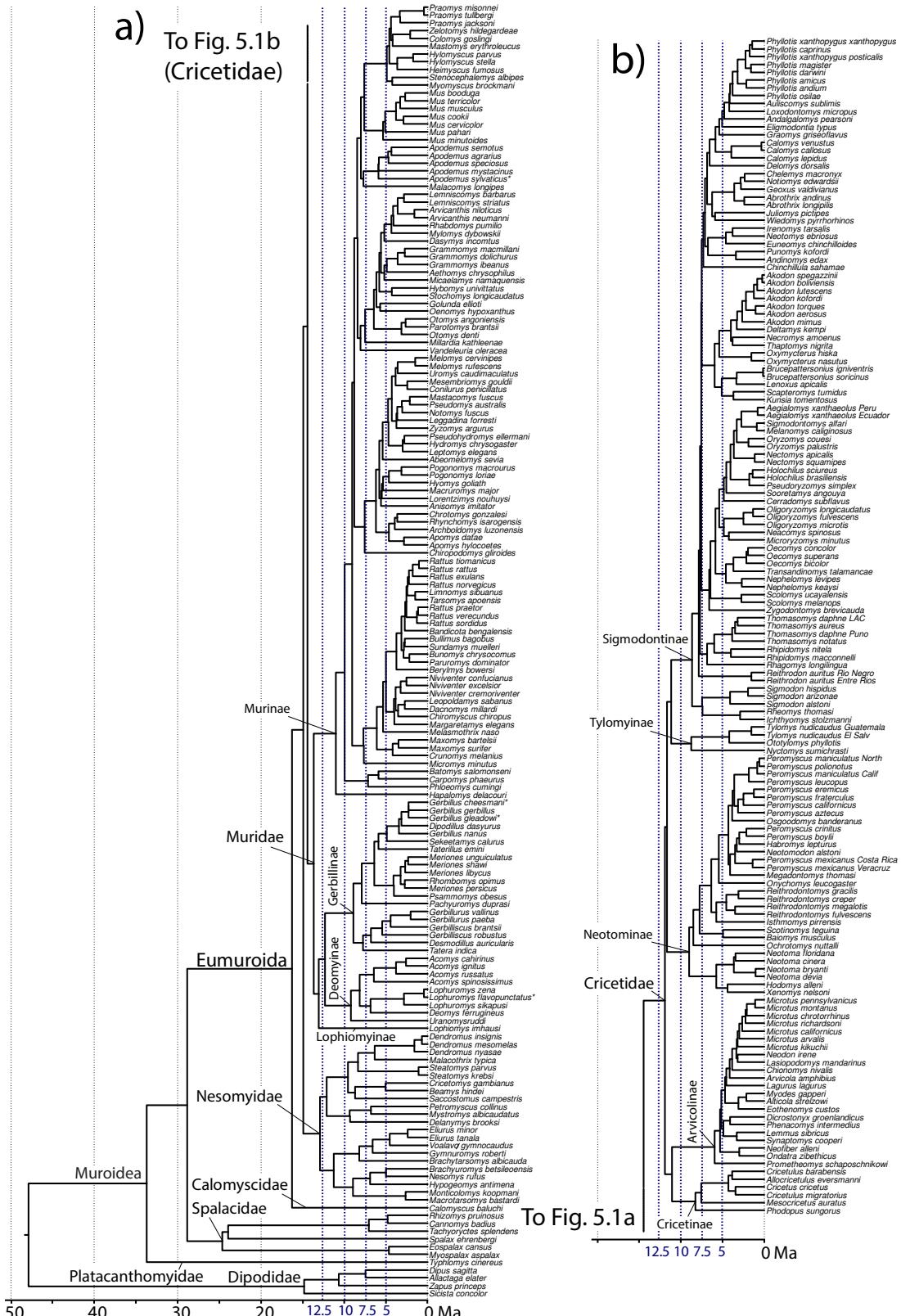


Figure 5.1. Myodont rodent chronogram modified from the molecular phylogeny of Steppan et al. (in prep). Most species are found in Schenk et al. (2013). Blue dashed lines indicate the four chronological sampling intervals. Some of the major taxonomic groups are indicated.

all clades present after the selected time for which at least three species appear in the morphological dataset. The number of suitable clades for comparison is maximized at 36 clades occurring at 5 mya and is reduced to 16 clades at 2.5 mya; although there are more clades at 2.5 mya, these have less than three species with morphological data. Clade comparisons were conducted at four origination times between 5 - 12.5 mya (Table 5.1; Figure 5.1). This was done because of the tradeoff between number of clades and accuracy of disparity estimates; young clades improve the power of the analyses due to the increase in sample size, but this comes at the expense of confidence in the disparity estimates due to less of the variance being captured per clade. In addition, the phylogeny of younger clades is less well established (i.e. many subgenera are not monophyletic); therefore, the number of species (total diversity) in younger subclades is harder to determine than older clades because genera are split across multiple young clades. For this reason, the most recent age at which clades were compared is at 5 mya.

Table 5.1. Clade information for the four chronological sampling intervals. Clade # is based on clades where at least three species appear in the morphological dataset, not total species number. The mean, range, and standard deviation of species numbers per clade are indicated.

Age (mya)	# clades	Mean	Range	S.D.
5	36	31.2	6 - 127	28.7
7.5	25	51.7	6 - 151	46.9
10	14	106.2	6 - 576	168.4
12.5	7	218	17 - 681	287.8

Diversity and Diversification Rate Estimates

Although many studies use diversification rates as a surrogate for clade diversity, this measure assumes that species number in clades increases unbounded through time; however, diversification rates are not always strongly correlated with species richness (Rabosky 2009a, 2009b). Consequently, species richness may be a better estimate for clade diversity than diversification rates (Rabosky 2009a, 2009b). In this study, I use both phylogenetic (diversification rate) and a non-phylogenetic (species richness) approaches to quantify clade diversity. The non-phylogenetic estimate is simply the log total extant species richness, including unsampled species. The phylogenetic estimate of diversification rates is based on total extant species richness and clade age from the aforementioned muroid chronogram; calculated using the method-of-moments estimator for crown groups (Magallón and Sanderson 2001) using the

Geiger library (Harmon et al. 2008) in R. Since extinction rates are unknown, I calculated diversification rates with no extinction (0.0), moderate extinction (0.5), and high extinction (0.9). The results were similar (data not shown) and I only present results using moderate relative extinction rate (0.5). For both diversity and diversification rate estimates, total species richness per clade is based on all known species, including species not sampled in the phylogeny, based on the taxonomy of Musser and Carleton (2005) with updates for newly described and unnamed species in Schenk et al. (2013) and Steppan et al. (in prep). Log richness, diversification rates, and associated variables are indicated in Table 5.2.

Table 5.2. Summary of diversity and diversification rate estimates. Descriptions of clades in the first columns are in Appendix Table D.1. Clades are listed in the same order as they appear from the bottom to the top of Figure 5.1, with the numbers preceding the clades indicating their identification number in the regression plots below (only outliers are highlighted in the plots).

	Species #					
	Sampled	Total	Proportion	Age	Log richness	Diversification rate
12.5 mya						
1. Dipodidae clade	3	38	0.08	10.27	1.57978	0.26086
2. Spalacidae clade	3	17	0.18	6.82	1.23045	0.27891
3. Nesomyinae	10	23	0.43	10.87	1.36173	0.20173
4. Nesomyidae clade I	12	38	0.32	11.68	1.57978	0.22947
5. Deomyinae+Gerbillinae	29	145	0.20	11.89	2.16137	0.33669
6. Murinae	102	584	0.17	10.61	2.76641	0.50787
7. Cricetidae	151	681	0.22	11.50	2.83315	0.48189
10 mya						
1. Spalacidae clade	3	17	0.18	6.82	1.23045	0.27891
2. Nesomyinae clade I	5	9	0.56	8.63	0.95424	0.15164
3. Nesomyinae clade II	5	14	0.36	7.90	1.14613	0.21750
4. Nesomyidae clade II	3	6	0.50	9.02	0.77815	0.10465
5. Dendromurinae+Cricetomyinae	9	32	0.28	9.23	1.50515	0.27209
6. Deomyinae	9	42	0.21	8.88	1.62325	0.31265
7. Gerbillinae	20	103	0.19	8.57	2.01284	0.42716
8. Murinae clade I	3	8	0.38	6.90	0.90309	0.17392
9. Murinae clade II	99	576	0.17	8.73	2.76042	0.61618
10. Cricetinae	6	18	0.33	7.97	1.25527	0.24568
11. Arvicolinae	22	151	0.15	5.75	2.17898	0.70353
12. Neotominae	31	124	0.25	8.70	2.09342	0.44209
13. Tylomyinae	4	10	0.40	8.44	1.00000	0.16641
14. Sigmodontinae	88	377	0.23	8.34	2.57634	0.59375
7.5 mya						
1. Spalacidae clade	3	17	0.18	6.82	1.23045	0.27891
2. Nesomyinae clade III	3	6	0.50	6.68	0.77815	0.14133
3. Nesomyinae clade IV	4	12	0.33	6.36	1.07918	0.24759
4. Dendromurinae clade	4	13	0.31	6.14	1.11394	0.26880
5. Deomyinae clade	4	22	0.18	6.63	1.34242	0.32441
6. <i>Acomys</i>	4	19	0.21	6.23	1.27875	0.32256
7. Gerbillinae clade I	5	16	0.31	6.57	1.20412	0.28094
8. Gerbillinae clade II	13	80	0.16	6.16	1.90309	0.55404
9. Murinae clade I	3	8	0.38	6.90	0.90309	0.17392
10. Murinae clade III	26	149	0.17	5.87	2.17319	0.68659
11. Murinae clade IV	25	119	0.21	5.99	2.07555	0.63494
12. Murinae clade V	19	86	0.22	6.25	1.93450	0.55738
13. <i>Apodemus</i>	5	20	0.25	5.67	1.30103	0.36322
14. <i>Mus</i>	7	38	0.18	5.18	1.57978	0.51763
15. Murinae clade VI	11	44	0.25	4.73	1.64345	0.59744
16. Cricetinae clade	4	9	0.44	4.17	0.95424	0.31391

Table 5.2-continued.

	Species #			Age	Log richness	Diversification rate
	Sampled	Total	Proportion			
17. Arvicolinae	22	151	0.15	5.75	2.17898	0.70353
18. Neotominae clade I	6	24	0.25	5.56	1.38021	0.40174
19. Neotominae clade II	22	93	0.24	6.15	1.96848	0.57952
20. Tylomyinae clade	3	8	0.38	4.04	0.90309	0.29708
21. Sigmodontinae clade I	5	24	0.21	7.18	1.38021	0.31110
22. Sigmodontinae clade II	7	55	0.13	6.64	1.74036	0.45817
23. Sigmodontinae clade III	27	129	0.21	6.37	2.11059	0.61028
24. Sigmodontinae clade IV	17	81	0.21	5.76	1.90849	0.59406
25. Sigmodontinae clade V	29	70	0.41	6.86	1.84510	0.47824
5 mya						
1. Nesomyinae clade V	3	11	0.27	4.41	1.04139	0.33884
2. <i>Dendromus</i>	3	12	0.25	1.53	1.07918	1.02812
3. <i>Lophuromys</i>	3	21	0.14	2.73	1.32222	0.76961
4. <i>Acomys</i> subclade	3	17	0.18	3.66	1.23045	0.52015
5. Gerbillinae clade III	3	14	0.21	4.31	1.14613	0.39867
6. Gerbillinae clade IV	6	20	0.30	3.92	1.30103	0.52505
7. Gerbillinae clade V	6	52	0.12	4.75	1.71600	0.62937
8. Murinae clade VII	3	21	0.14	4.06	1.32222	0.51823
9. Murinae clade VIII	26	127	0.20	4.79	2.10380	0.80769
10. Murinae clade IX	5	17	0.29	4.49	1.23045	0.42342
11. Murinae clade X	3	7	0.43	4.49	0.84510	0.24044
12. Murinae clade XI	13	94	0.14	4.55	1.97313	0.78425
13. Murinae clade XII	3	21	0.14	3.00	1.32222	0.70089
14. Murinae clade XIII	4	21	0.19	4.71	1.32222	0.44706
15. Murinae clade XIV	6	22	0.27	4.20	1.34242	0.51200
16. <i>Apodemus</i> subclade	3	18	0.17	4.55	1.25527	0.42968
17. <i>Mus</i> subclade	5	36	0.14	3.64	1.55630	0.72267
18. Murinae clade VI	11	44	0.25	4.73	1.64345	0.59744
19. Cricetinae clade	4	9	0.44	4.17	0.95424	0.31391
20. Arvicolinae clade I	4	17	0.24	4.71	1.23045	0.40392
21. Arvicolinae clade II	15	108	0.14	4.55	2.03342	0.81494
22. <i>Neotoma</i>	4	22	0.18	3.52	1.34242	0.61006
23. <i>Reithrodontomys</i>	4	20	0.20	4.40	1.30103	0.46814
24. Neotominae clade III	16	67	0.24	4.15	1.82607	0.78024
25. Tylomyinae clade	3	8	0.38	4.04	0.90309	0.29708
26. <i>Sigmodon</i>	3	14	0.21	3.94	1.14613	0.43626
27. <i>Thomasomys</i>	4	36	0.11	3.71	1.55630	0.70721
28. Sigmodontinae clade VI	6	30	0.20	4.42	1.47712	0.55428
29. Sigmodontinae clade VII	5	28	0.18	4.67	1.44716	0.51016
30. Sigmodontinae clade VIII	13	67	0.19	4.68	1.82607	0.69106
31. Sigmodontinae clade IX	5	13	0.38	4.95	1.11394	0.33341
32. Sigmodontinae clade X	10	52	0.19	3.85	1.71600	0.77621
33. Sigmodontinae clade XI	3	6	0.50	4.44	0.77815	0.21249
34. Sigmodontinae clade XII	5	14	0.36	3.49	1.14613	0.49205
35. <i>Calomys</i>	3	12	0.25	3.81	1.07918	0.41364
36. Sigmodontinae clade XIII	12	25	0.48	4.88	1.39794	0.46612

Morphological Data Collection

A detailed description of data collection and process is found in chapter 2 and will only be summarized here. I digitized one to six specimens (average = 4) per species to account for intraspecific variation and calculate species averages. Whenever possible, I sampled equal numbers of males and females of each species to account for sexual dimorphism, which is not common in most rodent species; preliminary analyses on the sampled species indicate that relative to the interspecific variation, sexual dimorphism was not significant and consequently male and female data were combined to calculate species averages. I digitized a total of 1,125 crania, representing 309 species of muroid rodents and outgroups (Figure 5.1), using a

Microscribe MX5 3D stylus digitizer (details below; Appendix Table A.1, chapter2). Eight sampled species were newly split (e.g. *Aegialomys xanthaeolus* Ecuador vs. *Aegialomys xanthaeolus* Peru), and therefore morphological data was applied to both (i.e. data collected for *Aegialomys xanthaeolus* in or outside of these regions was applied to both *Aegialomys xanthaeolus* Ecuador and *Aegialomys xanthaeolus* Peru).

Digitized specimens come from the Smithsonian Institution National Museum of Natural History (USNM), The Field Museum (FMNH), the Museum of Vertebrate Zoology (MVZ), the Florida Museum of Natural History (UF), the American Museum of Natural History (AMNH), Laboratorio de Citogenetica Mamiferos, Facultad de Medicina, Universidad de Chile (LCM), and the Oklahoma Museum of Natural History (OMNH). Only wild caught adult individuals were included as diagnosed by the basioccipital–basisphenoid epiphyseal fusion as in Robertson and Shadle (1954) and Samuels (2009) as well as the complete eruption of both 3rd molars as indicated by evidence of occlusal wear (Steppan 1997).

The three dimensional coordinates of 34 landmarks on the crania were captured using the microscribe digitizer which is accurate to 0.002 mm. Landmarks were chosen to cover most regions of the skull while prioritizing those that are conserved in most muroids, these are the: bregma, pterion, anterior petrous region of the temporal bone, dorsal zygomaxillary point, anterior nasal suture, nasion, lateral frontomaxillary suture, interorbital region, anterior naso-premaxillary suture, anterior zygomatic plate, ventral infraorbital foramen, squamosal-parietal-frontal-sphenoid suture, ventral zygomaxillary point, ventral temporo-zygomatic suture, lateral incisor socket, medial premaxilla-maxilla suture, anterior edge of the first molar, posterior edge of the third molar, maxillary tuberosity, alisphenoid-parapteregoid-temporal junction, medial edge of the bulla spine, posterior tip of the hamular process, interdental region, anterior edge of the incisive foramen, posterior edge of the incisive foramen, posterior edge of the interpalatine suture, basion, opisthion, posterior edge of the jugular process, lambda, medial parietal-interparietal suture, asterion, dorsal-external edge of the auditory meatus, and ventral-external edge of the auditory meatus (Table 2.2, chapter 2; landmarks described in chapter 2).

I digitized each landmark multiple times until a precision of 0.3 millimeters was achieved while retaining the two coordinates with the smallest Euclidean distance between each other. The crania were digitized in two orientations and the data points were merged using generalized procrustes analysis (GPA; Rohlf and Slice 1990) on common points digitized in both orientations

(see chapter 2) using Morpheus et al. (Slice 2009) followed by the restoration of scale. Analyses on the first 100 crania showed no significant asymmetry (data not shown), and therefore crania were subsequently digitized and analyzed on the left side only.

Geometric Morphometric Data Process

I vetted the crania to include only those that are in the best condition, however, 368 out of the 1,125 digitized specimens had at least one missing landmark (Appendix Table A.2, chapter 2) as a consequence of damage or due to not being identifiable in the particular species. These missing landmark coordinates were estimated in the Geomorph library (Adams and Castillo 2013) in R using thin-plate spline interpolation on landmarks common to both complete specimens and those with missing data (see chapter 2 for details).

The first step to obtain shape and size variables in a GM framework is to conduct GPA on the complete dataset, which translates the coordinate configurations to a common centroid by scaling them to unit centroid size and rotating them in order to minimize the sum of squared distances between the corresponding landmarks as well as account for the effects of translation (Zelditch et al. 2004). The output of this superimposition is a new set of procrustes coordinates (PrC) that describe size-independent shape differences within the sample as well as centroid-size (CS), which is sequestered in a separate variable. The first GPA outputted PrC and CS for all specimens. CS from this GPA were averaged and log transformed for each species and used as an estimate of GM size, while PrC was subjected to another GPA for each group of conspecifics to align specimens prior to estimating species average shape. Average shape was estimated using the method described in Claude (2008), which calculates the average coordinate positions of aligned specimens as implemented in the Geomorph library in R. The resulting species consensus shape were subjected to another GPA in order to re-align. The output of this GPA is a set of PrC that describe interspecific size-independent shape variation within the sample.

I applied a principal component analysis (PCA) on PrC (i.e. relative warp analysis) to reduce the number of shape variables (34 landmarks in 3D = 102 PrC) and to simplify interpretation. The resulting relative warps (RW) provide a summary of the greatest aspects of shape variation that are listed in decreasing importance and are also orthogonal (Appendix Table D.2). PCA was conducted in the Pcamethods library (Stacklies et al. 2007) in R using singular value decomposition. The distribution of families in morphospace was visualized on RW 1 - 6

which together explain 54.1% of the cranial shape variance (Table 5.3). The distribution of species in cranial shape morphospace based on all shape information (102 PrC) was visualized using a dendrograms based on hierarchical cluster analysis on the squared Euclidean distance matrix using Ward's method (Sneath and Sokal 1973) as implemented in R base package.

Table 5.3. Proportion of explained variance by RW1-102. Both the individual and the cumulative explained variance are indicated.

	R ²	Cumulative R ²
RW1	0.1651	0.1651
RW2	0.1025	0.2676
RW3	0.0791	0.3467
RW4	0.0754	0.4221
RW5	0.0700	0.4921
RW6	0.0492	0.5413
RW7	0.0415	0.5828
RW8	0.0382	0.6210
RW9	0.0367	0.6578
RW10	0.0320	0.6898
RW11	0.0280	0.7178
RW12	0.0256	0.7434
RW13	0.0200	0.7633
RW14	0.0188	0.7821
RW15	0.0157	0.7978
RW16-102	0.2022	1.0000

Extraction of Linear Distances

In addition to GM, I also quantified morphology by extracting linear distances from coordinate data. This was done by calculating distances between coordinates in raw specimen data that did not undergo any GM process prior to calculating species averages. Consequently, scale was preserved, and measurements are comparable to other studies that use distance-based approaches. Linear distances were based on Marroig and Cheverud (2001), Cheverud (1995), and Steppan (1997) and are summarized in Table 2.3 (chapter 2) and were log-transformed prior to PCA. PCA loadings indicate that PC1 is negatively correlated with size and suggest that PC2-39 are shape variables because they differ in magnitude and direction (Appendix Table D.3). As in the GM analyses above, the distribution of families in morphospace was visualized using PC1-6 which together explain 90.7% of the morphological variation (Table 5.4). The distribution of species in cranial shape morphospace based on PC 2-39 was visualized using a dendrograms.

Table 5.4. Proportion of variance explained by PC1-39. See Table 5.3 for more information.

	R ²	Cumulative R ²
PC1	0.7329	0.7329
PC2	0.0558	0.7887
PC3	0.0403	0.8290
PC4	0.0340	0.8630
PC5	0.0243	0.8873
PC6	0.0200	0.9073
PC7	0.0134	0.9207
PC8	0.0116	0.9323
PC9	0.0094	0.9416
PC10	0.0076	0.9493
PC11	0.0074	0.9566
PC12	0.0061	0.9627
PC13	0.0048	0.9675
PC14	0.0043	0.9718
PC15	0.0040	0.9757
PC16-39	0.0243	1.0000

Morphological Disparity and Evolution Rate Estimates

Morphological variance within clades was quantified using both phylogenetic (evolution rate) and a non-phylogenetic (disparity) approaches. Morphological disparity is defined as the variance in morphospace among species (Foote 1993) and total disparity for each clade is calculated as the average squared Euclidean distance among all pairs of species in the morphological datasets (the optimal method for datasets that are in the same units; Harmon et al. 2008) as implemented in the Geiger library in R. Depending on the distribution of morphological variation within subclades, the evolution rate (a measure of change through time) may result in a widely different value than disparity, with high rates indicating over-dispersion of similar morphologies and a low values indicating clustering of similar morphologies with disparity measures being unaffected (O'Meara et al. 2006); .

I compared the fit of the Brownian motion (BM) model of evolution to the Ornstein-Uhlenbeck (OU) model for each trait/clade combination in the Mvmorph library (Clavel 2014) in R using the Akaike Information Criterion (AIC; Akaike 1974). For all combinations, the BM model fit the data best and/or the rates of evolution estimated by the two models were similar (data not shown). Therefore, the BM model was used to calculate the maximum-likelihood estimates of morphological evolution rates (σ^2) for all trait/clade combinations. A multivariate BM model was fit to the two shape datasets (102 PrCs/PC2-39) and a univariate model was fit to the size datasets (log CS/PC1) as implemented in the Mvmorph library in R. For the multivariate

model, an estimate of the overall rate of evolution of the variables was calculated as the sum of the individual rates of each variable, or the trace of the rate matrix (as in Adams et al. 2009).

Log richness/diversification rates (Table 5.2) were regressed onto disparity/evolution rates (Table 5.5) calculated using: (1) GM shape based on all PrC data; (2) GM size based on log-transformed CS; (3) LM shape based on PC2-39; and (4) LM size based on PC1.

Table 5.5. Summary of disparity and evolution rate estimates based on four morphological datasets. PrC= 102 procrustes coordinates (GM shape); Log CS= centroid size (GM size); PC 2-39= LM shape; PC 1 = LM size; σ^2 = evolution rate. See Table 5.2 for more information.

	Disparity				σ^2			
	PrC	Log CS	PC 2-39	PC 1	PrC	Log CS	PC 2-39	PC 1
12.5 mya								
1. Dipodidae clade	0.02498	0.01333	0.23529	0.10435	0.00082	0.00043	0.00792	0.00356
2. Spalacidae clade	0.01684	0.01983	0.24071	0.73919	0.00099	0.00120	0.01436	0.04775
3. Nesomyinae	0.01255	0.03639	0.11491	1.52889	0.00080	0.00208	0.00843	0.08135
4. Nesomyidae clade I	0.01753	0.04495	0.32377	1.33408	0.00182	0.00212	0.06099	0.14736
5. Deomyinae+Gerbillinae	0.02033	0.01085	0.22352	0.43526	0.00162	0.00047	0.02434	0.04474
6. Murinae	0.01728	0.03523	0.22801	0.80083	0.00159	0.00244	0.02073	0.05433
7. Cricetidae	0.02092	0.01723	0.24364	0.50507	0.00221	0.00115	0.02632	0.03479
10 mya								
1. Spalacidae clade	0.01684	0.01983	0.24071	0.73919	0.00099	0.00120	0.01436	0.04775
2. Nesomyinae clade I	0.01326	0.05761	0.11926	2.20291	0.00084	0.00235	0.00924	0.09313
3. Nesomyinae clade II	0.00911	0.02297	0.09656	1.03058	0.00068	0.00180	0.00690	0.06789
4. Nesomyidae clade II	0.02258	0.04630	0.11954	1.16731	0.00088	0.00183	0.00513	0.05522
5. Dendromurinae+Cricetomyinae	0.01586	0.04866	0.39556	1.48454	0.00207	0.00212	0.07929	0.17504
6. Deomyinae	0.01142	0.00246	0.10704	0.15393	0.00113	0.00013	0.01795	0.07304
7. Gerbillinae	0.01497	0.01159	0.21262	0.49551	0.00177	0.00058	0.02665	0.03083
8. Murinae clade I	0.02645	0.06192	1.18144	1.88616	0.00126	0.00283	0.06350	0.08741
9. Murinae clade II	0.01683	0.03341	0.17340	0.78560	0.00159	0.00237	0.01840	0.05353
10. Cricetinae	0.01073	0.01993	0.28799	0.36782	0.00081	0.00179	0.02204	0.03377
11. Arvicolinae	0.01208	0.02030	0.13949	0.48303	0.00141	0.00157	0.01603	0.03684
12. Neotominae	0.00864	0.02558	0.11792	0.85787	0.00099	0.00113	0.01232	0.04247
13. Tylomyinae	0.00670	0.00883	0.16920	0.19559	0.00034	0.00031	0.00953	0.00676
14. Sigmodontinae	0.02000	0.01334	0.22871	0.37605	0.00298	0.00104	0.03442	0.03251
7.5 mya								
1. Spalacidae clade	0.01684	0.01983	0.24071	0.73919	0.00099	0.00120	0.01436	0.04775
2. Nesomyinae clade III	0.01452	0.04177	0.15361	1.93572	0.00077	0.00201	0.00867	0.08920
3. Nesomyinae clade IV	0.00713	0.01748	0.10170	0.56502	0.00064	0.00176	0.00763	0.05494
4. Dendromurinae clade	0.01253	0.00189	0.08074	0.07606	0.00322	0.00055	0.01396	0.00637
5. Deomyinae clade	0.00826	0.00206	0.08858	0.20501	0.00137	0.00010	0.02587	0.15896
6. <i>Acomys</i>	0.00608	0.00096	0.09216	0.02612	0.00070	0.00006	0.01159	0.00163
7. Gerbillinae clade I	0.01323	0.00838	0.11497	0.16236	0.00128	0.00057	0.01091	0.01186
8. Gerbillinae clade II	0.01498	0.01405	0.25234	0.68245	0.00206	0.00061	0.03520	0.04069
9. Murinae clade I	0.02645	0.06192	1.18144	1.88616	0.00126	0.00283	0.06350	0.08741
10. Murinae clade III	0.01099	0.01637	0.13465	0.34919	0.00154	0.00215	0.02109	0.04666
11. Murinae clade IV	0.02962	0.04834	0.23445	0.94575	0.00292	0.00535	0.02682	0.10173
12. Murinae clade V	0.01131	0.00593	0.14082	0.21977	0.00099	0.00037	0.01306	0.01963
13. <i>Apodemus</i>	0.00514	0.00192	0.05278	0.25736	0.00041	0.00013	0.00408	0.02302
14. <i>Mus</i>	0.00740	0.00523	0.08313	0.10224	0.00088	0.00048	0.00940	0.01039
15. Murinae clade VI	0.00581	0.00530	0.10764	0.15524	0.00077	0.00041	0.01496	0.02693
16. Cricetinae clade	0.00790	0.02137	0.26103	0.40344	0.00079	0.00217	0.02367	0.04315
17. Arvicolinae	0.01208	0.02030	0.13949	0.48303	0.00141	0.00157	0.01603	0.03684
18. Neotominae clade I	0.00740	0.00403	0.10147	0.20903	0.00091	0.00043	0.01466	0.01769
19. Neotominae clade II	0.00692	0.01013	0.09841	0.47840	0.00104	0.00096	0.01215	0.04203
20. Tylomyinae clade	0.00407	0.00123	0.14515	0.01595	0.00028	0.00008	0.00989	0.00109
21. Sigmodontinae clade I	0.03064	0.00635	0.24207	0.25490	0.00235	0.00037	0.01993	0.02569
22. Sigmodontinae clade II	0.00964	0.00408	0.10615	0.06373	0.00094	0.00053	0.00845	0.00678
23. Sigmodontinae clade III	0.01232	0.02066	0.15370	0.63612	0.00148	0.00155	0.02216	0.06091
24. Sigmodontinae clade IV	0.01961	0.01852	0.22999	0.48862	0.00568	0.00136	0.06474	0.03542

Table 5.5-continued.

	Disparity				σ^2			
	PrC	Log CS	PC 2-39	PC 1	PrC	Log CS	PC 2-39	PC 1
25. Sigmodontinae clade V	0.02050	0.00615	0.23376	0.10044	0.00339	0.00058	0.03789	0.01080
5 mya								
1. Nesomyinae clade V	0.00745	0.01944	0.10288	0.55576	0.00071	0.00198	0.00798	0.05800
2. <i>Dendromus</i>	0.00908	0.00131	0.06269	0.01160	0.00391	0.00067	0.01627	0.00429
3. <i>Lophuromys</i>	0.00280	0.00005	0.06422	0.28979	0.00146	0.00001	0.03193	0.21156
4. <i>Acomys</i> subclade	0.00688	0.00028	0.11754	0.00967	0.00083	0.00002	0.01457	0.00080
5. Gerbillinae clade III	0.01049	0.00859	0.09660	0.08742	0.00131	0.00060	0.01169	0.00798
6. Gerbillinae clade IV	0.01420	0.00355	0.25430	0.36175	0.00199	0.00042	0.03682	0.05504
7. Gerbillinae clade V	0.01484	0.00419	0.26176	0.06916	0.00220	0.00037	0.03630	0.00853
8. Murinae clade VII	0.01297	0.01034	0.20324	0.09627	0.00106	0.00081	0.01612	0.00757
9. Murinae clade VIII	0.00891	0.01517	0.20324	0.32051	0.00150	0.00224	0.02180	0.04824
10. Murinae clade IX	0.02034	0.01149	0.12420	0.22002	0.00197	0.00126	0.02000	0.02323
11. Murinae clade X	0.09223	0.08910	0.20666	1.83002	0.00634	0.00606	0.00852	0.12302
12. Murinae clade XI	0.01937	0.05052	0.10753	0.85657	0.00228	0.00619	0.03362	0.10790
13. Murinae clade XII	0.00866	0.00036	0.24149	0.06442	0.00104	0.00005	0.01379	0.00702
14. Murinae clade XIII	0.01105	0.00115	0.11659	0.10077	0.00096	0.00011	0.01469	0.00764
15. Murinae clade XIV	0.00587	0.00315	0.16805	0.12627	0.00069	0.00031	0.00994	0.02175
16. <i>Apodemus</i> subclade	0.00637	0.00032	0.05126	0.46464	0.00048	0.00002	0.00381	0.03580
17. <i>Mus</i> subclade	0.00837	0.00453	0.09415	0.08370	0.00104	0.00042	0.01101	0.00926
18. Murinae clade VI	0.00581	0.00530	0.10764	0.15524	0.00077	0.00041	0.01496	0.02693
19. Cricetinae clade	0.00790	0.02137	0.26103	0.40344	0.00079	0.00217	0.02367	0.04315
20. Arvicolinae clade I	0.01103	0.00784	0.12040	0.33311	0.00097	0.00069	0.01081	0.02706
21. Arvicolinae clade II	0.00966	0.00646	0.11650	0.18248	0.00140	0.00073	0.01602	0.01863
22. <i>Neotoma</i>	0.00664	0.00471	0.09803	0.04954	0.00099	0.00047	0.01735	0.00669
23. <i>Reithrodontomys</i>	0.00649	0.00616	0.07328	0.38444	0.00063	0.00066	0.00779	0.04395
24. Neotominae clade III	0.00612	0.00578	0.07342	0.29996	0.00114	0.00068	0.01272	0.02807
25. Tylomyinae clade	0.00407	0.00123	0.14515	0.01595	0.00028	0.00008	0.00989	0.00109
26. <i>Sigmodon</i>	0.00460	0.00207	0.04741	0.16186	0.00058	0.00016	0.00606	0.01229
27. <i>Thomasomys</i>	0.00912	0.00693	0.05020	0.04984	0.00104	0.00082	0.00546	0.00564
28. Sigmodontinae clade VI	0.00841	0.00688	0.15612	0.25246	0.00111	0.00109	0.02214	0.03809
29. Sigmodontinae clade VII	0.01446	0.00314	0.15661	0.18283	0.00158	0.00076	0.02253	0.01742
30. Sigmodontinae clade VIII	0.00876	0.00873	0.13990	0.32430	0.00147	0.00116	0.02105	0.04016
31. Sigmodontinae clade IX	0.03614	0.02743	0.29080	0.53888	0.01330	0.00168	0.12648	0.07051
32. Sigmodontinae clade X	0.00865	0.00191	0.17683	0.03385	0.00244	0.00063	0.04081	0.00744
33. Sigmodontinae clade XI	0.00983	0.00054	0.09449	0.03858	0.00084	0.00004	0.00781	0.00291
34. Sigmodontinae clade XII	0.03105	0.00539	0.55538	0.05809	0.00452	0.00092	0.08255	0.00724
35. <i>Calomys</i>	0.01848	0.00038	0.21942	0.10256	0.01138	0.00033	0.13118	0.02062
36. Sigmodontinae clade XIII	0.01378	0.00592	0.09334	0.10661	0.00229	0.00054	0.01159	0.01156

Correlation between Diversity and Morphological Variance

The association between diversity and morphological variance was tested using PGLS (Martins and Hansen 1997) regression to account for the non-independence of clades as a consequence of their phylogenetic relatedness, using subclade trees extracted from the chronogram described above as implemented in the Caper library (Orme et al. 2013) in R. This was done to test the null hypothesis that all measures of diversity are uncorrelated with measures of morphological variance and the alternate hypothesis, based on theory, of a positive correlation. I used PGLS to test the association between: (A) log richness vs. disparity calculated using GM and LM size and shape datasets (non-phylogenetic test) and at different clade designations; (B) diversification rate vs. evolution rate also calculated using GM and LM size and shape datasets (phylogenetic test) and similarly with different clade designations. This setup also facilitates testing whether the association between diversity and morphological variance is

affected by variation in: (1) morphological data acquisition methods (GM vs. LM); (2) size vs. shape datasets; (3) time intervals for extracting clades; and (4) estimates of diversity (log richness vs. diversification rates) and morphological variance (disparity vs. evolution rate). I also examined the relationship between: clade age vs. log richness and disparity; diversification rate vs. log richness and disparity; evolution rate vs. disparity and log richness; size disparity/evolution rate vs. shape disparity/evolution rate (both within and across GM and LM datasets).

Results

Dispersion in Morphospace

There was extensive overlap in cranial size both based on GM (Figure 5.2a) and LM (Figure 5.2b); both these approaches showed the same relative relationships in average size. Since all the linear distances load negatively onto PC1 (Appendix Table D.3), a decrease in the score of PC1 indicates an increase in cranial size. Spalacids have the greatest sized crania, followed jointly by murids+cricetids+dipodids+nesomyids, and lastly the sole calomyscid and placanthomyid, with the smallest sized crania (Figure 5.2a, b).

There was also extensive overlap in cranial shape based on both GM (Figure 5.3a, b, c) and LM (Figure 5.3d, e, f) approaches. The cricetids and the murids show the greatest morphological variation in all examined axes, with almost complete overlap in morphology. All other families, including the one sampled calomyscid, are mostly nested within this region of overlap, except for the sole placanthomyid in RW3 vs. RW4 (Figure 5.3b) where it falls out of this region. The other three families with more than one sampled representative (nesomyids, dipodids, and spalacids) have considerably less morphological diversity and more distinctive occupation in morphospace. Nesomyids overlapped extensively with all families (including dipodids and spalacids) in all examined axes except RW1 and RW2 where they are clearly separated from dipodids and spalacids (Figure 5.3a). Dipodids and spalacids overlapped less extensively with each other (although they did overlap considerably with other families). This is especially evident on RW1 and RW2 (Figure 5.3a), RW5 and RW6 (Figure 5.3c), PC1 and PC2 (Figure 5.3d), and PC4 (Figure 5.3e). When total data was visualized using dendograms, genera cluster together in morphospace in both GM (Appendix Figure D.1) and LM (Appendix Figure

D.2) more often than not. This pattern indicates that some component of the interspecific cranial shape variation is independent of size.

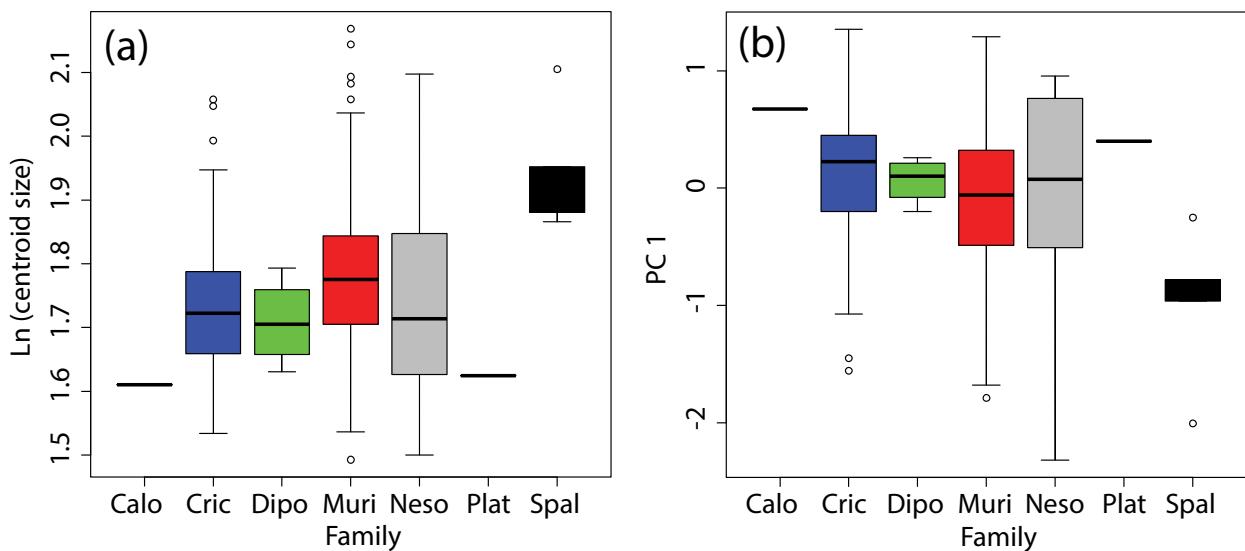


Figure 5.2. Dispersion of the seven myodont families in cranial size morphospace based on (a) GM (log CS) and (b) LM (PC1) datasets. Larger values indicate greater size in CS and smaller size in PC1. The first four letters of each family is shown and colors match those in Figure 5.3.

Diversity and Morphological Variance Regressions

Clade diversity was not significantly correlated with disparity (Table 5.6; Figure 5.4a, b, c, d) and diversification rate was not significantly correlated morphological evolution rate (Table 5.6; Figure 5.4e, f, g, h) for both GM and LM size and shape datasets and across all four investigated time periods (5-12.5 mya). Clade diversity was also not significantly correlated with morphological evolution rate and clade diversification rate was not significantly correlated with disparity (results not shown). Clade age was not significantly correlated with disparity (Table 5.6; Figure 5.5a, b, c, d) for both GM and LM size and shape datasets and across all time periods. Clade morphological evolution rate was highly correlated with disparity (Table 5.6; Figure 5.5e, f, g, h) for all the GM and LM size and shape datasets and across all time periods except for GM shape disparity vs. GM shape evolution rate at 12.5 and 10 mya. Clade age was not significantly correlated with diversity (Table 5.6; Figure 5.5i) across all time periods and diversification rates were significantly correlated diversity (Table 5.6; Figure 5.5j) for all time periods.

At 5 mya, GM shape disparity was highly correlated with GM size disparity ($p < 0.0001^*$, $R^2 = 0.701$) but LM shape disparity was not correlated with LM size disparity ($p =$

0.764, $R^2 = 0.0027$). GM shape disparity was correlated LM shape disparity ($p = 0.019^*$, $R^2 = 0.151$) and GM size disparity was highly correlated with LM size disparity ($p < 0.0001^*$, $R^2 = 0.860$). GM shape evolution rate was not correlated with GM size evolution rate ($p = 0.118$, $R^2 = 0.070$) and LM shape evolution rate was not correlated with LM size evolution rate ($p = 0.346$, $R^2 = 0.026$). GM shape evolution rate was also correlated LM shape evolution rate ($p < 0.0001^*$, $R^2 = 0.774$) and GM size evolution rate was highly correlated with LM size evolution rate ($p = 0.0008^*$, $R^2 = 0.283$). Similar results for GM vs. LM size and shape disparity and evolution rate comparisons were found across all time periods.

Discussion

Diversity and Morphological Variance in Muroid Rodents

The results of this study indicate that diversity and morphological variance are not significantly correlated in muroids. These two variables were not correlated despite (1) the different morphological data acquisition methods (GM vs. LM) employed; (2) the use of both shape and size datasets; (3) extracting clades from different time periods (5 mya, 7.5 mya, 10 mya, and 12.5 mya); and (4) the use of various indices of diversity and morphological variance (log richness, diversification rates, disparity, and evolution rate). Results from clades extracted from different time periods were largely consistent; the range of variation in diversity and diversification rates was much greater than that of disparity and morphological evolution rates, with most clades exhibiting relatively low values for the latter (Table 5.6; Figure 5.4; Figure 5.5). This suggests that in muroids, diversification is accompanied by little morphological divergence; this is supported by the fact that there are many more clades with both low diversity and morphological variance values than there are clades with high values in these two variables. The three most diverse sampled clades were: Arvicolinae clade II (a widespread vole radiation spanning *Eothenomys* to *Microtus*; Appendix Table D.1), Murinae clade VIII (a Southeast Asian radiation of mostly typical rat generalists spanning *Margaretamys* to *Rattus*), and Murinae clade XI (a highly ecologically diverse Sahulian radiation with highly derived desert, aquatic, and arboreal genera spanning *Leptomys* to *Melomys*). Despite this diversity, Arvicolinae clade II and Murinae clade VIII were no more disparate than the majority of the other sampled clades in all

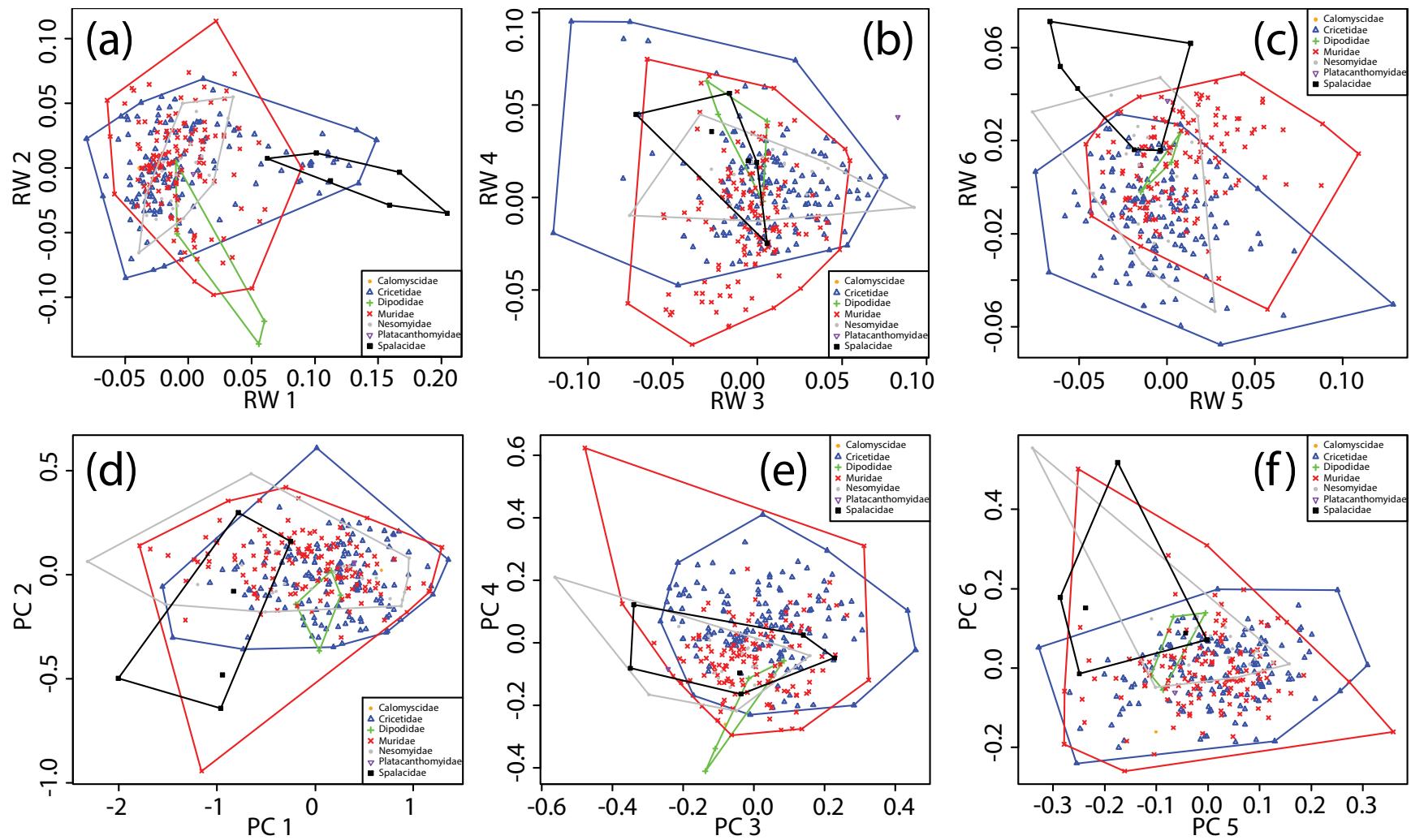


Figure 5.3. Dispersion of the seven myodont families in cranial shape morphospace based on (a, b, c) GM (RW 1-6) and (d, e, f) LM (PC 1-6) datasets. Unlike RW 1-6 which are all size independent shape variables, PC1 is a size variable (as in Figure 5.2) and PC2-6 are shape variables. Total variation in shape morphospace is indicated in the dendograms in Appendix Figures D.1 and D.2.

Table 5.6. PGLS regression analyses statistical summary. Time= clade designations at 4 time periods. Significant results are italicized. Scatterplots for 5 mya are shown in Figures 5.4 and 5.5.

	Time	Estimate	Std. Error	T-value	R ²	F-statistic	P-value
Diversity vs. geometric shape disparity	12.5 mya	0.003	0.002	1.305	0.254	1.703	0.2487
Diversity vs. geometric shape disparity	10 mya	-0.001	0.002	-0.204	0.003	0.042	0.8418
Diversity vs. geometric shape disparity	7.5 mya	0.002	0.003	0.634	0.017	0.402	0.5323
Diversity vs. geometric shape disparity	5 mya	-0.013	0.008	-1.683	0.077	2.832	0.1016
Diversity vs. geometric size disparity	12.5 mya	-0.003	0.009	-0.322	0.020	0.103	0.7608
Diversity vs. geometric size disparity	10 mya	-0.011	0.008	-1.463	0.151	2.141	0.1691
Diversity vs. geometric size disparity	7.5 mya	-0.003	0.007	-0.393	0.007	0.154	0.6982
Diversity vs. geometric size disparity	5 mya	-0.006	0.008	-0.746	0.016	0.557	0.4607
Diversity vs. linear shape disparity	12.5 mya	0.012	0.041	0.301	0.018	0.091	0.7755
Diversity vs. linear shape disparity	10 mya	-0.113	0.120	-0.945	0.069	0.893	0.3632
Diversity vs. linear shape disparity	7.5 mya	-0.114	0.099	-1.153	0.055	1.328	0.2609
Diversity vs. linear shape disparity	5 mya	-0.035	0.050	-0.698	0.014	0.487	0.4900
Diversity vs. linear size disparity	12.5 mya	-0.447	0.250	-1.791	0.391	3.208	0.1333
Diversity vs. linear size disparity	10 mya	-0.422	0.251	-1.683	0.191	2.832	0.1182
Diversity vs. linear size disparity	7.5 mya	-0.261	0.230	-1.137	0.053	1.292	0.2674
Diversity vs. linear size disparity	5 mya	-0.128	0.168	-0.763	0.017	0.583	0.4506
Diversification rate vs. geometric shape rate	12.5 mya	0.003	0.002	1.860	0.409	3.460	0.1219
<i>Diversification rate vs. geometric shape rate</i>	10 mya	<i>0.002</i>	<i>0.001</i>	<i>2.630</i>	<i>0.366</i>	<i>6.917</i>	<i>0.0220</i>
Diversification rate vs. geometric shape rate	7.5 mya	0.002	0.001	1.456	0.084	2.119	0.1590
Diversification rate vs. geometric shape rate	5 mya	-0.002	0.003	-0.981	0.028	0.963	0.3334
Diversification rate vs. geometric size rate	12.5 mya	0.001	0.003	0.222	0.010	0.049	0.8331
Diversification rate vs. geometric size rate	10 mya	-0.001	0.001	-0.473	0.018	0.224	0.6448
Diversification rate vs. geometric size rate	7.5 mya	0.001	0.001	0.764	0.025	0.584	0.4526
Diversification rate vs. geometric size rate	5 mya	0.000	0.001	0.098	0.000	0.010	0.9227
Diversification rate vs. linear shape rate	12.5 mya	-0.004	0.067	-0.060	0.001	0.004	0.9547
Diversification rate vs. linear shape rate	10 mya	-0.001	0.033	-0.020	0.000	0.000	0.9845
Diversification rate vs. linear shape rate	7.5 mya	0.010	0.019	0.539	0.012	0.290	0.5952
Diversification rate vs. linear shape rate	5 mya	-0.012	0.026	-0.466	0.006	0.217	0.6444
Diversification rate vs. linear size rate	12.5 mya	-0.171	0.137	-1.247	0.237	1.555	0.2677
Diversification rate vs. linear size rate	10 mya	-0.059	0.059	-0.997	0.076	0.994	0.3385
Diversification rate vs. linear size rate	7.5 mya	-0.021	0.046	-0.445	0.009	0.198	0.6606
Diversification rate vs. linear size rate	5 mya	0.010	0.038	0.266	0.002	0.070	0.7922
Clade age vs. diversity	12.5 mya	0.185	0.149	1.244	0.236	1.547	0.2688
Clade age vs. diversity	10 mya	0.012	0.188	0.062	0.000	0.004	0.9515
Clade age vs. diversity	7.5 mya	0.043	0.114	0.378	0.006	0.143	0.7089
Clade age vs. diversity	5 mya	0.110	0.080	1.386	0.053	1.921	0.1748
Clade age vs. geometric shape disparity	12.5 mya	0.001	0.001	0.624	0.072	0.390	0.5599
Clade age vs. geometric shape disparity	10 mya	-0.001	0.002	-0.359	0.011	0.129	0.7257
Clade age vs. geometric shape disparity	7.5 mya	0.005	0.002	3.089	0.293	9.544	0.0052
Clade age vs. geometric shape disparity	5 mya	0.004	0.004	1.015	0.029	1.029	0.3175
Clade age vs. geometric size disparity	12.5 mya	0.001	0.003	0.380	0.028	0.144	0.7199
Clade age vs. geometric size disparity	10 mya	0.001	0.005	0.144	0.002	0.021	0.8883
Clade age vs. geometric size disparity	7.5 mya	0.004	0.004	1.060	0.047	1.124	0.3000
Clade age vs. geometric size disparity	5 mya	0.006	0.004	1.578	0.068	2.490	0.1239
Clade age vs. linear shape disparity	12.5 mya	0.002	0.016	0.112	0.003	0.013	0.9151
Clade age vs. linear shape disparity	10 mya	-0.089	0.077	-1.154	0.100	1.331	0.2712
Clade age vs. linear shape disparity	7.5 mya	0.064	0.054	1.174	0.056	1.377	0.2526
Clade age vs. linear shape disparity	5 mya	0.004	0.024	0.154	0.001	0.024	0.8787
Clade age vs. linear size disparity	12.5 mya	0.027	0.129	0.208	0.009	0.043	0.8436
Clade age vs. linear size disparity	10 mya	0.033	0.182	0.181	0.003	0.033	0.8591
Clade age vs. linear size disparity	7.5 mya	0.202	0.123	1.643	0.105	2.698	0.1141
Clade age vs. linear size disparity	5 mya	0.140	0.078	1.780	0.085	3.168	0.0840
<i>Diversity vs. diversification rate</i>	12.5 mya	<i>4.856</i>	<i>0.601</i>	<i>8.083</i>	<i>0.929</i>	<i>65.340</i>	<i>0.0005</i>
<i>Diversity vs. diversification rate</i>	10 mya	<i>3.208</i>	<i>0.322</i>	<i>9.971</i>	<i>0.892</i>	<i>99.420</i>	<i><0.0001</i>
<i>Diversity vs. diversification rate</i>	7.5 mya	<i>2.546</i>	<i>0.168</i>	<i>15.180</i>	<i>0.909</i>	<i>230.400</i>	<i><0.0001</i>
<i>Diversity vs. diversification rate</i>	5 mya	<i>1.488</i>	<i>0.172</i>	<i>8.670</i>	<i>0.689</i>	<i>75.170</i>	<i><0.0001</i>
Geometric shape disparity vs. geometric shape rate	12.5 mya	4.321	2.174	1.988	0.441	3.950	0.1036
Geometric shape disparity vs. geometric shape rate	10 mya	3.743	2.143	1.747	0.203	3.051	0.1062
<i>Geometric shape disparity vs. geometric shape rate</i>	7.5 mya	<i>3.652</i>	<i>1.046</i>	<i>3.491</i>	<i>0.346</i>	<i>12.180</i>	<i>0.0020</i>
<i>Geometric shape disparity vs. geometric shape rate</i>	5 mya	<i>3.098</i>	<i>0.772</i>	<i>4.016</i>	<i>0.322</i>	<i>16.130</i>	<i>0.0003</i>
<i>Geometric size disparity vs. geometric size rate</i>	12.5 mya	<i>15.157</i>	<i>2.682</i>	<i>5.651</i>	<i>0.865</i>	<i>31.940</i>	<i>0.0024</i>
<i>Geometric size disparity vs. geometric size rate</i>	10 mya	<i>20.286</i>	<i>3.203</i>	<i>6.333</i>	<i>0.770</i>	<i>40.110</i>	<i><0.0001</i>
<i>Geometric size disparity vs. geometric size rate</i>	7.5 mya	<i>11.354</i>	<i>1.433</i>	<i>7.924</i>	<i>0.732</i>	<i>62.800</i>	<i><0.0001</i>
<i>Geometric size disparity vs. geometric size rate</i>	5 mya	<i>11.259</i>	<i>0.702</i>	<i>16.042</i>	<i>0.883</i>	<i>257.300</i>	<i><0.0001</i>

Table 5.6-continued.

	Time	Estimate	Std. Error	T-value	R ²	F-statistic	P-value
Linear shape disparity vs. linear shape rate	12.5 mya	2.954	0.884	3.343	0.691	11.170	0.0205
Linear shape disparity vs. linear shape rate	10 mya	9.100	2.559	3.556	0.513	12.640	0.0040
Linear shape disparity vs. linear shape rate	7.5 mya	9.863	2.025	4.870	0.508	23.720	0.0001
Linear shape disparity vs. linear shape rate	5 mya	2.000	0.467	4.281	0.350	18.330	0.0001
Linear size disparity vs. linear size rate	12.5 mya	9.343	2.690	3.474	0.707	12.070	0.0178
Linear size disparity vs. linear size rate	10 mya	10.145	3.333	3.044	0.436	9.265	0.0102
Linear size disparity vs. linear size rate	7.5 mya	7.836	2.310	3.393	0.334	11.510	0.0025
Linear size disparity vs. linear size rate	5 mya	5.040	1.037	4.863	0.410	23.640	<0.0001

four indices; however, Murinae clade XI was the second most disparate in both GM and LM size (Table 5.6; Figure 5.4a, b, c, d). Similarly, the three least diverse clades were also highly variable in disparities; while Sigmodontinae clade XI (South American group consisting of three genera: chinchilla mice, swamp rats, and climbing mice) and Tylomyinae clade (South American group consisting of two genera of climbing rats) were among the least disparate in all four indices, Murinae clade X (Sahulian group consisting of two genera of white-eared giant rats and tree mice) is the most disparate in three out of the four indices (GM size, LM size, and GM shape) (Table 5.6; Figure 5.4a, b, c, d). The most disparate clade in LM shape is Sigmodontinae clade XII (South American group consisting of four genera of grass mice, long-clawed mole mice, long-clawed Akodonts, and large long-clawed Akodonts), a clade with moderate to low diversity (Table 5.6; Figure 5.4c).

Similar patterns were observed for the association between the diversification and morphological evolution rates (Table 5.6; Figure 5.4e, f, g, h), despite the variation in the identity of the outlier clades. The three least diverse clades (Sigmodontinae clade XI, Tylomyinae clade, and Murinae clade X) also had the lowest diversification rates, however, their morphological evolution rates were not as highly variable as their disparity scores (i.e. Murinae clade X, while having the highest disparity score in most disparity indices, does not have the highest evolution rate, however, it has relatively high values for GM size, LM size, and GM shape) (Table 5.6; Figure 5.4e, f, g, h). However, the clade with the highest diversification rate was *Dendromus* (African climbing mice), which was considerably higher than the clades with the highest diversities (Arvicolinae clade II, Murinae clade VIII, and Murinae clade XI), a result most likely attributed to the relatively short branches that separate *Dendromus* members and its recent origin, given that it did not show exceptional diversity and has very low morphological evolution rate (Table 5.6; Figure 5.4e, f, g, h). Similarly, the most disparate clades were not

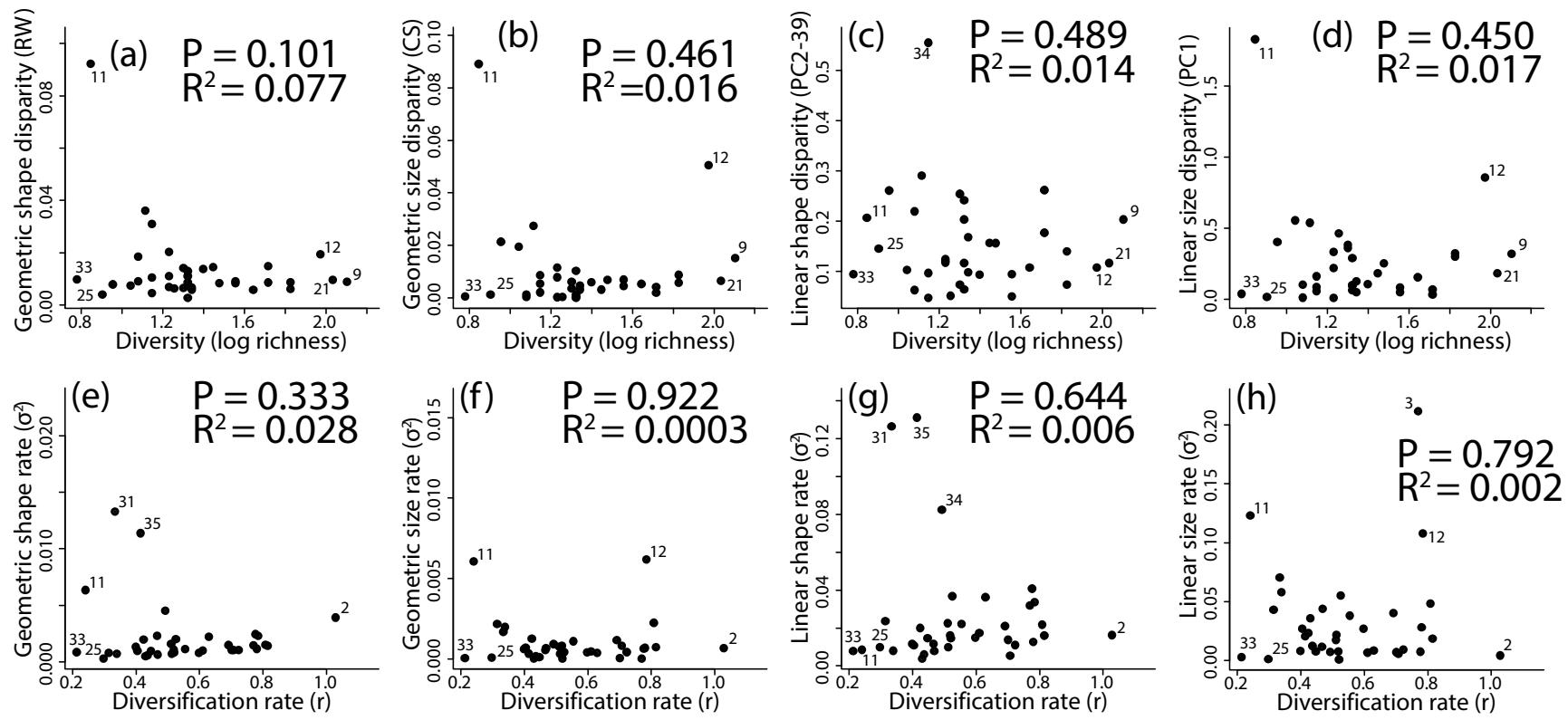


Figure 5.4. Linear relationships between (a, b, c, d) diversity vs. disparity and (e, f, g, h) diversification rate vs. morphological evolution rate of the clades at 5 mya. Several outlier clades are numbers following Tables 5.2 and 5.5 and are considered in the discussion. R² and p-values of the PGLS analyses are indicated as in Table 5.6. The best fit line is shown for significant slopes.

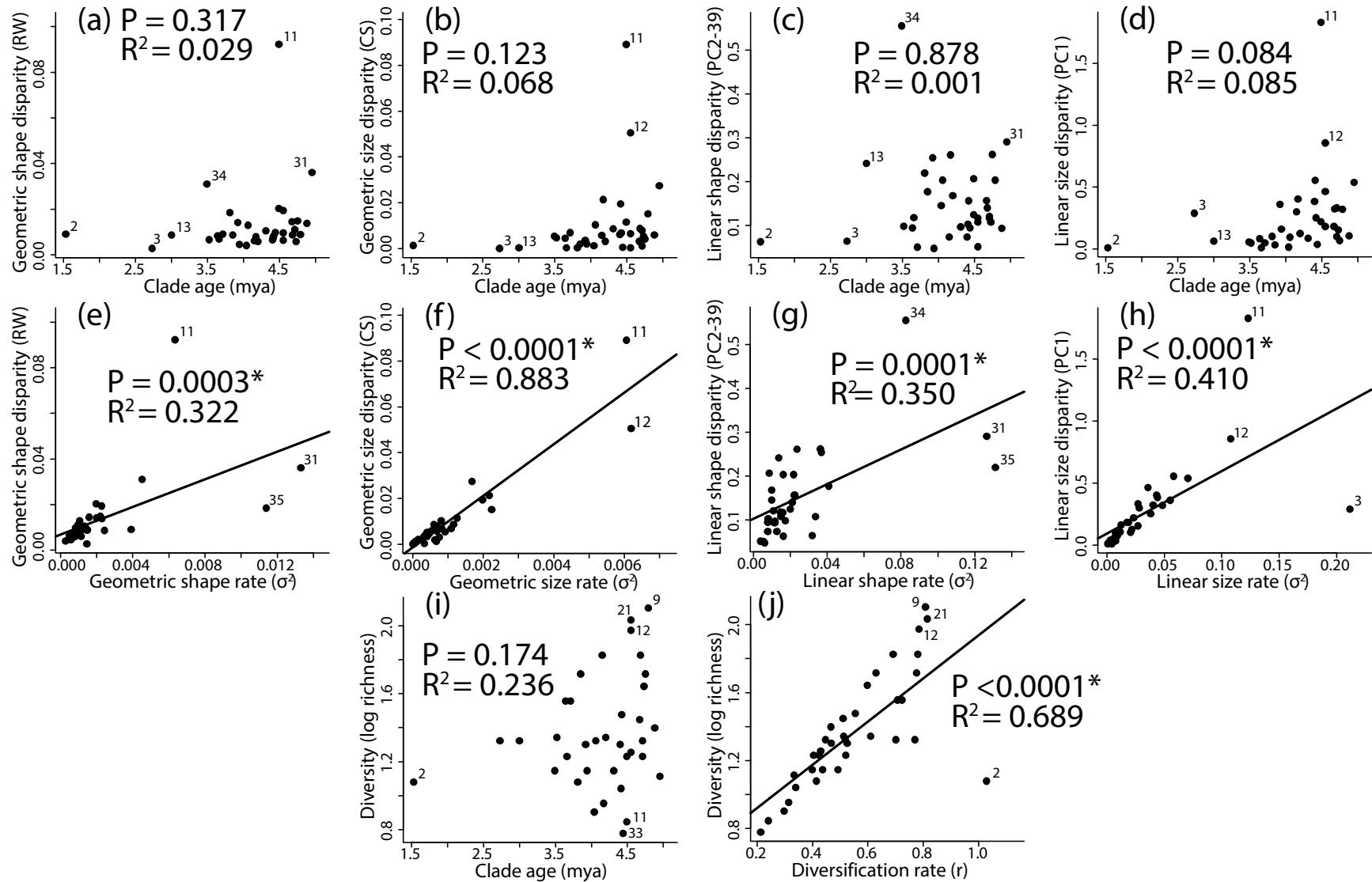


Figure 5.5. Linear relationships between (a, b, c, d) clade age vs. disparity, (e, f, g, h) morphological evolution rate vs. disparity, (i) clade age vs. diversity and (j) diversification rate vs. diversity of the clades at 5 mya. See Figure 5.4 legend for more information.

necessarily the clades with the greatest morphological evolution rates. While Sigmodontinae clade XII and Murinae clade XI had both high disparity and morphological evolution rate, Sigmodontinae clade IX (South American group consisting of four genera: giant rats, swamp rats, Andean rats, and brucies), *Calomys*, and *Lophuromys* showed high evolution rates but unremarkable disparities (Table 5.6; Figure 5.4e, f, g, h).

The consistent results observed across GM/LM/size/shape datasets reflect the fact that, except for LM shape disparity/evolution rate vs. LM size disparity/evolution rate contrasts, all other variables were correlated (GM shape disparity/evolution rate vs. GM size disparity/evolution rate; GM shape disparity/evolution rate vs. LM shape disparity/evolution rate; GM size disparity/evolution rate vs. LM size disparity/evolution rate). The correlation between size and shape evolution/disparity can be explained by shared allometric relationships, whereby cranial shape is highly dependent on size leading similar sized crania to have similar shapes. However, this correlation can also occur if different subclades within a focal clade undergo decoupled increases size and shape evolution rates (Adams et al. 2009).

Given the similar patterns between the diversification vs. morphological evolution contrasts and the diversity vs. disparity contrasts, it is perhaps not surprising that diversification rates were highly correlated with net diversity ($p < 0.0001^*$, $R^2 = 0.689$; Table 5.6; Figure 5.5j) and that the rates of morphological evolution were highly correlated with disparity (all p values $< 0.0003^*$, $R^2 = 0.332$ to 0.883 ; Table 5.6; Figure 5.5e, f, g, h). The fact that clade age was not correlated with disparity (Table 5.6; Figure 5.5a, b, c, d) or diversity (Table 5.6; Figure 5.5i) implies that the variation in origination times of sampled clades (from 1.5 to 5 mya) did not have a major effect on the observed patterns of association between diversity and morphological variance. This decoupling may also indicate that 4.5 mya is not sufficient time to accumulate significant variation in diversity and morphological variance in muroids, however, there was some evidence that clades with exceptional disparity were relatively old (e.g. Murinae clade X, Murinae clade XI, Sigmodontinae clade IX, and Sigmodontinae clade XII) and that recently evolved clades had the lowest disparities (e.g. *Dendromus* and *Lophuromys*).

Causes of Decoupled Diversity and Morphological Variance

Despite using the GM approach, which is especially successful at detecting relatively low levels of morphological variation between morphologically similar species (Zelditch et al. 2004),

I found no correlation between morphological variance and diversity. Moreover, this result is based on perhaps the most important morphological index of ecology and niche in mammals, the cranium organ system, which houses most sensory and masticatory structures and is among the most variable structures in muroids (Nowak 1999), and therefore, the most likely to show a pattern if it does exist than other morphological traits. For example, cranial size and shape are more useful indicators of general feeding ecology than body size and shape because they more directly measure gape size and feeding adaptations. It is unlikely that the decoupling of diversity and morphological variance is a consequence of methodological artifacts since the pattern was robust to the use of multiple indices of morphology and clades extracted from different time periods. Furthermore, the range of variation in morphological variance and diversity was sufficient enough to detect correlations between morphological variance and other variables (e.g. GM and LM disparity vs. evolution rate; GM vs. LM size and shape variables) and between diversity and other variables (e.g. diversification rate vs. net diversity).

The decoupling of diversity and morphological variance is perhaps less surprising in more recent than older clades because many recent clades have species with very similar external morphologies (e.g. *Rattus*, Rowe et al. 2011) with morphologically cryptic species being increasingly described solely based on molecular data (e.g. *Niviventer*, He et al. 2013). This explanation might explain some of the pattern, since clades such as Murinae clade VIII (includes both *Rattus* and *Niviventer*) have high diversity/diversification rate and low disparity/evolution rate (Table 5.2; Table 5.5; Figure 5.4). However, it is unlikely to explain the overall pattern since similar results were observed in clades extracted at different time intervals. Furthermore, the relatively recent genus, with known morphologically cryptic species, *Calomys* (e.g. González Ittig 2002), had high GM and LM shape evolution rates but low diversity/diversification rates (Table 5.2; Table 5.5; Figure 5.4e, g); opposite of the expected pattern if the prevalence of cryptic species explain the lack of relationship between diversity and morphological variance.

Variation in both diversity and morphological variance could be explained by other factors such as ecological opportunity mediated by biogeographic transitions. There is some evidence for this presented by Schenk et al. (2013) and the present dissertation (chapter 3), where the primary colonizations of South America, Sahul, and Southeast Asia were associated with increased phylogenetic and phenotypic diversification in muroid rodents, although this pattern cannot be generalized to other primary and secondary colonizations. Other unexamined

triggers of ecological opportunity may also explain patterns of diversity and morphological variance in muroids such as mass extinctions of protagonists and the evolution of key innovations (Simpson 1953; Schluter 2000; Grant and Grant 2008). There is also some evidence that diversity/diversification rates in muroids is associated with intrinsic and extrinsic ecological and ecomorphological factors including average body size, increased elevation, average relative tail length, appendage proportions, specialized diet, nesting site, and activity period (chapter 4).

An extrinsic factor that is yet to be examined and that potentially could better explain both phylogenetic and phenotypic diversity in muroids is the latitudinal diversity gradient, a biogeographic trend of increased diversity from the poles to the tropics (i.e. a negative correlation between latitudinal position of clades and diversity). This pattern has been documented in butterflies (Cardillo 1999), birds (Cardillo 1999; Ricklefs 2006b), amphibians (Wiens 2007), flowering plants (Jansson and Davies 2008), and mammals (Rolland et al. 2014; but see Soria-Carrasco and Castresana 2012). There is some indication that the latitudinal diversity gradient does explain some of the diversity patterns in muroids as the two clades with among the highest log richness and diversification rates occur near the tropics (Murinae clade VIII, a Southeast Asian radiation and Murinae clade XI, a Sahulian radiation; Table 5.2; Figure 5.5j). Moreover, the aforementioned positive correlation between muroid diversification rates and elevation (i.e. elevational diversity gradient; chapter 4), similar to the latitudinal diversity gradient, is a consequence of the ecological manifestations of increased net primary productivity and temperature (Brown 2014), such as increased habitat complexity and biotic interactions including competition (McCain 2005). Increased diversity at higher altitudes/lower latitudes can occur without increased morphological variance via allopatric speciation caused by geographic isolation. However, if the geographically isolated clades adapt their morphologies to differences in climates, then diversity is expected to be correlated with directional morphological change. Alternatively, lineages can adapt their physiologies to new climates independent of morphology, leading to a pattern of non-association between morphological evolution with diversity.

The predictions of Schluter's (2000) theory of ecological adaptive radiation is based on the assumption that increased diversification rates are precipitated by reduced niche overlap between the diversifying lineages and closely related, sympatric groups, leading the aforementioned to undergo adaptive divergence as recently diverged species occupy new ecological niches (Simpson 1944; Freckleton and Harvey 2006). Such a pattern is not observed

in muroids; rather all families were highly overlapping in morphospace in both size (Figure 5.2) and shape (Figure 5.3); a pattern that could cause clades to constrain each other's diversification rates. However, the fact that the families with the most divergent morphospace occupation (nesomyids, dipodids, and spalacids; Figure 5.2; Figure 5.3) are among the least diverse may indicate that muroid diversification occurs within a shared region of morphospace, a pattern that has been documented in other taxa (e.g. birds, Ricklefs 2005; plethodon salamanders, Adams et al. 2009). Other potential causes of increased diversification rates in clades that are not investigated in the present study include clade allopatry relative to others, which in theory could allow lineages sufficient freedom to diversify into adaptive zones without being crowded by close competitors; a similar explanation to the biogeographically induced ecological opportunity model tested by Schenk et al. (2013). However, it is unlikely, that allopatry enhances diversification and morphological evolution rates in muroids considering that the allopatric Nesomyid clades in Madagascar are unremarkable in both indices whereas Murinae clades (Southeast Asian clade VIII and Sahulian clade XI) have among the highest diversification rates while being sympatric with other clades in that region.

Conclusions

Muroid diversity does not appear to be correlated with morphological variance, a result that is robust with regard to variation in morphological datasets and clade designations. This result contradicts most well-known evolutionary theories that predict a correlation such as the punctuated equilibrium and the ecological adaptive radiation models. However, other recent empirical studies conducted on other taxa, similarly show a decoupling of diversity and morphological variance which indicates that increased diversification is not always accompanied by increased morphological divergence and vice versa. Recent results (chapter 4) indicate that directional morphological evolution (i.e. adaptation) may be more important in explaining muroid diversity than extrinsic factors (chapter 3) or morphological divergence (this study). I also found that phylogenetic and non-phylogenetic estimates of diversity/morphological variance are highly correlated, and consequently led to similar results. Clade age was not significantly correlated with diversity/morphological variance which suggests that diversity cannot be explained by clade age. Another result is that GM and LM size and shape variables are highly

correlated within and between frameworks which is indicative of allometric relationships. Finally, the great extent of the overlap in morphospace in myodont families suggests an overall similar cranial morphology and that muroid diversification occurs within a shared region of morphospace.

CHAPTER SIX

VARIATION IN SKULL MORPHOLOGY OF RODENTS ACROSS ARIDITY ASSOCIATED ECOLOGICAL GRADIENTS: A PHYLOGENETIC TEST OF DESERT ADAPTATION

Summary

Understanding how organisms adapt to aridity is a central theme in traditional desert ecology research. However, many of the pioneering studies were conducted before detailed phylogenies were available to provide evolutionary context and before the accumulation of accurate bioclimatic and species distribution data to provide geographic and environmental context. I use a composite molecular phylogeny of rodents to apply phylogenetic correction in testing the correlation between cranial, mandibular, and dental characters with measures of habitat aridity in a sample of desert and mesic rodents in order to identify the adaptive value of changes in skull morphology. In addition, I use habitat information on all extant rodent species available from the International Union for Conservation of Nature Red List (IUCN) to investigate the general pattern of rodent transition between desert and mesic ecosystems, which I find to be very frequent throughout their evolutionary history. There was a directional bias favoring transition from mesic to desert ecosystems which is consistent with the derived desert specialization being an “evolutionary dead-end” that limits further evolution. Although there is significant phylogenetic signal in almost all of the examined morphological characters, I still find a strong correlation with habitat aridity after phylogenetic correction in characters associated with auditory (tympanic bulla inflation) and water retention (nasal passage elongation) specialization but not in characters associated with dietary (lower incisor index) specialization. However, both desert and mesic rodents overlapped extensively in overall skull morphology and multivariate analyses did not find a significant difference between these two groups. Nonetheless, among the examined morphological characters chosen to represent overall skull morphology, measurements associated with bulla dimensions (length, height, and width) and reduced mesopterygoid breadth (correlated with increased bulla width) were the most strongly associated with climatic measures of aridity, consistent with an increase in bulla size in more arid

environments. This result indicates that bullar hypertrophy is among the strongest patterns of convergent cranial desert adaptation in rodents, and indicates that adaptation plays a similar role in shaping the evolution of this structure in different desert rodent clades.

Introduction

Understanding how organisms adapt to their environment is a central theme in traditional ecological research where morphology is assumed to reflect both habitat specific adaptations (Wainwright and Reilly 1994) and phylogenetic history. This is especially true for convergent desert adaptations in rodents, including those for fossoriality and bipedality, which have long interested naturalists, but mostly adaptations to water and energy conservation that enable rodents to survive these “extreme” habitats (Vial 1962; Mares 1975, 1976). Rodents are particularly amenable to adaptation studies since, with over 2,261 species and 474 genera, they are by far the largest order of mammals, representing nearly half of the extant mammalian diversity (Wilson and Reeder 2005). Moreover, they are found on all continents with the exception of Antarctica and occupy variable habitats ranging from mesic rainforests to arid deserts (Fabre et al. 2012), and convergence in ecological and morphological traits is common in species living in similar habitats on different continents (Wood 1947).

Deserts constitute the largest terrestrial biome, covering one-fifth of dry land (Hickman et al. 2004) and while varying greatly in temperature, are defined by their aridity which is caused by low and unpredictable rainfall that erodes the soil and renders it unusable to plants and animals because annual drought cycles prevent plant growth and thus greatly reduce food resources for animals (Louw and Seely 1982). Adaptations to deserts are either direct adaptations to aridity or indirect adaptations to the habitat manifestations of aridity such as low plant cover (where perennials cover less than 10% of total area) and low food and water resources most of the year (Sowell 2001; Ward 2009).

One of the most extreme cases of convergent adaptations to equivalent desert niches in different continents are those shared by Palearctic jerboas and gerbils, Australian hopping mice, and North American kangaroo rats (Shenbrot et al. 1999). Despite being distantly related, these four taxa share numerous traits including small and round bodies, elongated hindlimbs/shortened forelimbs, long tails, large bullae, long and complex nasal passages, high basal metabolic rate,

bipedality, burrowing behavior, and granivorous diet (Hart 1971; Berman 1985; Rocha 1995; Diaz and Ojeda 1999; Diaz 2001; Diaz et al. 2001; Bozinovic and Gallardo 2005; Bozinovic et al. 2007; Rocha et al. 2007; Sassi et al. 2007). Similar, although less extreme, convergences have also been observed in South American hystricognaths (e.g. Mares 1975, 1976; Ojeda et al. 1999).

Among the most studied convergent desert adaptive structures in mammals, that are also characteristic of fossorial species, is the hypertrophied tympanic bulla which is a bony cranial chamber that houses the middle ear bones and amplifies low-frequency sounds (e.g. kangaroo rats, Webster and Webster 1975; gerbils, Lay 1972; neotropical spiny rats, Gardner and Emmons 1984; mole-rats, Burda et al. 1990; marsupials, Mason 2001; sand cats, Huang et al. 2002; tuco-tucos, Schleich and Vassallo 2003, Francescoli 1999, Francescoli et al. 2012; golden moles, Mason 2003; and armadillos, Squarcia et al. 2007). In a comparison of 13 gerbil species, Lay (1972) found that more arid environments are correlated with increased anatomical specialization of middle and inner ear anatomy and as a consequence, increased auditory sensitivity. The increased auditory sensitivity that accompanies tympanic bulla enlargement is described as an adaptation for both prey capture and predator avoidance in open habitats where sound dissipates quickly and early detection is key to escape more effective predators (Lay 1972; Webster and Webster 1975). Many desert rodents are fossorial because open habitats have few natural shelters and increased sound sensitivity is important for subterranean vocalizations that use low frequency sounds (Lay 1972; Webster and Webster 1975). Francescoli et al. (2012) compared the interspecific variation in bulla volume in one genus of fossorial rodents, the tuco-tucos, with 60 species, and considered the interspecific variation in bulla volume to be adaptive as it was not explained by phylogenetic relationship. They reasoned that an increase in bulla size is associated with increased sensitivity to low frequencies, the primary means of communication in fossorial rodents, at the expense of sensitivity to high frequency sounds, in which smaller bulla are more sensitive (Francescoli et al. 2012), however, they did not test the association with aridity.

The shape of the lower incisors, measured as the ratio of the width across both lower incisors to their length (lower incisor index), has also been proposed to be a desert adaptation in various groups of rodents, where higher values are associated with a “squarer” shape (i.e. relatively wide and shallow incisors) and with the ability to remove salt from desert saltbush epidermis in various rodent groups (Ojeda et al. 1999). However, apart from the aforementioned

study, the association between incisor shape and aridity have never been directly tested in a large sample of rodent species.

Internal nasal passage (nasoturbinate) morphology have also been proposed to be desert adaptive in desert mammals, with narrow, extremely convoluted nasoturbinates being associated with aridity (Feldhamer et al. 2007). Longer and narrower nasoturbinates are more efficient at cooling exhaled air and therefore better in water conservation through condensation and reabsorption of exhaled air (e.g. kangaroo rats, Schmidt-Nielsen and Schmidt-Nielsen 1951; degus, Cortes et al. 1988, 1990). Due to the morphological complexity of the nasoturbinates, this structure is sometimes estimated using external nasal measurements, more specifically the nasal index (ratio of the breadth to the length of the nasals), with narrower more protruded nasals being associated with colder and drier regions; this measurement is also commonly used in anthropological studies when testing the association with climate and testing adaptive hypotheses (reviewed in Leong and Eccles 2009). The adaptive significance of nasal index variation to climate have not been extensively studied in rodents or other mammals. However, Agrawal (1967) showed that there is a tendency of decreased nasal length as a digging adaptation in fossorial rodents because projecting nasals hinder burrowing and have a greater chance of injury, which could confound the potential relationship in rodents, since most desert species are subterranean. Since the nasal index does not take into account the height of the rostrum, which is also expected to reflect nasoturbinate morphology in rodents, I use an estimate of nasal volume that is expected to better reflect the size of the nasoturbinates as the product the nasal breadth, nasal length, and rostral depth.

In this study, the adaptive values of the tympanic bulla, lower incisors, and nasal morphology are tested at a broad taxonomic scale that includes desert and mesic representatives from most rodent families. Most comparative morphological studies of desert adaptation are based on very limited taxonomic scales and small sample sizes, and most of the documented associations with deserts have been anecdotal and not rigorously tested. This study is the first to use an order level molecular phylogeny of rodents to correct for evolutionary relationships when testing the correlation between skull morphology and aridity. In this study, I test the correlation between putative desert adaptive skull morphological traits (bullar index, bullar volume, lower incisor index, nasal index, and nasal volume; see methods) with aridity (mean annual precipitation, mean annual temperature, aridity index, and discrete IUCN habitat classifications;

see methods). The aim is to determine if desert species have significantly different skull morphology than mesic species. All measurements (bullar index, bullar volume, lower incisor index, and nasal index) except for nasal volume (as estimated via external cranial measurements) are based on prior studies of desert adaptation (see methods). I follow earlier studies by focusing on the tympanic portion of the bulla in the comparative analyses even though many desert species (e.g. kangaroo rats and jerboas) also exhibit a greatly inflated mastoid bulla.

A secondary focus of this study is to explore the correlation between other regions of the skull with no prior evidence of desert adaptation (standard rodent skull measurements that cover major regions of the skull) with aridity. In addition, this test serves as a benchmark to compare to results from analyses of putative desert adaptive traits. Since skull morphology reflects the ecology of species in the habitat in which they reside, some skull regions are expected to show evidence of desert adaptation. For instance, jaw and dental characters are expected to reflect diet (e.g. molar hypsodonty can reflect a diet consisting of extensive abrasive material and grit), with desert rodents expected to have jaw and dental characters that are more adaptive to granivory, the most common diet in desert rodents; however, there are many exceptions to granivorous diets in deserts (Palminteri et al. 2012). Another secondary aim of this study is to explore the general pattern of transition between desert and mesic ecosystems in rodents, a question that has never been tested before in a phylogenetic framework.

Materials and Methods

Composite Rodent Chronogram

For subsequent analyses, I use a modified chronogram adapted from Fabre et al.'s (2012) diversification analyses tree, which includes all extant rodent species. Fabre et al.'s (2012) tree was estimated using maximum likelihood inferred using a molecular supermatrix of 11 mitochondrial and nuclear genes of 1,265 rodent species with multiple fossil calibrations. Species lacking molecular data were grafted onto the tree closest to the species that shares the most recent common ancestor (e.g. same genus, same subfamily) based on the taxonomy of Carleton and Musser (2005), resulting in a tree with 2,260 rodent species (Fabre et al. 2012).

The superfamily Muroidea, with 1,516 species (including grafted species) was dropped from Fabre et al.'s (2012) tree and replaced by an unpublished 913 muroid species chronogram

from Steppan et al. (in prep). This was done because the grafted muroid chronogram includes more species with molecular data and is based primarily on nuclear sequences and excludes misidentified sequences included in Fabre et al. (2012). The crown age for muroids in Steppan et al.'s (in prep) tree is 32.6 my and the stem lineage from Fabre et al.'s (2012) tree spans from 51.12 to 48.77 my. In order standardize the divergence times in the composite rodent chronogram, after pruning the muroid crown group from Fabre et al.'s (2012) tree (at 48.77 my), 16.17 my were added to the stem age ($48.77\text{ my} - 16.17\text{ my} = 32.6\text{ my}$) before adding the muroid crown group from Steppan et al.'s (in prep) tree. This allows all tips from both phylogenies to align at zero, restoring the ultrametricity of the chronogram which was confirmed prior to subsequent analyses by computing the distances from each tip to the root.

All muroid species lacking molecular data were grafted back into Steppan et al.'s (in prep) muroid clade in the composite tree based on taxonomic information from Carleton and Musser (2005) using the same criteria as Fabre et al. (2012). Because there are new muroid species described in the Steppan et al. (in prep) that are not found in Carleton and Musser (2005) or in Fabre et al. (2012), the final composite rodent chronogram includes more species than the initial Fabre et al. (2012) supermatrix tree (2,357 species). If morphological/habitat data was obtained from more than one subspecies, then the species tip was split mid-branch, creating polytomies, and data was applied separately to each tip in subsequent analyses, conducted using a final tree that includes 2,414 OTUs. Tree pruning, grafting, and ultrametricity checks were conducted in the Ape library (Paradis et al. 2004) in R (R Development Core Team 2013).

Binary Habitat Categories and Quantification of Habitat Transition

All 2,414 OTUs were classified as desert or mesic based on information from the literature (Appendix Table E.3), primarily using information from IUCN (2013). IUCN relies on experts to classify the habitat of each species based on its distribution; species that were classified as '8. Desert' in the habitat classification scheme were categorized as desert species in this study. This includes species that live in '8.1 Hot,' '8.2 Temperate,' and '8.3 Cold' deserts. In instances where species live in more than one habitat type (e.g. a desert and a mesic region), the species were classified as desert if their range includes a desert. Species that live in any other habitat type ('1. Forest,' '2. Savanna,' '3. Shrubland,' '4. Grassland,' '5. Wetlands,' '6. Rocky areas,' '7. Caves and Subterranean,' '9. Marine Neritic,' '12. Marine Intertidal,' '13. Marine

'Coastal,' and '14. Artificial'), excluding deserts, are classified as mesic. Therefore, desert species are not those that live exclusively in deserts, but rather those whose habitat classification includes a desert, and mesic species are those whose habitat classification does not include a desert. In addition to this classification scheme, analyses were also conducted on a classification based on Shenbrot et al. (1999) and results of the two schemes were compared. Shenbrot et al. (1999) consider desert rodents to be species with >50% of their range in an arid region while excluding species restricted to mesic refugia such as oases and species with exclusive subterranean lifestyle such as naked mole rats. By implication, all other species not found in this list are considered to be mesic species.

The frequency and general pattern of transition between desert and mesic environments in rodents was estimated using ancestral character reconstruction using both maximum likelihood (ML) as implemented in the Ape library and Bayesian (BI) stochastic character mapping (Huelsenbeck et al. 2003) as implemented in the Phytools library (Revell 2012) in R using binary habitat categories ('desert' vs. 'mesic') derived from IUCN (2013). Stochastic character mapping in Phytools is based on the method described in SIMMAP (Bollback 2006). Both ML and BI approaches used the all rates different matrix (ARD), two-parameter model (different rates estimated for forward and reverse transitions) which fit the data significantly better than both the equal rates (ER) and the symmetric (SYM), one-parameter models (same rate estimated for forward and reverse transition; ER and SYM are identical for binary traits) as determined by the likelihood ratio test ($\Delta \ln L = 36.98$, $p < 0.0001^*$).

Habitat transitions are inferred as occurring along the branch where the ancestral node is more likely (>50%) to be one habitat type (e.g. 'mesic') and the decedent node is most likely (>50%) to be another habitat type (e.g. 'desert'). The BI analysis uses the best-fit evolutionary model (ARD) and tip states ('desert' vs. 'mesic') to simulate stochastic character histories of the habitat using the fitted continuous time reversible Markov model of evolution (Huelsenbeck et al. 2003; Revell 2012). Because by itself, a single stochastic character history map is meaningless, habitat transition inferences were based on the average of 1,000 history maps; this was also done to account for mapping uncertainty, as recommended by Revell (2013).

Extraction of Continuous Environmental Data

Bioclimatic variables were obtained for the habitat of each species from WORLDCLIM 2.5-min geographical information system (GIS) layer (Hijmans et al. 2005) using DIVA-GIS v7.5 (Hijmans et al. 2012) by cross-referencing geographic localities (range distribution maps) of each species (polygon shape files from IUCN) with the WORLDCLIM 2.5-min database. I used the average value of each grid cell observation (range = 2 - 1,318,798 grid cells) that falls within the boundary of the polygon range file. Mean annual temperature and mean annual precipitation were extracted for comparative analyses in addition to average temperature and precipitation of the driest quarters which were used to calculate the aridity index (Appendix Tables E.1 and E.2) following the method of de Martonne (1942), which is also known as the De Martonne-Gottman aridity index and the Pinna Combinative Index (Zambakas 1992):

$$AI = \frac{\frac{P}{T+10} + \frac{12p}{t+10}}{2}$$

Where P is mean annual rainfall in millimeters, T is mean annual temperature in degrees Celsius, p is the average rainfall of the driest month in millimeters, and t is average temperature of the driest month in degrees Celsius. This index was expanded from the formula that was introduced by de Martonne (1927) where the temperature and the rainfall of the driest months are not accounted for. In Martonne's (1942) aridity index temperature is used as a proxy for potential evapotranspiration which is not available from DIVA-GIS and otherwise might be preferred (Maliva and Missimer 2012). While evaporation is calculated as a function of temperature alone, in reality it is related to many other factors including the amount of moisture in the soil, the type of soil, wind velocity, atmospheric pressure, and plant cover (Walton 1969). Because DIVA-GIS does not output the average temperature of the driest month (t), the aridity index was modified to use quarterly data (i.e. t = average temperature of the driest quarter; p = average rainfall of the driest quarter) following Eckert et al. (2010). Aridity here captures water availability as a function of temperature and precipitation and is arguably the best measure of the abiotic variables that desert organisms adapt to. This index is unitless, with lower values indicating increased aridity, and ranges from very dry to very humid regions (Baltas 2007).

In order to meet the assumptions of normality of subsequent analyses, mean annual rainfall was log transformed. The aridity index was also log transformed, but only after the calculation of the index from the raw data (e.g. Arroyo et al. 2006). In addition, since the raw aridity index scores are usually positive values with a larger value indicating a more mesic region, the negative raw aridity index scores were dropped from the analyses (a value of 0 is the lowest possible aridity index score in Martonne's (1942) method). The negative aridity index is a known problem in cold regions, where very low temperatures lead to negative aridity indices, regardless of aridity. This led to dropping 12 species, many of whom are mesic species with average annual precipitation in their range being > 106.84 mm. In addition, to be more conservative, 5 outlier species with extremely high aridity index scores (> 200 units) were dropped from the analyses to reduce their effect on driving the pattern.

Morphological Data Collection

One to nine specimens of 591 rodent OTUs (mostly different species) were examined for a total of 2,075 specimens and an average of 4 specimens per OTU (Appendix Table A.3, chapter 2). Multiple specimens with equal representation of males and females were examined when possible in order to account for the potential effect of intraspecific variation and sexual dimorphism (but see chapter 2). Most of the available desert rodent species from the visited museums (see below) were sampled in addition to a selection of close mesic relatives; a sample that is optimal for testing desert adaptation but does not provide a true representation of rodent species diversity. Representatives from all five suborders and 79% of the families of rodents were sampled; all families with desert representatives were included.

Morphological measurements were obtained from the skulls of voucher specimens from the collections of the American Museum of Natural History (AMNH) in New York, the Field Museum of Natural History (FMNH) in Chicago, the Museum of Vertebrate Zoology (MVZ) in Berkeley, the Smithsonian Institution in Washington D.C. (USNM), and the Florida Museum of Natural History (UF) in Gainesville, Laboratorio de Citogenetica Mamiferos, Facultad de Medicina, Universidad de Chile (LCM) in Chile, and the Oklahoma Museum of Natural History (OMNH). Only wild caught adult individuals were chosen. Adult status was assessed by the basioccipital–basisphenoid epiphyseal fusion as in Robertson and Shadle (1954) and Samuels

(2009) as well as the complete eruption of 3rd molars, reaching the occlusal surface (Steppan 1997) and the examination of the size of the associated skins.

Cranial measurements were extracted from photographs captured with a Nikon D3200 digital SLR camera using a Nikon 40mm f/2.8G AF-S DX Micro-Nikkor Lens (Nikon, Tokyo) at 24 megapixels (resolution = 6016 x 4000; JPEG) in a standardized manner (see chapter 2 for more detailed information on standardized photography procedure). Up to 10 photographs were taken per individual and include multiple magnifications (zoom settings) of the dorsal, ventral, and lateral orientations of the skull with a scale bar included in each photograph. All measurements were taken from images using Tpsdig v2.16 (Rohlf 2010) of the left side of the skull; if the left side was damaged, the right side was measured instead.

Morphological Characters

Species averages were calculated for all morphological characters from distances extracted from the ventral (Appendix Table E.4; Appendix Figure E.1), lateral (Appendix Table E.5; Appendix Figure E.2), and dorsal (Appendix Table E.5; Appendix Figure E.3) views of crania as well as the occlusal (Appendix Table E.6; Appendix Figure E.4) and lateral (Appendix Table E.6; Appendix Figure E.5) views of the mandibles. If distances could be observed from multiple views of the crania or mandibles (e.g. molar length can be observed in both the lateral and the occlusal views of the mandibles), then they were measured in all views and averaged before calculating subsequent derivative characters such as bulla volume and nasal index (Appendix Table E.7) in order to reduce the effects of flattening a 3D structure to 2D images. The following 47 measurements were obtained from each skull.

Ventral cranial characters. (1) *Skull length* (SL) is a common measure of skull size taken from the antero-medial most inferior border of the foramen magnum to the antero-medial most border of the premaxillaries. It is also known as the basilar length and is somewhat shorter than the other common size measurement, the condylobasal length. (2) *Skull width* (SW) is the maximum width of the skull perpendicular to SL. This measurement, also known as the zygomatic breadth/width, captures the greatest distance across zygomatic arches. (3) *Incisor width* (IW) measured at the insertion of the incisors to the premaxilla (widest part). (4) *Diastema length* (DL) measured at the alveoli. (5) *Molar tooth row length* (ML) measured at the occlusal region. (6) *First molar width* (MW) measured at the occlusal region. (7) *Pterygoid region length*

(PR) measured as the widest distance across the structure. (8) *Mesopterygoid breadth* (MB) is the distance between the tympanic bulla as measured across the mesopterygoid region. (9) *Basioccipital length* (BO) is the antero-posterior extent of the basioccipital. (10) *Bulla length* (BL) is the maximum length of only the tympanic portion of the auditory bulla from the anterior point of insertion into the basioccipital to the posterior-most of the tympanic bulla, not including the mastoid part of the auditory bulla. (11) *Bulla width* (BW) approximately perpendicular to BL and across the auditory meatus. (12) *Condyle breadth* (CB) measures the widest distance across the occipital condyles. Measurements (2) to (10) and (12) follow Steppan (1997), measurements (1) and (10) follow Squarcia et al. (2007), and measurements (1), (2), and (10) follow Francescoli et al. (2012). Ventral cranial measurements are depicted in Appendix Figure E.1.

Lateral cranial characters. (13) *Incisor depth* (ID) is the antero-posterior extent of the incisors. (14) *Incisor height* (IH) is the longest distance from the tip of the incisors to their insertion into the premaxillaries. (15) *Rostral depth* (RD) is the deepest part of the rostrum. (16) *Lateral molar row length* (LML) is the same as ML, viewed laterally (measured again to calculate averages; see above). (17) *First molar height* (MH) is the maximum height of the first molar. (18) *Maximum lateral bulla length* (LBL) is the same as BL, viewed laterally (measured again to calculate averages). (19) *Bulla height* (BH) is approximately perpendicular to the plane defined by BL and BW across the auditory meatus (perpendicular to LBL). Measurements (13), (15), and (16) follow Steppan (1997), and measurements (18) and (19) follow Francescoli et al. (2012). All lateral cranial characters are depicted in Appendix Figure E.2.

Dorsal cranial characters. (20) *Nasal breadth* (NB) is the widest distance across the nasals. (21) *Nasal length* (NSL) is the antero-posterior extent of the nasals. (22) *Interorbital breadth* (IOB) is the minimum distance between the upper edges of the orbits across the dorsal side of the skull. (23) *Dorsal skull width* (DSW) is also known as the zygomatic breadth and is another measure of skull width similar to SW. (24) *Dorsal skull length* (DSL) another measure of skull length similar to SL. Measurements (20) to (24) follow Steppan (1997), measurement (21) also follows Agrawal (1967), and measurement (23) also follows Francescoli et al. (2012). All dorsal cranial characters are depicted in Appendix Figure E.3.

Occlusal mandible characters. (25) *Lower incisors width* (LIW) is the width across both lower incisors; in mandibles disarticulated at the symphysis, the width across one incisor was multiplied by 2. (26) *Incisor length* (IL) is the maximum length of the incisors. (27) *Jaw*

diastema length (JDL) is the distance between the molar tooth row and the incisor at the alveoli. (28) *Jaw molar tooth row length* (JML) measured at the occlusal region. (29) *Jaw first molar width* (JMW) measured at the occlusal region. (30) *Total jaw length* (TJL) is the distance from the anterior tip of the incisor to the posterior extreme of the jaw at the condyloid process. Measurements (25) and (26) follow Ojeda et al. (1999), measurement (26) also follows Agrawal (1967), measurement (27) to (29) follow Steppan (1997), and measurement (30) follows Ndiaye et al. (2012). All occlusal mandible characters are depicted in Appendix Figure E.4.

Lateral mandible characters. (31) *Jaw incisor depth* (JID) is the antero-posterior extent of the incisors. (32) *Incisor length* (IL2) is the maximum length of the incisors viewed from the lateral side of the mandible. (33) *Jaw length measurement I* (JLS) from the incisor to the angular process; similar to TJL. (34) *Moment arm of the masseter* (MAM) is the distance from angular to condyloid process. (35) *Jaw length measurement II* (JLB) is the distance from the incisor to the condyloid process; similar to TJL. (36) *Jaw molar 1 height* (JMH) is the maximum height of the first molar of the mandible. Measurements (31), (33), and (34) follow Steppan (1997), measurement (32) follows Ojeda et al. (1999), and measurement (35) follows Ndiaye et al. (2012). All lateral mandible characters are depicted in Appendix Figure E.5.

Derived characters. (37) *Average jaw length* (AJL) is the average of TJL, JLS, and JLB. (38) *Average incisor length* (AIL) is the average of IL and IL2. (39) *Average skull length* (ASL) is the average of SL and DSL. (40) *Average skull width* (ASW) is the average of SW and DSW. (41) *Average molar length* (AML) is the average of ML and LML. (42) *Average bulla length* (ABL) is the average of BL and LBL. (43) *Bulla index* (BI) is calculated as the ratio of ABL to ASL. (44) *Bulla volume* (BV) is the 3D measure calculated following Schleich and Vassallo (2003) and Francescoli et al. (2012) using the formula of an elliptical cone where:

$$BV = \frac{(\pi)(\frac{ABL}{2})(\frac{BW}{2})(BH)}{3}$$

Similar to BI, this character only accounts for the inflation of the tympanic portion of the bulla and not the mastoid portion of the bulla. (45) *Nasal index* (NI) is a measure of the shape of the nasals calculated as the ratio of NB to NSL. (46) *Nasal volume* (NV) is an estimate of shape/size of the nasal passages/nasoturbinate calculated as the product of NB, NSL, and RD. (47) *Lower*

incisor index (LII) is the ratio of LIW to AIL and estimates the shape of the lower incisors. Measurements (43) and (47) follow Ojeda et al. (1999), measurement (43) also follows Squarcia et al. (2007), measurement (44) follows Schleich and Vassallo (2003) and Francescoli et al. (2012), and measurement (45) is a standard anthropological measurement. All morphological variables were log transformed prior to subsequent phylogenetic and/or size correction.

Phylogenetic and Size Correction

Phylogenetic signal (tendency for related species to look more alike than species randomly drawn from the phylogeny) was computed by calculating the K-statistic under a Brownian motion (BM) model of evolution with statistical significance calculated by 1,000 randomizations (Blomberg et al. 2003). The K value is a measure of the magnitude of the phylogenetic signal; values close to zero indicate no phylogenetic signal (close relatives do not look more similar than distant relatives) and K values significantly greater than zero indicate the presence of phylogenetic signal ($K < 1$ indicate less resemblance of relatives than predicted by BM; $K > 1$ indicate more resemblance than expected by BM) (Blomberg et al. 2003).

Several methods can be used to correct for size. A common method is conducting an analysis of covariance (ANCOVA) with the covariate being a univariate measure of body size such as mass; another simpler, less desirable approach is to simply take the ratio of the measure of interest to a size measure such as skull length (McCoy et al. 2006). I use a method that includes information from all the data (shearing). Shearing is conducted by calculating the residuals from a least squares regression analyses of each trait against the first principal component of the pooled data, the latter used as a size measure (McCoy et al. 2006).

I tested the correlation between environmental and morphological variables, both with and without correcting for phylogeny. The tree used in phylogenetic correction contains 591 OTUs (Figure 6.1; Appendix Figure E.6) extracted from the 2,414 OTU rodent phylogeny described above. In analyses where phylogeny was accounted for, shearing and PCA were conducted *after* correcting for phylogenetic non-independence among species. This is important because not accounting for phylogeny at the preliminary transformations can increase variance and type I error, even if phylogeny was accounted for in subsequent analyses leading to spurious results in phylogenetic comparative methods (Revell 2009). Phylogenetic signal calculation, phylogenetic size correction, and phylogenetic PCA were conducted following Revell (2009) using the Phytools library in R.

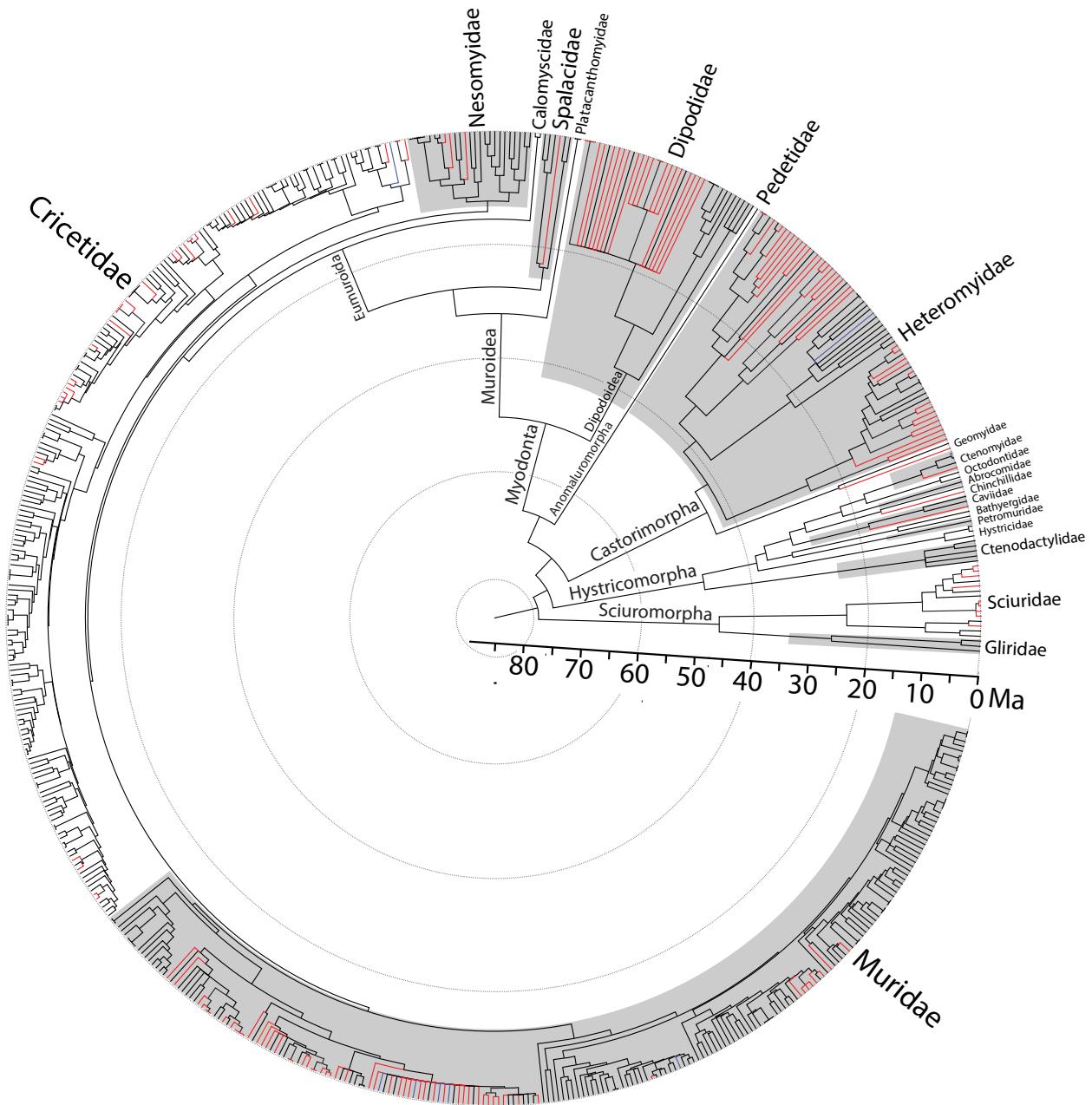


Figure 6.1. Summarized composite chronogram of 591 rodent OTUs with collected morphological data. Molecular phylogeny modified from Fabre et al. (2012) and Steppan et al. (in prep). Major taxonomic groups are indicated. Red tips indicate desert species, black tips indicate mesic species, and blue tips indicate species with ambiguous habitat; black branches do not signify habitat. Figure provided for illustrative purposes and was used for ancestral state reconstruction (full 2,414 OTU tree used). Species labels are in Appendix Figure E.6 and trees summarizing results of ancestral state reconstruction are in Appendix Figures E.7 and E.8.

Univariate Analyses of Putative Desert Adaptive Characters

The associations between the five derived morphological traits with prior evidence of desert adaptation with climate and habitat data were tested in a univariate framework as follows. Data where only size correction was performed were tested for desert adaptation by: (1) conducting generalized least squares analyses of each character onto the aridity index (AI), mean annual temperature (BIO1), and mean annual rainfall (BIO12). These regressions were conducted on each climatic variable separately. In addition, (2) an analysis of variance (ANOVA) was conducted while classifying species as desert or mesic using IUCN data (Appendix Table E.3). Both these analyses were conducted in the R base package.

Data where both size and phylogenetic correction was performed were tested for desert adaptation by: (1) conducting phylogenetic generalized least squares (PGLS) analyses of each character onto the three bioclimatic variables following the method of Freckleton et al. (2002). PGLS was used instead of independent contrasts because they can tolerate polytomies better. Analyses on discrete data (desert vs. mesic) were conducted using (2) phylogenetic analyses of variance (PhyANOVA) with 1,000 phylogenetic simulations following the method of Garland et al. (1993). PhyANOVA was conducted in the Phytools library and PGLS was conducted using the Caper library (Orme et al. 2013) in R.

Multivariate Analyses of Overall Skull Morphology

In order to test the generality of skull adaptation to deserts in rodents, the association between a suite of twenty-nine standard linear measurements intended to capture overall skull morphology (not including derived putative desert adaptive characters tested above or multiple measurements of the same structure) with climate and habitat data was tested in a multivariate framework as follows. (1) Morphological data were subjected to principal component analysis (PCA) and the first six principal components, were inspected for separation of desert vs. mesic rodents in all three datasets (raw, size corrected, and phylogenetic size corrected). (2) A discriminant function analysis (DFA) was performed to provide information as to the relative contribution of each morphological variable in the discrimination between these two groups. (3) A multivariate analysis of variance (MANOVA) was performed to see if these two groups have significantly different overall morphologies. Non-phylogenetic PCA was conducted using singular value decomposition in the Pcamethods library (Stacklies et al. 2007), phylogenetic

PCA was conducted in the Phytools library, linear discriminant function analysis was conducted in the Mass library (Venables and Ripley 2002), and PhyMANOVA was conducted in the Geiger library (Harmon et al. 2008) in R. (4) The correlation between continuous climatic variables and morphological variables was also tested using canonical correlations analysis (CCA) in order to quantify the associations between overall morphology and climate. CCA calculates a set of canonical variates, which are orthogonal linear combinations of the variables within each set that have the maximum correlation with each other (Härdle and Simar 2012) with the maximum number of canonical dimensions extracted being equal to the number of variables in the smallest dataset (Afifi et al. 2011). CCA was conducted in both the Cca library (González et al. 2008) and the Yacca library (Butts 2012) in R. CCA also used code from the UCLA webpage (2013).

Questions and Hypotheses

The main question asked in this study is: (1) is the variation in the tympanic bulla, lower incisors, and nasal morphology in rodents desert-adaptive? These characters were chosen because they appear to be adaptive at studies with more limited taxonomic scales that do not apply phylogenetic correction (putative desert-adaptive traits). Based on these studies I predict that increased aridity (decrease in aridity index, decrease in mean annual precipitation, and increase in mean annual temperature) will be directly correlated with an: (a) increase in bullar index (BI) and bullar volume (BV) reflecting an increase in absolute/relative size; (b) increase in lower incisor index (LII) indicating a “squarer” shape; (c) decrease in nasal index (NI) and nasal volume (NV) reflecting longer and narrower nasal passages that are more efficient at water conservation of exhaled air. This question was tested using univariate analyses of characters derived from morphological distances. An alternative explanation for interspecific variation in these traits is phylogenetic relationship/drift. This alternative is supported if traits are more similar in closely related species than distantly related species. Another explanation for interspecific variation in these traits is adaptation to other untested abiotic and biotic factors.

Other explored secondary questions include: (2) is the variation in other aspects of skull morphology not previously hypothesized to be desert adaptive (henceforth ‘desert-neutral’ traits; based on standard skull measurements) also desert-adaptive? This question is tested using multivariate analyses and is exploratory, and therefore I do not predict a directional pattern. I

also explore (3) the pattern of transition between mesic and desert habitats using ancestral state reconstruction of a dataset that includes all extant rodent species with IUCN habitat information.

Results

Habitat Classification and Transition in Rodents

Results from analyses using Shenbrot et al.'s (1999) habitat scheme were largely concordant with those from the IUCN habitat scheme; therefore only analyses using the latter are presented here. Out of the 2,277 described extant species of rodents, 243 (11%) are classified as 'desert' by the IUCN (2013). Out of the 5 suborders of rodents, most desert species are myodont ($172/1569 = 11\%$), followed by castorimorphs ($40/102 = 40\%$), and then sciromorphs ($26/307 = 8\%$). There are negligible hystricomorph and anomaluromorph desert species. Most sciromorph desert rodents are from Marmotini (ground squirrels; $22/92 = 24\%$), whereas most of the castorimorph desert rodents are from Dipodomysinae (kangaroo rats and mice; $14/21 = 67\%$) and Perognathinae (pocket mice; $22/26 = 85\%$). Desert myodonts come from diverse groups, mostly in Dipodinae (three-toed jerboas and relatives; $8/9 = 89\%$), Allactaginae (five-toed jerboas and relatives; $13/16 = 81\%$), Cardiocraniinae (five-toed pygmy jerboas and relatives; $7/7 = 100\%$), Spalacinae (spalacids; $5/13 = 38\%$), Gerbillinae (gerbils; $51/103 = 50\%$), Murinae (mostly *Notomys*; $4/9 = 44\%$), and Neotominae (mostly *Neotoma*: $11/22 = 50\%$ and *Peromyscus*: $17/56 = 30\%$). There are negligible desert species in other myodont groups.

Scaled likelihood (SL) refers to the percentage likelihood of the node being the habitat indicated based on the ML analysis (Appendix Figure E.7) and posterior probability (PP) refers to the average probability of the node being the habitat indicated based on 1,000 BI simulations (Appendix Figure E.8). Both the ML and the BI ancestral state reconstruction analyses show marginal support for the ancestral habitat of rodents being desert (SL = 52.8%, PP = 0.51). The BI analysis detected an average of 276.6 transitions between habitats (mesic to desert = 141.7, desert to mesic = 134.9) with 85% more time spent in the mesic habitat. Similarly, the ML analysis detected a faster forward transition rate from mesic to desert (0.073 ± 0.0074) than the reverse desert to mesic transition rate (0.013 ± 0.0011).

While most of the mesic to desert transitions were relatively recent and were not associated with the evolution of major desert rodent clades, a small number did, including: (1)

Marmotini clade (*Spermophilus*, *Cynomys*, *Marmota*, and *Ammospermophilus*) where both analyses estimate their common ancestor to be desert (SL = 56.7%, PP = 51.4%) while the ancestral node to this clade (Marmotini subclade+*Sciurotamias* and *Tamias*) is mesic (SL = 56.7%, PP = 0.63); (2) Murid clade (Gerbillinae, Deomyinae, and Lophiomyinae) where only the ML analysis estimates their common ancestor to be desert (SL = 70.8%, PP = 0.0) while the ancestral node to this clade (Muridae) is mesic (SL = 68.4%, PP = 1.0); (3) Gerbillinae clade (*Pachyuromys*, *Desmodilliscus*, *Taterillus*, *Sekeetamys*, *Gerbillus*, *Dipodillus*, *Brachiones*, *Psammomys*, *Meriones*, and *Rhombomys*) where both analysis estimates their common ancestor to be desert (SL = 99.3%, PP = 0.89), however, only BI analyses detects that this clade transitioned to desert from an ancestor that is mesic (SL = 0.05%, PP 0.93); (4) *Neotoma* where only the ML analysis estimates their common ancestor to be desert (SL = 80.0%, PP = 0.02) while the ancestral node to this clade (*Neotoma*+*Hodomys* and *Xenomys*) is mesic (SL = 60.8%, PP = 0.82). Notably absent from this list are heteromyids and dipodoids which were not associated with a mesic to desert transition but rather constitute a retention of the ancestral desert habitat condition of the common ancestor of rodents.

Difference in Climate between Desert and Mesic Environments

There is a significant difference in the aridity index scores between desert species (according to IUCN classifications) and mesic species (Figure 6.2a; $t = 13.82$, $p < 0.0001^*$). The average desert species aridity index score (0.97 ± 0.41 units) were significantly lower than the average aridity index scores of mesic species (1.54 ± 0.42 units). Similarly, there is a significant difference between desert and mesic species in mean annual precipitation (Figure 6.2b; $t = 17.98$, $p < 0.0001^*$). The average mean annual precipitation in the habitat of desert species (2.43 ± 0.28 ln mm) is significantly lower than in mesic species (2.97 ± 0.33 ln mm). The average mean annual temperature in the habitat of desert species is significantly different from that in the habitat of mesic species (Figure 6.2c; $t = 2.18$, $p = 0.03^*$). The average mean annual temperature in the habitat of desert species (16.9 ± 5.62 °C) is significantly lower than in the habitat of mesic species (18.2 ± 6.64 °C). This 1.3 °C difference illustrates that many deserts are cold with aridity being the main criterion for classifying a region as desert. This also shows that several of the desert species in the sample live in relatively cold regions.

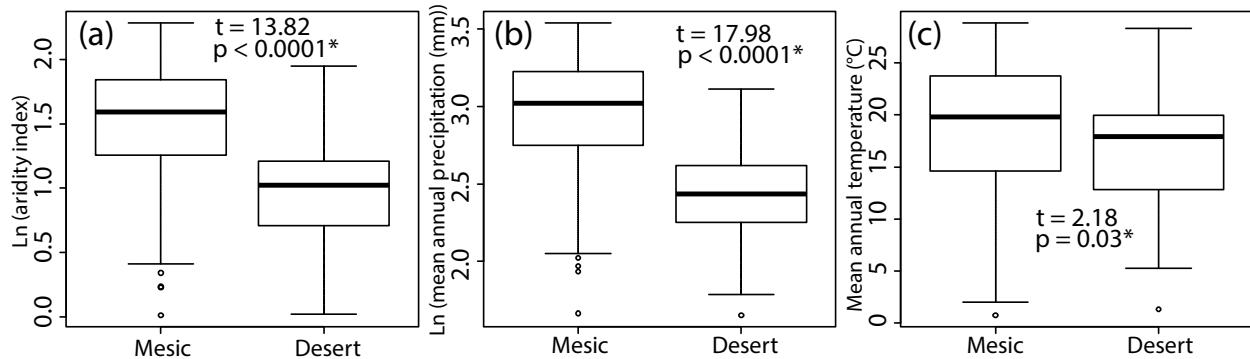


Figure 6.2. Association between binary habitat data with (a) aridity index (unit-less), (b) mean annual precipitation in millimeters, and (C) mean annual temperature in °C. Indicated statistics are based on a t-test. Inner boxplot lines are median values, box margins are 25th and the 75th percentiles, whiskers are 5th and 95th percentiles, and points beyond the whiskers are outliers.

Dataset Comparison and Phylogenetic Signal

The results of the (a) non-size, non-phylogenetically corrected data; the (b) size-corrected, non-phylogenetically corrected data; and the (c) size-corrected, phylogenetically-corrected data are consistent in both the univariate analyses of the five putative desert-adaptive traits and the multivariate analyses of the twenty-nine desert-neutral characters. The addition of size correction tends to reduce the significance of the correlations and the addition of phylogenetic correction tends to reduce it much more. All non-size and size corrected morphological data and environmental variables, showed statistically significant phylogenetic signal at $p < 0.001^*$ and K values ranging from 0.015 to 0.66. The only exceptions were LIW and LII for the size corrected dataset ($p = 0.3$, $K = 0.01$ and $p = 0.15$, $K = 0.23$ respectively), however, results in subsequent analyses were consistent with phylogenetically corrected data. Significant phylogenetic signal argues for the importance of using phylogenetic correction in comparative analyses of rodents. For these reasons and because (c) is the most conservative test, only the results of the size-corrected, phylogenetically-corrected data will be presented.

Contrasts of Putative Desert Adaptive Traits with Habitat and Environmental Data

PhyANOVA indicates that desert rodents have significantly greater bullar index scores than mesic rodents (Figure 6.3a; $F = 141.39$, $p = 0.001^*$) indicating that desert rodents have greater relative bulla size. PGLS indicates that bullar index scores are significantly negatively correlated with both aridity index scores (Figure 6.3b; Coef = -0.012, $R^2 = 0.077$, $p = 0.028^*$)

and mean annual precipitation (Figure 6.3c; Coef = -0.034, $R^2 = 0.034$, $p < 0.0001^*$) indicating increased relative bulla size is correlated with more arid environments that receive lower rainfall. PGLS indicates that bullar index scores are not significantly correlated with mean annual temperature (Figure 6.3d; Coef = 0.003, $R^2 = 0.001$, $p = 0.509$). The same patterns was observed in bullar volume scores, which according to PhyANOVA, were significantly greater in desert than mesic rodents (Figure 6.4a; $F = 162.28$, $p = 0.001^*$) which is associated with greater volumes in desert rodents. Similarly, PGLS indicates that bullar volume scores are significantly negatively correlated with both aridity index scores (Figure 6.4b; Coef = -0.034, $R^2 = 0.019$, $p = 0.001^*$) and mean annual precipitation (Figure 6.4c; Coef = -0.069, $R^2 = 0.027$, $p = 0.0001^*$) indicating increased overall bulla size is correlated with more arid environments with lower mean annual rainfall. PGLS indicates that bullar volume scores are not significantly correlated with mean annual temperature (Figure 6.4d; Coef < -0.001, $R^2 = 0.002$, $p = 0.963$).

PhyANOVA indicates that nasal index scores are not significantly different between desert and mesic rodents (Figure 6.5a; $F = 4.29$, $p = 0.669$). However, PGLS indicates that nasal index scores are significantly positively correlated with aridity index scores (Figure 6.5b; Coef = 0.016, $R^2 = 0.008$, $p = 0.024^*$) and marginally significantly negatively correlated with mean annual temperature (Figure 6.5d; Coef = -0.001, $R^2 = 0.005$, $p = 0.057$) indicating that nasals are relatively longer and narrower in more arid and warmer environments. PGLS indicates that nasal index scores are not significantly correlated with mean annual precipitation (Figure 6.5c; Coef = 0.019, $R^2 = 0.004$, $p = 0.084$). PhyANOVA indicates that desert rodents have significantly lower nasal volumes than mesic rodents (Figure 6.6a; $F = 84.11$, $p = 0.002^*$) indicating that desert rodents have lower nasal volumes. PGLS indicates that nasal volume scores are significantly positively correlated with aridity index (Figure 6.6b; Coef = 0.026, $R^2 = 0.019$, $p = 0.001^*$) and mean annual precipitation (Figure 6.6c; Coef = 0.044, $R^2 = 0.023$, $p = 0.0003^*$) indicating that more arid environments that receive lower mean annual rainfall are correlated with lower overall nasal volumes. PGLS indicates that nasal volume scores are not significantly correlated with mean annual temperature (Figure 6.6d; Coef < -0.001, $R^2 = 0.001$, $p = 0.544$).

PhyANOVA indicates that lower incisor indices are not significantly different between desert and mesic rodents (Figure 6.7a; $F = 2.34$, $p = 0.778$) and PGLS indicates that lower incisor index scores are not significantly correlated with aridity index (Figure 6.7b; Coef = -0.026, $R^2 =$

0.002, $p = 0.139$), mean annual precipitation (Figure 6.7c; Coef = -0.016, $R^2 = 0.001$, $p < 0.563$), or mean annual temperature (Figure 6.7d; Coef = -0.002, $R^2 < 0.001$, $p = 0.311$).

Multivariate Association of Overall Skull Morphology with Habitat and Environment

The morphospace represented by the first six phylogenetic principal components of the twenty-nine characters do not clearly separate species based on binary habitat classification (Figure 6.8; Table 6.1). Similarly, based on a visual inspection of the sole linear discriminant function, there does not seem to be clear separation between desert and mesic groups (Figure 6.9; Table 6.2). Despite this result, the reclassification of species based on the discriminant function was highly successful with 82% of all species being correctly reclassified into their original habitat categories in the original dataset and 79% of correct reclassification based on the cross validated dataset using jackknife resampling (Table 6.3). The fact that the discriminant function was highly successful at reclassifying species into their original habitat categories (Table 6.3) despite high overlap in discriminant function scores (Figure 6.9) may indicate that the discriminant function analysis is recovering clades and not habitat groups. Furthermore, PhyMANOVA, which tests whether the cranial morphologies of these two groups are significantly different, indicates no significant difference (Wilks' $\lambda = 0.65$, $p = 0.96$), which was unlike the non-phylogenetic MANOVA which did find a significant difference ($F = 8.65$, $p < 0.0001^*$). Taken together, the phylogenetic results indicate that desert and mesic species do not differ significantly in the twenty-nine desert-neutral characters.

The canonical correlations analysis, which tests the multivariate association between morphological and climatic variables, indicates strong associations between the morphological and the climatic variables in all three dimensions (Figure 6.10a, Cor1 = 0.598, $R^2 = 0.079$, $p < 0.0001^*$; Figure 6.10b, Cor2 = 0.500, $R^2 = 0.378$, $p < 0.0001^*$; Figure 6.10c, Cor3 = 0.430, $R^2 = 0.187$, $p < 0.0001^*$). Furthermore, the aforementioned results indicate that all three dimensions are significant together (Cor1-3) and separately (R^2 of canonical variates 1-3). The canonical coefficients of the first dimension indicates that it is most strongly associated with the aridity index (0.97) and mean annual precipitation (0.89) in the climate dataset and bulla length (-0.78), height (-0.78), and width (-0.71) in the negative direction, and mesopterygoid breadth (0.77) and incisor width (0.72) in the positive direction in the morphological dataset (Figure 6.11a; Table 6.4). This result indicates that the strongest association detected between these two datasets is a

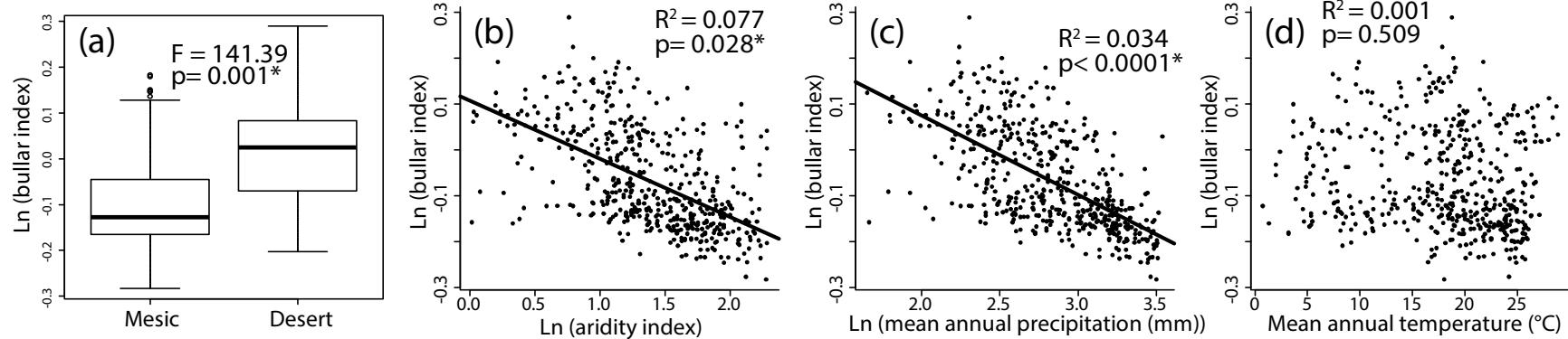


Figure 6.3. Association between bulla index scores with (a) habitat, (b) aridity index, (c) mean annual precipitation, and (d) mean annual temperature. The association between morphological variables with the binary habitat data was tested using PhyANOVA whereas the association with continuous environmental variables were tested using PGLS. Boxplots and scatterplots indicate phylogenetic and size corrected residuals of morphological variables. Indicated R^2 values, as in the text, are adjusted for the number of explanatory terms in the model relative to the number of data points (more conservative than unadjusted R^2). A best fit line is only included in significant and marginally significant regressions.

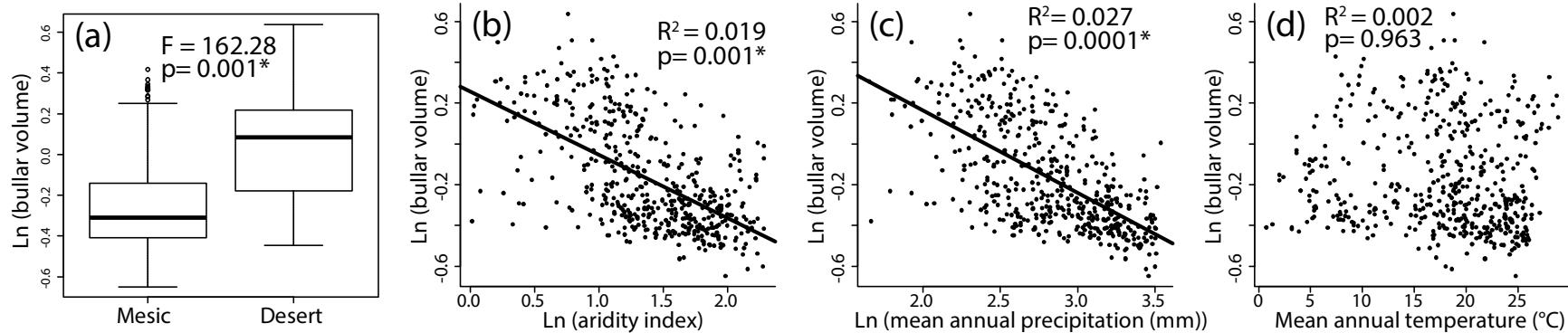


Figure 6.4. Association between bulla volume scores with (a) habitat, (b) aridity index, (c) mean annual precipitation, and (d) mean annual temperature. See Figure 6.3 legend for information.

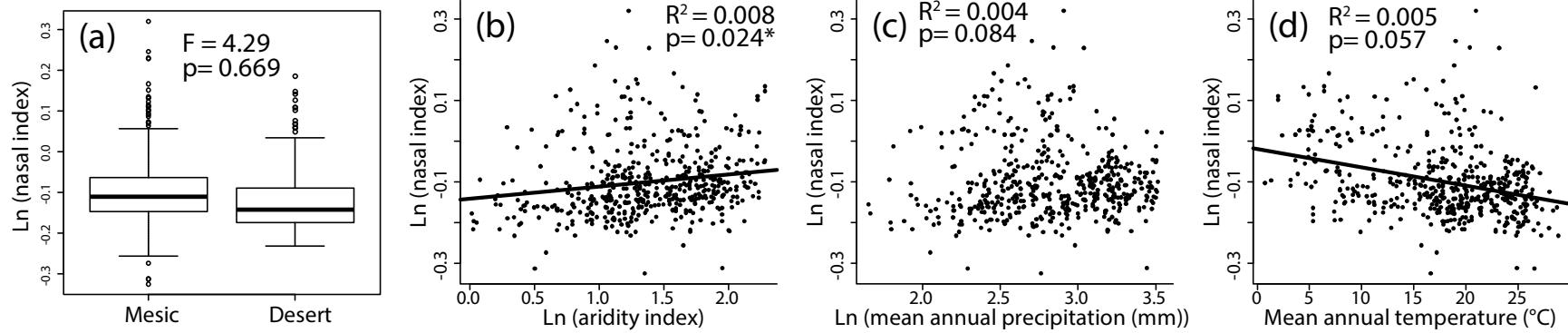


Figure 6.5. Association between nasal index scores with (a) habitat, (b) aridity index, (c) mean annual precipitation, and (d) mean annual temperature. See Figure 6.3 legend for information.

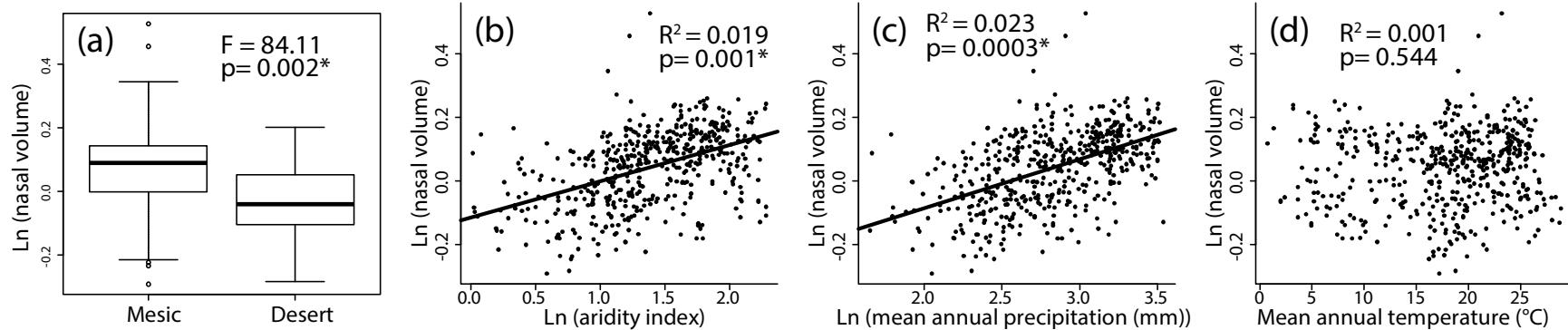


Figure 6.6. Association between nasal volume scores with (a) habitat, (b) aridity index, (c) mean annual precipitation, and (d) mean annual temperature. See Figure 6.3 legend for information.

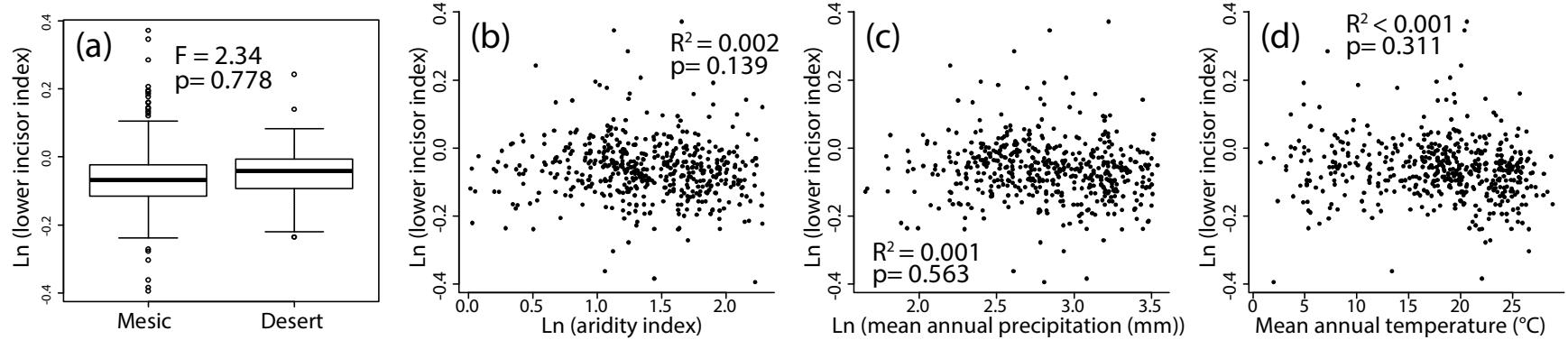


Figure 6.7. Association between lower incisor index scores with (a) habitat, (b) aridity index, (c) mean annual precipitation, (d) mean annual temperature. See Figure 6.3 legend for information.

negative correlation between increased aridity index (more mesic environments) and mean annual precipitation with decreased bulla dimensions and increased mesopterygoid breadth (region sandwiched between the tympanic bulla) and incisor breadth. However, all other morphological variables, except for bulla length, width, and height as well as interorbital breadth and first molar width, were also positively associated with the aridity and precipitation. The second canonical dimension, which explains residual variation, is most strongly associated with temperature (0.98) and somewhat with mean annual precipitation (0.45) in the climate dataset and somewhat with skull length (0.51), pterygoid length (0.47), incisor depth (0.46), and nasal length (0.40) in the morphological dataset (Figure 6.11b; Table 6.4). The residual variation explained by the third canonical dimension, while significant, was weak and indicates mostly correlations among the morphological variables and not environmental variables (Figure 6.11c; Table 6.4).

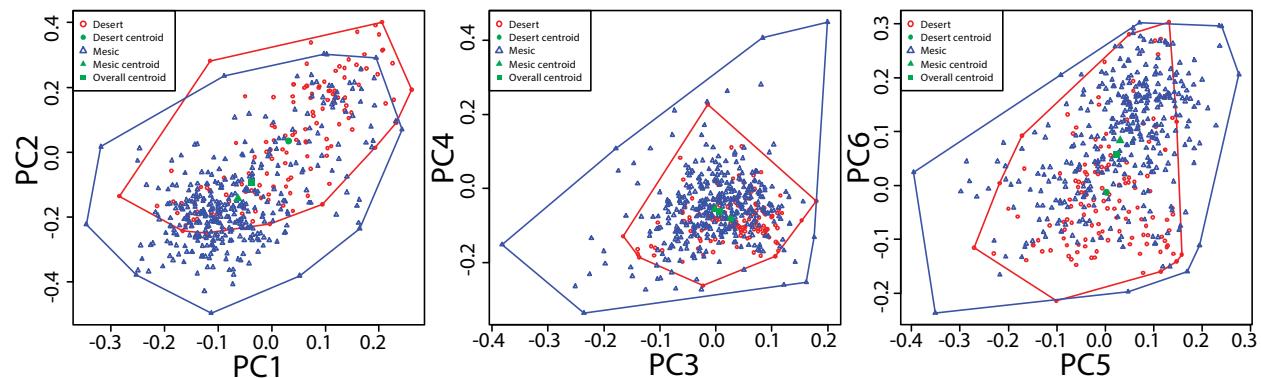


Figure 6.8. Variation in desert and mesic rodents in the first six phylogenetic principal component morphospace of the twenty-nine desert-neutral cranial characters. Principal components 1-6 explain 19.6, 12.0, 10.5, 9.6, 8.0, and 5.7% of the variation respectively.

Table 6.1. The first six phylogenetic principal component loadings of the twenty-nine desert-neutral characters indicating the relative contribution of each morphological character.

	PC1	PC2	PC3	PC4	PC5	PC6
ABL	0.450	0.500	0.133	-0.004	-0.035	-0.067
AIL	0.102	-0.262	-0.095	0.007	-0.018	0.503
AJL	-0.176	-0.250	-0.136	0.139	-0.355	0.581
AML	0.151	-0.326	-0.380	-0.129	-0.200	-0.311
ASL	0.143	-0.102	0.115	0.320	0.509	0.048
ASW	-0.071	-0.088	-0.026	0.191	0.270	0.090
BH	0.488	0.612	0.069	-0.030	-0.233	-0.219
BO	0.004	-0.031	0.431	0.249	0.051	0.037
BW	0.063	0.265	-0.034	0.130	-0.018	-0.196
CB	0.268	-0.287	-0.356	0.264	0.218	0.135
DL	0.047	-0.125	-0.053	0.131	0.234	0.365

Table 6.1—continued.

	PC1	PC2	PC3	PC4	PC5	PC6
ID	0.132	-0.109	0.383	0.060	-0.111	-0.227
IH	0.150	0.171	-0.071	-0.142	0.412	0.002
IOB	0.240	-0.025	-0.073	0.176	0.343	-0.181
IW	-0.036	-0.453	-0.029	0.037	0.217	-0.147
JDL	-0.103	-0.126	-0.288	0.059	-0.134	0.484
JID	-0.206	0.011	0.479	-0.135	-0.081	0.094
JMH	-0.372	-0.122	0.070	-0.889	0.150	0.073
JML	0.042	-0.493	-0.400	-0.044	-0.558	0.043
JMW	-0.173	-0.365	-0.128	0.007	-0.701	0.064
LIW	-0.954	0.167	-0.137	0.170	0.008	-0.096
MAM	-0.227	0.165	0.162	0.047	-0.519	0.237
MB	-0.079	-0.735	-0.230	0.247	0.436	0.119
MH	0.252	0.111	-0.837	-0.177	0.086	-0.277
MW	-0.096	-0.665	0.409	0.027	-0.067	-0.487
NB	-0.006	-0.137	0.115	-0.026	-0.074	0.161
NSL	-0.164	0.066	0.256	0.054	0.461	0.139
PR	0.019	0.203	0.146	0.381	0.354	0.297
RD	0.110	-0.093	0.038	0.006	-0.007	0.174

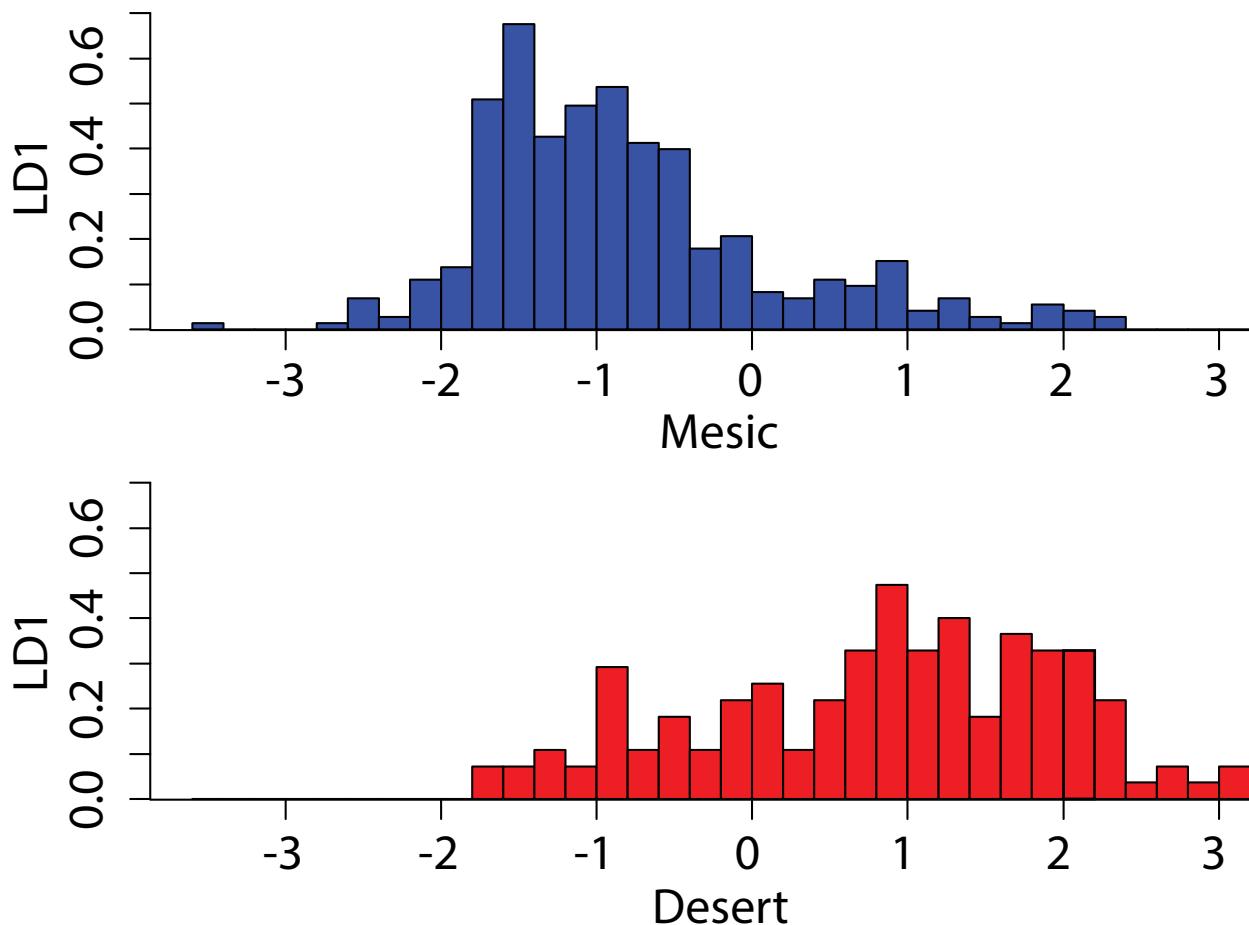


Figure 6.9. Variation in desert and mesic rodents in the morphospace represented by the sole discriminant function of the twenty-nine desert-neutral cranial characters.

Table 6.2. Discriminant function coefficients of the twenty-nine desert-neutral cranial characters indicating the relative contribution of each morphological character.

	LD1	LD1	
ABL	-11.17	JDL	0.27
AIL	-4.59	JID	-1.99
AJL	-7.99	JMH	-1.23
AML	-3.20	JML	-3.39
ASL	-7.65	JMW	1.99
ASW	7.89	LIW	-1.83
BH	-7.14	MAM	-7.45
BO	-4.34	MB	-2.81
BW	-3.59	MH	-3.66
CB	-1.28	MW	-4.36
DL	-2.25	NB	-15.01
ID	-1.44	NSL	-10.19
IH	-0.24	PR	0.01
IOB	-2.67	RD	-7.87
IW	-6.00		

Table 6.3. Proportion of correct habitat classifications based on the linear discriminant function of the 29 desert-neutral characters using both the original data and cross-validated data based on jackknife resampling. Observed and predicted habitat categories are indicated in the rows and columns respectively.

Observed habitat		Predicted habitat					
		Original			Cross-validated		
		Mesic	Desert	Total	Mesic	Desert	Total
Count	Mesic	324	39	363	319	44	363
	Desert	49	88	137	56	81	137
Proportion	Mesic	0.89	0.11	1	0.88	0.12	1
	Desert	0.64	0.36	1	0.59	0.41	1
Proportion correct		-	-	0.82	-	-	0.79

Discussion

Habitat Transition and Desert Specialization in Rodents

Rodents are highly adaptable, with a relatively broad niche and generalized skull morphology and masticatory apparatus (Nowak 1999). Consequently, they are globally distributed (found on all major landmasses except Antarctica and New Zealand) and inhabit most terrestrial ecosystems ranging from tropical rainforests to hyper-arid deserts (Fabre et al. 2012). Deserts are commonly described “extreme” habitats and desert rodents, with their common suite

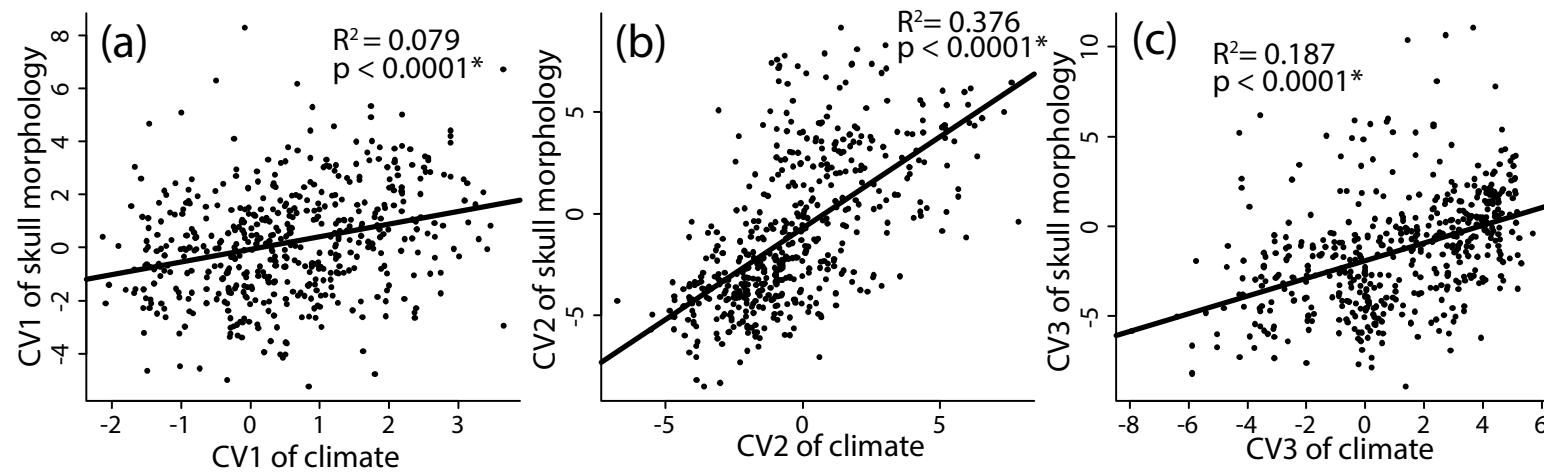


Figure 6.10. Canonical correlations of climate (mean annual precipitation, mean annual temperature, and the aridity index) vs. skull morphology (twenty-nine desert-neutral characters) in three dimensions (a, b, c). R^2 values and best fit line are results of regressions of the canonical scores in the indicated dimensions (not canonical correlations which are based on multiple dimensions, see text).

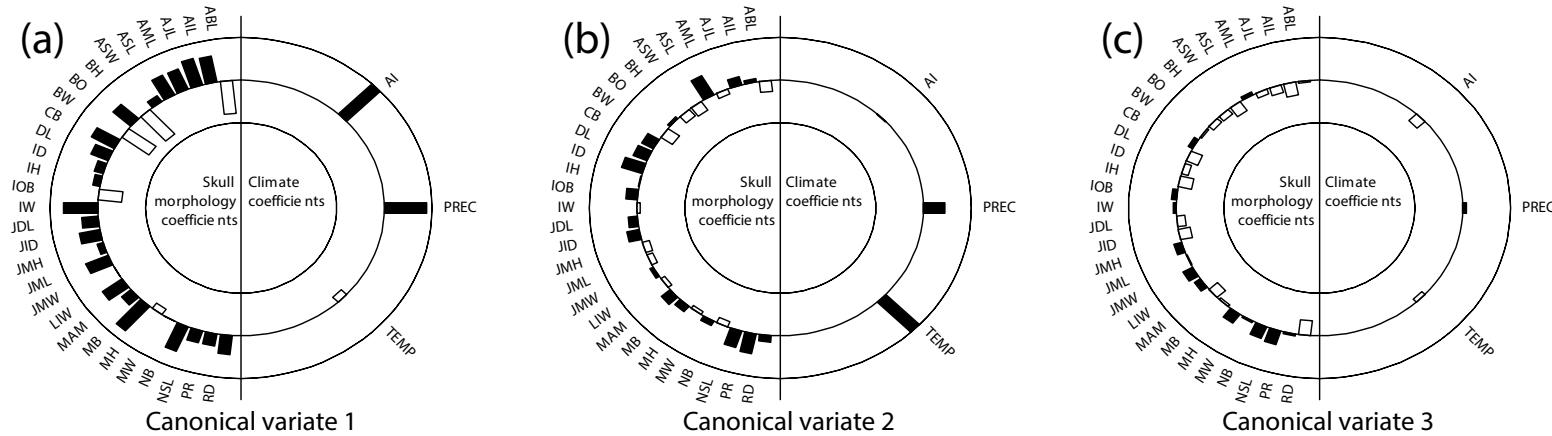


Figure 6.11. Canonical coefficients of correlations between climate (log mean annual precipitation (PREC), mean annual temperature (TEMP), and the log aridity index (AI)) and skull morphology (twenty-nine desert-neutral characters) in all three dimensions displayed in a circular fashion (a, b, c). Larger (positive) values are indicated by the radial bars that are pointing outward from the base of the inner circle and the smaller (negative) values are pointing inward.

Table 6.4. Canonical coefficient values of correlations between climate (mean annual precipitation, mean annual temperature, and the aridity index) and skull morphology (twenty-nine desert-neutral characters) in all three dimensions. See Figure 6.11 for more information.

	Canonical variate 1	Canonical variate 2	Canonical variate 3
Climate			
AI	0.97	-0.01	-0.23
PREC	0.89	0.45	0.08
TEMP	-0.16	0.98	-0.09
Skull morphology			
ABL	-0.78	-0.26	-0.04
AIL	0.62	0.08	-0.31
AJL	0.65	0.20	-0.18
AML	0.52	-0.13	-0.12
ASL	0.53	0.51	0.07
ASW	0.17	-0.25	-0.26
BH	-0.78	-0.20	-0.15
BO	0.50	0.06	-0.13
BW	-0.71	-0.30	-0.04
CB	0.56	0.28	0.10
DL	0.39	0.32	-0.26
ID	0.20	0.46	-0.15
IH	0.16	0.02	-0.29
IOB	-0.50	0.25	0.11
IW	0.72	-0.07	0.06
JDL	0.35	0.19	-0.18
JID	0.44	0.27	-0.25
JMH	0.13	-0.15	0.17
JML	0.51	-0.13	-0.02
JMW	-0.01	0.08	0.23
LIW	0.51	-0.10	0.15
MAM	0.26	0.24	-0.24
MB	0.77	0.16	-0.05
MH	-0.16	-0.08	0.26
MW	0.00	0.11	0.04
NB	0.63	-0.14	0.30
NSL	0.29	0.40	0.34
PR	0.29	0.47	0.05
RD	0.45	0.15	-0.35

of convergent adaptations, including those for fossoriality, bipedality, water conservation, and energy conservation, as extremely specialized (Vial 1962; Lay 1972; Mares 1975, 1976).

The BI analysis indicates that rodents spent 85% more time in the mesic habitat state and that the desert lineages are concentrated near the tips of the tree, indicating frequent, recent desert transitions. The strong bias favoring transition from mesic to desert ecosystems in the ML analysis (5.6 fold difference) and the weak bias in the BI analysis (1.1 fold difference), may indicate that it is easier for rodent lineages to transition from mesic to desert ecosystems than the reverse, which may indicate that desert specialization limits the capacity for rodents to revert to a generalized mesic condition. This result seems consistent with the “evolutionary dead-end” hypothesis, which describes the tendency for directional evolution towards increased ecological specialization that limits further evolution (Simpson 1953; Kelley Farrell 1998). While some recent studies show a similar trend of increased transition from a generalized to a specialized ecological condition (e.g. host-plant use in phytophagous insects, Nosil 2002, Nosil et al. 2005; habitat specialization of avian malaria parasites, Loiseau et al. 2012) others show the reverse pattern (e.g. parasitoid flies, Stireman 2005). Trade-offs in performance between different habitats (as a consequence of habitat-specific adaptations) have been described as a factor that promotes specialization (e.g. pea aphids, Via 1991; walking sticks, Sandoval 1994, Joshi and Thompson 1995, Fry 1996; stickbacks, Schluter 1993, 1995) and may explain the trend of biased transition from mesic to desert habitats in rodents.

Both the ML and the BI analyses did not unambiguously place the common ancestor of rodents into a habitat category, but weakly suggested deserts to be the ancestral habitat of rodents, and that rodents colonized deserts from mesic ecosystems independently multiple times. The results also indicate that while the common ancestors of most characteristically desert-adapted clades (gerbils, heteromyids, and dipodoids) did occupy desert habitats, the evolution of these clades did not coincide with the mesic to desert transition but rather the transition occurred at a more ancestral node. In gerbils, the mesic to desert transition occurred at the node that includes Gerbillinae+Deomyinae+Lophiomyinae, and similar results were found for heteromyids and dipodoids, where the desert transition did not coincide with the evolution of these two clades but rather constituted a retention of the ancestral desert condition of the common ancestor of rodents. This result indicates that many mesic clades closely related to characteristically desert

rodent clades (e.g. Gerbillinae vs. Deomyinae+Lophiomyinae) may constitute the reversion of desert specialists to mesic environments.

Desert Adaption in the Tympanic Bulla, Lower Incisors, and Nasals

The fact that desert rodents have enlarged bullae, squarer shaped lower incisors, and longer more complex nasal passages have been argued in multiple studies (e.g. Webster and Webster 1975; Lay 1972; Ojeda et al. 1999; Schmidt-Nielsen and Schmidt-Nielsen 1951; Cortes et al. 1988, 1990). However, because most of these studies were conducted with a descriptive goal with limited functional interpretations, evidence for desert adaptation in these structures have been anecdotal, based on limited taxonomic scale, with small sample sizes, and without correcting for phylogenetic relationships. Here, I present the first quantitative, phylogenetically correct, order-level investigation of desert adaptation of skull morphology in rodents. The results show that while morphological variation of the bullae, lower incisors, and nasals have significant phylogenetic signal, phylogeny alone does not completely explain interspecific variation.

The results indicate that both the relative and absolute size of the tympanic bulla is greater in desert than in mesic rodents and that the size of this structure increases with increasing aridity. This correlation is observed in the residual interspecific variation after the application of both phylogenetic and/or size correction. This result is consistent with results observed in earlier studies (e.g. gerbils, Lay 1972, Pavlinov and Rogovin 2000, Momtazi et al. 2008; heteromyids, Webster and Webster 1975, Randall 1993; sand cats, Huang et al. 2002; Xenarthra, Squarcia et al. 2007) despite the different methods used. The enlargement of the tympanic bulla has been shown to be correlated with improved hearing of low-frequency sounds in desert and/or subterranean rodents (e.g. gerbils, Lay 1972; kangaroo rats, Webster and Webster 1975; neotropical spiny rats, Gardner and Emmons 1984; tuco-tucos, Francescoli 2000; caviomorphs, Schleich and Vassallo 2003). Improved hearing at low-frequency bands is especially useful for desert rodents because deserts are open habitats where sound dissipates quickly, and increased auditory sensitivity improves both prey capture and predator avoidance rates (Lay 1972; Webster and Webster 1975) as well as conspecific communication in burrows (Francescoli et al. 2012).

Bullar hypertrophy has been described as both a desert and a fossorial adaptation, sometimes in the same species. This is unsurprising because many desert rodents are fossorial (e.g. gerbils, Lay 1972; tuco-tucos, Francescoli et al. 2012) because deserts are open habitats

with relatively few natural shelters (Lay 1972). Burrows also allow desert rodents to escape fatally high daytime temperatures in some regions since the microclimate of the burrow is significantly cooler in the day than aboveground and exhibits less temperature fluctuations; burrows are also moister, which facilitates water conservation (Ward 2009). Interestingly, I found a general pattern of increased bullar hypertrophy in desert rodents despite the inclusion of fossorial species that achieve enhanced low-frequency hearing through adaptations of the inner ear, without the inflation of the tympanic bulla (e.g. naked mole rats, Heffner and Heffner 1992). This may indicate that the case exhibited by the naked mole rats is an uncommon exception, with the general trend observed in fossorial desert rodents being that of bullar hypertrophy.

I do not find evidence for a significant difference in the shape of the lower incisors between desert and mesic rodent species or any association between this structure with other climatic variables, both with and without phylogenetic and/or size correction. The association between this structure with aridity has been never been directly studied before. Kenagy (1972) was the first to propose that the broad, flat, and chisel-shaped lower incisors of *Dipodomys microps* is an adaptation to remove the salt-coated epidermis of halophytic plants that occur in their habitat before ingestion, a character/behavior that was thought to be unique among rodents. In a comparison of seven species of desert rodents (*Microcavia australis*, *Ctenomys mendocinus*, *Octodontomys gliroides*, *Otomys mimax*, *Dipodomys merriami*, *Dipodomys microps* and *Psammomys obesus*), Ojeda et al. (1999) showed that in addition to *Dipodomys microps*, *Typanoctomys barrerae* and *Psammomys obesus* which occur in different deserts (Great Basin, Monte, and Sahara respectively) have evolved similar shaped incisors which are also associated with the ability to remove salt from desert saltbush epidermis before ingesting the green mesophyll tissue, with increased specialization being correlated with increased ‘squareness’ of the lower incisors. Perhaps it is unsurprising that I do not find a correlation, since the sample of rodents display a very large range of dietary variation both within and between habitat groups (e.g. see chapter 4), with many of the sampled desert rodents not being found in habitats that contain saltbush. Therefore, an association may be observed if analyses were limited to folivorous species and excluded other dietary types including granivorous species.

The results indicate that both the nasal index and the nasal volume scores are significantly positively correlated with mean annual precipitation and/or aridity index scores, which indicate that more arid environments are correlated with longer and narrower nasals and

lower nasal volumes, a pattern robust to phylogenetic and/or size correction. If the nasal index and nasal volume measures approximate nasoturbinate morphology, then the results are consistent with the expectation of desert adaptation in rodents, where long, narrow, and extremely convoluted nasoturbinates are the most effective at conserving water from exhaled air (Schmidt-Nielsen and Schmidt-Nielsen 1951; Cortes et al. 1988, 1990; Feldhamer et al. 2007).

One of the most important functions of the nasal cavity is to moisten and warm inhaled air to prevent damage of sensitive mucosal lung tissues and to cool and dry exhaled air facilitating water retention (Inthavong et al. 2007; Noback et al. 2011). Both these processes are more efficient in longer and narrower than in shorter and broader nasoturbinate systems because both the surface to volume ratio of the nasal passages and the resistance time (time air is spends in the nasal cavity) increases in elongated nasal passages with reduced (narrow) cross-sectional area (Inthavong et al. 2007). The lengthening and narrowing of the nasoturbinate system is associated with increased mucosal contact surface per unit volume of inhaled air, enhancing water and heat exchange between air and mucosal tissue (Inthavong et al. 2007). This pattern is common in anthropological studies that document a significant correlation between nasal cavity shape, estimated using external nasal measurements, with temperature and humidity in a clinal fashion; nasal cavities in cold-dry regions are relatively higher (longer) and narrower (more protruded) than those from hot-humid climates, in agreement with the adaptive increased contact between air and mucosal tissue in cold-dry climates (Leong and Eccles 2009; Noback et al. 2011).

When compared to the nasal volume, which takes into account rostral height, the association with aridity in the nasal index was weaker, which could reflect an adaptive trade-off/constraint with fossoriality (which is not expected to be reflected in the rostral height) since most small desert rodents avoid heat by burrowing (e.g. gerbils, kangaroo rats, and dipodoids, Nowak 1999), where projecting, long nasals hinder digging efficiency and have a greater chance of injury (Agrawal 1967). Many desert animals have also evolved a counter-current heat exchange system in their nasal passages to further enhance water retention (Schmidt-Nielsen 1972), a structure that is not adequately captured by cranial measurements.

Desert Adaption in Overall Skull Morphology

The results show that desert and mesic species have extensive overlap in overall skull morphology; this was among the few instances where phylogenetic tests clearly disagreed with non-phylogenetic tests with the latter showing a significant difference between the two groups. However, the multivariate association between overall morphology and climate was significant, indicating strong correlations between some morphological traits with climatic variables. The strongest pattern of association between the morphological and the climatic variables was that of increased tympanic bulla dimensions (length, height, and width) and reduced mesopterygoid breadth (region sandwiched between the tympanic bulla which tends to decrease with increasing bulla width) and reduced (upper) incisor breadth in more arid environments. With the exception of incisor breadth, all these regions are correlated with bulla hypertrophy and/or are directly used in the calculation of bulla index and/or volume. Surprisingly, the association between the breadth of the upper incisors with aridity was stronger than that of the lower incisors, even though the latter is used in the calculation of the lower incisor index, with wider incisors associated with arid environments (e.g. Ojeda et al. 1999); while unclear, this may be associated with tooth-digging adaptations in fossorial rodents (e.g. Becerra et al. 2013). Other linear measurements, including the components in the calculation of the lower incisor index and the nasal index/volume, were much more weakly correlated with aridity than those in bullar dimensions.

Therefore, while there is support for general differences in overall skull morphology between desert and mesic species, this difference is contingent on the analyses conducted with a difference observed in the binary analyses (i.e. MANOVAs of desert vs. mesic rodents) only in non-phylogenetically corrected dataset, but a difference is found in all datasets with continuous bioclimatic variables (i.e. CCAs of clinal morphological variation across environmental variables) with the most consistent outcome being the association between bullar dimensions with aridity. Interestingly, other than the upper incisor width, dental characters (e.g. molar dimensions and other incisor dimensions) were not associated with aridity despite many examples of dietary specialization in desert rodents. This is perhaps explained by the fact that different desert rodents have different specializations ranging from being exclusively folivorous (some with the capacity to shave and consume halophytic plants) to exclusively granivorous, only the prior of which are associated with the evolution of “squarer” lower incisors (e.g. Ojeda et al. 1999) and neither is associated with molar hypsodonty (Williams and Kay 2001).

Conclusions

Rodents transitioned very frequently between desert and mesic habitats throughout their evolutionary history, indicating flexible habitat choice and frequent habitat switches. Despite this pattern, there is a bias towards a transition from a mesic to a desert habitat, consistent with the “evolutionary dead-end” hypothesis. It also appears that rodents colonized desert environments independently, multiple times and that the evolution of characteristically desert-adapted clades (gerbils, heteromyids, and dipodoids) did not coincide with a desert transition but occurred after the desert transition took place. Phylogenetic signal does not appear to completely account for interspecific morphological variation in rodents relative to habitat and climate. Both the relative and absolute size of the tympanic bullae is significantly greater in desert than in mesic rodents, with the size increasing with increased aridity, a result consistent with previous studies conducted in more limited scales. Similarly, there was a significant positive correlation between increased lengthening and narrowing of the nasals (and reduced nasal volume) with increased aridity, a result consistent with studies conducted on other taxa, and may reflect more lengthened, narrowed, and convoluted nasal passages that are more effective at conserving water from exhaled air. The shape of the lower incisors was not significantly associated with habitat or climate, indicating no common pattern in the evolution of this trait across desert rodent clades, perhaps due to different responses to dietary selective pressures in different deserts. Desert and mesic rodents overlap extensively in the morphospace represented by other skull characters indicating no significant difference between desert and mesic species in overall skull morphology. However, there was a significant correlation between climatic variables and most of the examined skull measurements, the strongest of which convey a pattern of increased tympanic bulla dimensions in more arid environments, confirming that bullar hypertrophy is the strongest pattern of cranial desert adaptation in rodents, and supports the theory that adaptation plays a similar role in shaping the evolution of this structure in various desert rodent clades.

CHAPTER SEVEN

MORPHOLOGICAL AND PHYLOGENETIC COMMUNITY STRUCTURE IN ECOLOGICAL ASSEMBLAGES OF DESERT RODENTS

Summary

The main objective of community ecology is to understand the mechanisms that facilitate coexistence in species assemblages. For the most part, classical studies of coexistence in desert rodent communities document a structured pattern of body size over-dispersion which is typically interpreted in terms of competition theory. However, because most of these studies were conducted in relatively small scales, depauperate systems, and are restricted to North American deserts, the generality of this pattern to other deserts or to mesic communities is yet to be determined. In this study I use the community phylogenetic approach to test the prediction that desert rodent provinces around the world are non-randomly assembled from species pools of desert regions, which in turn are non-randomly assembled from species pools of larger biogeographic regions. I test this prediction both using a composite molecular phylogeny of rodents to calculate phylogenetic structure and a skull geometric morphometric and body mass dataset to calculate morphological structure. The results indicate that desert rodent assemblages differ in community structure; the majority are not phylogenetically structured at the provincial and the regional scales, while most provinces are morphologically over-dispersed in resource acquisition traits. This pattern of non-phylogenetic structure and over-dispersion morphological structure suggests interspecific competition between distant relatives. The most diverse desert provinces consist of phylogenetically distant relatives which indicates that niche partitioning facilities coexistence in diverse assemblages. I also find a strong positive correlation between metrics of phylogenetic and morphological structure which supports the usage of phylogenies as indirect measures of niche in phylogenetic community studies of desert rodents.

Introduction

Ecologists, evolutionary biologists, and biogeographers share an interest in understanding patterns of species diversity and assembly (Harmon-Threatt and Ackerly 2013). Furthermore, the

main objective of community ecology is to understand the mechanisms that facilitate coexistence in local assemblages (i.e. community structure), or whether neutral or deterministic processes limit local assemblages to subsets of regional species pools (Cardillo 2011). Assemblages are defined here as groups of species occupying the same region, whether or not they are sympatric or locally syntopic. Traditionally, this question is addressed by determining whether species are non-randomly assembled into communities from regional species pools (lists of all species in the next-highest spatial scale) in terms of ecological traits and taxonomic composition (Webb et al. 2002; Cardillo 2011).

Webb (2000) and Webb et al. (2002) introduced a new research field known as “phylogenetic community ecology” which precipitated interest in use of phylogenies in community ecology. While this field has generally not instigated new questions, it has provided new methods to ask fundamental ecological questions, with the main advantage being that of improved estimation of species relatedness provided by phylogenies over taxonomic classifications (Cardillo 2011). Moreover, interest in using phylogenies in community ecology is also attributed to their usefulness as indirect measures of niche and overall ecology; phylogenetic proximity is often assumed to reflect ecological similarity as a consequence of phylogenetic niche conservatism (Webb et al. 2002; Stevens et al. 2012). This usefulness stems from the difficulty in quantifying the Hutchinsonian niche (Hutchinson 1959) or in determining whether enough important characters have been measured to adequately determine niche overlap (Ricklefs 2010; Stevens et al. 2012). Furthermore, while morphological traits can accurately estimate resource use, phylogenetic information can provide a more general estimate of niche that takes into account non-morphological axes of niche variation (Stevens et al. 2012).

Ecological studies that use the community phylogenetic approach start off by determining whether focal communities are significantly structured or are randomly assembled from regional species pools (i.e. neutrally assembled, Hubbell 2001). This determination is based on one of many possible null models, which subsample taxa from the regional species pool and calculate metrics of phylogenetic structure (see below) multiple times and then compare results of these “null communities” to the result of the observed community (Webb 2000; Webb et al. 2002). If focal communities are found to be significantly structured (relative to null communities) then the dominant ecological force responsible for this pattern is determined, which at small spatial scales it is usually attributed to one of two alternative forces. Phylogenetic clumping/clustering of

communities (community members are more closely related to each other than expected by chance) is usually attributed to habitat/environmental filtering which selects for species with similar niche requirements inherited from their common ancestor (Webb et al. 2002).

Conversely, phylogenetic over-dispersion/evenness of communities (community members are more distantly related to each other than expected by chance) is attributed to competitive exclusion/species sorting (Grant 1972) favoring coexistence of species with divergent niches (Webb et al. 2002).

Most phylogenetic community ecology studies are performed at small spatial scales; however, some studies have recently used this approach to investigate patterns of community assembly at biogeographical scales (e.g. carnivores, Cardillo 2011; ruminants, Cantalapiedra et al. 2013; bumble bees, Harmon-Threatt and Ackerly 2013; Australian desert vertebrates, Lanier et al. 2013), where historical processes may explain patterns of community structure better than ecological processes. For example, phylogenetic clumping at large spatial scales may be attributed to local diversification with no subsequent dispersal across biogeographic barriers; and phylogenetic over-dispersion may be attributed to colonization of species from distant origins as a consequence of community connections by favorable habitat (Cardillo 2011; Brown 2012).

The limited spatial scale of most phylogenetic community ecology studies may be attributed to the disproportionate usage of taxa with limited mobility such as plants and microbes; Vamosi et al. (2009) reviewed 24 phylogenetic community structure studies and found that 22 were conducted on taxa that cannot move freely between local assemblages (Harmon-Threatt and Ackerly 2013). Highly mobile taxa are expected to interact over much larger scales than those considered in community ecology (Cavender-Bares et al. 2009) because they are able to overcome competition more easily through dispersal and therefore may appear to be randomly assembled at small scales (Weiher et al. 2011). Therefore, in addition to historical forces, ecology may also direct community assembly at much larger spatial scales in mobile taxa than in relatively immobile taxa. For example, at large spatial scales, habitat filtering can be explained in terms of the abiotic range limits that lead to a discrepancy between fundamental and realized niches. These abiotic range limits are in turn estimated by the range of the species (Cardillo 2011). Similarly, interspecific competition can also be expanded to large spatial scale assemblages, as in studies that show that even in the absence of abiotic barriers to dispersal,

interspecific competition can lead to stable geographic range limits (e.g. Case et al. 2005; Price and Kirkpatrick 2009).

Granivorous desert rodent communities are a classic model system in the study of community assembly patterns and played a central role in the development of theories and approaches in community ecology (e.g. Bowers and Brown 1982; Kotler and Brown 1988; Brown 1989). Most of the evidence indicates that interspecific competition is the most dominant force in non-randomly structuring heteromyid communities in North American deserts (e.g. Munger and Brown 1981; Bowers and Brown 1982; Brown and Munger 1985; Heske et al. 1994). However, other mechanisms that facilitate coexistence have also been considered, including disparate microhabitat selection and temporal variation in resource abundance (Brown 1989). While North American desert rodent communities have been relatively well studied, few studies are done elsewhere. In a comparison of community structure of small desert mammals, across four continents, Kelt et al. (1996) has shown that patterns of community structure derived from studies of North American deserts (which are generally structured by interspecific competition) are not generalizable to other deserts around the world which are structured differently. This difference may be attributed to the investigated traits (e.g. Leibold 1998), which mostly dealt with body mass and locomotion; which while shown to be important in structuring granivorous desert rodent communities in North America, may not play a dominant role in mediating interspecific competition in the deserts of Africa, Asia, and Australia (Kelt et al. 1996; Weiher and Keddy 2001). Because other deserts include much less granivorous rodent species, coexistence may be facilitated more by dietary differences and other mechanisms, than differences in body mass and locomotion (Kelt et al. 1996; Weiher and Keddy 2001).

So far, only one study uses the phylogenetic community ecology approach to study desert rodent community assembly. Stevens et al. (2012) examined the pattern in phylogenetic community structure in rodent communities in the central Mojave Desert and found that communities in general are over-dispersed in less productive habitats and clumped in more productive habitats. This pattern is interpreted in terms of ‘diversity begets diversity’ facilitated by packing ecologically similar species in more diverse habitats (Brown 2012). This result is concordant with studies that use non-phylogenetic approaches and find a positive correlation between species richness and environmental heterogeneity in desert rodent communities (e.g. Rosenzweig and Winakur 1969; M’Closkey 1976, 1978; Kotler and Brown 1998).

In the present study, I conduct the first global comparative test of phylogenetic community structure of desert rodent assemblages at two spatially nested scales (regional and subregional (provincial)). Regions are typically continents or major landmasses separated from other regions by sea water, and provinces are contiguous desert habitats, typically named deserts characterized by distinctive flora. I also test morphological structure (i.e. using the same methods and metrics of phylogenetic community ecology on morphological distance between species based on ecologically relevant traits; see methods) in different datasets with expected differences in association with resource acquisition and abiotic tolerance, which therefore may show conflicting patterns of community structure (i.e. clumping of traits related to abiotic tolerance and over-dispersion in traits related to resource acquisition) (e.g. Davies et al. 2012; Merwin et al. 2012). I also directly compare phylogenetic and morphological community structure, a topic of recent interest in this field (e.g. Merwin et al. 2012; Harmon-Threatt and Ackerly 2013). Since both phylogenies and morphological traits are used as surrogate measures of niche, concordance between phylogenetic and morphological structure is expected when ecological traits are phylogenetically conserved (i.e. habitat filtering leads to both phylogenetic and morphological clustering, and competitive exclusion leads to both phylogenetic and morphological over-dispersion) (Webb et al. 2002). However, discordance between these two niche measures is expected when ecological traits are phylogenetically convergent among distant relatives that share a habitat (Webb et al. 2002). In these cases habitat filtering may lead to phylogenetic over-dispersion and morphological clustering, while competitive exclusion may lead to a phylogenetically random and a morphologically over-dispersed pattern (Webb et al. 2002).

I expect discordance between phylogenetic and morphological community structure in desert rodent communities because adaptive convergence is very common in desert rodents, where aridity led to the evolution of various morphological adaptations to water and energy conservation (Mares 1975, 1976; Louw and Seely 1982; Sowell 2001; Ward 2009). These convergences are observed both within and among communities in different continents. For example, both jerboas and gerbils in Eurasia, hopping mice in Australia, and North American kangaroo rats, have convergently evolved small bodies, elongated hindlimbs, shortened forelimbs, long tails, large bullae, long and complex nasal passages, high basal metabolic rate, bipedal/ricochetal saltation, burrowing behavior and granivorous diet (Hart 1971; Berman 1985;

Rocha 1995; Diaz and Ojeda 1999; Diaz 2001; Diaz et al. 2001; Bozinovic and Gallardo 2005; Bozinovic et al. 2007; Rocha et al. 2007; Sassi et al. 2007).

Testing phylogenetic community structure in desert rodent communities is advantageous because rodents are the most diverse mammal group both in and out of deserts, and are found in all continents (in at least one desert in all continents) with the exception of Antarctica (Wilson and Reeder 2005). Furthermore, this research is precipitated by the recent publication of a molecular phylogeny of rodents (Fabre et al. 2012) and the accumulation of species range data and species lists in various assemblages (e.g. Shenbrot et al. 1999; International Union for Conservation of Nature Red List (IUCN) 2013).

The primary purpose of this study is to test the prediction that (1) desert rodent species are assembled non-randomly from regional species pools in the following manner. I expect that at (a) small spatial scales, due to competition for limited resources and because rodents are mobile, interspecific competition/competitive exclusion will be the predominate ecological force structuring the assemblages, leading to a pattern of both phylogenetic and morphological over-dispersion; and at (b) large spatial scales, due to similar extreme abiotic environmental selective pressures experienced in desert ecosystems, environmental filtering will be the strongest ecological force structuring the assemblages, leading to a pattern of both phylogenetic and morphological clumping. I test these predictions by examining community assembly at two spatially nested scales: (a) provincial assemblages (e.g. Sonoran, Chihuahuan, and Great Basin desert provinces) within regional source pools (e.g. Nearctic desert region); (b) regional assemblages (e.g. Nearctic desert region) within a biogeographic source pools (e.g. North American biogeographic region). I also test the predictions that (2) increased taxonomic diversity in assemblages is correlated with increased mean phylogenetic distance (i.e. more diverse communities are composed of phylogenetically distant relatives that as a consequence compete less); and that (3) phylogenetic and morphological community structure (based on estimates of average phylogenetic and morphological distance) in desert rodent assemblages are correlated, which is expected if both these indices are adequate indicators of niche.

Materials and Methods

Phylogenetic Data

I estimate metrics of phylogenetic structure using community subtrees extracted from a composite chronogram of rodents (see chapter 6) that contains 2,357 rodent species (2,414 OTUs) based on Fabre et al. (2012) and Steppan et al. (in prep). Details on generating this chronogram are discussed elsewhere (chapter 6). A pruned 289 species tree of desert rodents extracted from the aforementioned chronogram is shown in Figure 7.1.

Assemblages and Biogeographic Regions

Assemblages refer to species co-occurring in the same region (place). The terms communities and species pools were used in similar fashion to the definitions in Webb et al. (2002). A community is an assemblage of species co-occurring at a spatial scale where species could potentially disperse within a few generations (Webb et al. 2002). A regional species pool is the list of all species in an area at a spatial scale that is higher than the one under consideration (Webb et al. 2002). Species were assigned to desert assemblages based on Shenbrot et al.'s (1999) species lists which in turn are based on original distribution data that includes information from Russian monographs, especially for Eurasian desert regions. Original species lists were restricted to desert adaptive species with >50% of their range occurring in an assemblage, however, since non-desert adaptive species with <50% of their range occurring in an assemblage can still interact with other species in that assemblage, I amended original species lists to include non-desert adaptive species as well as species with <50% of their range occurring in an assemblage. This was done by using species distribution maps from IUCN (2013) to add species with significant range overlap with the desert assemblages delineated by Shenbrot et al. (1999) to the original species lists. Species with narrow ranges and/or are isolated on islands (e.g. *Peromyscus sejugis* and *Peromyscus stephani*) were excluded because their interaction with other species in those assemblages are minimal; this process led to the inclusion of 73 additional species to one or more of the assemblage species lists that were described by Shenbrot et al. (1999). I sampled 17 out of the 29 desert rodent assemblages defined by Shenbrot et al. (1999) (Figure 7.2). To maintain the independence of the sample, subregions were sampled in such a way as to preserve the largest set of non-overlapping assemblages. If provinces overlap

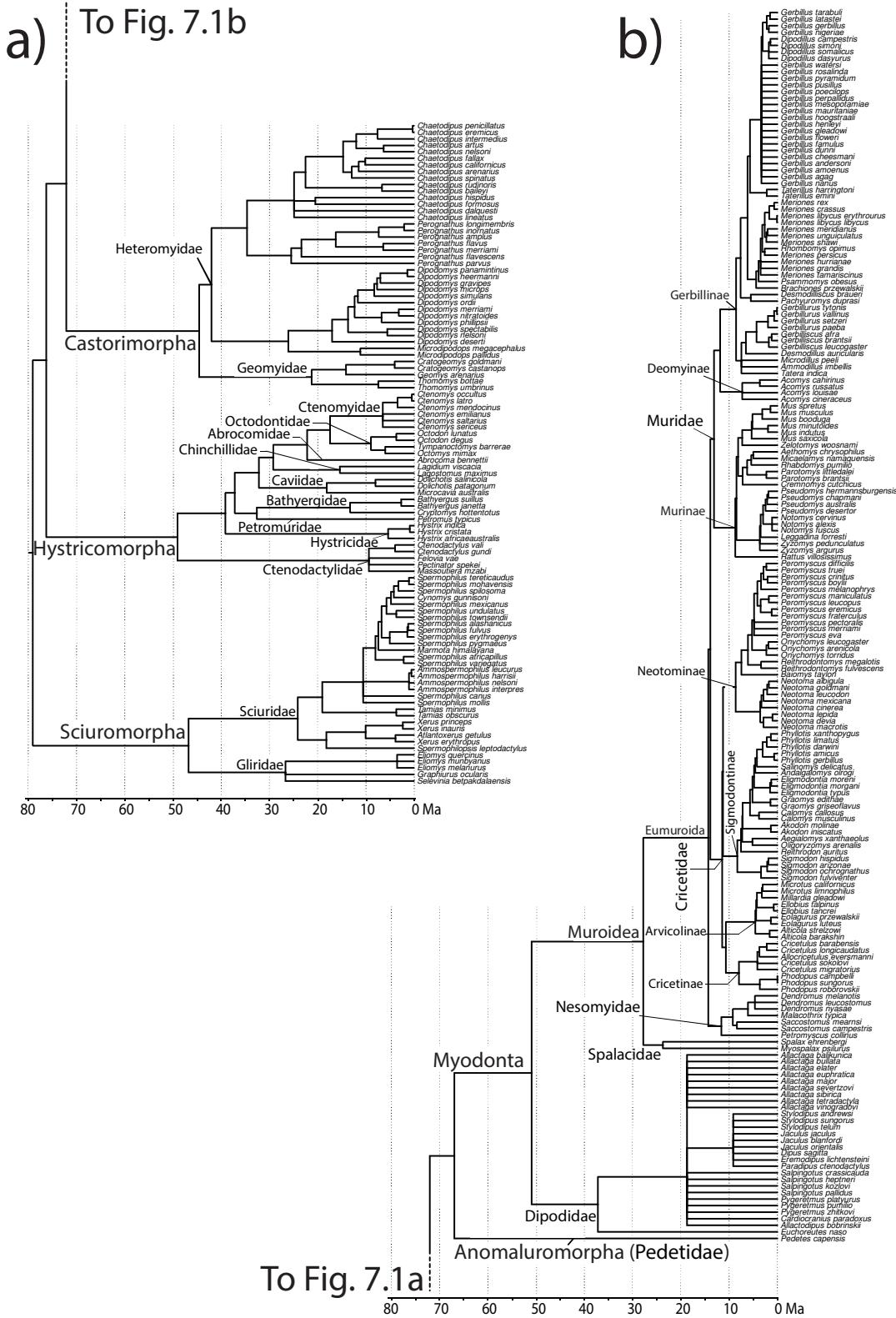


Figure 7.1. Composite chronogram of 289 desert rodent species found in one or more of the 17 sampled desert rodent provinces. This chronogram is extracted from a larger phylogeny modified from Fabre et al. (2012) and Steppan et al. (in prep). Major taxonomic groups are indicated and the tree is partitioned by provinces/regions in Appendix Figures F.2, F.3, F.4, and F.5.

significantly, then the larger province is sampled and the smaller one is omitted. In a few cases where all provinces in a realm have considerable overlap, then the realm that subsumes these provinces was sampled instead of the provinces. Since subregional biogeographic qualifiers such as ‘province’ and ‘realm’ are not correlated with the spatial size or diversity of assemblages across continents (e.g. the Atacama realm is identical to the Atacama province and the central Saharan province is much larger than the Neotropic region), I refer to all subregional assemblages of potentially interacting species (implied by range overlap) as provinces.

The regional species pools for the 17 desert rodent provinces were determined by assigning them to one of five desert regions as defined by Shenbrot et al. (1999) which correspond to continents/biogeographic regions: (1) North American provinces grouped in the Nearctic region; (2) South American provinces grouped in the Neotropic region; (3) single Australian province grouped in the Australian region; (4) single South African province grouped in the Paleotropic region; (5) all Eurasian provinces grouped in the Palaearctic region (Appendix Figure F.1). The biogeographic/continental species pools for the five desert regions were determined by assigning all 2,414 rodent OTUs in the composite rodent phylogeny to one or more of seven biogeographic regions that correspond largely to conventional realms and previous studies (e.g. Schenk et al. 2013; Appendix Figure B.1, chapter 3). Following Schenk et al. (2013), North America (450 species) includes Central America southward to the Panamanian suture; South America (634 species) south of the Panamanian suture; Eurasia (444 species) includes the Middle East and North Africa; Southeast Asia (346 species) from southern India to the Philippines and Sulawesi; Sahul (164 species) includes Australia and New Guinea; Africa (413 species) south of the Sahara; and Madagascar (25 species). IUCN (2013) distribution data was used to assign species to biogeographic regions. After the two biogeographic regions with no deserts (Southeast Asia and Madagascar) were dropped, the five remaining biogeographic regions correspond with the desert regions in Shenbrot et al. (1999) (Palaearctic, Paleotropic, Australian, Nearctic, and Neotropic) with the exception that the horn of Africa is included in the Palearctic desert region (which otherwise corresponds with Eurasia) and not in sub-Saharan Africa due to its greater proximity to other deserts in that region. I adopt this scheme by including the horn of Africa in Eurasia (Appendix Figures F.6, F.7, F.8, F.9, and F.10).

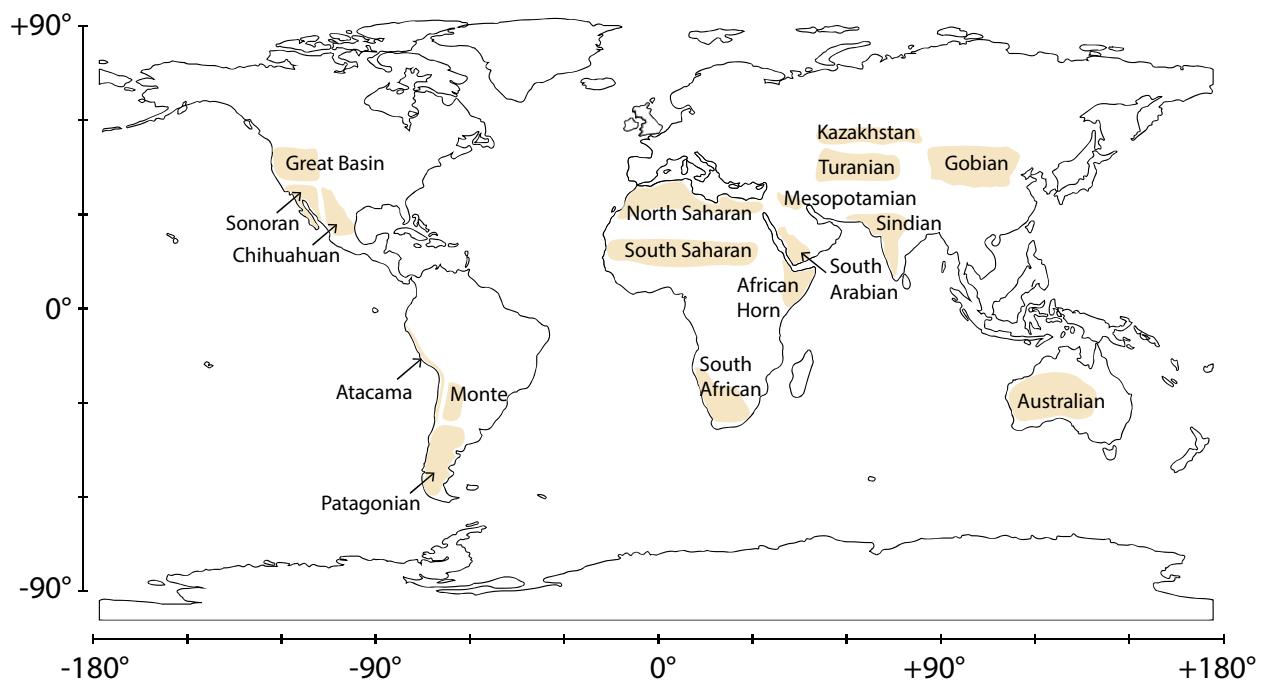


Figure 7.2. Map of 17 desert rodent provinces defined in Shenbrot et al. (1999). Provinces are not drawn to scale and are defined based on the distribution of rodent species, not the full extent of the deserts, and does not include all deserts (e.g. the central Saharan province is not sampled because it overlaps significantly with the North and South Saharan provinces).

Morphological Data Collection

Skull morphology was quantified in 1-9 specimens of 234 desert rodent species for a total of 956 specimens and an average of 4 specimens per species (Appendix Table A.4, chapter 2). Multiple specimens and equal representation of males and females were examined when possible to account for intraspecific variation and sexual dimorphism by calculating species averages (see chapter 2). I photographed skulls of voucher specimens of most available desert species in the American Museum of Natural History (AMNH), The Field Museum (FMNH), the Museum of Vertebrate Zoology (MVZ), the Smithsonian Institution National Museum of Natural History (USNM), the Florida Museum of Natural History (UF), Laboratorio de Citogenetica Mamiferos, Facultad de Medicina, Universidad de Chile (LCM), and the Oklahoma Museum of Natural History (OMNH). Only wild caught adult individuals were chosen with adult status diagnosed by the basioccipital–basisphenoid epiphyseal fusion as in Robertson and Shadle (1954) and Samuels (2009) as well as the complete eruption of 3rd molars which is assessed by the fact that it has reached the occlusal surface (Steppan 1997) and by examining the size of the associated skins.

Cranial landmarks were digitized on photographs captured with a Nikon D3200 digital SLR camera using a Nikon 40mm f/2.8G AF-S DX Micro-Nikkor Lens (Nikon, Tokyo, Japan) at 24 megapixels (resolution = 6016 x 4000; JPEG) in a standardized manner (see chapter 2). Five photographs were taken per individual to capture all the relevant orientations for landmark digitization with a scale bar included in each photograph. Landmarks were digitized on the left side of the skull, except when the left side of the skull is damaged then the right side is used instead and reflected. Landmark digitization was conducted in Tpsdig v2.16 (Rohlf 2010).

Body mass data was collected for all available rodent species (1,411 species) in the 2,414 rodent OTU tree using the PanTHERIA database (Jones et al. 2009). Body mass for species with no data available (1,003 species) was estimated using ancestral state reconstruction as implemented in the Picante library (Kembel et al. 2010) in R (R Development Core Team 2013). Body mass data from the five sampled biogeographic regions with deserts was retained and log transformed prior morphological structure analyses.

Description of Landmarks

At the provincial scale, morphological structure is based on landmarks digitized from the aforementioned photographs. Landmarks were chosen in such a way as to cover most of the important elements in the cranium and jaw and are expected to be associated with ecology. Chosen landmarks come from various literature sources including: Samuels (2009), Colangelo et al. (2010), Hautier et al. (2011), Yazdi et al. (2011), Álvarez and Pérez (2013), and Casanovas-Vilar and Dam (2013); as well as standard landmarks collected on mammalian skulls and (i.e. end points of standard caliper measurements). Some of these landmarks appeared in the 3D dataset described in chapter 2. Numbers preceding landmarks described below match Figure 7.3.

Ventral cranial landmarks. (1) Anterior-medial tip of suture between nasals in front of incisors. (2) Lateral edge of incisor junction with the premaxilla. (3) Inferior edge of infraorbital foramen. (4) Frontal notch of the zygomatic arch (anterior-most insertion point). (5) Lateral-most of zygomatic arch (zygomatic breadth measurement). (6) Posterior-most of the zygomatic process notch curvature (posterior-most insertion point). (7) Anterior-lateral edge of the external auditory meatus. (8) Posterior-most of junction between tympanic and occipital (posterior extremity of bulla). (9) Lateral-posterior most of occipital condyle. (10) Anterior-most edge of tympanic bulla at lateral junction with pterygoid process. (11) Posterior edge of the molar tooth

row alveolus. (12) Lateral junction between the first and second molars. (13) Anterior edge of the molar tooth row alveolus. (14) Anterior extreme of incisive foramen. (15) Posterior extreme of incisive foramen. (16) Anterior extreme of the greater palatine foramen. (17) Posterior extreme of the greater palatine foramen. (18) Posterior-midsagittal extreme of the palate (or spine) at the anterior limit of the mesopterygoid fossa. (19) Anterior-midsagittal margin of foramen magnum. (20) Posterior-midsagittal margin of foramen magnum.

Lateral cranial landmarks. (1) Anterior-most edge of the nasals along the midsagittal. (2) Anterior tip of the suture between the nasal and premaxilla. (3) Ventral most of the infraorbital foramen. (4) Dorsal most of infraorbital foramen. (5) Suture between the lacrimal and zygomatic plate. (6) Junction between parietal-squamosal suture with frontal-squamosal suture. (7) Intersection between parietal-occipital suture and suprameatal triangle. (8) Posterior-most of the occipital condyle. (9) Anterior-most of paroccipital process. (10) Anterior-most of stylomastoid suture posterior of the auditory meatus. (11) Posterior most of suture between root of zygomatic arch and jugal. (12) Posterior-most of the optic canal. (13) Posterior edge of the molar tooth row alveolus. (14) Anterior edge of the molar tooth row alveolus. (15) Junction point between the posterior of the incisor and the premaxilla. (16) Distal extreme of the incisor. (17) Point of insertion of anterior-medial edge of the incisor into the premaxilla.

Dorsal cranial landmarks. (1) Anterior-most tip of inter-nasal suture along the midsagittal. (2) Anterior tip of the nasal-premaxilla suture. (3) Anterior edge of suture between the premaxilla and the maxilla in front of the zygomatic plate. (4) Posterior tip of maxillary-frontal suture lateral to the zygomatic plate and the lacrimal. (5) Anterior notch of the zygomatic arch. (6) Posterior zygomatic notch at the root of the arch. (7) Posterior-most extreme of the zygomatic arch at the root. (8) Junction between the parietal-interparietal and interparietal-occipital sutures with the squamosal. (9) Posterior extreme of the occipital at the midline. (10) Medial-most of the suture between the interparietal and the occipital near occipital tip. (11) Junction between inter-parietal suture and parietal-interparietal suture. (12) Junction between the frontal-parietal suture and the inter-parietal suture. (13) Junction between the parietal-squamosal suture and frontal-squamosal suture. (14) Narrowest breadth of the frontal curvature at the inter-orbital constriction. (15) Junction between the inter-nasal and frontal sutures.

Occlusal mandible landmarks. (1) Antero-medial edge of the incisor. (2) Postero-medial edge of the incisor alveolus. (3) Anterior edge of the molar tooth row alveolus. (4)

Posterior edge of the molar tooth row alveolus. (5) Anterior edge of the base of the coronoid process. (6) Distal tip of coronoid process. (7) Maximum curvature of the mandibular notch, posterior of the base of the coronoid. (8) Superior-medial tip of the condyloid process.

Lateral mandible landmarks. (1) Anterior-distal most edge of the incisor. (2) Antero-dorsal edge of the incisor alveolus. (3) Point of maximum curvature of the diastema. (4) Anterior edge of the molar tooth row alveolus. (5) Anterior edge of the base of coronoid process. (6) Distal tip of coronoid process. (7) Maximum curvature of the mandibular notch, posterior of the base of the coronoid. (8) Anterior edge of condyloid process. (9) Posterior edge of condyloid process. (10) Point of maximum curvature between condyloid process and angular process. (11) Posterior most tip of angular process. (12) Ventral most tip of angular process. (13) Maximum curvature at ventral boarder of the ramus. (14) Outer posterior extreme of mandibular symphysis. (15) Antero-ventral edge of the incisor alveolus.

Geometric Morphometric Data Process

A total of 302 out of the 956 digitized specimens had at least one missing landmark (Appendix Table A.5, chapter 2) as a consequence of damaged material or being unidentifiable in the particular species. These missing landmark coordinates were estimated in the Geomorph library (Adams and Castillo 2013) in R which conducts a thin-plate spline interpolation using landmarks common to complete specimens and specimens with missing data (Adams and Castillo 2013), using the same process described previously for the 3D dataset (see chapter 2). A list of all target specimens (with at least 1 missing landmark) and the reference specimens used to estimate their missing landmarks is found in Appendix Table A.5 (chapter 2).

A generalized procrustes analysis (GPA) was conducted on the complete dataset to obtain geometric morphometric shape variables (Rohlf and Slice 1990) by translating coordinate configurations to a common centroid and by scaling them to unit centroid size and rotating them in order to minimize the sum of squared distances between the corresponding landmarks (Zelditch et al. 2004). The output of GPA is a new set of procrustes coordinates that describe size-independent morphological shape differences within the sample.

For each of the five morphological datasets, the following analyses were conducted separately. An initial GPA was conducted in order to align specimens prior to estimating average species shapes (procrustes coordinates) using the method described in Claude (2008) which



Figure 7.3. Positions of the cranial and mandibular landmarks used to calculate morphological structure metrics at the provincial scale shown on the (a) ventral cranial, (b) lateral cranial, (c) dorsal cranial, (d), occlusal mandibular, and (e) lateral mandibular views of the Mexican woodrat (*Neotoma mexicana*; USNM 127314).

calculates the average coordinate positions of aligned specimens as implemented in the Geomorph library in R. This in turn outputs average shape (procrustes coordinates) for each species which are then subjected to another GPA to re-align and output a new set of procrustes coordinates that describe interspecific size-independent morphological shape variation.

Out of the 289 species in the 17 sampled desert provinces, 55 species have no morphological data collected. Omitting these species from the analyses may underestimate the extent of morphological structure in the community when compared to phylogenetic structure. Therefore, morphological data for these species was estimated prior to the morphological structure analyses by using ancestral state reconstruction as implemented in the Picante library in R. The pairwise Euclidean distance between all species based on the five morphological shape datasets was calculated separately and used to estimate morphological structure in desert rodent provinces (see below).

Estimation of Phylogenetic and Morphological Structure

Phylogenetic structure of desert rodent assemblages was estimated using the Picante library in R. Ten subtrees were extracted from the 2,414 OTU chronogram described above, one for each of the five desert regions (Palaearctic, Palaeotropic, Australian, Nearctic, and Neotropic; Appendix Figure F.5) and one for each of the five biogeographic regions (North America, South America, Eurasia, Africa, and Sahul; Appendix Figures F.6, F.7, F.8, F.9, and F.10) and were used as the regional species pool for the provincial scale analyses (Appendix Figures F.2, F.3, F.4) and the desert regional scale analyses respectively.

For each of the 17 desert rodent provinces and the five desert regions, the mean phylogenetic distance between all pairwise combinations of taxa (mean pairwise distance, MPD) and the mean phylogenetic distance between each taxon and its closest relative (mean nearest taxon distance, MNTD) was calculated (Webb 2000; Webb et al. 2002). The standardized effect sizes (SES) of the MPD and MNTD were calculated for each assemblage using all the available null models; however, because the results were largely concordant, I only show the results for the ‘phylogeny pool’ null community model, which randomizes the community data matrix by drawing species randomly with equal probability from the regional species pool (i.e. from the phylogeny or morphological distance matrix) (Kembel et al. 2010).

SES are measures of tree-wide (SES-MPD) or branch-tip (SES-MNTD) phylogenetic clumping or over-dispersion with a negative value indicating clumping and a positive value indicating over-dispersion, relative to null communities (Kembel et al. 2010). The SES values (standardized effect size of MPD or MNTD relative to the null communities) are calculated as follows (Kembel et al. 2010):

$$SES = \frac{observed\ MPD\ or\ MNTD - mean\ MPD\ or\ MNTD\ in\ null\ communities}{standard\ deviation\ of\ MPD\ or\ MNTD\ in\ null\ communities}$$

The statistical significance of the SES values was calculated by comparing the observed data to data generated from a sample of 1,000 simulated null assemblages drawn from regional species pools (Z values, calculated as the difference between the observed distance metric in the community and the mean of the distance metric in the 1,000 null communities generated by randomizations divided by the standard deviation of the distance metric in the null communities; Kembel et al. 2010). P-values of the observed distance metric versus the null communities were calculated as the rank of the observed distance metric vs. null communities divided by the number of randomizations +1 (=1,001) (Kembel et al. 2010). Significantly clustered assemblages were those with SES values ≤ -1.645 ($\alpha = 0.05$) and significantly over-dispersed assemblages were those with SES values ≥ 1.645 ($p \geq 0.95$).

The SES mean pairwise distance (SES-MPD) and the SES mean nearest trait distance (SES-MNTD), the morphological equivalents of the phylogenetic metrics described above, were also calculated for each assemblage using the same methods described above, while substituting the phylogenetic distance with the Euclidean morphological distance between taxa. At the provincial scale, these metrics were calculated using the 5 morphological (shape) datasets, whereas in the regional scale, these metrics were calculated using the log body mass dataset.

Results

Community Structure at the Provincial Scale

Only three out of the 15 desert provinces were significantly phylogenetically structured, all of which were clumped (negative SES-MPD and/or SES-MNTD values): the North Saharan

province (Table 7.1; SES-MNTD = -1.742, p = 0.036*), the Sindian province (Table 7.1; SES-MPD = -2.081, p = 0.025*), and the Chihuahuan province (Table 7.1; SES-MPD = -3.018, p = 0.009*; SES-MNTD = -2.546, p = 0.007*). The phylogenetically over-dispersed provinces (positive SES-MPD and/or SES-MNTD values) were all non-significant (Table 7.1).

Out of the 15 desert rodent provinces, 11 were significantly morphologically structured in at least one region of the skull (Table 7.2; Table 7.3). Significant clumping in cranial morphology occurs in the South Arabian province (Table 7.2; lateral cranium, SES-MPD = -1.668, p = 0.048*), the Sindian province (Table 7.2; lateral cranium, SES-MPD = -1.757, p = 0.041*), the African Horn province (Table 7.2; lateral cranium, SES-MPD = -2.299, p = 0.013*; lateral cranium, SES-MNTD = -1.819, p = 0.030*), and the Chihuahuan province (Table 7.2; dorsal cranium, SES-MPD = -1.784, p = 0.037*; dorsal cranium, SES-MNTD = -1.639, p = 0.047*). Significant clumping in mandibular morphology occurs in the Turanian province (Table 7.3; lateral mandible, SES-MNTD = -1.570, p = 0.042*), the Kazakhstan province (Table 7.3; lateral mandible, SES-MNTD = -1.581, p = 0.036*), and the Chihuahuan province (Table 7.3; lateral mandible, SES-MNTD = -1.989, p = 0.023*).

Significant over-dispersion in cranial morphology occurs in the Turanian province (Table 7.2; dorsal cranium, SES-MPD = 2.340, p = 0.985*; lateral cranium, SES-MPD = 2.003, p = 0.976*; ventral cranium, SES-MPD = 1.823, p = 0.967*), the Kazakhstan province (Table 7.2; dorsal cranium, SES-MPD = 2.051, p = 0.975*; lateral cranium, SES-MPD = 2.143, p = 0.988*; ventral cranium, SES-MPD = 2.076, p = 0.984*), the Gobian province (Table 7.2; dorsal cranium, SES-MPD = 1.720, p = 0.955*), the Great Basin province (Table 7.2; ventral cranium, SES-MPD = 2.047, p = 0.986*), the Sonoran province (Table 7.2; dorsal cranium, SES-MNTD = 2.505, p = 0.993*; lateral cranium, SES-MNTD = 2.113, p = 0.980*; ventral cranium, SES-MNTD = 1.696, p = 0.952*), and the Patagonian province (Table 7.2; dorsal cranium, SES-MPD = 1.979, p = 0.995*; dorsal cranium, SES-MNTD = 1.830, p = 0.967*). Significant over-dispersion in mandibular morphology is found in the Sonoran province (Table 7.3; lateral mandible, SES-MNTD = 2.136, p = 0.986*), the Chihuahuan province (Table 7.3; lateral mandible, SES-MPD = 1.644, p = 0.962*; occlusal mandible, SES-MPD = 2.268, p = 0.994*), the Monte province (Table 7.3; occlusal mandible, SES-MPD = 1.586, p = 0.958*), and the Patagonian province (Table 7.3; occlusal mandible, SES-MPD = 2.047, p = 0.994*; occlusal mandible, SES-MNTD = 2.094, p = 0.987*). The Chihuahuan province is the only case where

results from SES-MNTD disagreed with SES-MPD; lateral mandible SES-MNTD was significantly clumped and SES-MPD was significantly over-dispersed.

Community Structure at the Regional Scale

Only two out of the five desert regions were significantly phylogenetically structured: the Neotropic region exhibited a clumped pattern (Table 7.4; SES-MNTD = -1.757, p = 0.019*) and the Palearctic region showed an over-dispersed pattern (Table 7.4; SES-MNTD = 2.084, p = 0.980*). Similarly, only two out of the five desert regions were significant morphologically structured in body mass: the Nearctic region showed a clumped pattern (Table 7.4; SES-MPD = -1.707, p = 0.045*; SES-MNTD = -1.701, p = 0.032*) and the Paleotropic region was over-dispersed (Table 7.4; SES-MPD = 2.696, p = 0.993*; SES-MNTD = 2.019, p = 0.958*).

Table 7.1. Phylogenetic structure metrics for 15 desert rodent provinces in 3 desert regions using the ‘phylogeny pool’ null model. Species number in each province and desert region are also indicated. Z and P indicate the standardized effect size and the p-value of MPD/MNTD vs. null communities respectively. $Z \geq 1.645$ ($p \geq 0.95$) indicate phylogenetic evenness; $Z \leq -1.645$ ($p \leq 0.05$) indicate phylogenetic clustering. Significantly structured provinces are italicized. The Australian and Palaeotropic deserts were omitted because the species lists in the regional species pools are equivalent to species lists of the provinces in Shenbrot et al. (1999).

Diversity	SES-MPD		SES-MNTD	
	Z	P	Z	P
Palearctic region	131			
<i>North Saharan</i>	32	-0.070	0.435	<i>-1.742</i> 0.036
<i>South Saharan</i>	19	-0.561	0.289	0.157 0.552
<i>South Arabian</i>	14	-1.018	0.154	0.902 0.782
<i>Mesopotamian</i>	14	-0.391	0.351	0.898 0.784
<i>Sindian</i>	11	<i>-2.081</i>	0.025	-0.910 0.191
<i>Turanian</i>	20	1.219	0.901	0.284 0.607
<i>Kazakhstan</i>	30	1.414	0.919	0.291 0.604
<i>Gobian</i>	34	-0.191	0.416	<i>-0.722</i> 0.245
<i>African Horn</i>	15	-0.912	0.186	0.461 0.682
Nearctic region	88			
<i>Great Basin</i>	26	0.525	0.635	1.109 0.862
<i>Sonoran</i>	59	-0.307	0.339	<i>-0.808</i> 0.213
<i>Chihuahuan</i>	47	<i>-3.018</i>	0.009	<i>-2.546</i> 0.007
Neotropic region	35			

Table 7.1—continued.

	Diversity	SES-MPD		SES-MNTD	
		Z	P	Z	P
Atacama	11	-0.410	0.184	-1.052	0.142
Monte	22	0.448	0.612	-0.549	0.282
Patagonian	19	0.836	0.816	0.079	0.503

Table 7.2. Cranial morphological structure metrics for 15 desert rodent provinces in 3 desert regions using the ‘phylogeny pool’ null model. See legend of Table 7.1 for more information.

	Dorsal cranium				Lateral cranium				Ventral cranium			
	SES-MPD		SES-MNTD		SES-MPD		SES-MNTD		SES-MPD		SES-MNTD	
	Z	P	Z	P	Z	P	Z	P	Z	P	Z	P
Palearctic region												
North Saharan	-0.612	0.291	-0.676	0.268	-0.309	0.377	0.411	0.661	-1.467	0.084	-0.577	0.281
South Saharan	0.041	0.517	0.361	0.675	-0.112	0.450	0.430	0.689	-0.515	0.296	-0.007	0.510
<i>South Arabian</i>	-0.717	0.264	-0.085	0.490	-1.668	0.048	-0.765	0.226	-1.332	0.097	-0.510	0.308
Mesopotamian	-0.175	0.451	0.657	0.750	-0.643	0.253	0.257	0.623	-0.429	0.345	0.443	0.666
<i>Sindian</i>	-0.912	0.192	-0.193	0.467	-1.757	0.041	-1.319	0.090	-1.021	0.152	-0.570	0.297
<i>Turanian</i>	2.340	0.985	1.321	0.902	2.003	0.976	-0.328	0.370	1.823	0.967	-0.280	0.395
<i>Kazakhstan</i>	2.051	0.975	0.403	0.652	2.143	0.988	0.143	0.550	2.076	0.984	-0.586	0.286
<i>Gobian</i>	1.720	0.955	0.792	0.779	0.350	0.636	-0.686	0.246	0.522	0.696	-0.519	0.311
African Horn	-1.225	0.100	-0.796	0.222	-2.299	0.013	-1.819	0.030	-1.401	0.090	-1.329	0.109
Nearctic region												
<i>Great Basin</i>	0.970	0.829	0.287	0.622	-0.201	0.408	0.249	0.583	2.047	0.986	0.463	0.678
<i>Sonoran</i>	1.170	0.862	2.505	0.993	0.563	0.713	2.113	0.980	-0.473	0.289	1.696	0.952
<i>Chihuahuan</i>	-1.784	0.037	-1.639	0.047	-1.011	0.152	-1.570	0.057	-1.104	0.152	-1.479	0.078
Neotropic region												
Atacama	-1.001	0.169	-1.117	0.141	-0.783	0.227	-0.985	0.160	-1.022	0.152	-0.932	0.186
Monte	1.199	0.883	1.131	0.876	1.405	0.938	1.316	0.905	0.517	0.657	1.259	0.904
Patagonian	1.979	0.995	1.830	0.967	1.336	0.922	1.105	0.863	1.071	0.835	1.306	0.891

Table 7.3. Mandibular morphological structure metrics for 15 desert rodent provinces in 3 desert regions using the ‘phylogeny pool’ null model. See legend of Table 7.1 for more information.

	Lateral mandible				Occlusal mandible			
	SES-MPD		SES-MNTD		SES-MPD		SES-MNTD	
	Z	P	Z	P	Z	P	Z	P
Palearctic region								
North Saharan	-0.487	0.359	-0.725	0.247	0.504	0.703	0.604	0.722
South Saharan	-0.720	0.215	-0.582	0.282	-0.383	0.362	0.621	0.759
<i>South Arabian</i>	-1.078	0.089	-0.130	0.496	-0.946	0.162	-0.080	0.500
Mesopotamian	-0.004	0.584	0.584	0.764	-0.201	0.443	0.369	0.673
<i>Sindian</i>	-0.908	0.144	0.127	0.620	-1.141	0.094	-0.351	0.362
<i>Turanian</i>	-0.209	0.486	-1.570	0.042	-0.257	0.428	-0.980	0.159
<i>Kazakhstan</i>	-0.191	0.502	-1.581	0.036	-0.577	0.293	-1.289	0.103
<i>Gobian</i>	-0.818	0.216	-1.110	0.128	-1.346	0.091	-0.962	0.169
African Horn	0.659	0.839	0.156	0.624	-0.453	0.332	-0.445	0.344
Nearctic region								
Great Basin	-0.860	0.208	-0.311	0.381	-0.229	0.428	-0.027	0.493

Table 7.3-continued.

	Lateral mandible				Occlusal mandible			
	SES-MPD		SES-MNTD		SES-MPD		SES-MNTD	
	Z	P	Z	P	Z	P	Z	P
<i>Sonoran</i>	0.201	0.556	2.136	0.986	-1.077	0.145	0.440	0.660
<i>Chihuahuan</i>	1.644	0.962	-1.989	0.023	2.268	0.994	-0.812	0.218
Neotropic region								
<i>Atacama</i>	1.000	0.834	0.212	0.576	-0.195	0.456	0.064	0.530
<i>Monte</i>	0.433	0.651	0.965	0.825	1.586	0.958	1.441	0.924
<i>Patagonian</i>	1.247	0.889	1.500	0.934	2.047	0.994	2.094	0.987

Table 7.4. Phylogenetic and morphological structure metrics for 5 desert regions within 5 biogeographic regions using the ‘phylogeny pool’ model. See Table 7.1 for more information.

Regional (biogeographic) diversity	Phylogenetic				Morphological				
	SES-MPD		SES-MNTD		SES-MPD		SES-MNTD		
	Z	P	Z	P	Z	P	Z	P	
<i>Palearctic (Eurasia)</i>	131 (444)	0.340	0.633	2.084	0.980	-0.924	0.182	0.320	0.608
<i>Nearctic (North America)</i>	88 (450)	1.044	0.861	-1.461	0.068	-1.707	0.045	-1.701	0.032
<i>Neotropic (South America)</i>	35 (634)	0.472	0.644	-1.757	0.019	1.486	0.931	-0.239	0.438
<i>Australian (Sahul)</i>	12 (164)	-0.851	0.199	0.380	0.646	-1.533	0.061	0.270	0.622
<i>Palaeotropic (Africa)</i>	31 (413)	1.195	0.880	0.118	0.546	2.696	0.993	2.019	0.958

Association between Phylogenetic Structure with Morphological Structure and Diversity

The observed mean phylogenetic distance between the desert province species is significantly positively correlated with log species richness for the MPD metric (Figure 7.4a; $R^2 = 0.24$, $p = 0.0276^*$) but not the MNTD metric (Figure 7.4a; $R^2 = 0.02$, $p = 0.401$). For both MPD and MNTD, I found a significant positive correlation between the mean phylogenetic distance and mean morphological distance based on the dorsal cranium (Figure 7.4b; MPD, $R^2 = 0.65$, $p < 0.0001^*$; MNTD, $R^2 = 0.66$, $p < 0.0001^*$), the lateral cranium (Figure 7.4c; MPD, $R^2 = 0.75$, $p < 0.0001^*$; MNTD, $R^2 = 0.51$, $p = 0.0008^*$), the ventral cranium (Figure 7.4d; MPD, $R^2 = 0.87$, $p < 0.0001^*$; MNTD, $R^2 = 0.53$, $p = 0.0005^*$), and the lateral mandible (Figure 7.4e; MPD, $R^2 = 0.42$, $p = 0.0030^*$; MNTD, $R^2 = 0.23$, $p = 0.0308^*$). For both MPD and MNTD, mean phylogenetic distance is not significantly correlated with mean morphological distance based on the occlusal mandible (Figure 7.4f; MPD, $R^2 = 0.18$, $p = 0.0525$; MNTD, $R^2 = 0.02$, $p = 0.434$). Although the Australian province was an outlier in all the aforementioned regressions, having generally low values for mean phylogenetic and morphological distance as well as low species richness; the removal of the Australian province prior to conducting the regression analyses did not alter the significance or the direction of the observed patterns (results not shown).

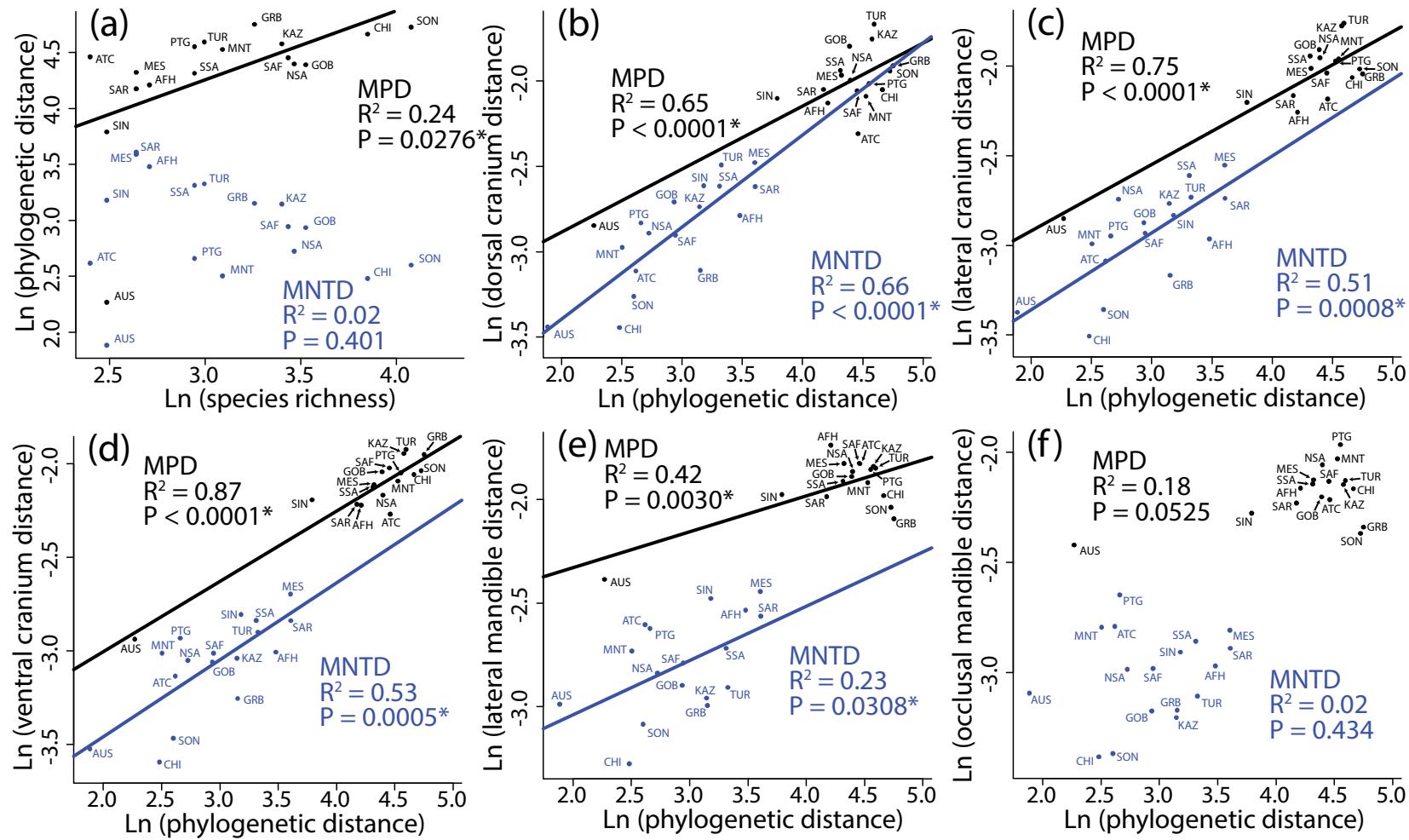


Figure 7.4. Regressions between mean phylogenetic distance and (a) log species richness, (b) mean dorsal cranial distance, (c) mean lateral cranial distance, (d) mean ventral cranial distance, (e) mean lateral mandibular distance, and (f) occlusal mandibular distance. A best fit regression line is included in significant relationships. R^2 values, as in the text, are adjusted values (see chapter 6). Mean phylogenetic and morphological distance are calculated using observed values of MPD (black) and MNTD, (blue) and not SES values. Province abbreviations are: NSA= North Saharan; SSA= South Saharan; SAR= South Arabian; MES= Mesopotamian; SIN= Sindian; TUR= Turanian; KAZ= Kazakhstan; GOB= Gobian; AFH= African Horn; GRB= Great Basin; SON= Sonoran; CHI= Chihuahuan; ATC= Atacama; MNT= Monte; PTG= Patagonian; AUS= Australian; SAF= South African.

Discussion

Community Structure at the Provincial Scale

The present study is the first attempt to directly test and compare desert rodent assemblage structure and the patterns that facilitate coexistence in these assemblages in different continents using the community phylogenetic approach, at two spatially nested scales. Moreover, I also test the association between phylogenetic and morphological structure, and the association between phylogenetic structure with taxonomic diversity. The results of this study are important because phylogenetic community structure is usually studied in plant communities and other taxa with limited mobility (e.g. British meadows, Silvertown et al. 2001; Caribbean *Anolis*, Glor et al. 2003; Florida oak, Cavender-Bares et al. 2006; Australian *Banksia*, Merwin et al. 2012) and rarely studied in mammals which are relatively more mobile. The use of desert rodents is especially important because they are highly mobile as a consequence of the evolved adaptations for long distance travel leading to large ranges. Vagile organisms, being able to disperse and interact over very large spatial scales, may exhibit different patterns of community structure than less mobile organisms, such as over-dispersion in large spatial scales as a consequence of competition, or even random assembly at large spatial scales since vagile species can mediate competition more readily (Harmon-Threatt and Ackerly 2013).

The results indicate that desert rodent assemblages differ from other taxa in community structure, in accord with results from similar previous studies (e.g. Kelt et al. 1996). I generally find that at the provincial scale, with the exception of 3 desert provinces that are significantly phylogenetically clumped (North Saharan, Sindian, and Chihuahuan), most of the desert rodent assemblages (12) are not significantly structured (i.e. neutrally assembled from regional species pools). Recent evidence compiled on mobile taxa on similar large spatial scales show a pattern of clumping, presumably a consequence of environmental filtering (e.g. carnivores, Cardillo 2011; ruminants, Cantalapiedra et al. 2013; bumble bees, Harmon-Threatt and Ackerly 2013; Australian desert vertebrates, Lanier et al. 2013). This pattern is partially consistent with my results, since while only three provinces were significantly clumped, 11 out of 15 showed a trend towards clumping as indicated by negative phylogenetic SES-MPD and/or SES-MNTD values (Table 7.1). I also found that while most desert rodent provinces are not significantly structured based on all morphological datasets, the number of provinces that were significantly clumped in

at least one skull region were slightly lower than those that were significantly over-dispersed (6 vs. 8). Moreover, I found 3 provinces that were morphologically clumped at some regions of the skull and over-dispersed in others (see below). I found similar results at the regional scale, with most biogeographic regions (3) being non-significantly structured in phylogeny and only 1 biogeographic region being significantly clumped (Neotropic) and 1 being significantly over-dispersed (Palearctic). Similarly, at this scale most biogeographic regions (3) were not significantly structured in morphology and only 1 region being significantly clumped (Nearctic) and 1 being significantly over-dispersed (Paleotropic).

While the phylogenetic structure analyses do not support the general prediction that desert rodent species are assembled non-randomly from regional species pools at the provincial and regional scales, the morphological structure analyses does lend some support to this prediction. I predicted that at relatively small spatial scales (desert provinces), interspecific competition will be the predominate structuring ecological force leading to both phylogenetic and morphological over-dispersion; instead the observed pattern was that of phylogenetic non-structure with morphological over-dispersion and/or clumping. Phylogenetic non-structure (i.e. randomness) with morphological over-dispersion of resource acquisition traits is consistent with interspecific competition between distant relatives leading to competitive exclusion (Webb et al. 2002). Whereas, phylogenetic non-structure with morphological clumping of key traits related to abiotic adaptation (i.e. aridity survival) could be due to morphological convergence in distant relatives, a pattern that is very common in the cranium of desert rodents (see chapter 6).

The fact that different regions of the skull show different patterns of clumping and over-dispersion in different provinces may indicate that regions most adaptive to resource acquisition and to abiotic survival could differ in different assemblages. However, almost all of the provinces that exhibit significant over-dispersion (7 out of the 8) do so in at least one region of the skull that is associated with dental characters, the predominant measure of resource acquisition in mammals (i.e. the mandibular and the ventral cranial datasets). In other words, in the Sonoran province, over-dispersion occurs in the dorsal, lateral, and ventral cranium as well as the lateral mandible; in the Turanian and Kazakhstan provinces, over-dispersion occurs in the dorsal, lateral, and ventral cranium; in the Chihuahuan province over-dispersion occurs in the lateral and occlusal mandible; in the Patagonian province, over-dispersion occurs in the occlusal mandible and the dorsal cranium; in the Monte and Great Basin provinces, over-dispersion

occurs in the occlusal mandible and ventral cranium respectively; and only in the Gobian province does over-dispersion occur in a region of the skull not generally associated with resource acquisition (dorsal cranium). This was not the case for provinces that exhibited significant clumping, where only 3 out of the 6 provinces are clumped in skull regions associated with resource acquisition (Chihuahuan clumping in the dorsal cranium and lateral mandible; Kazakhstan and Turanian clumping in the lateral mandible), all 3 of which also show a pattern of significant over-dispersion in other regions of the skull associated with resource acquisition (see above); therefore no provinces are clustered solely in resource acquisition traits. The South Arabian, Sodian, and African Horn are significantly clumped in the lateral cranium, a region of the skull not generally associated with resource acquisition, and may be explained by environmental filtering in distant relatives in the South Arabian and African Horn provinces which do not exhibit phylogenetic structure; or environmental filtering in close relatives in the Sodian province that also exhibits significant phylogenetic clumping.

Of all the examined provinces, the Chihuahuan province had the strongest evidence of community structure. The general pattern in this assemblage is that of phylogenetic clustering, morphological clustering of regions of the skull mostly associated with adaptation to abiotic conditions, and morphological over-dispersion of regions of the skull most associated with resource acquisition. This pattern suggests that habitat filtering is selecting for the coexistence of taxa with certain morphological attributes (dorsal cranium morphological clumping) which are shared by close relatives (phylogenetic clumping) but also that competition is leading to the exclusion of taxa with similar resource acquisition traits (mandibular over-dispersion). Although I do not directly test it, this pattern is also suggestive of character displacement in close relatives as a consequence of interspecific competition. The Sodian province had the second strongest evidence of community structure, with both phylogenetic clumping and morphological clumping of the lateral cranium (and no over-dispersion in any other traits), suggesting that environmental filtering is the dominant structuring ecological force in this community leading to the coexistence of close relatives with similar cranial morphology. The Sonoran and the Patagonian provinces are predominantly structured by interspecific competition between distant relatives that converged on similar resource acquisition traits; this is suggested by the random (non-structured) pattern observed in the phylogeny and the over-dispersed pattern observed in the mandibular region of the skull and parts of the cranial region of the skull. The Turanian and the

Kazakhstan provinces showed similar patterns of being phylogenetically non-structured, morphologically clumped in the mandible, and morphologically over-dispersed in the cranium, a pattern that may indicate interspecific competition between distant relatives.

Community Structure at the Regional Scale

I predicted that at relatively large spatial scales (desert regions), environmental filtering will be the predominate structuring ecological force leading to both phylogenetic and morphological clumping; instead I found no general pattern, where out of the 5 examined desert regions, 2 exhibited phylogenetic or morphological clumping and 2 exhibited phylogenetic or morphological over-dispersion. Phylogenetic clumping in the Neotropic desert region can be explained by habitat filtering (in terms of differential expansion of the geographical ranges of species) of close relatives and morphological clumping in the Nearctic desert region can be explained by habitat filtering of distant relatives (e.g. Cardillo 2011), both of which arise as a consequence of the tolerance to aridity limiting species that exist in these desert regions to those with shared desert adaptive traits. Alternatively, localized rapid speciation and/or reduced extinction can also lead to phylogenetic clumping (Cardillo 2011), a pattern that is very prevalent in the broader South American biogeographic region (Schenk et al. 2013; chapter 3).

Phylogenetic over-dispersion in the Palearctic desert may be explained by interspecific competition of close relatives at large geographical scales leading to competitive exclusion and morphological over-dispersion; whereas in the Paleotropic desert it may be due to evolutionary divergence of distant relatives (character displacement) (e.g. Cardillo 2011) a pattern that was documented in the body mass of granivorous desert rodents (Bowers and Brown 1982).

Taken together these results indicate that although no generalizations can be made about the pattern of phylogenetic and/or morphological community structure at the examined provincial and regional scales in desert rodent assemblages; there is a trend of phylogenetic non-structure and morphological over-dispersion at the provincial scale, which suggests a pattern of interspecific competition of distant relatives. Stevens et al. (2012) suggests that the pattern of over-dispersion in body mass, the “hallmark of competition theory” observed in many of the North American deserts (e.g. Brown 1973; Brown and Kurzius 1987; Ernest et al. 2008) may be the exception rather than the rule, pointing to habitat specificity as a potential explanation for the high degree of variation in phylogenetic structure (most of which are not significantly structured,

but include some that are clumped and others that are over-dispersed) that they observed in their analyses of the Mojave Desert rodent communities. Here, I show that although phylogenies do capture some aspects of niche well (see below) a thorough investigation of alternative measures of niche (i.e. morphology) are important to confirm/reject results detected by phylogenies, and to test the potential for interspecific competition between distant relatives.

Association between Phylogenetic Structure and Diversity

The prediction that more diverse desert provinces are composed of phylogenetically distant relatives that overlap less in niche space appears to hold as indicated by the significant positive correlation between the observed mean phylogenetic distance and log species richness. The fact that there was a positive correlation in MPD but not MNTD suggests that this positive correlation is associated with the addition of distant relatives that presumably differ more in niche and not the addition of sister taxa (Webb et al. 2002). Interestingly this result is the opposite of what Stevens et al. (2012) found when they examined this association at much smaller community scales. This may indicate that this pattern is scale dependent where the increase in diversity at small spatial scales is associated with more clumped communities and the increase in diversity at large spatial scales is associated with a more over-dispersed assemblages. Additional insights that can be drawn from the results include the striking difference in diversity of the examined provinces, which could not be attributed to the absolute size of the province (e.g. the Sonoran province is the most diverse yet is smaller than the least diverse assemblage, the Australian province, Figure 7.2; Figure 7.4a). The high diversity in the Sonoran province can be attributed to greater resource diversity and increase in heterogeneity which could allow more species to coexist (as evidenced by the associated increase in phylogenetic distance, Figure 7.4a) and exploit the different resources facilitated by the increase in niche space (MacArthur and MacArthur 1961; Stevens and Tello 2011).

Association between Phylogenetic and Morphological Structure

The results strongly support the prediction that phylogenetic and morphological structure indices are correlated in desert rodent assemblages, due to the observed significant positive correlation between mean phylogenetic distance and the mean morphological distance (for both MPD and MNTD) for all skull regions (4) except the occlusal mandible. The association

between phylogenetic and morphological structure generally support to the contention that using the phylogeny and metrics of phylogenetic structure as a surrogate for niche does capture this concept well in desert rodent communities. Harmon-Threatt and Ackerly (2013) recently conducted a similar study in bumblebees, a highly mobile taxon at large spatial scales, and noticed similar patterns of correlation between morphological and phylogenetic structure which they interpret as arising due to the examined traits having strong phylogenetic signal or convergence of community members due to shared resources (they observed that morphological clumping was associated with phylogenetic clumping).

Despite the association between empirical phylogenetic and morphological structure indices (MPD and MNTD), many assemblages differed in statistical support for phylogenetic and morphological structure (i.e. based on the significance of the SES-MPD and SES-MNTD values) which may simply reflect habitat specificity where different traits differ in importance in different habitats (e.g. displacement/divergence in certain aspects of cranial morphology may provide advantages in some communities while variation in other aspects in cranial morphology may provide more advantages for other communities, depending on the available resources). Moreover, discordance between the significance of phylogenetic and morphological structure indices may indicate that the phylogeny is capturing other non-morphological aspects of niche/phenotype that may be important for structuring the focal community that are not captured by the examined morphological traits, or that the morphological dataset is capturing non-phylogenetically conserved traits that may be important for structuring certain assemblages.

Conclusions

Desert rodent assemblages appear to differ in community structure at both the provincial and regional scales. The majority of assemblages are not significantly phylogenetically structured and seem to be neutrally assembled from source species pools. However, at the provincial scale, most assemblages do show evidence of morphological structure, mostly a pattern of over-dispersion in resource acquisition traits. Phylogenetic non-structure with morphological over-dispersion in resource acquisition traits suggests interspecific competition and competitive exclusion in distant relatives, which seems to be the predominant ecological force structuring assemblages at this scale. Of all the examined provinces, the Chihuahuan

province had the strongest evidence of community structure, where the pattern of phylogenetic clustering, clustering of abiotically-associated regions of the skull, and over-dispersion of resource-acquisition-associated regions of the skull, suggests that habitat filtering is selecting for phylogenetically close as well as morphologically similar species in certain cranial attributes associated with arid adaptations, whereas interspecific competition is leading to the competitive exclusion of taxa that significantly overlap in resource acquisition traits. Moreover, the results suggest that more diverse assemblages are composed of phylogenetically distant relatives that overlap less in niche space, a pattern that is the opposite to the one found in previous studies conducted on smaller spatial scales of desert rodent communities. Finally, the results strongly indicate that the observed phylogenetic and morphological structure metrics are correlated, which support the use of phylogenetic structure metrics as surrogates for niche in desert rodent communities. However, because the significance of community structure results differed between phylogenetic and morphological datasets, it seems that comparing results obtained from alternative measures of niche is still important.

CHAPTER EIGHT

MOLECULAR SYSTEMATICS AND DESERT ECOLOGY OF GERBILS (RODENTIA, GERBILLINAE) AND DEOMYINES (RODENTIA, DEOMYINAE): A TEST OF GEOMETRIC VARIATION IN TYMPANIC BULLA MORPHOLOGY ACROSS ARIDITY GRADIENTS

Summary

Recent molecular studies in gerbils found multiple instances of discordance between molecular and morphological phylogenies. In this study, I compile the largest molecular dataset of gerbils and deomyines to date, to estimate the phylogeny of the group. Maximum likelihood and Bayesian analyses were largely concordant and both had high levels of node support. The results were also highly concordant with previous molecular phylogenies based on allozymes, chromosomes, DNA/DNA hybridization, and DNA sequences; and discordant with morphological phylogenies. All traditional gerbil tribes and subtribes were paraphyletic. In addition paraphyly was found in the genera *Gerbillus*, *Gerbilliscus*, and *Meriones* as well as in 5 subgenera within *Dipodillus*, *Gerbillurus*, and *Meriones*. Short branches separating species groups within *Dipodillus* and *Meriones* suggest synonymy. Within Deomyines, all polytypic genera and subgenera were monophyletic, however, 2 species groups within *Acomys* appear to be synonymous. I also find support for the prediction that discordance between molecular and morphological phylogenies in gerbils is due to convergent adaptations to arid environments. Most of the association between bulla morphology with aridity appears to be in size rather than in shape, and morphology varies more strongly along bioclimatic clines than among two binary habitat classifications. However, the most variable aspects of bullar shape is that of increased anterior-posterior elongation and medio-lateral flattening in desert relative to mesic species.

Introduction

Muridae is the most diverse family of mammals, consisting of over 700 species and 150 genera (Musser and Carleton 2005) in four subfamilies: Murinae, Lophiomyinae, Deomyinae,

and Gerbillinae, where there is evidence that the latter two are sister subfamilies (Michaux and Catzeflis 2000; Michaux et al. 2001; Jansa and Weksler 2004; Steppan et al. 2004a; Chevret and Dobigny 2005; Schenk et al. 2013). Murids are found throughout the Old World including Africa, Asia, Europe, and Australia; living in most types of habitats ranging from hyper-arid deserts hyper-mesic rainforests (Nowak 1999). Murid systematics have changed drastically in the past 100 years, as a consequence of molecular phylogenetic studies (Musser and Carleton 2005). While these studies unambiguously support the sister status of gerbils and deomyines (e.g. Jansa and Weksler 2004; Steppan et al. 2004a), relationships within these two clades are less understood, with great discordance observed between morphological and molecular phylogenies of gerbils (Musser and Carleton 2005). Few molecular studies focus exclusively on deomyines, which is usually investigated within larger taxonomic groups that includes other murid subfamilies (e.g. Jansa and Weksler 2004; Steppan et al. 2004a).

Members of Deomyinae, a subfamily that consists of 42 species and 4 genera of spiny mice and relatives (Musser and Carleton 2005), are found mostly in Africa, however, their range also covers part of the Middle East including the Arabian Peninsula and Turkey; within this range they occupy various habitats including grasslands, forests, savannahs, and deserts (Figure 8.1; Nowak 1999). Deomyines vary in behavior, with diurnal, crepuscular, and fully nocturnal species; and also vary in nesting habits with both borrowing and non-burrowing species (Nowak 1999). This group does not share a large suite of morphological traits and are only assembled recently based on molecular evidence (Musser and Carleton 2005). Before this assembly, *Deomys* was placed in Dendromurinae by Thomas (1896) and remained there until two decades ago when a variety of molecular phylogenetic analyses (Denys et al. 1995; Verheyen et al. 1995; Michaux and Catzeflis 2000, Michaux et al. 2001; Chevret et al. 2001) robustly placed this genus in the same clade as the ‘acomynes’ (*Acomys*, *Lophuromys*, and *Uranomys*) (Musser and Carleton 2005). Similar to *Deomys*, acomynes were only recently isolated from murines based on non-morphological data (e.g. chromosomes, Viegas-Péquignot et al. 1986; allozymes, Bonhomme et al. 1985; DNA/DNA hybridization, Chevret et al. 1993; mtDNA and rRNA 12S sequences, Hänni et al. 1995; mtDNA cytochrome b sequences, Verheyen et al. 1995) which strongly support their monophyly and isolation from other murines (Musser and Carleton 2005).

Gerbillinae, an Old World subfamily that consists of 103 species and 16 genera of gerbils, jirds, and relatives (Musser and Carleton 2005), have a much larger geographic

distribution than deomyines, covering most of Africa and a larger extent of Asia, from the Middle East to central Asia; wherein they occupy mostly arid, unproductive, open regions including deserts, grasslands, and savannahs (Figure 8.1; Nowak 1999). One of the most characteristic features of gerbils is their largely inflated tympanic bulla (cranial chamber that houses middle ear bones) which functions in sound amplification (aids in detecting interspecific vocalizations and foot drumming, as well as sounds from predators) in open, mostly desert, habitats where sound dissipates quickly (Lay 1972). Members of this group share a large suite of morphological and behavioral traits; the majority are diurnal, have varying degrees of ricochet locomotion (associated elongated tails and narrow hind legs), and are mostly desert adapted, which is evident by their efficient burrowing, well developed vision (large eyes), and efficient water conservation (Nowak 1999). Unlike deomyines, gerbils have long been grouped together and defined based on derived skeletal, dental, and male genital characters (e.g. similar tympanic bulla morphology and mastoid pneumatization; shared dental formula, enamel patterns, and overall teeth morphology; small or absent coronoid process; reviewed in Lay 1972, Petter 1973, Carleton and Musser 1984, Pavlinov et al. 1990, Pavlinov 2001).

Despite sharing a large suite morphological synapomorphies, relationships within gerbils are highly debated, with the two most inclusive morphological phylogenies (all 16 genera, Pavlinov 2001; 14 genera, Tong 1989) having low resolution at deep nodes and disagreements in a great deal of the systematic inferences (Musser and Carleton 2005). No one molecular phylogeny includes all extant gerbil genera (Musser and Carleton 2005) and most of the early phylogenies suffered from low generic sampling (e.g. the two studies with the largest sampled genera: 7 genera using DNA/DNA hybridization, Chevret 1994; 6 genera using chromosome data, Benazzou 1984), low overlap in sampled species, methodological problems, lack of outgroups, small datasets, and small sample sizes, making comparisons between studies difficult (Chevret and Dobigny 2005). A recent molecular phylogeny by Chevret and Dobigny (2005) based on mtDNA cytochrome b and 12S rRNA, included the greatest number of species and genera sampled to date (29 species in 11 recognized genera) and led the authors to suggest major taxonomic revisions at the tribal, subtribal, generic, and subgeneric levels. The concordance between this mtDNA sequence phylogeny with previous molecular phylogenies based on non-sequence data (e.g. DNA/DNA hybridization and chromosomes; see above) is greater than the concordance between previous morphological phylogenies, which led Chevret and Dobigny

(2005) to hypothesize that most of the characters used in morphological phylogenies are homoplastic, and evolved as a consequence of strong constraints imposed by arid environments.

Since the Chevret and Dobigny's (2005) publication, no subsequent molecular phylogeny incorporates more gerbil species or genera; studies were more narrowly focused on relationships within genera and/or were confined to certain geographic locations. These include the study of the phylogenetic relationships within *Gerbilliscus* based on cytochrome b and 16S mitochondrial genes from 9 *Gerbilliscus* species and 5 species within *Gerbillurus*, *Gerbillus*, and *Desmodillus* (Colangelo et al. 2007), followed by the study of the morphological variation in several of the aforementioned *Gerbilliscus* species (Colangelo et al. 2010). These studies have led to the recognition of three major clades within *Gerbilliscus* that correspond to major geographical subdivisions, and supported the synonymy of the *Gerbillurus* and *Gerbilliscus*, placing the former within the latter (Colangelo et al. 2007). By examining the phylogenetic relationships within *Gerbillus* based on cytochrome b mitochondrial gene from 7 mostly Tunisian *Gerbillus* species, Abiad et al. (2010) found evidence for the synonymy of *Dipodillus* and *Gerbillus* at the genus level. Moreover, they recognize the separation of *Gebillus nanus* from other sampled species into *Hendecapleura*, the latter of which are divided into the subgenera *Dipodillus* and *Gerbillus*, with all subgeneric designations being congruent with prior morphological and karyological evidence (Abiad et al. 2010). Ito et al. (2010) used mtDNA cytochrome b and cytochrome c oxidase subunit II sequences to estimate the phylogenetic relationships in 7 gerbil species collected in China from 3 genera (*Meriones*, *Brachionomys*, and *Rhombomys*) along with 24 species in 9 genera extracted from GenBank. Their results indicate that *Meriones* is paraphyletic, with *Meriones tamariscinus* being sister to a clade that includes other *Meriones* in addition to *Brachionomys*, *Psammomys*, and *Rhombomys*; they also recognize a possible synonymy between *Meriones chengi* and *Meriones meridianus* based on short branches (Ito et al. 2010).

In this study, I use the supermatrix approach to combine most published DNA sequence data for gerbils and deomyines with unpublished sequences to provide the most comprehensive estimation of the systematics of the group to date. I perform both maximum likelihood and Bayesian analyses on thirteen loci, including nuclear and mitochondrial protein-coding genes, mitochondrial ribosomal RNA-coding genes, and introns, of 57 gerbil species from 14 genera, as well as 25 deomyine species from all 4 genera. This phylogeny was used for two main purposes, the first is to suggest taxonomic revisions in these two subfamilies. The second purpose is to test

the prediction that discordance between molecular and morphological phylogenies is a consequence of rapid morphological convergent adaptation in gerbils to aridity (e.g. Chevret and Dobigny 2005). I test this prediction using a fossil calibrated chronogram based on the aforementioned molecular dataset and an expanded morphological dataset that includes both mesic and desert gerbils, deomyines, and outgroups, in order to test the association between tympanic bulla morphology (the most widely studied mammalian desert adaptive character (see chapter 6) and is widely used in traditional gerbil systematics) and multiple climatic measures of aridity, after applying phylogenetic correction. Due to the lack of clear homologous landmarks in the tympanic bulla, I use sliding semilandmarks to outline the structure (Rohlf 1990; Bookstein 1997) using the geometric morphometric approach (Zelditch et al. 2004) to quantify bullar morphology as in previous studies conducted in *Meriones* (e.g. Momtazi et al. 2008).

Morphological variation in the tympanic bulla has long been attributed to desert adaptation in mammals (e.g. Lay 1972), however, no study used both phylogenetic correction and continuous bioclimatic variables to test this hypothesis. Gerbils are particularly suited for this study considering the great range of variation in the tympanic bulla morphology. In a comparison of 13 gerbil species, Lay (1972) found that species that live in more arid environments have increased auditory sensitivity as a consequence of increased anatomical specializations in the middle and inner ear anatomy (i.e. of the tympanic bulla). This increased auditory sensitivity that accompanies tympanic bulla enlargement is described as an adaptation for predator avoidance in open xeric habitats where sound dissipates quickly and early detection is necessary to improve chances of escaping more effective predators (Lay 1972; Webster and Webster 1975). The use of phylogenetic correction allows for isolating the effect of phylogeny from adaptation in interspecific comparisons of bullar morphology. In a previous study (chapter 6), I showed that among a large sample cranial and mandibular linear measurements, measurements associated with the tympanic bulla were the most strongly associated with aridity in rodents, even after phylogenetic correction.

By using geometric morphometrics in the present study, I can examine size variation in the tympanic bulla independent of shape, and vice versa. This facilitates testing whether bullar variation is a dichotomous change associated with size enlargement in deserts (e.g. due to a discrete shift in lifestyle associated with the need for increased auditory sensitivity in open habitats) and/or is a more complex adaptation of overall bullar shape to aridity. Furthermore, the

use of both discrete and continuous climatic variables allows for testing whether desert adaptation occurs in a continuous or binary fashion, the latter of which suggests two adaptive optima representing the bullar condition of mesic vs. desert species.

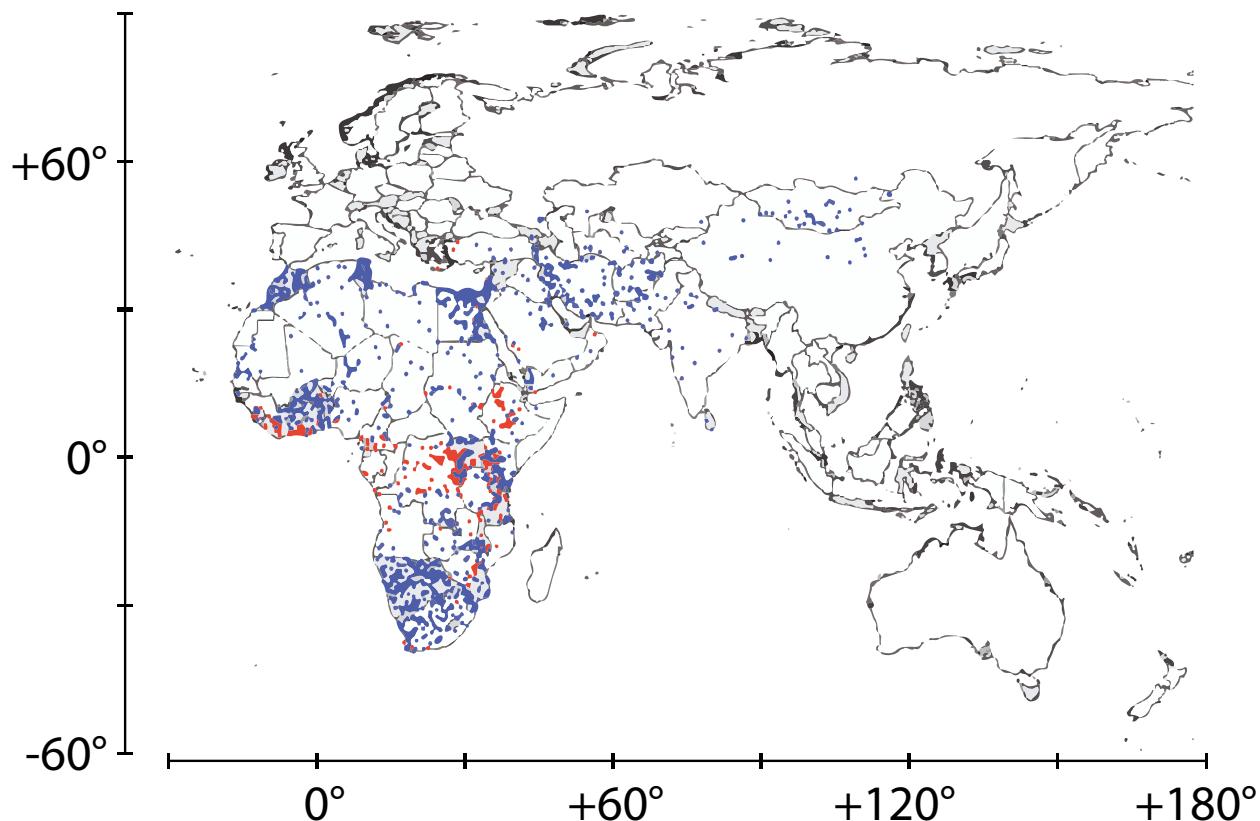


Figure 8.1. Geographical distribution of gerbils and deomyines. Blue points= gerbils; red points= deomyines. Points indicate all species occurrence records from the Global Biodiversity Information Facility (GBIF 2013) data portal using collections from the following institutions (abbreviations described in <http://data.gbif.org/>): AM, AMNH, CAS, CCM, CI, CSIRO, CUMV, DMNS, FLMNH, FMNH, GNM, IICT, INPA, ISEA, ISU, LSUMNS, MACN, MCZ, MHNB, MNB, MRI, MSB, MSI, MSUM, MVZ, NHMLC, NLBIF, NMBCC, NMNH, NMNS, NMS, NYSM, OMNH, OSU, RBINS, ROM, SAM, SANBI, SBMNH, SMNH, SNSB, TCWC, TTU, UAFMC, UAMN, UCD, UCMNH, UCSB, UKBI, UMBMNH, UMMZ, UMNH, UMZC, UNIBIO, UTEP, UWBM, UWMV, WNMU, YUPB, and YUPM.

Materials and Methods

Phylogenetic Sampling

A total of 95 species were included in the phylogenetic analyses. These represent all gerbil and deomyine species with published sequence data as well as most species with material readily available, in addition to a small number of murids and cricetids, sampled as outgroups.

All 4 deomyine and most gerbil (14 out 16) genera were sampled, including ~52% of gerbil species and ~44% of deomyine species (Musser and Carleton 2005). The unsampled genera (*Ammodillus* and *Microdillus*) are monotypic and rare (found only in Somalia). Outgroups were sampled to maximize the inclusion of murid and cricetid fossil calibrations from Schenk et al. (2013). I sampled the monotypic Lophiomyinae, the sister group of gerbils and deomyines, in addition to six murine species (sister to the Gerbillinae+Deomyinae+Lophiomyinae clade): *Tokudaia osimensis*, *Apodemus agrarius*, *Mus pahari*, *Rattus tiomanicus*, *Batomys granti*, and *Phloeomys* sp. Outside of Muridae, I included six cricetid species from three subfamilies: *Phyllotis xanthopygus*, *Sigmodon hispidus*, *Rheomys thomasi* (Sigmodontinae), *Ondatra zibethicus*, *Microtus chrotorrhinus* (Arvicolinae), and *Cricetus cricetus* (Cricetinae). All taxonomy followed Musser and Carleton (2005).

DNA Extraction and Sequencing

The final supermatrix used in the phylogenetic analyses is a concatenation of 2 mitochondrial ribosomal genes (1,019 base pairs (bp) of 12S rRNA; 513 bp of 16S rRNA), 7 nuclear protein-coding genes (148 bp of exon 3 and 101 bp of exon 4 of acid phosphatase 5 (ACP5); 754 bp of exon 2 and 79 bp of exon 3 of arginine vasopressin receptor 2 (AVPR2); 2,388 bp of exon 11 of breast cancer 1 (BRCA1); 878 bp of exon 10 of growth hormone receptor (GHR); 1,122 bp of exon 1 of interphotoreceptor retinoid binding protein (IRBP); 2,025 bp of the single large exon of recombination activation gene 1 (RAG1); 1,264 bp of exon 28 of von Willebrand factor (VWF)), 3 mitochondrial protein-coding genes (324 bp of cytochrome c oxidase I (COI); 684 bp of cytochrome c oxidase II (COII); 1,140 bp of cytochrome b (CYTB)), and 3 nuclear introns (253 bp of intron 2 of ACP5; 220 bp of intron 2 of AVPR2; 1,214 bp of intron 3 of benzodiazepine receptor gene (BZRP)) for a total of 14,126 sites. Sequences were obtained from studies published in GenBank (most 12S, Chevret and Dobigny 2005; most 16S, Colangelo et al. 2007; all AVPR2, Bösel et al. 2009; most BRCA1, Steppan et al. 2004a and Rowe et al. 2008; all COI, Steppan et al. 2005; most COII, Steppan et al. 2005 and Ito et al. 2010; most CYTB, Chevret and Dobigny 2005 and Ndiaye et al. 2014; most GHR, Steppan et al. 2004a, 2005, Schenk et al. 2013; most IRBP, and Jansa and Weksler 2004 and Schenk et al. 2013; most RAG1, Schenk et al. 2013; most VWF, Michaux et al. 2001) in addition to

unpublished sequences from Steppan et al. (in prep) and sequences collected for this study (25 ACP5, 10 BZRP, 28 CYTB, 5 GHR, 2 IRBP, and 5 RAG1) (Appendix Table G.1).

For newly generated sequences (ACP5, BZRP, CYTB, GHR, IRBP, and RAG1), total genomic DNA was extracted from vouchered museum tissues using standard phenol–chloroform–isoamyl alcohol extraction procedure as described by Sambrook et al. (1989). Polymerase chain reactions (PCR) included 10× GoTaq buffer (Promega, Madison, Wisconsin, USA), 1 unit of GoTaq polymerase, 10 µM of forward and reverse primers, 0.15 mM of dNTPs, 3 mM of MgCl₂, 0.2 µg BSA, 20–25 ng of DNA template, and ddH₂O to a total volume of 25 µl. A negative control without template DNA was included in all PCRs to test for DNA contamination of reagents. Amplification and sequencing were completed with primer sequences under reaction conditions described previously depending on specific taxa (Jansa and Voss 2000; Adkins et al. 2001; DeBry and Seshadri 2001; Steppan et al. 2004a, b, 2005; Rowe et al. 2008; Schenk et al. 2013). ACP5 was amplified using a combination of the primer sequences 120FWD, 139FWD, 545REV, 564REV, and S223 (DeBry and Seshadri 2001; Rowe et al. 2008). All BZRP amplifications used the primers S221 and S222 (Rowe et al. 2008). CYTB was amplified using a combination of the primer sequences S199, P484, and P485 (Rowe et al. 2008). GHR was amplified with the primers GHREXON10 and GHREND (Adkins et al. 2001). The IRBP region was amplified using a combination of the primers 119A2, B2, and 878F (Jansa and Voss 2000; Weksler 2003). RAG1 was amplified using a combination of the primers S70, S142, S73, S278, and S279 (Steppan et al. 2004b; Schenk et al. 2013).

PCRs were visualized on 1% agarose gels with ethidium bromide and successful reactions were prepared by enzymatic digestion with EXO-SAP-IT (Affymetrix, Cleveland, Ohio, USA). Both the 5' and 3' directions of the sequences were generated using the aforementioned primers at the FSU core facilities or at the DNA Analysis Facility on Science Hill at Yale University. Sequencher v4.7 (Gene Codes Corporation, Ann Arbor, MI, USA) was used to assemble single sequence reads into a contiguous sequence with heterozygous sites scored as polymorphic. Sequences that contained protein-coding genes (ACP5, AVPR2, BRCA1, COI, COII, CYTB, GHR, IRBP, RAG1, and VWF) were assembled manually using Mesquite v2.75 (Maddison and Maddison 2010) using the codon structure as a guide by consolidating indels and resulted in an unambiguous alignment. Remaining sequences (12S, 16S, and BZRP)

were aligned using MUSCLE (Edgar 2004). Species were represented in the concatenated data matrix by 1 to 11 loci (Appendix Table G.1).

Phylogenetic Analysis

Phylogenetic estimation was conducted using maximum likelihood (ML) and Bayesian inference (BI) using RAxML v7.6.3 (Stamatakis 2006) and MrBayes v3.2.2 (Huelsenbeck and Ronquist 2001) respectively; both run on the CIPRES Science Gateway (Miller et al. 2010). ModelTest (Posada and Crandall 1998) was used to estimate the best-fit DNA substitution model for each locus separately, for each data type partition separately (e.g. codon positions, introns; see below), and for the concatenated data using the Akaike information criterion (AIC; Akaike 1974). The GTR+ Γ +I model was used in all the phylogenetic analyses because it was the best-fit model for all the data type partitions, the concatenate data, and all loci except for BRCA1 and RAG1 (where GTR+ Γ was the preferred model); BZRP and GHR (where HKY+ Γ fit the data best); ACP5 (where K81uf+I fit the data best); and IRBP (where TrN+ Γ +I fit the data best). In cases where the best fit model was not implemented in RAxML, MrBayes, and/or Beast analyses (see below), the most similar available model was used instead (in all cases, GTR+ Γ +I).

For the concatenated data, I conducted phylogenetic analyses using three partitioning schemes: (1) no partition, (2) 13 partitions corresponding to loci, and (3) 8 partitions corresponding to across-gene codon position and data type (i.e. mitochondrial ribosomal, nuclear introns, 3 mitochondrial codon positions, and 3 nuclear codon positions). Trees estimated using these alternative partitioning schemes were similar (data not shown) and only trees estimated using the 8 partition (across-gene codon position and data type) scheme are shown because it fit the data best in previous phylogenetic studies of muroid rodents (e.g. Schenk et al. 2013). Parameter values among all partitions were unlinked during analyses.

RAxML searches were run ten times from different random starting trees for individual loci and for the concatenation in order to escape local optima (Morrison 2007). The resulting trees for the multiple searches looked indistinguishable and the results of only one search is presented here. Clade support for the ML trees was determined using standard nonparametric bootstrapping (BS) as implemented in RAxML in CIPRES Science Gateway, using rapid bootstrap inferences each optimized with ML, which resulted in 100-1,000 replicated bootstrap searches, with results summarized on the best-scoring ML tree.

For the MrBayes analyses, a flat Dirichlet prior was applied on all trees and the GTR+ Γ +I DNA substitution model for all partitions with clade support determined using Bayesian posterior probabilities (PP). Metropolis-coupled Markov chain Monte Carlo (MC³) was run independently four times, using different random starting trees, for 36 million generations each, sampling every 5,000 generations from the posterior distribution. All the trees where the standard deviation of the split frequencies was > 0.01 were discarded as burn-in generations (first 5-11% of the MC³ chains); convergence and stationary of the post-burn-in trees was confirmed by evaluating all parameter values in the MC³ chains in Tracer v1.5 (Rambaut and Drummond 2005) and no additional trees were excluded as burn-in. All four independent MC³ chains had a post-burn-in effective sample size (ESS) of > 600 for all parameters and the combined MC³ chain (see below) had an ESS $> 3,000$ for each parameter. The post-burn-in trees from the four independent runs were combined manually and summarized with TreeAnnotator v1.8.0 (Drummond and Rambaut 2007) using the maximum-clade credibility tree criterion.

Divergence-Time Analysis

Divergence-times were estimated simultaneously with topology and branch lengths using an uncorrelated lognormal relaxed-clock model in Beast v1.7.5 (Drummond and Rambaut 2007) using the CIPRES Science Gateway. A GTR+ Γ +I DNA substitution model was applied for all 8 partitions (as in the MrBayes analyses above) with clade support determined using Bayesian PP. The MC³ chain was run for 50 million generations, sampling every 5,000 generations from the posterior distribution. Tracer was used to determine appropriate burn-in based on convergence and stationary leading to the exclusion of the first 10% of the of the MC³ chain as burn-in. Out of 119 parameters; 113 had ESS > 200 ; 115 had ESS > 100 ; and only 4 had ESS < 100 : the posterior, prior, and the mitochondrial codon position 3 CG and GT substitution rate parameters, which did not reach an ESS > 100 after 100 million generations. The post-burn-in trees were summarized with TreeAnnotator using the maximum-clade credibility tree criterion. Five fossil calibrations were used to calibrate the chronogram (Table 8.1) all of which were used previously (see Schenk et al. 2013 and references therein for justification). Lognormal prior distributions were applied to all calibrations with means and standard deviations chosen to construct 95% confidence intervals (for the origination of the taxon based on first occurrence and stratigraphic

sampling) spanning 95% Marshall indices (Marshall 1994) as reported by the Paleobiology Database (PDB 2013). Only the Beast chronogram was used in subsequent comparative analyses.

Table 8.1. Calibration-point distributions including estimates for the Beast analysis. All Beast calibrations were assigned lognormal prior distributions. Node numbers correspond to those in Figure 8.5. The ages are in million years before present. StDev = standard deviation.

Node	Clade	StDev	Offset	5%	95%
5	<i>Acomys</i>	1.93	5.26	5.3	29.05
3	<i>Apodemus</i>	0.48	4.85	5.3	7.06
4	Gerbillinae	1.25	15.87	16	23.70
2	Murinae	0.89	9.77	10	14.05
1	Sigmodontini	1.41	4.80	4.9	14.93

Morphological Data Collection

Morphological data was collected from 1 to 10 crania of 102 species of muroids (mostly gerbils and deomyines) for a total of 429 specimens and an average of 4 specimens per species (Appendix Tables A.6, chapter 2). When sufficient material was available, multiple specimens and equal representation of males and females were examined in order to account for intraspecific variation and sexual dimorphism (see chapter 2). I sampled all the available gerbil species and most of the deomyine species in the visited institutions (see below). All 16 of the gerbil genera were sampled except for the rare Somali pygmy gerbil, *Microdillus peeli*, which was not available; all 4 deomyine genera were sampled. The morphological sample includes ~71% of gerbil species and ~24% of deomyine species (Musser and Carleton 2005).

Ventral cranial photographs were captured from skulls of voucher specimens from the American Museum of Natural History (AMNH), the Field Museum of Natural History (FMNH), the Museum of Vertebrate Zoology (MVZ), the Smithsonian Institution National Museum of Natural History (USNM), the Florida Museum of Natural History (UF), and the Laboratorio de Citogenetica Mamiferos, Facultad de Medicina, Universidad de Chile (LCM). Wild caught adults were chosen, as determined by basioccipital–basisphenoid epiphyseal fusion as in Robertson and Shadle (1954) and Samuels (2009) and the complete eruption 3rd molars assessed by reaching the occlusal surface (Steppan 1997) and the examination of the size associated skins.

Ventral cranial semilandmarks were digitized on photographs taken with a Nikon D3200 digital SLR camera using a Nikon 40mm f/2.8G AF-S DX Micro-Nikkor Lens (Nikon, Tokyo,

Japan) at 24 megapixels (resolution = 6016 x 4000; JPEG) in a standardized manner (see chapter 2). All photographs included a scale bar. The left side of the cranium was digitized unless it was damaged; in these instances the right side is reflected and digitized instead. Semilandmarks of curves were digitized using Tpsdig v2.16 (Rohlf 2010).

Geometric Morphometric Processing and Analyses

Coordinates marking the outline of the ventral outer edge of the cranium and the tympanic bulla were digitized following a method modified from Momtazi et al. (2008). For the tympanic bulla, the outline was estimated from points digitized along the structure in a clockwise fashion starting with the anterior-medial most of the junction between tympanic bulla and pterygoid process (Figure 8.2). The points were then resampled along the curve by length, resulting in 200 semilandmarks. The same process was repeated for the ventral view of the left side of the cranium starting from the anterior most region of the mid-sagittal plane, between incisors/nasal bones (Figure 8.2), with the points resampled to give 400 semilandmarks.

A generalized procrustes analysis (GPA; Rohlf and Slice 1990) was conducted on the dataset to obtain shape variables. GPA translates the coordinate configurations to a common centroid by scaling them to unit centroid size (CS) and rotating them in order to minimize the sum of squared distances between the corresponding landmarks as well as account for the effects of translation (Zelditch et al. 2004). GPA outputs procrustes coordinates (PrC) that describe size-independent shape differences and CS, which are sequestered in separate variables.

All GPA analyses were conducted by treating coordinates as sliding semilandmarks on boundary curves; semilandmarks were slid along their tangent directions using the Procrustes distance criterion (Adams and Castillo 2013). A GPA was conducted to align specimens prior to estimating species averages; this outputted both shape (PrC) and size (CS) variables for each specimen. CS were averaged to estimate species average size, and the average procrustes coordinate positions of aligned specimens were used to estimate average shape for each species (Claude 2008) as implemented in the Geomorph library (Adams and Castillo 2013) in R (R Development Core Team 2013). A second GPA was conducted on the consensus shape for each species in order to re-align and output a new set of PrCs that describe interspecific shape differences that are independent of size within the sample. GPA analyses were conducted separately for the cranium and bulla datasets.

PrCs were further processed into relative warps (RW) by performing principal component analysis (PCA) in order to reduce the number of shape variables (400 skull semilandmarks and 200 bulla semilandmarks in 2D = 800 and 400 PrCs respectively) and simplify interpretation. PCA was conducted in the Pcamethods library (Stacklies et al. 2007) in R using singular value decomposition. Since PCA (relative warp analysis) is conducted on PrCs which are size corrected, all RWs are shape variables that are independent of size. In order to visualize the distribution of species in morphospace, and compare desert to mesic species (see below), scores on the first six RWs which together explain 88.6 and 88.0% of the bullar and cranial outline shape variation respectively were plotted along with thin-plate splines (TPS) used to show shape differences using deformation grids. Deformation grids show shape differences between the consensus configuration of landmarks and the most extreme values along each relative warp axis (minimum and maximum values) using the bending energy criterion, which shows the energy needed to bend each landmark in the consensus landmark positions to the most extreme values along each RW axis. TPS deformation grids were plotted using the Geomorph library in R. CS were log transformed prior to subsequent comparative analyses; three size measures were analyzed: (1) bulla CS, (2) cranium CS, and (3) relative bulla CS (= log (bulla CS/cranium CS)).

Extraction of Habitat Categories and Continuous Environmental Data

The process of extracting binary habitat categories and continuous environmental variables have been described previously (chapter 6) and will be summarized here. IUCN (2013) was used to group species into desert vs. mesic groups (Appendix Figure G.2). Climatic variables were obtained for each species from WORLDCLIM 2.5-min geographical information system (GIS) layer (Hijmans et al. 2005) using DIVA-GIS v7.5 (Hijmans et al. 2012). A total of four bioclimatic variables were extracted and used to calculate the aridity index, where a low value indicates more arid regions (see chapter 6). In addition to the aridity index, annual mean temperature and annual mean precipitation were also extracted for comparative analyses, similarly by cross-referencing geographic localities (range distribution maps downloaded as polygon shape files from IUCN (2013)) of each species with the WORLDCLIM 2.5-min database using DIVA-GIS. In order to meet the assumptions of normality of subsequent

analyses, mean annual precipitation was log transformed. The aridity index was also log transformed, after the calculation of the index from raw data (e.g. Arroyo et al. 2006).

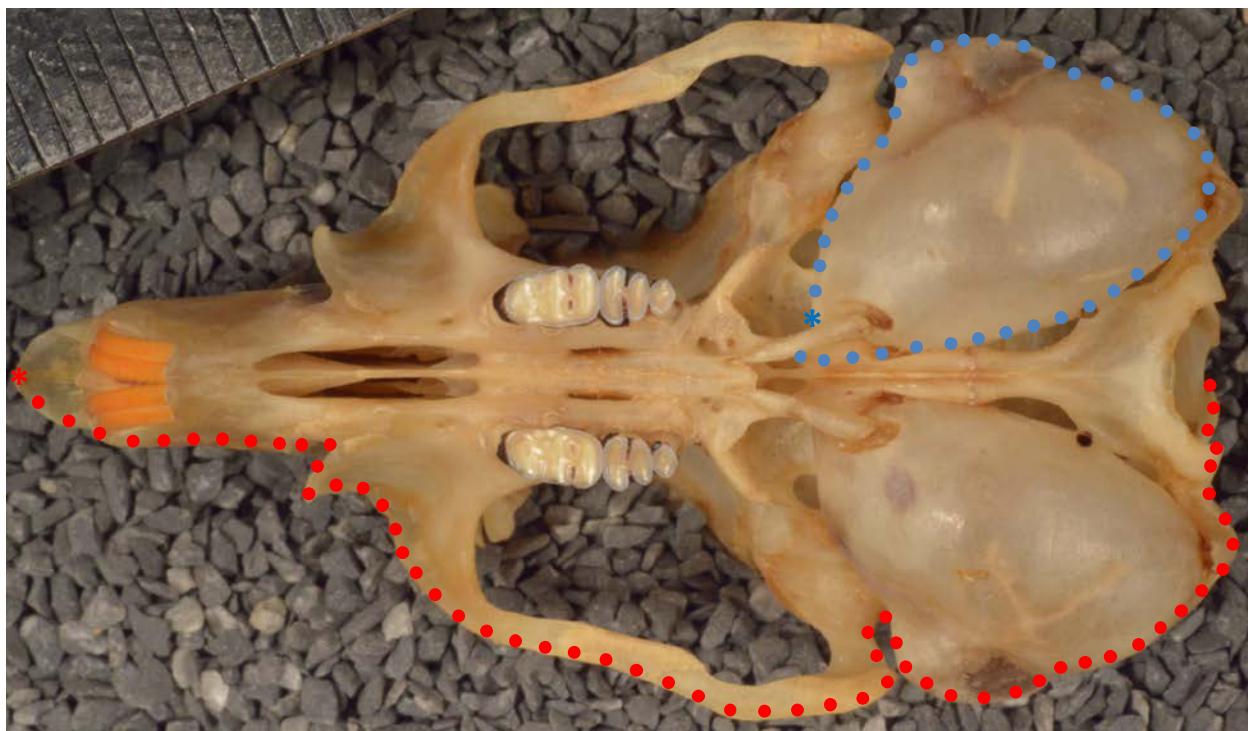


Figure 8.2. Positions of the cranial semilandmarks used in the geometric morphometric analyses of morphological variation (blue= bulla, red= cranium) shown on the ventral view of Shaw's jird (*Meriones shawi*; USNM 474187). Not all semilandmarks are shown (bulla= 200; skull= 400); cranial semilandmarks are shown on the right side but were digitized on the left.

Comparative Analyses

To test the association between morphology and climate/habitat, I analyzed the data both with and without phylogenetic correction. Phylogenetic correction reduced the significance of all correlations (more conservative) and all morphological and environmental variables had significant phylogenetic signal (data not shown), for these reasons, I only discuss the results of the phylogenetically correct analyses below. Two trees were used for phylogenetic correction, the Beast chronogram (1) with species missing morphological data pruned off, and (2) tree (1) with species that have morphological data and lack molecular data grafted onto their closest relatives based on the taxonomy of Carleton and Musser (2005) (Appendix Figure G.2; see chapter 6). Grafting and pruning were conducted in the Ape library (Paradis et al. 2004) in R.

The correlation between cranial/bullar size with habitat/climate was tested by conducting: (1) phylogenetic analyses of variance (PhyANOVA) of CS vs. habitat; (2) phylogenetic

generalized least squares (PGLS) analyses of CS vs. mean annual precipitation, mean annual temperature, and the aridity index. The correlation between cranial/bullar shape with habitat/climate was tested by conducting: (1) phylogenetic multivariate analysis of variance (PhyMANOVA) of the first 70 RWs, which account for most of the shape variation, of the bulla/cranium vs. habitat; (2) multiple phylogenetic generalized least squares analyses (mPGLS) of the first 70 RWs of the bulla/cranium vs. the three aforementioned climatic variables. Both analyses of variance were conducted with 1,000 Brownian motion simulations following the method of Garland et al. (1993). PhyANOVA was conducted in the Phytools library (Revell 2012), PhyMANOVA was conducted in the Geiger library (Harmon et al. 2008), and PGLS (including mPGLS) was conducted in the Caper library (Orme et al. 2013) in R. PGLS was conducted on each climatic variable separately following the method of Freckleton et al. (2002); this was used instead of phylogenetic independent contrasts because it can tolerate polytomies.

Results

Phylogenetic Analyses

Replicated ML searches of individual loci led to a single ML tree each (Appendix Figure G.1). All individual loci trees had at least one area of incongruity with the concatenated dataset tree (Figure 8.3) in the estimated relationships among genera and are summarized as follows. (1) In 12S *Taterillus* is placed as sister to *Sekeetamys* whereas Murniae is reconstructed as sister to Gerbillinae. (2) In 16S *Taterillus* is paraphyletic and includes *Gerbillus*, and Deomyinae is also reconstructed as being paraphyletic. (3) In COI *Taterillus* is sister to *Meriones*, and *Gerbilliscus* is less closely related to *Desmodillus* than in the concatenated dataset, and Deomyinae is paraphyletic. (4) In COII *Meriones* is monophyletic, and *Gerbilliscus* is less closely related to *Gerbillurus* than in the concatenated dataset, and Murinae is paraphyletic. (5) In BZRP *Taterillus* is sister to *Psammomys*. (6) In VWF *Deomys* is sister to *Uranomys*; *Gerbillus* is closely related to *Gerbilliscus*; and *Dipodillus* is closely related to *Meriones*. (7) In BRCA1 *Taterillus* is sister to *Gerbillus*, and *Deomys* is sister to *Acomys*. (8) In ACP5 *Sekeetamys* is sister to *Meriones+Psammomys+Dipodillus+Gerbillus+Taterillus*, and Lophiomyinae is sister to Murinae. (9) In CYTB *Meriones* is monophyletic, *Deomys* is sister to *Uranomys*, Lophiomyinae is sister to part of Murinae; Cricetidae and Murinae are both paraphyletic.

Other conflicts between phylogenies based on the concatenated dataset vs. individual loci include: (10) in GHR *Taterillus* is sister to *Gerbillus+Dipodillus*, and *Gerbilliscus* is more closely related to *Desmodillus* than *Gerbillurus*. (11) In IRPB *Taterillus* is sister to *Meriones+Psammomys*, *Desmodilliscus* is sister to *Meriones+Psammomys+Taterillus+Gerbillus+Dipodillus*, and *Deomys* is sister to the rest of the deomyines. (12) In RAG1 *Dipodillus* is paraphyletic, *Taterillus* is sister to *Gerbillus+Dipodillus*. (13) In AVPR2 *Desmodillus* is sister to the rest of Gerbillinae. Most of the aforementioned incongruities in the relationships among genera in loci trees occur in nodes with low BS values and/or short branches and represent a shift in the placement of the clades by a few nodes, which may be attributed to differential partitioning. In most of the loci trees the five sampled subfamilies were monophyletic.

Replicated ML searches using the concatenated dataset led to a single ML tree with an lnL score of -98,173.514 (Figure 8.3). Apart from the incongruities described above, the individual loci trees were concordant with the concatenated trees based on both ML (Figure 8.3) and BI (Figure 8.4; Figure 8.5) and with recently published results (e.g. Chevret and Dobigny 2005; Schenk et al. 2013); I found strong concordance in BS and PP values from both MrBayes and the Beast analyses. Most differences between the ML and the BI trees occurred within genera (e.g. the exact placement of *Gerbillus latastei*). The only among genus difference concerned the monophyly of *Meriones* where the ML and the Beast BI analyses found the genus to be paraphyletic while the MrBayes BI analysis found it to be monophyletic. However, the monophyly of *Meriones* has low support in MrBayes (PP, 0.50; Figure 8.4) whereas the paraphyly of the genus has high support in both Beast and RAxML (PP, 1.0; BS, 100%; Figure 8.3; Figure 8.5). Other PP values from the Beast and the MrBayes analyses were highly similar and the PP values in the following results are based on MrBayes only (Figure 8.4).

Most clades in the concatenated data analyses were strongly supported (76% of nodes \geq 85% BS, 84% \geq 0.95 PP) including all three of the polytypic subfamilies and both families (PP, 1.0; BS, 100%), the sister relationship between Gerbillinae and Deomyinae (PP, 1.0; BS, 100%), the Gerbillinae+Deomyinae sister relationship to Lophiomyinae (PP, 1.0; BS, 93%), the Gerbillinae+Deomyinae+Lophiomyinae sister relationship to Murinae (PP, 1.0; BS, 100%), and the monophyly of Muridae (PP, 1.0; BS, 100%). Most nodes with low PP and BS scores coincide with short branches within genera (e.g. within *Gerbillus*, *Meriones*, *Acomys*, and *Lophuromys*) and/or in regions with most conflict in the individual loci trees (e.g. within the

Meriones+Psammomys+Brachiontes+Rhombomys clade). Although the placement of *Taterillus* showed the most incongruence in the individual loci trees, its placement as a sister to Gerbillini I clade (Figure 8.3) was strongly supported in the concatenated dataset (PP, 1.0; BS, 100%).

Within Deomyinae, both polytypic genera were monophyletic with moderate support (*Acomys*, PP, 0.85; BS, 53%; *Lophuromys*, PP, 0.51; BS, 73%). Deomyinae consisted of a basal split between the monotypic genus *Uranomys* and the remaining three genera (PP, 1.0; BS, 100%), followed by a split between *Acomys* and *Lophuromys+Deomys* (PP, 1.0; BS, 93%). The split between the monotypic *Deomys* and *Lophuromys* was weakly supported (Figure 8.3; Figure 8.4). Within *Acomys*, there was moderate support for the basal split between the subgenus, *Subacomys*, consisting of only *A. subspinosus*, from the rest of the sampled species which form the subgenus, *Acomys* (PP, 0.85; BS, 53%). The monophyly of the subgenus *Acomys* and its exact placement within the genus is yet to be determined as *A. louisae*, which forms the monotypic subgenus *Peracomys*, was not sampled. Within *Lophuromys*, based on the only sampled member of the *Kivumys* subgenus (*L. woosnami*), the basal split between *Kivumys* and the subgenus *Lophuromys* (all other sampled species) had moderate support (PP, 0.51; BS, 73%).

Although I found strong support for the paraphyly of *Acomys minous* (PP, 0.72; BS, 86%) based on geographic distributions (i.e. GroupA clusters with *A. nesiotes* both found in Cyprus and GroupB clusters with *A. cilicicus* both found in Turkey; as in Barome et al. (2001)), members of the whole *Acomys* subclade that consists of *A. minous* GroupA+A. *nesiotes*+A. *cahirinus*+*A. minous* GroupB+A. *cilicicus* are separated by very short branches suggesting that they are all synonymous species; *A. chudeaui* and *A. airensis* are also potentially synonymous species, because they are similarly separated by very short branches (Figure 8.3; Figure 8.4).

Within Gerbillinae, both tribes Taterillini (*Tatera+Taterillus+Gerbilliscus+Gerbillurus+Desmodillus*) and Gerbillini (all other genera) were paraphyletic with Taterillini nested within Gerbillini. Within Taterillini, the two subtribes Gerbillurina (*Gerbillurus+Desmodillus*) and Taterillina (*Tatera+Gerbilliscus+Taterillus*) were also paraphyletic (Figure 8.3; Figure 8.4) as in Chevret and Dobigny (2005) and Schenk et al. (2013). *Gerbillus*, *Meriones*, and *Gerbilliscus* were paraphyletic. *Gerbillus* has *Dipodillus* nested within it (as in Chevret and Dobigny 2005 and Schenk et al. 2013; considered as synonyms in Nowak 1999), *Meriones* has *Brachiontes+Rhombomys+Psammomys* nested within it (as in Ito et al. 2010) in the ML tree (Figure 8.3) but is monophyletic in the BI tree (Figure 8.4), and *Gerbilliscus* has *Gerbillurus* nested in it.

Gerbillinae consisted of a basal split between a highly supported clade that consists of the two monotypic genera *Pachyuromys* and *Desmodilliscus* (PP, 1.0; BS, 99%) and the rest of *Gerbillinae*, followed by a split between *Tatera+Desmodillus+Gerbilliscus+Gerbillurus* and *Taterillus+Psammomys+Rhombomys+Brachiones+Meriones+Sekeetamys+Gerbillus+Dipodillus* (as in Chevret and Dobigny 2005). The first clade consisted of a basal split between the monotypic *Tatera* and *Desmodillus+Gerbilliscus+Gerbillurus* followed by a split between the monotypic *Desmodillus* and *Gerbilliscus+Gerbillurus*, the latter forming a paraphyletic group.

The second clade consists of a basal split between *Taterillus* and *Psammomys+Rhombomys+Brachiones+Meriones+Sekeetamys+Gerbillus+Dipodillus* followed by a split between *Psammomys+Rhombomys+Brachiones+Meriones* and *Sekeetamys+Gerbillus+Dipodillus*. The relationships among *Psammomys+Rhombomys+Brachiones+Meriones* are ambiguous (as in Ito et al. 2010) and were incongruent between the ML and BI analyses. In the ML analysis, this group consists of a basal split between *M. tamariscinus* and *Psammomys+Rhombomys+Brachiones+Meriones* (as in Ito et al. 2010) followed by a split between *Meriones* and *Psammomys+Rhombomys+Brachiones* with *Psammomys* and *Rhombomys+Brachiones* as sister clades. In the BI analysis, this group consisted of a basal split between *Rhombomys+Brachiones* and *Psammomys+Meriones*. *Sekeetamys+Gerbillus+Dipodillus* consisted of a basal split between the monotypic *Sekeetamys* and *Gerbillus+Dipodillus*, the latter being paraphyletic.

Within *Dipodillus*, both subgenera are paraphyletic; subgenus *Dipodillus* (represented in the sample by *D. simoni*) is nested within subgenus *Petteromys* (all other sampled *Dipodillus*). The extremely short branches separating *D. rupicola* and *D. campestris* indicates that these two species may be synonymous. *Gerbillurus* consisted of a basal split between the monotypic subgenus *Progerbillurus* (*G. paeba*) and the other two subgenera where the polytypic subgenus *Gerbillurus* is paraphyletic having *G. tytonis* (subgenus *Paratatera*) nested within it. Within *Gerbillus*, both subgenera are monophyletic with the genus consisting of a basal split between subgenus *Hendecapleura* (represented in the sample by *G. henleyi*, *G. nanus*, and *G. poecilops*) and *Dipodillus+Gerbillus* (the latter consisting of all other sampled *Gerbillus*) which in turn form two monophyletic groups. Despite the ambiguity of the relationships among genera close to *Meriones* (see above), in all instances, subgenus *Meriones* (consisting of only *M. tamariscinus*) is clearly separated from all other *Meriones* representing the basal split within the genus or within a larger clade that subsumes the genus. However, the other two sampled subgenera are

paraphyletic with *M. rex* (which along with *M. persicus* form subgenus *Parameriones*) nested within *Pallasiomys* (all other sampled *Meriones*); *M. persicus* is however divergent from other *Meriones*. The very short branches separating *M. shawi* and *M. unguiculatus* also suggests that these two species may be synonymous. Although *M. chengi* and *M. meridianus* are strongly supported sister groups (PP, 1.0; BS, 100%) they are clearly separated by relatively long branches which would argue against their synonymy (a synonymy proposed by Ito et al. 2010).

Univariate Association of Cranial Size with Climate

Species classified by IUCN as occurring in desert habitats lived in regions that were significantly more arid (low aridity index scores), received significantly less mean annual precipitation, and had slightly colder temperatures (by about 1°C) than species classified as mesic (see chapter 6). Similar results were found for the comparative analyses using both the pruned and the grafted (expanded) trees (Appendix Figure G.2); as well as when using the full dataset or when restricting analyses to gerbils, therefore, unless otherwise specified (in cases of discordance in significance), all results will refer to the full dataset, grafted tree analyses.

PhyANOVA indicates that cranial CS does not significantly differ between desert and mesic species (Figure 8.6a; $F = 0.059$, $p = 0.931$). However, PGLS shows that cranial CS is significantly positively correlated with the aridity index (Figure 8.6b; Coef = 0.026, $R^2 = 0.063$, $p = 0.007^*$) and significantly negatively correlated with mean annual temperature (Figure 8.6d; Coef = -0.002, $R^2 = 0.047$, $p = 0.0167^*$) indicating that cranial size is greater in more mesic and colder regions. PGLS indicates that cranial CS is not significantly correlated with mean annual precipitation (Figure 8.6c; Coef = 0.015, $R^2 = 0.002$, $p = 0.371$).

PhyANOVA indicates that desert species have significantly greater bullar CS than mesic species (Figure 8.7a; $F = 14.58$, $p = 0.032^*$); however, this result was not significant in the pruned full dataset analysis ($F = 11.60$, $p = 0.113$) or in both the grafted ($F = 2.49$, $p = 0.169$) and the pruned ($F = 0.22$, $p = 0.699$) gerbil only analyses. PGLS indicates that bullar CS is significantly negatively correlated with the aridity index (Figure 8.7b; Coef = -0.029, $R^2 = 0.071$, $p = 0.004^*$) and mean annual temperature (Figure 8.7d; Coef = -0.003, $R^2 = 0.143$, $p < 0.0001^*$) indicating that bullar size is greater in more arid and colder environments. PGLS indicates that bullar CS is not significantly correlated with mean annual precipitation (Figure 8.7c; Coef = -0.021, $R^2 = 0.004$, $p = 0.236$). PhyANOVA indicates that desert species have significantly greater relative

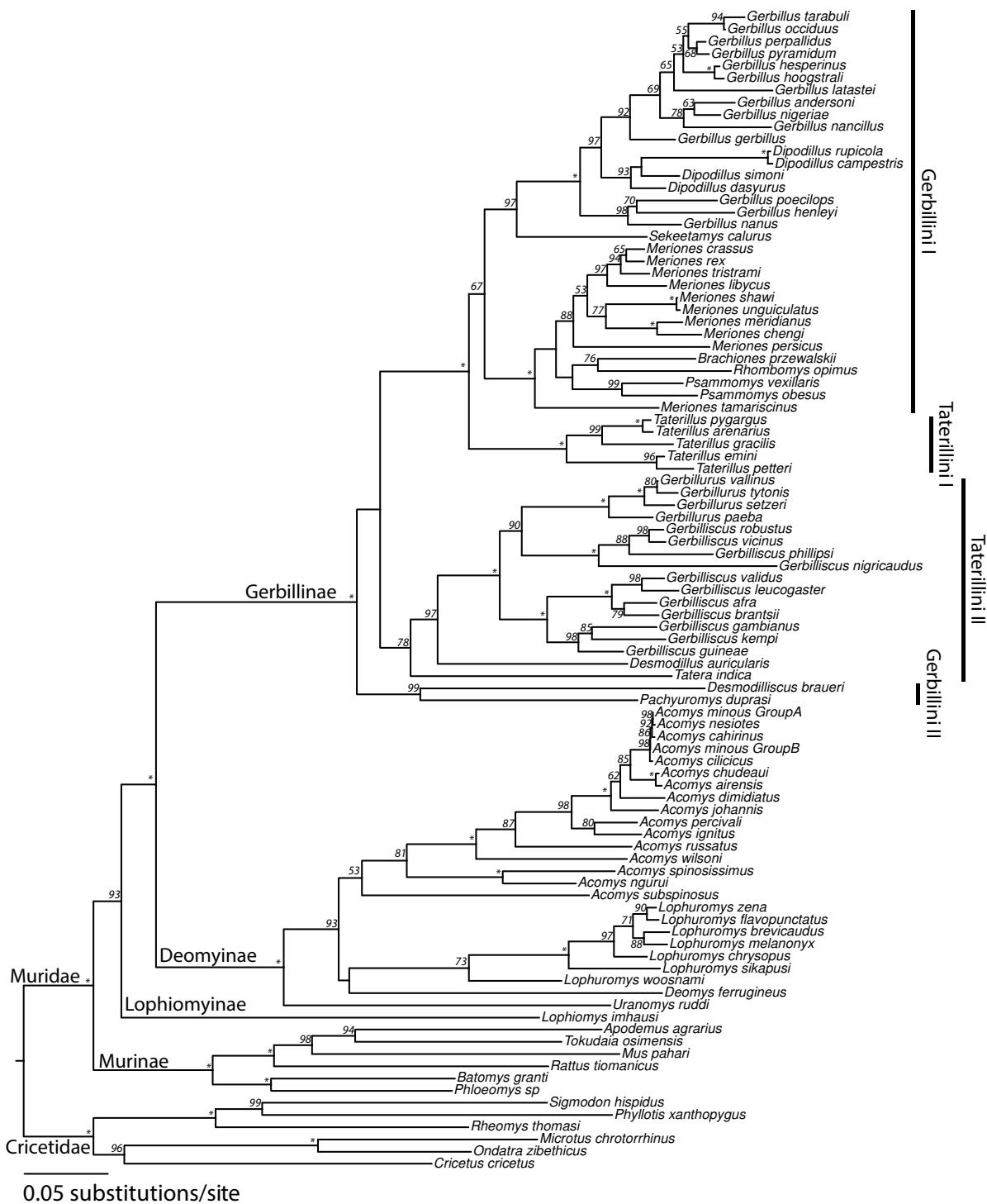


Figure 8.3. ML phylogram of the concatenated dataset. BS values are indicated if > 50%; those = 100% are marked with asterisks. Traditional tribal designations for gerbils based on the morphological phylogenies of Pavlinov et al. 1990 and Pavlinov 2001 are also indicated.

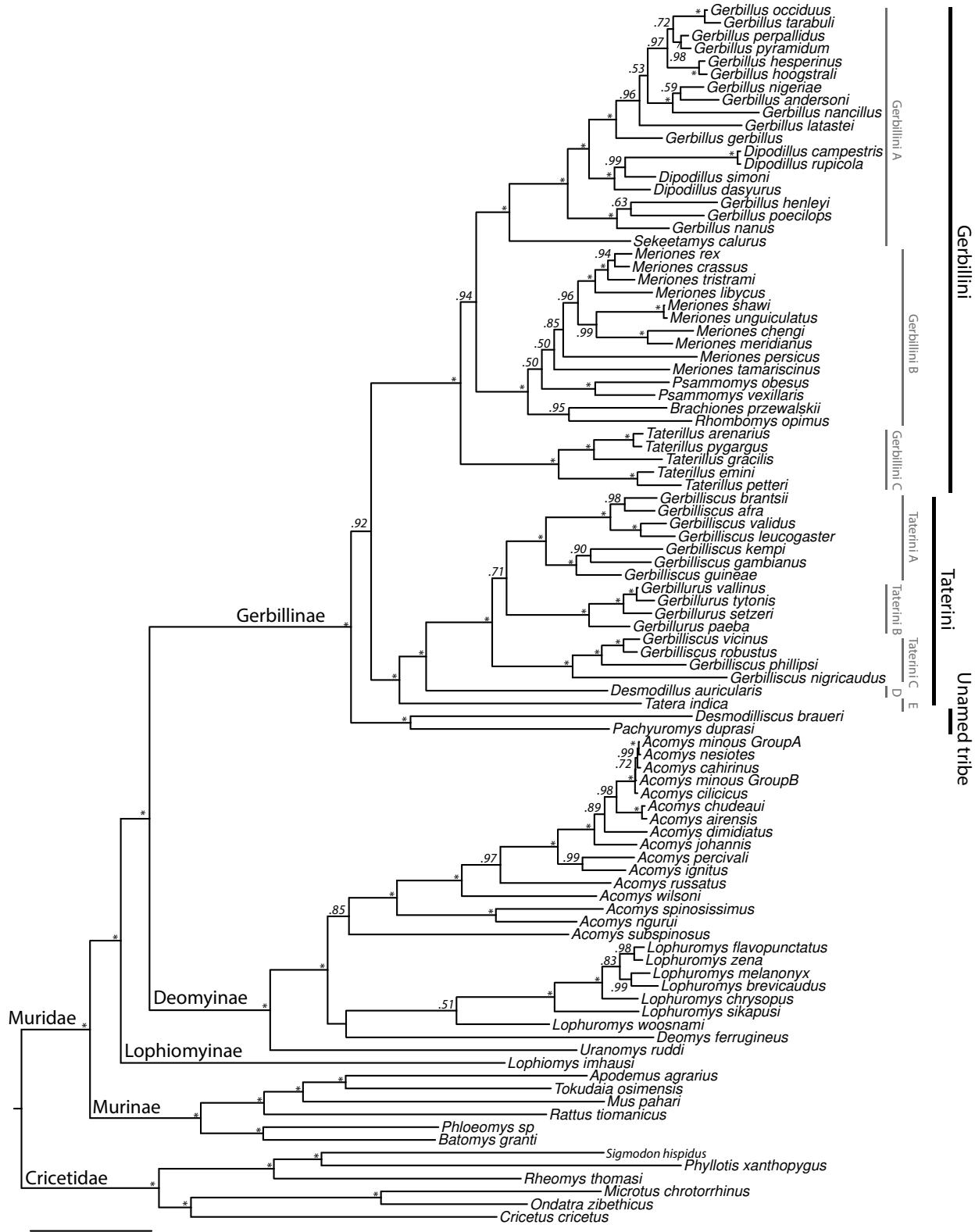


Figure 8.4. BI phylogram of the concatenated dataset from the MrBayes analysis. PP values are indicated if > 0.5 ; those = 1.0 are marked with asterisks. Proposed tribal and subtribal designations for gerbils based Chevret and Dobigny (2005) and this study are also indicated.

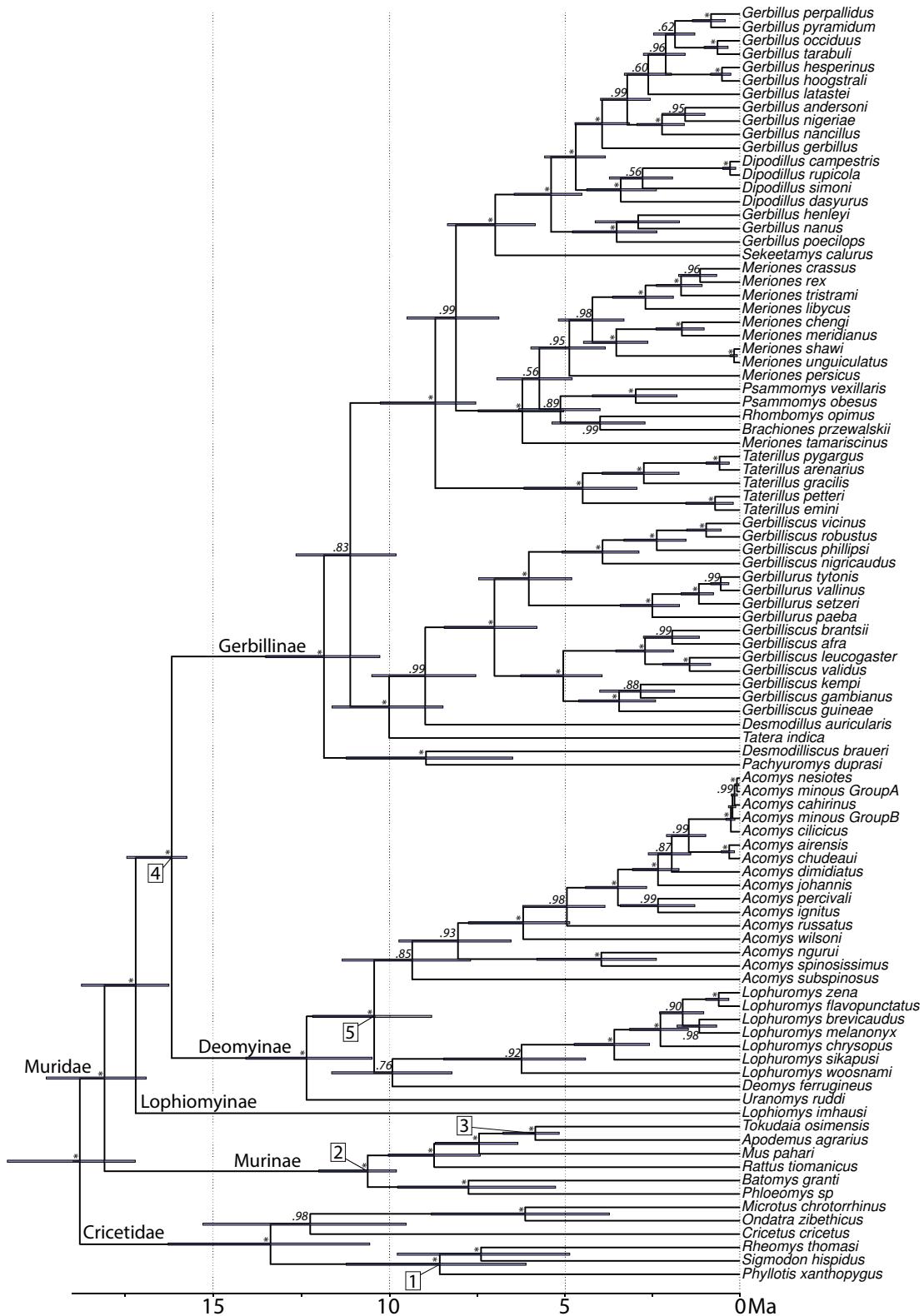


Figure 8.5. Time-calibrated ultrametric chronogram from the Beast analysis of the concatenated dataset. PP values are indicated if > 0.5; those = 1.0 are marked with asterisks. Node bars denote the 95% highest posterior densities. Nodes constrained in the analysis based on fossil calibrations are indicated with numbers inside squares that correspond with the fossils described in Table 8.1.

bullar CS than mesic species (Figure 8.8a; $F = 35.88$, $p = 0.001^*$). PGLS indicates that relative bullar CS is significantly negatively correlated with the mean annual precipitation (Figure 8.8c; Coef = -0.036, $R^2 = 0.107$, $p = 0.0005^*$) and mean annual temperature (Figure 8.8d; Coef = -0.001, $R^2 = 0.065$, $p = 0.0059^*$) indicating that relative bullar size is greater in environments that receive less rainfall and are colder. PGLS indicates that relative bullar CS is not significantly correlated with aridity index scores (Figure 8.8b; Coef = 0.003, $R^2 = 0.008$, $p = 0.628$).

Multivariate Association of Cranial Shape with Climate

Desert and mesic species do not form two distinct clusters in the morphospace represented by the first 6 RWs of both the cranium and the bulla (Figure 8.9). Furthermore, the PhyMANOVA, indicates that both the bullar and the cranial shape of these two groups are not significantly different (Table 8.2; Wilks' $\lambda = 0.17$, $p = 0.98$; Wilks' $\lambda = 0.21$, $p = 0.80$, respectively). However, a PhyANOVA conducted separately for the first six RWs indicates that desert species have significantly greater cranial RW1 scores (mean, desert = 0.013, mesic = -0.011; $F = 17.5$, $p = 0.014^*$) which is associated with a slight anterior-posterior compression of the cranium, an asymmetrical medio-lateral elongation, especially in the posterior region of the cranium which is suggestive of tympanic bulla inflation, as well as a slight medio-lateral compression of semilandmarks close to the rostrum (Figure 8.9d). Desert species also have significantly greater cranial RW5 scores (mean, desert = 0.003, mesic = -0.003; $F = 15.5$, $p = 0.028^*$) which is associated with a slight symmetrical medio-lateral compression (Figure 8.9f). Similarly, desert species have significantly lower bullar RW1 scores (mean, desert = -0.018, mesic = 0.015; $F = 19.2$, $p = 0.009^*$) which is associated with anterior-posterior elongation of the tympanic bulla (especially along the lateral side of the structure close to the mesopterygoid) as well as medio-lateral flattening of this structure in desert relative to mesic species (Figure 8.9a).

The mPGLS analyses indicate that cranial shape is significantly associated with aridity (Table 8.2; $F = 4.578$, $R^2 = 0.710$, $p < 0.0001^*$) as well as mean annual temperature (Table 8.2; $F = 7.012$, $R^2 = 0.805$, $p < 0.0001^*$) but not mean annual precipitation (Table 8.2; $F = 1.705$, $R^2 = 0.326$, $p = 0.051$). However, cranial shape was not significantly associated with all three climatic variables in the pruned full dataset analysis ($F = 55.247$, $R^2 = 0.982$, $p = 0.107$; $F = 96.744$, $R^2 = 0.989$, $p = 0.081$; $F = 7.982$, $R^2 = 0.873$, $p = 0.275$; for aridity, mean annual precipitation, and mean annual temperature respectively) or the pruned gerbil only analysis ($F = 150.05$, $R^2 =$

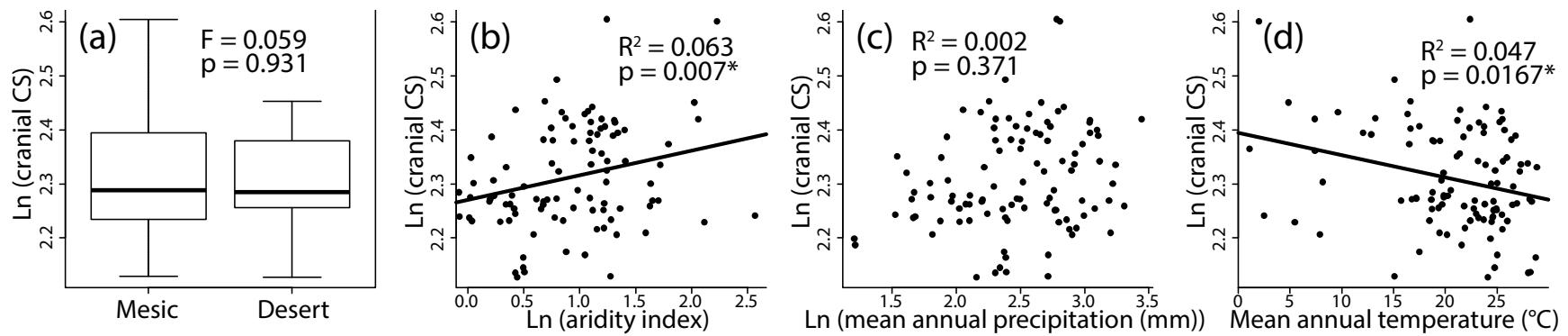


Figure 8.6. Association between cranial CS with (a) habitat, (b) aridity index, (c) mean annual precipitation, and (d) mean annual temperature. The association between morphological variables with the binary habitat was tested using PhyANOVA whereas the association between morphological variables with the three continuous environmental variables were tested using PGLS; both on the grafted phylogeny. A best fit line is shown in significant regressions. R^2 values, as in the text, are adjusted values (see chapter 6).

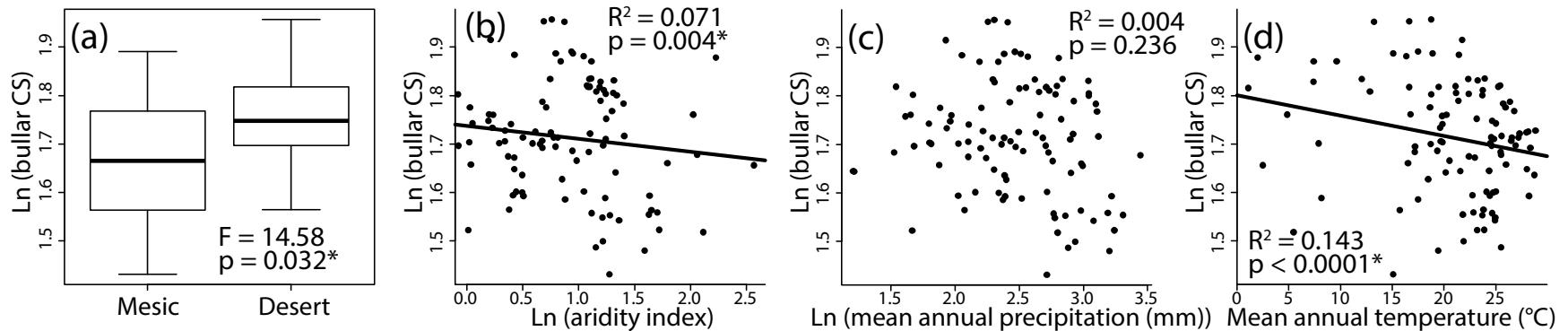


Figure 8.7. Association between bullar CS with (a) habitat, (b) aridity index, (c) mean annual precipitation, and (d) mean annual temperature. See Figure 8.6 legend for information.

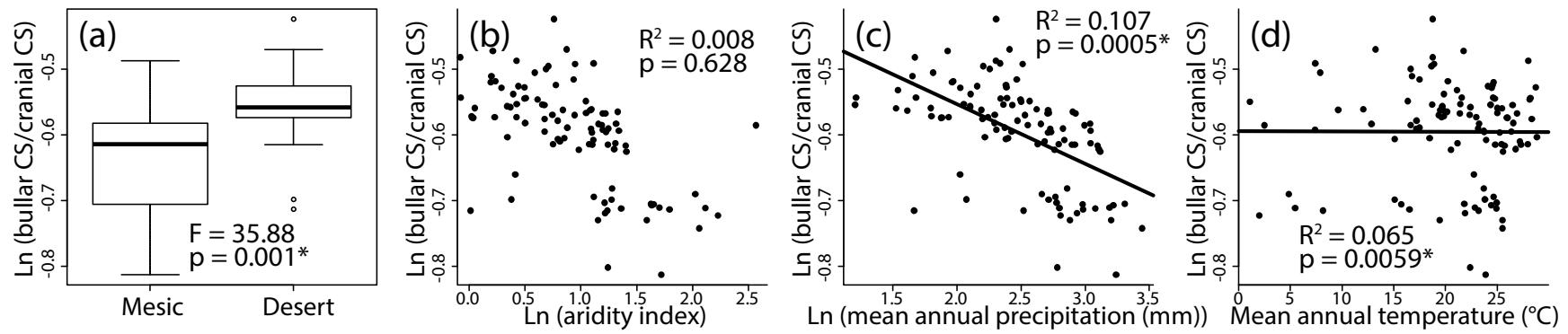


Figure 8.8. Association between relative bullar CS (bullar CS/cranial CS) with (a) habitat, (b) aridity index, (c) mean annual precipitation, and (d) mean annual temperature. See Figure 8.6 legend for information.

0.993 , $p = 0.064$; $F = 2.026$, $R^2 = 0.501$, $p = 0.514$; $F = 4.115$, $R^2 = 0.753$, $p = 0.375$; for aridity, mean annual precipitation, and mean annual temperature respectively).

Bullar shape is significantly associated with aridity (Table 8.2; $F = 3.027$, $R^2 = 0.582$, $p = 0.0005^*$), mean annual precipitation (Table 8.2; $F = 3.119$, $R^2 = 0.592$, $p = 0.0004^*$), and mean annual temperature (Table 8.2; $F = 2.902$, $R^2 = 0.566$, $p = 0.0008^*$) in the mPGLS analyses. However, bullar shape was not significantly associated with aridity ($F = 0.723$, $R^2 = 0.375$, $p = 0.756$) or mean annual precipitation ($F = 1.174$, $R^2 = 0.146$, $p = 0.640$) in the pruned full dataset analysis; or with mean annual precipitation ($F = 2.404$, $R^2 = 0.553$, $p = 0.077$) and mean annual temperature ($F = 2.563$, $R^2 = 0.580$, $p = 0.063$) in the grafted gerbil only analysis; or all three climatic variables in the pruned gerbil only analysis ($F = 20.840$, $R^2 = 0.951$, $p = 0.172$; $F = 1.129$, $R^2 = 0.112$, $p = 0.648$; $F = 112.241$, $R^2 = 0.991$, $p = 0.075$; for aridity, mean annual precipitation, and mean annual temperature respectively).

Table 8.2. Statistical summary of PhyMANOVA and mPGLS analyses of cranial/bullar shape vs. habitat/climate based on the grafted full dataset analyses. Shape is based on RW 1-70 which explain 99.9% of both cranial and bullar variation. Significant contrasts are italicized.

	Analysis	Wilks λ	F	R^2	p-value
Cranial shape vs. habitat	PhyMANOVA	0.1718	2.5211	-	0.9810
<i>Cranial shape vs. aridity</i>	<i>mPGLS</i>	-	<i>4.5777</i>	<i>0.7108</i>	<i><0.0001*</i>
Cranial shape vs. precipitation	mPGLS	-	1.7052	0.3263	0.0513
<i>Cranial shape vs. temperature</i>	<i>mPGLS</i>	-	<i>7.0125</i>	<i>0.8051</i>	<i><0.0001*</i>
Bullar shape vs. habitat	PhyMANOVA	0.2143	1.8332	-	0.8042
<i>Bullar shape vs. aridity</i>	<i>mPGLS</i>	-	<i>3.0274</i>	<i>0.5820</i>	<i>0.0005*</i>
<i>Bullar shape vs. precipitation</i>	<i>mPGLS</i>	-	<i>3.1193</i>	<i>0.5928</i>	<i>0.0004*</i>
<i>Bullar shape vs. temperature</i>	<i>mPGLS</i>	-	<i>2.9026</i>	<i>0.5665</i>	<i>0.0008*</i>

Discussion

Gerbillinae and Deomyinae Systematics

Deomyinae and Gerbillinae are strongly supported sister groups (PP, 1.0; BS, 100%), as in previous molecular phylogenies (e.g. Agulnik and Silver 1996; Michaux and Catzeffis 2000; Michaux et al. 2001; Martin et al. 2000; Jansa and Weksler 2004). For Gerbillinae, Chevret and Dobigny (2005), using mtDNA cytochrome b and 12S rRNA of 29 species of gerbils in 11 genera, recovered the same three major groups (which they label as tribes) that I did: a basal lineage (i.e. tribe I) consisting of the two monotypic genera *Pachyuromys*+*Desmodilliscus*;

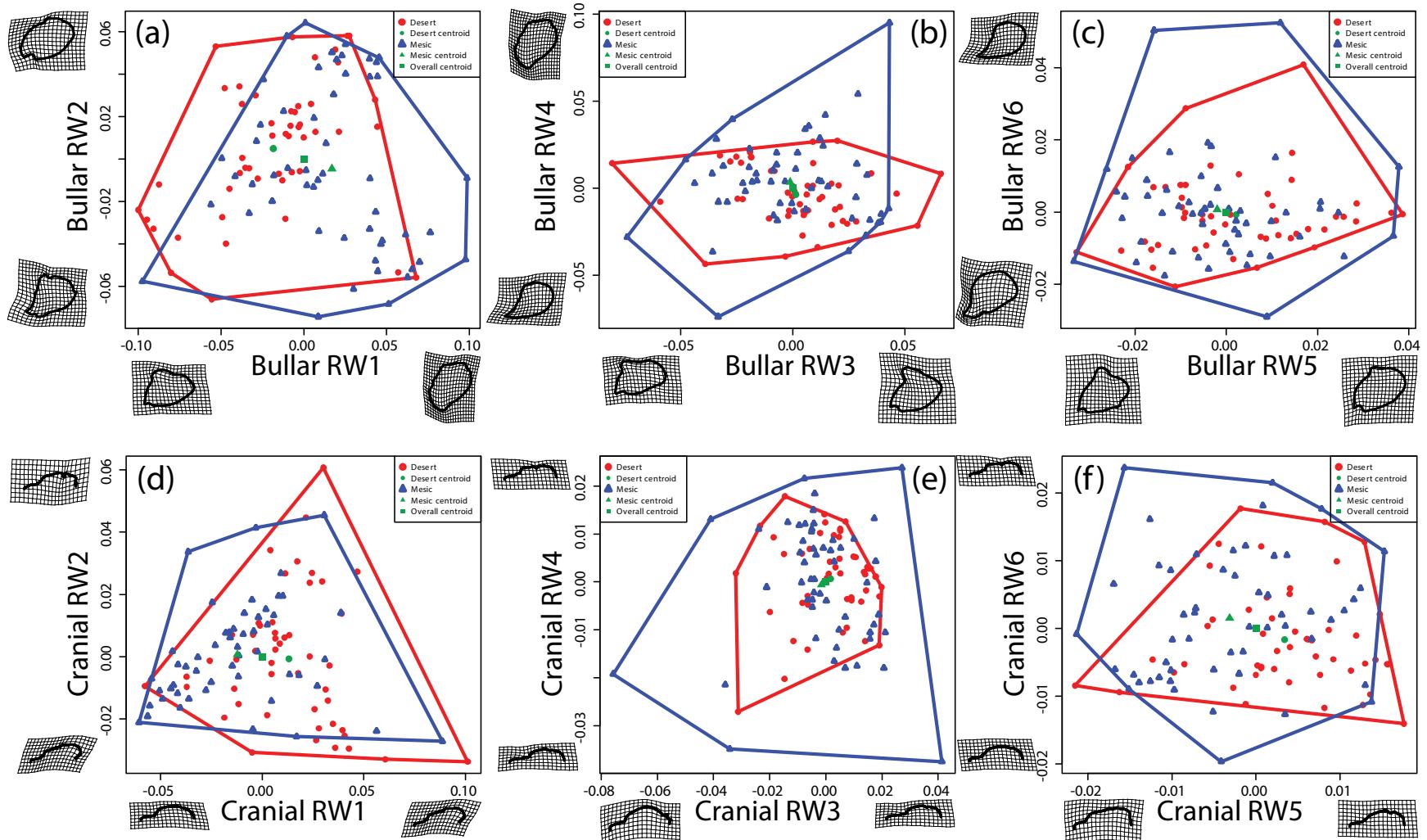


Figure 8.9. Relative warp plots and TPS for the ventral views of (a, b, c) the bulla and (d, e, f) the cranium of desert and mesic species. Bullar RW 1-6 explain 34.0, 24.1, 13.2, 9.2, 4.8, and 3.0% of the bullar shape variation respectively; cranial RW 1-6 explain 45.8, 16.4, 12.0, 6.1, 4.1, and 3.5% of the cranial shape variation respectively. Points indicate species means. TPS correspond with the maximum observed deformations along each RW axis relative to the overall consensus configurations.

which is sister to two clades that consist of (tribe II) *Tatera*+*Desmodillus*+*Gerbilliscus*+*Gerbillurus* and (tribe III) consisting of *Taterillus*+*Rhombomys*+*Brachiontes*+*Psammomys*+*Meriones*+*Sekeetamys*+*Gerbillus*+*Dipodillus* (they do not sample *Brachiontes*). Furthermore, I also recover the same two groups (i.e. subtribes) within tribe III that were found by Chevret and Dobigny (2005): (subtribe a) *Sekeetamys*+*Gerbillus*+*Dipodillus* (they assume *Dipodillus* as a synonym of *Gerbillus* a priori) and (subtribe b) *Psammomys*+*Rhombomys*+*Brachiontes*+*Meriones*. I find that the closest relative of *Brachiontes* within the sample is *Rhombomys* which form a relatively strongly supported clade (PP, 0.95; BS, 76%).

Similar to most previous molecular studies (e.g. Steppan et al. 2005; Chevret and Dobigny 2005; Schenk et al. 2013), traditional tribal designations, based on the morphological phylogenies of Tong (1989) and Pavlinov et al. (1990) have not been recovered, with both tribes Taterillini and Gerbillini being paraphyletic, with Taterillini nested within Gerbillini; even within Taterillini, the two subtribes Gerbillurina and Taterillina were also paraphyletic (Figure 8.3; Figure 8.4). Furthermore, I also found three paraphyletic genera: *Gerbillus*, *Meriones*, and *Gerbilliscus*; a total of 5 paraphyletic subgenera (within *Dipodillus*, *Gerbillurus*, and *Meriones*); and 2 possible synonymous species groups (*Dipodillus rupicola* and *Dipodillus campestris*; *Meriones shawi* and *Meriones unguiculatus*) which are separated by very short branches.

All the molecular studies, while largely consistent with each other (e.g. Benazzou 1984; Chevret 1994; Chevret and Dobigny 2005; Steppan et al. 2005; Ito et al. 2010; Schenk et al. 2013; this study), are strongly discordant with the morphology-based classification based on a combination of skeletal, dental, and genital traits (e.g. Tong 1989; Pavlinov et al. 1990). This reflects the need for major revisions within all taxonomic levels (tribal, subtribal, generic, and subgeneric) in the current morphologically based taxonomy of gerbils.

At the tribal and subtribal levels, I find strong support for the three new tribal and two new subtribal designations proposed by Chevret and Dobigny (2005) and thus support these new groupings with slight modifications (Figure 8.4). The present analyses indicate that *Brachiontes* should be included in the new Gerbillini tribe (i.e. tribe III) and in the Gerbillini B subtribe (i.e. subtribe b) (see above). I also propose grouping *Taterillus* into a third separate monotypic subtribe within Gerbillini and the division of the new Taterini tribe into five subtribes, two composed of *Gerbilliscus*, and one composed of *Gerbillurus*, and two monotypic tribes composed of *Desmodillus* and *Tatera*. The division of the Taterini tribe into five subtribes is based on the

strong support for the monophyly of two *Gerbilliscus* clades, one consisting of *G. robustus*+*G. vicinus*+*G. phillipsi*+*G. nigricaudus* (PP, 1.0; BS, 100%) and one consisting of all other sampled *Gerbilliscus* (PP, 1.0; BS, 100%); the monophyly of *Gerbillurus* (PP, 1.0; BS, 100%); and their clear separation from the two monotypic subtribes consisting of *Desmodillus* and *Tatera*.

However, I find conflicting support for the relationships within the aforementioned three polytypic subtribes with the ML analysis indicating that *Gerbillurus* is more closely related to the *G. robustus*+*G. vicinus*+*G. phillipsi*+*G. nigricaudus* subtribe (BS, 90%; Figure 8.3) and the BI analysis indicating that *Gerbillurus* is more closely related to the subtribe consisting of all other *Gerbilliscus* species (PP, 0.71; Figure 8.4). This grouping is supported by this study's expanded taxonomic sampling within *Gerbilliscus*, which allows for the observation of two distinctive clades of *Gerbilliscus* and therefore I do not support Chevret and Dobigny (2005) in the proposition to consider *Gerbillurus* to be a synonym of *Gerbilliscus*, but rather to preserve *Gerbillurus* as a genus and to split the *Gerbilliscus* species into two genera (i.e. forming the two monotypic *Gerbilliscus* subtribes described above). In all instances, I find strong support for the monophyly of a clade that consists of all *Gerbilliscus* and *Gerbillurus* (PP, 1.0; BS, 100%) which is consistent with previous morphological (Pavlinov et al. 1990; Pavlinov 2001) and molecular studies (Qumsiyeh et al. 1991; Chevret 1994; Chevret and Dobigny 2005).

At the generic and the subgeneric levels, within the new Gerbillini A subtribe (Figure 8.4), the results support considering *Dipodillus* to be a synonym of *Gerbillus* (e.g. Nowak 1999); however, the fact that all the sampled *Dipodillus* species cluster together within *Gerbillus* suggests that *Dipodillus* should be considered as a subgenus within *Gerbillus*, and the two other *Gerbillus* clades be considered as two additional separate subgenera, the latter two of which are consistent with the traditional two subgenera *Hendecapleura* and *Gerbillus* (i.e. Musser and Carleton 2005). The situation within the Gerbillini B subtribe is much more tenuous as I found conflicting groupings based on different analyses; the ML analysis supports three subgenera consisting of (1) *Meriones tamariscinus*; (2) all other *Meriones*; (3) *Brachiontes*+*Rhombomys*+*Psammomys* (as in Ito et al. 2010); whereas the BI analysis supports two subgenera consisting of (1) *Meriones*+*Psammomys* and (2) *Brachiontes*+*Rhombomys*. Therefore the monophyly of *Meriones* and consequently whether or not to synonymize *Brachiontes*+*Rhombomys*+*Psammomys* with *Meriones* cannot be determined; however, the two traditional sampled polytypic subgenera (*Parameriones* and *Pallasiomys*) are clearly paraphyletic.

The data strongly support the monophyly of Deomyinae (PP, 1.0; BS, 100%) as a clade that consists of the two monophyletic genera *Acomys* and *Lophuromys* and two monotypic genera *Uranomys* and *Deomys* as in previous molecular phylogenies based on DNA/DNA hybridization (Denys et al. 1995) mtDNA cytochrome b sequences, (Verheyen et al. 1995), nuDNA VWF and/or LCAT sequences (Michaux and Catzeflis 2000, Michaux et al. 2001) a combination of DNA/DNA hybridization, mtDNA and nuDNA sequences (Chevret et al. 2001), and nuDNA BRCA1, GHR, IRBP, and RAG1 (Schenk et al. 2013).

The monophyly of Deomyinae and its isolation from Murinae is also supported by some morphological traits including pelage texture, palatal and molar occlusal patterns, and reproductive biology (Musser and Carleton 2005). Deomyine species are not traditionally grouped at the suprageneric level, however, the results support the division of deomyines into three tribes: (1) a moderately supported monotypic clade (Acomyini) consisting of all *Acomys* (PP, 0.85; BS, 53%); (2) a weakly supported clade (Deomyini) consisting of all *Lophuromys+Deomys* (PP, 0.47; BS, 41%); (3) a monotypic clade (Uranomyini) consisting of *Uranomys ruddi*. All three aforementioned groups are supported by Schenk et al. (2013) albeit with stronger support for all three groups/tribes in their phylogeny, which consists of nearly half the number of taxa sampled in this study. Unlike, Gerbillinae, the present results do not reject the monophyly of all of the deomyine genera and all of the sampled deomyine subgenera. I also find two possible synonymous species groups (*Acomys minous Group A+Acomys nesiotes+Acomys cahirinus+Acomys minous Group B+Acomys cilicicus* and *Acomys chudeaui+Acomys airensis*) both of which are separated by very short branches.

Desert Adaptation of the Tympanic Bulla

Gerbillinae is the most diverse subfamily of mammals inhabiting the Palaearctic Desert, which extends from Asia to Africa, with over 46 species in 8 genera being endemic to this arid region (Lay 1972). Chevret and Dobigny (2005) suggested that the discordance between morphological and molecular phylogenies in Gerbillinae is a result of convergence as a consequence of strong adaptive pressures in arid environments, including in traits located at the posterior part of the skull, which along with teeth characters, is the basis of gerbil classification. For example, features of the middle ear were considered as derived character states in the morphological phylogeny of Tong (1989) and used to determine the relationships among genera.

Even earlier, subgeneric relationships within gerbils have been based on tympanic bulla morphology in addition to dental characters (e.g. Petter 1973). These traits have been used to group genera (e.g. *Gerbillus* and *Gerbillurus*) that previous molecular phylogenies and this study find to be part of divergent lineages. Lay (1972) argued that the increase in bullar hypertrophy in gerbils, which he also found to be associated with arid environments, is a useful adaption for predator avoidance in open habitats. Pavlinov and Rogovin (2000) similarly argued that tympanic bulla hypertrophy (which they found to be statistically significant in several specialized desert rodents) was useful in increasing auditory sensitivity at low frequencies. However, these studies did not apply phylogenetic correction and therefore may have over-estimated the strength of the association between bullar morphology with aridity when testing for desert adaptation.

I found support for the prediction that convergent adaptation to aridity led to discordance between molecular and morphological phylogenies in both the morphology of the tympanic bulla and the overall cranium. The results indicate that even after correcting for phylogenetic relationships, the size of the cranium is significantly smaller in more arid and in warmer environments; whereas the size of the tympanic bulla is significantly larger in more arid and in colder environments. Furthermore, the relative size of the tympanic bulla to the rest of the cranium is also significantly greater in environments that receive less rainfall and are colder. However, evidence for the association between the overall size-independent shape variation of the cranium and the tympanic bulla with climate was more tenuous and depended on the dataset (i.e. full dataset vs. gerbils only; grafted vs. pruned) with the grafted analysis generally finding a significant association with most aridity indices and the pruned analyses showing no significant association. Nonetheless, I found evidence of a significant difference between desert and mesic species when binary habitats were compared along several shape variation axes. Differences were associated with asymmetrical medio-lateral elongation of the cranium of desert species, especially in the posterior region of the cranium, which is associated with bullar inflation, and a change in the shape of the rostrum. More specifically, the shape of the tympanic bulla in desert species is more anterior-posteriorly elongated along the lateral side of the structure close to the mesopterygoid, and more medio-laterally flattened when compared to the mesic species.

Considering that tympanic bulla morphology is widely used in morphological phylogenies of gerbils that serve as a basis for the taxonomy of the group, convergence in this trait along with other cranial structures that are prone to desert adaption would explain part of the

discordance between molecular and morphological phylogenies and the frequent paraphyly at tribal, subtribal, generic, and subgeneric levels. The association between tympanic bulla morphology with aridity and its propensity for convergence in diverse taxa has been demonstrated before in a much larger order-level taxonomic scale (chapter 6). The use of homoplastic characters in place of synapomorphies in morphological phylogenies of gerbils explain the many inaccuracies of the taxonomic divisions within Gerbillinae (morphological phylogenies are the basis for the current taxonomy of the group). Although I focus on the bulla, other linear cranial characters common in traditional morphological phylogenetics of rodents, are also expected to experience convergent adaptation to aridity in rodents. Cranial convergence is very common in rodents due to their small size, short dispersal distances, and short generation times, enabling them to rapidly respond to environmental pressures (Samuels 2009).

By using the geometric morphometric approach, I was able to test the association between climatic variables with cranial/bullar size and shape separately. The stronger association between bullar size with climatic variables relative to bullar shape suggests that bullar variation is mostly dichotomous, associated with size enlargement in deserts, as a consequence of a discrete shift in life style, associated with the need for increased auditory sensitivity in open habitats (e.g. Lay 1972) rather than a more complex and direct adaptation of the overall bullar shape to aridity. Moreover, this change in size occurs along continuous aridity gradients rather than among binary habitat categories which suggests that desert adaptation is occurring in a continuous fashion where relative bullar size is increasing as aridity increases and there are more than two adaptive optima representing the bullar condition of mesic vs. desert species.

Despite the fact that overall cranial/bullar shape did not show strong association with climatic variables, the use of geometric morphometrics allowed for the determination that the major difference in both bullar and cranial shape between desert and mesic species is that of increased anterior-posterior elongation and more medio-lateral flattening in desert species. Colangelo et al. (2010) found a similar association in *Gerbilliscus*; although they did not apply phylogenetic correction, they found a significant association between overall dorsal and ventral cranial shape with rainfall, especially in landmarks associated with the overall shape of the tympanic bulla. They argued that the different shapes of the tympanic bulla may correspond to the capacity to recognize different sound frequencies and may be associated with pre-mating reproductive barriers in *Gerbilliscus* (Colangelo et al. 2010). The association between bullar

shape with the capacity for conspecific mate recognition have been argued before in other gerbil genera where an inverse relationship between population density and the degree of bulla hypertrophy have been demonstrated (Petter 1961; Lay 1972). However, given the larger taxonomic scale of the present study, the adaptive signal for bullar inflation relative to aridity (i.e. environmental filtering) seems to trump the signal for interspecific competition, more so for bullar size than for bullar shape.

Conclusions

In this study, I use the largest molecular dataset for gerbils and deomyines to date (in terms of characters examined and taxa sampled) to estimate the phylogeny of the group. I find multiple paraphyletic taxonomic groupings in gerbils, at the tribal, subtribal, generic, and subgeneric levels and consequently recommend taxonomic revision at all taxonomic scales. Most of these recommendations have been made before by other authors. All traditional tribal and subtribal groups were invalid due to their paraphyly, and consequently new monophyletic tribal and subtribal groups were recommended. I also find 3 paraphyletic genera, 5 paraphyletic subgenera, and 2 possible synonymous species groups. Perhaps as a consequence of the recency of the description of the deomyine subfamily and the fact that this group is mostly based on molecular data, the taxonomic situation within this subfamily is much more stable, with all polytypic genera and subgenera being monophyletic. However, I identified two possible synonymous species groups within *Acomys*. The paraphylies within Gerbillinae, at all taxonomic scales, may be a consequence of traditional taxonomic groups being based on morphological phylogenies which in turn are based on convergent morphological traits rather than synapomorphies. This was supported by the pattern of convergent cranial adaptations to aridity found in this study, which was present after phylogenetic correction. The association between aridity with bullar/cranial size was stronger than the association with shape; this association is evident along climatic clines rather than among the two binary habitat classifications, which implies that morphology is varying in a dichotomous fashion between an enlarged bulla/reduced cranium in desert regions vs. a reduced bulla/enlarged cranium in mesic environments. However, this variation is also continuous along aridity gradients rather than representing two adaptive optima for desert vs. mesic environments. Aspects of cranial and bullar shape most variable

between habitats is that of bullar hypertrophy of desert species and specifically increased anterior-posterior elongation and medio-lateral flattening of the bulla relative to mesic species.

CHAPTER NINE

CONCLUSION

In this dissertation, I use comparative morphology informed by molecular systematics and geometric morphometrics to address fundamental questions at the intersection of ecology and evolution including how ecology and evolution interact to lead to the current observed pattern of taxonomic and morphological diversity; a topic of shared interest to ecologists and evolutionary biologists (Ricklefs 2006, 2007). Diversity patterns are usually studied by investigating the patterns of speciation, extinction, competition, niche variation, and biogeographic transition (Keddy 1992; Brown 1995 Weiher et al. 2011), depending on the spatial and temporal scale of the study. I study this topic in the most diverse order and superfamily of mammals (Rodentia and Muroidea respectively) which facilitates an unprecedented look at what drives diversity patterns in mammals in general as well as within the context of desert habitats.

The main question in this dissertation is “why are muroid rodents so diverse?” In order to answer this question, I quantified the fit of several models of variation in diversity among clades, including the ecological opportunity model of adaptive radiation, or more specifically that biogeographic transitions between continents trigger increased diversification rates (chapter 3); the hypothesis that ecological and ecomorphological attributes drive differential diversification rates within clades (chapter 4); and the hypothesis that increased diversity is associated with increased disparity (chapter 5). In the second part of the dissertation, I studied the interaction between rodents and desert environments, including their morphological adaptations to aridity (chapter 6); how past and present interactions of rodents have shaped their assembly patterns within desert communities (chapter 7); and the systematics of the largest radiation of desert mammals (Gerbillinae) and their closest relatives, the deomyines, while conducting a more focused test of desert adaptation (chapter 8).

Similar to Schenk et al. (2013), where they showed that only one of the six investigated primary continental colonizations, South America, fit all the predictions of the ecological opportunity model (based on *taxonomic* predictions of the ecological opportunity model), I also found that among all the primary biogeographic transitions, only the colonization of South America showed strong support for the *phenotypic* predictions of the model; indicating that extrinsic factors contribute little to the observed diversity pattern in muroid rodents, at least in

the large scale employed. I also show that directional shifts in the evolution of body size, appendage proportions, relative tail length, elevation, diet, and other ecological attributes show support for association with diversification rates. This may indicate that intrinsic factors are more important than extrinsic factors in the diversification of muroid rodents. I also showed that diversity/diversification rates and disparity/morphological evolution rates are decoupled in muroids, which indicates that this clade does not fit predictions of evolutionary theories including the punctuated equilibrium model (Gould and Eldredge 1977) and the ecological adaptive radiation model (Schluter 2000).

I detected very frequent transitions between desert and mesic habitats in rodents and also a strong pattern of correlation between bullar and nasal morphology with aridity, a result that is consistent with previous studies that were investigated at a narrower scope. I also show that the majority of desert rodent assemblages are not *phylogenetically* structured at both the provincial and regional scales (i.e. they seem to be neutrally assembled from source species pools) while most are *morphologically* structured at the provincial scale (i.e. over-dispersed pattern in resource acquisition traits) indicative of interspecific competition/competitive exclusion between distant relatives. By estimating the largest molecular phylogeny of gerbils and deomyines to date, I show paraphyly is common at the tribal, subtribal, generic, and subgeneric level in Gerbillinae; which I attribute to convergent adaptations to aridity causing discordance between morphological phylogenies, which are the basis of the taxonomic classification, and molecular phylogenies, in accord with the prediction of Chevret and Dobigny (2005).

The main novelty of this dissertation is using a broad scale to answer questions that are commonly addressed in narrow scales. In addition, an updated systematic understanding of gerbils and deomyines induced by the newly estimated molecular phylogeny, is important to ecological and evolutionary studies that require an accurate understanding of species identities and the evolutionary relationships among them.

APPENDIX A

SUPPORTING MATERIAL FOR CHAPTER 2

Table A.1. List of specimens digitized in three dimensions for chapter 5. AMNH= American Museum of Natural History (NY, USA); FMNH= Field Museum of Natural History (IL, USA); LCM= Laboratorio Citogenetica Mammiferos (Chile); MVZ= Museum of Vertebrate Zoology (CA, USA); OMNH= Oklahoma Museum of Natural History (OK, USA); UF= Florida Museum of Natural History (FL, USA); USNM= National Museum of National History (DC, USA).

	Museum tag
Calomyscidae	
Calomyscinae	
<i>Calomyscus baluchi</i>	UF 28486, 28503, 28504, 28502
Cricetidae	
Arvicolinae	
<i>Alticola strelzowi</i>	AMNH 178819; FMNH 34034
<i>Arvicola amphibius</i>	FMNH 112222, 112223, 112224; UF 22400
<i>Chionomys nivalis</i>	MVZ 198808; USNM 369657, 104527, 105816
<i>Dicrostonyx groenlandicus</i>	UF 24163, 24407, 24167, 24116
<i>Eothenomys custos</i>	AMNH 44140, 44150, 44156, 44147
<i>Lagurus lagurus</i>	AMNH 87095, 176250, 176249, 257134
<i>Lasiopodomys mandarinus</i>	AMNH 25438, 45439; USNM 172586, 299098
<i>Lemmus sibiricus</i>	MVZ 128863, 128857, 128855, 128854
<i>Microtus arvalis</i>	FMNH 103131, 103132, 103133; USNM 85655
<i>Microtus californicus</i>	FMNH 10743, 10745, 10750; USNM 41607
<i>Microtus chrotorrhinus</i>	AMNH 147362; MVZ 54425, 54427, 54426
<i>Microtus kikuchii</i>	USNM 358625, 332965, 332967, 332964
<i>Microtus montanus</i>	FMNH 12653, 12649, 12664; UF 12732
<i>Microtus pennsylvanicus</i>	UF 3887, 3888, 3911; USNM 150132
<i>Microtus richardsoni</i>	USNM 81384
<i>Myodes gapperi</i>	MVZ 56815, 56816, 56813, 56814
<i>Neodon irene</i>	USNM 449167, 449168, 449172, 449173
<i>Neofiber allenii</i>	UF 7418, 7421, 7445, 7440
<i>Ondatra zibethicus</i>	UF 1791, 1793, 1795, 2415
<i>Phenacomys intermedius</i>	USNM 557668, 174477, 557669, 174432
<i>Prometheomys schaposchnikowi</i>	AMNH 174334, 257138, 206579; USNM 547937
<i>Synaptomys cooperi</i>	UF 3839, 3841, 6436, 7946
Cricetinae	
<i>Allocricetus eversmanni</i>	AMNH 176255, 59753; FMNH 33959, 33964
<i>Cricetus barabensis griseus</i>	FMNH 33980, 33981, 33982, 33985
<i>Cricetus migratorius</i>	UF 14594, 27124, 27145, 27142
<i>Cricetus cricetus</i>	AMNH 176483, 176484; MVZ, 41457, 129377
<i>Mesocricetus auratus</i>	FMNH 63951; MVZ 102642, 102643; UF 3987
<i>Phodopus sungorus</i>	AMNH 206570; MVZ 174380, 41239, 174379
Neotominae	
<i>Habromys lepturus</i>	USNM 68615, 68618, 68609, 68619
<i>Hodomys allenii</i>	USNM 44633, 44634, 44626, 44627
<i>Isthmomys pirrensis</i>	USNM 338302, 338269, 338306, 338270
<i>Megadontomys thomasi</i>	MVZ 113564, 113558, 113559, 113562
<i>Neotoma bryanti</i>	MVZ 186295, 195326, 186296, 186297
<i>Neotoma cinerea</i>	UF 31327, 3166
<i>Neotoma devia</i>	USNM 215546, 226400, 202463, 226399
<i>Neotoma floridana</i>	UF 14691, 12778, 166, 167
<i>Neotomodon alstoni</i>	MVZ 91979, 91978, 91986, 91984
<i>Ochrotomys nutalli</i>	UF 112, 12421, 2710, 801
<i>Onychomys leucogaster</i>	FMNH 123451, 123450; UF 24175, 12613
<i>Osgoodomys banderanus</i>	USNM 45334, 45335, 45333, 33305
<i>Peromyscus aztecus</i>	USNM 392010; UF 24035, 24030, 24036
<i>Peromyscus boylii</i>	UF 6221, 6224, 6225, 6121
<i>Peromyscus californicus</i>	USNM 569214
<i>Peromyscus crinitus</i>	USNM 53283

Table A.1—continued.

	Museum tag
<i>Peromyscus eremicus</i>	UF 9445, 9447, 9448; USNM 60100
<i>Peromyscus fraterculus</i>	USNM 81017, 69556, 81016, 91566
<i>Peromyscus leucopus</i>	UF 9298, 9303, 1968; USNM 157114
<i>Peromyscus maniculatus</i>	UF 3637, 2802, 2803; USNM 530844
<i>Peromyscus mexicanus</i>	UF 23931, 23930, 23929; USNM 314413
<i>Peromyscus polionotus</i>	UF 13035, 5167, 786; USNM 308898
<i>Reithrodontomys creper</i>	MVZ 164894, 164898, 164892, 164897
<i>Reithrodontomys fulvescens</i>	FMNH 73418, 13115, 54147; USNM 70255
<i>Reithrodontomys gracilis</i>	MVZ 98443, 98442; USNM 108143
<i>Reithrodontomys megalotis</i>	FMNH 12273, 12271, 12270; UF 6080
<i>Scotinomys teguina</i>	FMNH 128560, 128561; UF 27717, 27712
<i>Xenomys nelsoni</i>	USNM 45287, 45285
<i>Biomys musculus</i>	FMNH 54084, 54085, 54086; UF 6039
Sigmodontinae	
<i>Abrothrix andinus</i>	MVZ 115690, 115691, 115689, 115697
<i>Abrothrix longipilis</i>	MVZ 163783, 163784, 163782, 163783
<i>Aegialomys xanthaeolus</i>	FMNH 194444, 19445; USNM 304528, 551641
<i>Akodon aerosus</i>	FMNH 52529, 52524, 43232; USNM 507279
<i>Akodon boliviensis</i>	FMNH 107917; MVZ 172907, 172953; UF 9190
<i>Akodon kofordi</i>	MVZ 171660, 171662, 171661, 171663
<i>Akodon lutescens</i>	USNM 259623
<i>Akodon mimus</i>	MVZ 116109, 171748, 171751
<i>Akodon spegazzinii</i>	UF 27623, 27625, 27629, 27633
<i>Akodon torques</i>	MVZ 171713, 171724, 174054; USNM 194638
<i>Andalgalomys pearsoni</i>	FMNH 164184, 164188, 157341; MVZ 145278
<i>Andinomys edax</i>	FMNH 162761; MVZ 120224, 120225, 141617
<i>Auliscomys sublimis</i>	MVZ 139474, 139475, 115912, 139477
<i>Brucepattersonius igniventris</i>	MVZ 191467, 183036, 191468, 183037
<i>Calomys callosus</i>	UF 27606, 27625, 27629, 27633
<i>Calomys lepidus</i>	MVZ 115752, 174016, 116018, 115754
<i>Calomys venustus</i>	USNM 259264
<i>Cerradomys subflavus</i>	MVZ 197609, 197542, 1970610, 197541
<i>Chelemys macronyx</i>	MVZ 151013, 154583, 174384, 174382
<i>Chinchillula sahamae</i>	MVZ 116034, 172675, 116181, 174023
<i>Delomys dorsalis</i>	MVZ 183048, 183047, 183064, 183065
<i>Deltamys kempfi</i>	AMNH 206118, 206105, 206163, 206097
<i>Eligmodontia typus</i>	AMNH 262812; FMNH 124314, 124313, 124322
<i>Euneomys chinchilloides</i>	FMNH 50736, 134181; MVZ 186039, 186038
<i>Geoxus valdivianus</i>	MVZ 162249, 159389, 154603, 154607
<i>Graomys griseoflavus</i>	FMNH 28423, 50920, 46125; UF 27630
<i>Holochilus brasiliensis</i>	AMNH 210253; FMNH 136891, 87988, 88919
<i>Holochilus sciurus</i>	FMNH 55476, 118813, 93050; UF 13357
<i>Ichthyomys stolzmanni</i>	AMNH 10109
<i>Irenomys tarsalis</i>	MVZ 155837, 154620, 184955, 152171, 201154
<i>Juliomys pictipes</i>	MVZ 182079, 197565, 197563, 197564
<i>Kunsia tomentosus</i>	FMNH 122710, 122711; USNM 584515, 584516
<i>Lenoxus apicalis</i>	MVZ 172657, 171511, 172656, 171513
<i>Loxodontomys micropus</i>	MVZ 155836, 158475, 158474, 155827
<i>Melanomys caliginosus</i>	MVZ 164873, 164871, 164870, 124057
<i>Microryzomys minutus</i>	MVZ 115636, 171472, 173974, 166666
<i>Neacomys spinosus</i>	MVZ 136626, 136629, 136625, 136627
<i>Necromys amoenus</i>	MVZ 172884, 172886, 172881, 172885
<i>Nectomys apicalis</i>	MVZ 153544, 153542, 153534, 153539
<i>Nectomys squamipes</i>	FMNH 26741; UF 6581, 6583, 30468
<i>Neotomomys ebriosus</i>	FMNH 75580; MVZ 114749, 114747, 172661
<i>Nephelomys keaysi</i>	MVZ 173987, 171460, 171445, 171446
<i>Nephelomys livipes</i>	FMNH 52703, 52702, 52705, 52708
<i>Notiomys edwardsii</i>	MVZ 182132
<i>Oecomys bicolor</i>	FMNH 117010, 116920, 116919; UF 635
<i>Oecomys concolor</i>	FMNH 87968; USNM 374321
<i>Oecomys superans</i>	MVZ 155007, 200944, 153524, 155008
<i>Oligoryzomys fulvescens</i>	UF 6148, 28847, 6149, 6152
<i>Oligoryzomys longicaudatus</i>	UF 25933, 27622, 27671; USNM 259583
<i>Oligoryzomys microtis</i>	FMNH 84349, 84350, 84351; USNM 584565
<i>Oryzomys couesi</i>	UF 9869, 29867, 29868, 6901
<i>Oryzomys palustris</i>	UF 23558, 23560, 23561; USNM 510842
<i>Oxymycterus hiska</i>	AMNH 91602, 91601; MVZ 172660, 171520

Table A.1—continued.

	Museum tag
<i>Oxymycterus nasutus</i>	USNM 460550, 484395, 461881, 460551
<i>Phyllotis amicus</i>	MVZ 138034, 145548
<i>Phyllotis andium</i>	MVZ 135748, 135749, 135752, 135753
<i>Phyllotis caprinus</i>	OMNH 30081, 30082
<i>Phyllotis darwini</i>	LCM 3047, 3338, 4038, 4057, 4037, 4061
<i>Phyllotis magister</i>	MVZ 174036, 174038
<i>Phyllotis osilae</i>	FMNH 52579, 107828, 107831; USNM 194576
<i>Phyllotis xanthopygus</i>	LCM 3009, 3143, 3351, 3021
<i>Pseudoryzomys simplex</i>	AMNH 262048; USNM 584585, 584586, 390668
<i>Punomys kofordi</i>	MVZ 1147557, 114758, 116193
<i>Reithrodon auritus auritus</i>	MVZ 163411, 172218, 171163, 165853
<i>Rhagomys longilingua</i>	FMNH 170687
<i>Rheomys thomasi</i>	MVZ 98811, 98814, 98798, 98808
<i>Rhipidomys macconnelli</i>	MVZ 160085, 160088, 160082, 160086
<i>Rhipidomys nitela</i>	MVZ 197548, 197549, 197550, 197551
<i>Scapteromys tumidus</i>	AMNH 235431; MVZ 183268, 183267, 183269
<i>Scolomys melanops</i>	AMNH 67522
<i>Scolomys ucayalensis</i>	MVZ 183166, 183169, 183167, 183168
<i>Sigmodon alstoni</i>	FMNH 20040, 20042, 20045; USNM 442581
<i>Sigmodon arizonae</i>	MVZ 62573, 62576, 62574, 62575
<i>Sigmodon hispidus</i>	UF 143, 1588, 1584, 1589
<i>Sigmodontomys alfarri</i>	FMNH 70536, 70535, 70534; MVZ 164891
<i>Sooretamys angouya ratticeps</i>	FMNH 136919, 136920, 136922
<i>Thaptomys nigrita</i>	FMNH 26820; MVZ 183043, 183040, 183044
<i>Thomasomys aureus</i>	MVZ 166710, 166708, 166709, 166711
<i>Thomasomys daphne</i>	AMNH 72128, 72112, 248283; FMNH 172378
<i>Thomasomys notatus</i>	FMNH 170696; USNM 582122, 194898, 194897
<i>Transandinomys talamancae</i>	FMNH 69207, 69211; MVZ 164879, 164878
<i>Wiedomys pyrrhorhinos</i>	FMNH 136942; MVZ 197566, 197567
<i>Zygodontomys brevicauda</i>	MVZ 106227, 113383; UF 13359, 6574
Tylomyinae	
<i>Nyctomys sumichrasti</i>	MVZ 98817, 98818; UF 7566, 7568, 7569, 7564
<i>Ototylomys phyllotis</i>	FMNH 42043, 64564, 64567; UF 6910
<i>Tylomys nudicaudus</i>	FMNH 64569; MVZ 131365, 131364, 223323
Muridae	
Deomyinae	
<i>Acomys cahirinus</i>	MVZ 107726, 118298, 118306; UF 15101
<i>Acomys ignitus</i>	USNM 181744, 182888, 181750, 182889
<i>Acomys russatus</i>	USNM 317002, 317007, 316997, 317006
<i>Acomys spinosissimus</i>	AMNH 162547, 162546, 219041, 162545
<i>Deomys ferrugineus</i>	FMNH 167789, 167781, 167780; MVZ 196252
<i>Lophuromys flavopunctatus</i>	USNM 259508, 537876, 259515, 537875
<i>Lophuromys zena</i>	USNM 589948, 589952, 589943, 589947
<i>Lophuromys sikapusi</i>	FMNH 81935, 81937, 81938; MVZ 196260
<i>Uranomys ruddi</i>	USNM 438783, 367021, 438782, 367020
Gerbillinae	
<i>Desmodillus auricularis</i>	AMNH 165455, 165453, 165451, 165456
<i>Dipodillus dasyurus</i>	USNM 350041, 316662, 316658, 350037
<i>Gerbilliscus brantsii</i>	AMMNH 83696, 83693, 83694, 83695
<i>Gerbilliscus robusta</i>	MVZ 186208, 186204, 186205
<i>Gerbillurus paeba</i>	AMNH 219001, 219002; MVZ 149573, 149576
<i>Gerbillurus vallinus</i>	USNM 424171, 424172, 424173, 424175
<i>Gerbillus cheesmani</i>	UF 29029
<i>Gerbillus gerbillus</i>	FMNH 87664, 87675; MVZ 34212, 34213
<i>Gerbillus gladowi</i>	UF 15106
<i>Gerbillus nanus</i>	UF 14577, 25903, 28564, 28562
<i>Meriones libycus</i>	UF 28537
<i>Meriones persicus</i>	UF 28527
<i>Meriones shawi</i>	USNM 474209, 474187, 474208, 474185
<i>Meriones unguiculatus</i>	FMNH 32712, 32715, 32716; MVZ 145685
<i>Pachyuromys duprasi</i>	FMNH 74976, 89621, 80021, 80048
<i>Psammomys obesus</i>	AMNH 203215; FMNH 78611, 91277, 91279
<i>Rhombomys opimus</i>	AMNH 88865, 88868, 88871, 88875
<i>Sekeetamys calurus</i>	FMNH 101021, 101025, 101024, 101033
<i>Tatera indica</i>	AMNH 240846; UF 30352, 30266, 30245, 30260
<i>Taterillus emini</i>	USNM 165288, 299721, 165289, 299718

Table A.1—continued.

	Museum tag
Lophiomyinae	
<i>Lophiomys imhausi</i>	USNM 291766, 172694, 184114, 184115
Murinae	
<i>Abeomelomys sevia</i>	AMNH 191963, 191965, 191966, 191964
<i>Aethomys namaquensis</i>	MVZ 117521, 117524, 117519, 117520
<i>Anisomys imitator</i>	AMNH 194893, 194894, 194892, 194891
<i>Apodemus agrarius</i>	MVZ 120896, 120898, 125183, 121103
<i>Apodemus mystacinus</i>	USNM 327654; MVZ 100019, 72459, 72461
<i>Apodemus semotus</i>	USNM 261057, 333017, 361053, 333014
<i>Apodemus speciosus</i>	MVZ 119797; USNM 299360
<i>Apodemus sylvaticus</i>	FMNH 74411, 74409, 74412; USNM 153235
<i>Apomys datae</i>	FMNH 188427, 188448, 188280; USNM 574889
<i>Apomys hylocoetes</i>	FMNH 147871, 147872; USNM 125243, 125244
<i>Archboldomys luzonensis</i>	USNM 573837, 573835, 573838, 573840
<i>Arvicathis neumanni</i>	FMNH 158037; MVZ 101023
<i>Arvicathis niloticus</i>	FMNH 105595, 105596, 105597; MVZ 154335
<i>Bandicota bengalensis</i>	MVZ 181303, 181305; UF 14630, 27590
<i>Batomys salomonensi</i>	FMNH 147940, 148163, 148170, 148172
<i>Berylmus bowersi</i>	MVZ 186483, 186484, 186482, 186490
<i>Bullimus bagobus</i>	USNM 462203, 459923, 462206, 458789
<i>Bunomys chrysocomus</i>	AMNH 224769, 224767; MVZ 225697, 225810
<i>Carpomys phaeurus</i>	FMNH 62291
<i>Chiromyscus chiropus</i>	AMNH 268333; FMNH 32010; USNM 321507, 308218
<i>Chiropodomys gliroides</i>	AMNH 106684, 106681, 106687; USNM 283681
<i>Chrotomys gonzalesi</i>	USNM 356290, 458955
<i>Colomys goslingi</i>	AMNH 55219, 55220; USNM 537872, 375903
<i>Conilurus penicillatus</i>	AMNH 183587; FMNH 120704; USNM 141486, 141487
<i>Crunomys melanius</i>	FMNH 147106, 167889
<i>Dacnomys millardi</i>	FMNH 84892, 76519, 84881; MVZ 186519
<i>Dasymys incomitus</i>	AMNH 118839, 118837, 118835; MVZ 88742
<i>Golunda ellioti</i>	FMNH 83032, 83034, 83036; UF 14613
<i>Grammomys dolichurus</i>	MVZ 117387, 117389, 117386, 118168
<i>Grammomys ibeanus</i>	USNM 183754, 162530, 162529, 162528
<i>Grammomys macmillani</i>	FMNH 73916, 73917, 79469; USNM 299736
<i>Hapalomys delacouri</i>	FMNH 32463
<i>Heimyscus fumosus</i>	USNM 585164, 584972, 585169, 585173
<i>Hybomys univittatus</i>	USNM 84522, 580737, 545844, 580207
<i>Hydromys chrysogaster</i>	MVZ 119719, 121748, 119419, 129303
<i>Hylomyscus parvus</i>	USNM 585202, 585208, 584752, 584754
<i>Hylomyscus stella</i>	FMNH 165219, 165221, 165223; MVZ 196244
<i>Hyomys goliath</i>	MVZ 129941; 194909, 194899, 194910
<i>Leggadina forresti</i>	USNM 284270
<i>Lemniscomys barbarus</i>	USNM 475121, 475161, 475122, 475165
<i>Lemniscomys striatus</i>	FMNH 17280, 86192, 123809; UF 20537
<i>Leopoldamys sabanus</i>	FMNH 98587, 98585, 98584; MVZ 186495
<i>Leptomys elegans</i>	AMNH 158203, 104200, 108447, 104199
<i>Limnomyss sibuanus</i>	FMNH 148174, 147947, 147950, 148175
<i>Lorentzimys nouhuysi</i>	USNM 585614, 585616, 585612
<i>Macruromys major</i>	AMNH 152068, 152066, 152069, 152067
<i>Malacomys longipes</i>	MVZ 196255, 196280, 196254, 196279
<i>Margaretamys elegans</i>	AMNH 223697, 223696, 225146, 223695
<i>Mastacomys fuscus</i>	USNM 574492
<i>Mastomys erythroleucus</i>	FMNH 42353, 42354; MVZ 196261, 196262
<i>Maxomys bartelsii</i>	USNM 481468, 481516, 481465, 496858
<i>Maxomys surifer</i>	MVZ 155535, 155537, 155534, 155539
<i>Melasmotherrix naso</i>	AMNH 225087, 225112, 225103, 225110
<i>Melomys cervinipes</i>	MVZ 134084, 134069, 126567, 126568
<i>Melomys rufescens</i>	FMNH 54064; USNM 295069
<i>Mesembriomys gouldii</i>	USNM 284348, 284344, 141489
<i>Micromys minutus</i>	AMNH 160524; MVZ 123584, 123585, 174890
<i>Millardia kathleenae</i>	AMNH 163761; FMNH 82944
<i>Mus booduga</i>	FMNH 35292; USNM 533774
<i>Mus cervicolor</i>	FMNH 105715, 105714; MVZ 154456, 154455
<i>Mus cookii</i>	FMNH 105731, 76796, 99769; MVZ 154450
<i>Mus minutoides</i>	AMNH 168548; MVZ 162503, 162508, 165138
<i>Mus musculus</i>	UF 27595, 14562, 1840, 7588
<i>Mus pahari</i>	MVZ 166472, 221555, 221556; USNM 355553

Table A.1—continued.

	Museum tag
<i>Mus terricolor</i>	USNM 533850, 533851, 398777, 279167
<i>Myomys dybowskii</i>	USNM 317996, 183598, 183604, 183608
<i>Myomyscus brockmani</i>	USNM 183495, 259902, 183502, 162472
<i>Niviventer confucianus</i>	AMNH 58972; MVZ 174887, 174871, 174888
<i>Niviventer cremoriventer</i>	USNM 292782, 488957, 292790, 488962
<i>Niviventer excelsior</i>	USNM 574373, 574372
<i>Notomys fuscus</i>	MVZ 124313, 124312, 124314, 124315
<i>Oenomys hypoxanthus</i>	USNM 183631, 220534, 437349, 297526
<i>Otomys angoniensis</i>	USNM 437517, 382382, 318084, 382383
<i>Otomys denti</i>	USNM 381484, 381486, 259555, 340925
<i>Parotomys brantsii</i>	AMNH 168509, 168510; MVZ 117756, 118405
<i>Paruromys dominator</i>	AMNH 225744, 225742; MVZ 225784, 225788
<i>Phloeomys cumingi</i>	UF 22381
<i>Pogonomys loriae</i>	USNM 357495, 357496
<i>Pogonomys macrourus</i>	MVZ 140443, 138620, 140447, 140450
<i>Praomys jacksoni</i>	AMNH 82454; MVZ 196286, 196289, 196287
<i>Praomys misonnei</i>	FMNH 149595, 149597, 149598, 149601
<i>Praomys tullbergi</i>	MVZ 133098, 133099; USNM 463056
<i>Pseudohydromys ellermani</i>	MVZ 129794, 129796, 129798
<i>Pseudomys australis</i>	AMNH 65998; MVZ 134044, 134115, 133681
<i>Rattus exulans</i>	UF 27816, 28982, 30104; USNM 321152
<i>Rattus norvegicus</i>	UF 3945, 12719, 39452, 2885
<i>Rattus praetor</i>	USNM 277303, 290540, 277304, 277067
<i>Rattus rattus</i>	USNM 356509, 465, 1250, 468
<i>Rattus sordidus</i>	MVZ 133641, 133606, 133637, 133639
<i>Rattus tiomanicus</i>	FMNH 171919, 171920, 171917; USNM 590331
<i>Rattus verecundus</i>	USNM 357439, 357437, 357431, 357438
<i>Rhabdomys pumilio</i>	MVZ 88824, 88823, 88820, 117468
<i>Rhynchosomys isarogensis</i>	USNM 573906, 573905, 573912, 573911
<i>Stenocephalemys albipes</i>	USNM 515391, 516174, 516155, 516179
<i>Stochomys longicaudatus</i>	FMNH 29471, 29472, 74223; MVZ 196264
<i>Sundamys muelleri</i>	USNM 113035, 115593, 104838, 121764
<i>Tarsomys apoensis</i>	FMNH 148177, 148176; USNM 144619
<i>Uromys caudimaculatus</i>	MVZ 175371, 175372, 140440, 134112
<i>Vandeleuria oleracea</i>	AMNH 242257; USNM 279309, 277861, 279310
<i>Zelotomys hildegardae</i>	USNM 183912, 183913, 181804, 183911
<i>Zyzomys argurus</i>	USNM 284323, 578555, 284328, 384336
 Nesomyidae	
Cricetomyinae	
<i>Beamys hindei</i>	USNM 183107, 183109, 183103, 183108
<i>Cricetomys gambianus</i>	FMNH 128237; MVZ 196236, 196237; UF 29051
<i>Saccostomus campestris</i>	MVZ 118335, 118371, 118364, 118365
Delanomyinae	
<i>Delanymys brooksi</i>	AMNH 181210, 181208, 181209; FMNH 148417
Dendromurinae	
<i>Dendromus insignis</i>	USNM 164387, 184067, 164392, 164454
<i>Dendromus mesomelas</i>	MVZ 117690
<i>Dendromus nyasae</i>	FMNH 196686, 191596, 191597, 191598
<i>Malacothrix typica</i>	USNM 343711, 423199, 343708, 423204
<i>Steatomys krebsi</i>	FMNH 153193
<i>Steatomys parvus</i>	USNM 367225, 428962, 295978, 164468
Petromyscinae	
<i>Petromyscus collinus</i>	AMNH 165437, 165438, 165439, 165408
Mystromyinae	
<i>Mystromys albicaudatus</i>	USNM 468440, 422538, 422540, 468445
Nesomyinae	
<i>Brachytarsomys albicauda</i>	AMNH 100692; MVZ 217015; USNM 449215, 449214
<i>Brachyuromys betsileoensis</i>	AMNH 100802; MVZ 216974; USNM 328818, 328815
<i>Eliurus minor</i>	USNM 448974, 578678, 328827, 449246
<i>Eliurus tanala</i>	USNM 448986, 449251, 448987, 449253
<i>Gymnuromys roberti</i>	FMNH 5632, 151694, 151695; MVZ 221230
<i>Hypogeomys antimena</i>	AMNH 119705
<i>Macrotarsomys bastardi</i>	USNM 328795, 328802, 328796, 578717
<i>Monticolomys koopmani</i>	AMNH 275217, 275214
<i>Nesomys rufus</i>	AMNH 100679; MVZ 217006; USNM 449239, 449245
<i>Voalavo gymno caudus</i>	FMNH 156162, 159648, 159725, 159727

Table A.1—continued.

Museum tag	
Platacanthomyidae	
Platacanthomyinae	
<i>Typhlomys cinereus</i>	AMNH 84762, 84769, 84761; FMNH 39131
Spalacidae	
Myospalacinae	
<i>Eospalax fontanieri cansas</i>	FMNH 19070, 19069
<i>Myospalax aspalax</i>	FMNH 49900, 49901
Spalacinae	
<i>Spalax ehrenbergi</i>	FMNH 101009, 101010, 101014, 101011
Rhizomyinae	
<i>Cannomys badius</i>	FMNH 104207, 104211, 104212; MVZ 183902
<i>Rhizomys pruinosus</i>	FMNH 84849; MVZ 186543, 186544, 186548
Tachyoryctinae	
<i>Tachyoryctes splendens</i>	MVZ 163968, 183904, 183908, 183907
Dipodidae	
Allactaginae	
<i>Allactaga elater</i>	AMNH 88749; FMNH 103865, 103867, 103868
Dipodinae	
<i>Dipus sagitta</i>	AMNH 84135, 58608, 84121, 58623
Sicista	
<i>Sicista concolor</i>	UF 26942, 26941
Zapodinae	
<i>Zapus princeps</i>	AMNH 124327; UF 12734, 12741, 12731
Abrocomidae	
<i>Abrocoma bennettii</i>	UF 23915

Table A.2. List of reference and target specimens used in the missing data estimation procedure for chapter 5. See Table A.1 legend for more information.

Target	Reference
FMNH 23169	FMNH 103865, FMNH 103867, FMNH 103868, AMNH 88749
MVZ 115690	MVZ 115689, MVZ 115697
MVZ 115691	MVZ 115689, MVZ 115697
MVZ 137883	MVZ 115689, MVZ 115697
MVZ 163782	MVZ 115689, MVZ 115697
MVZ 163783	MVZ 115689, MVZ 115697
MVZ 163784	MVZ 115689, MVZ 115697
MVZ 118298	MVZ 107726, MVZ 118306
UF 15101	MVZ 107726, MVZ 118306
AMNH 162547	AMNH 162545, AMNH 162546, AMNH 219041
USNM 304528	FNMH 19444, FNMH 19445
USNM 551641	FNMH 19444, FNMH 19445
MVZ 117521	FNMH 147940, FNMH 148163, FNMH 148170
FNMH 43232	FNMH 52524, USNM 507279
FNMH 52529	FNMH 52524, USNM 507279
FNMH 107917	MVZ 172907, MVZ 172953
UF 9190	MVZ 172907, MVZ 172953
MVZ 171660	MVZ 171663
MVZ 171661	MVZ 171663
MVZ 171662	MVZ 171663
USNM 259623	FNMH 52524, USNM 507279, MVZ 172907, MVZ 172953, MVZ 171663, MVZ 171748, MVZ 171748, UF 27629, UF 27633, MVZ 171724, MVZ 174054
MVZ 116109	MVZ 171748
MVZ 171751	MVZ 171748
UF 27625	UF 27623, UF 27629, UF 27633
MVZ 171713	MVZ 171724, MVZ 174054
USNM 194638	MVZ 171724, MVZ 174054
AMNH 59753	FNMH 33959
FNMH 33964	FNMH 33959
AMNH 176255	FNMH 33959
MVZ 145278	FNMH 157341, FNMH 164188
FNMH 164184	FNMH 157341, FNMH 164188
MVZ 141617	MVZ 120224, MVZ 120225, FNMH 162761
AMNH 194894	AMNH 194891, AMNH 194892, AMNH 194893
USNM 261053	USNM 261057, USNM 333014, USNM 333017
USNM 299360	MVZ 119797
FNMH 147871	FNMH 147872
USNM 125243	FNMH 147872
USNM 125244	FNMH 147872

Table A.2—continued.

Target	Reference
FMNH 105596	FMNH 105595
FMNH 105597	FMNH 105595
MVZ 154335	FMNH 105595
UF 22400	FMNH 112222, FMNH 112223, FMNH 112224
FMNH 54085	FMNH 54084, FMNH 54086
UF 6039	FMNH 54084, FMNH 54086
UF 14630	MVZ 181303, MVZ 181305, UF 27590
FMNH 148172	FMNH 147940, FMNH 148163, FMNH 148170
MVZ 186482	MVZ 186483, MVZ 186484, MVZ 186490
AMNH 100802	USNM 328815, USNM 328818, MVZ 216974
MVZ 191467	FMNH 52524, USNM 507279, MVZ 172907, MVZ 172953, MVZ 171663, MVZ 171748, UF 27623, UF 27629, UF 27633, MVZ 171724, MVZ 174054
MVZ 191468	FMNH 52524, USNM 507279, MVZ 172907, MVZ 172953, MVZ 171663, MVZ 171748, UF 27623, UF 27629, UF 27633, MVZ 171724, MVZ 174054
MVZ 183036	FMNH 52524, USNM 507279, MVZ 172907, MVZ 172953, MVZ 171663, MVZ 171748, UF 27623, UF 27629, UF 27633, MVZ 171724, MVZ 174054
MVZ 183037	FMNH 52524, USNM 507279, MVZ 172907, MVZ 172953, MVZ 171663, MVZ 171748, UF 27623, UF 27629, UF 27633, MVZ 171724, MVZ 174054
USNM 462203	USNM 458789, USNM 459923
USNM 462206	USNM 458789, USNM 459923
AMNH 224767	AMNH 224769, MVZ 225697, MVZ 225810
UF 20682	UF 27674
UF 27606	UF 27674
UF 27672	UF 27674
UF 28486	UF 28503, UF 28504
UF 28502	UF 28503, UF 28504
MVZ 116018	MVZ 115752, MVZ 115754, MVZ 174016
USNM 259264	MVZ 115752, MVZ 115754, MVZ 174016
MVZ 183902	FMNH 104207, FMNH 104211, FMNH 104212
FMNH 62291	FMNH 147940, FMNH 148163, FMNH 148170
MVZ 197541	UF 6901, UF 29867, UF 29868, UF 23558, UF 23560, UF 23561, USNM 510842
MVZ 197542	UF 6901, UF 29867, UF 29868, UF 23558, UF 23560, UF 23561, USNM 510842
MVZ 197609	UF 6901, UF 29867, UF 29868, UF 23558, UF 23560, UF 23561, USNM 510842
MVZ 197610	UF 6901, UF 29867, UF 29868, UF 23558, UF 23560, UF 23561, USNM 510842
MVZ 116034	MVZ 138034, MVZ 145548, MVZ 135748, MVZ 135749, MVZ 135752, MVZ 135753, OMNH 30081, OMNH 30082, LCM 4037, LCM 4038, LCM 4057, LCM 4061, MVZ 174036, MVZ 174038, FMNH 52579, FMNH 107828, FMNH 107831, USNM 194576, LCM 3009, LCM 3021, LCM 3143
MVZ 116181	MVZ 138034, MVZ 145548, MVZ 135748, MVZ 135749, MVZ 135752, MVZ 135753, OMNH 30081, OMNH 30082, LCM 4037, LCM 4038, LCM 4057, LCM 4061, MVZ 174036, MVZ 174038, FMNH 52579, FMNH 107828, FMNH 107831, USNM 194576, LCM 3009, LCM 3021, LCM 3143
MVZ 172675	MVZ 138034, MVZ 145548, MVZ 135748, MVZ 135749, MVZ 135752, MVZ 135753, OMNH 30081, OMNH 30082, LCM 4037, LCM 4038, LCM 4057, LCM 4061, MVZ 174036, MVZ 174038, FMNH 52579, FMNH 107828, FMNH 107831, USNM 194576, LCM 3009, LCM 3021, LCM 3143
MVZ 174023	MVZ 174036, MVZ 174038, FMNH 52579, FMNH 107828, FMNH 107831, USNM 194576, LCM 3009, LCM 3021, LCM 3143
MVZ 198808	USNM 105816, USNM 369657
USNM 104527	USNM 105816, USNM 369657
FMNH 32010	AMNH 268333, USNM 321507
USNM 308218	AMNH 268333, USNM 321507
USNM 283681	AMNH 106681, AMNH 106684, AMNH 106687
AMNH 55220	AMNH 55219, USNM 375903, USNM 537872
USNM 141486	AMNH 183587, FMNH 120704
USNM 141487	AMNH 183587, FMNH 120704
UF 29051	FMNH 128237, MVZ 196236, MVZ 196237
FMNH 33981	FMNH 33980, FMNH 33982, FMNH 33985
UF 14594	UF 27124, UF 27142, UF 27145
MVZ 41451	AMNH 176483, AMNH 176484
MVZ 129377	AMNH 176483, AMNH 176484
AMNH 118835	FMNH 147940, FMNH 148163, FMNH 148170
AMNH 118837	FMNH 147940, FMNH 148163, FMNH 148170
AMNH 118839	FMNH 147940, FMNH 148163, FMNH 148170
MVZ 88742	FMNH 147940, FMNH 148163, FMNH 148170
AMNH 181209	AMNH 181208, FMNH 148417
AMNH 181210	AMNH 181208, FMNH 148417
MVZ 183064	MVZ 166708, MVZ 166709, MVZ 166710, MVZ 166711, AMNH 72112, AMNH 72128, AMNH 248283, FMNH 172378, FMNH 170696, USNM 194897, USNM 582122
MVZ 183065	MVZ 166708, MVZ 166709, MVZ 166710, MVZ 166711, AMNH 72112, AMNH 72128, AMNH 248283, FMNH 172378, FMNH 170696, USNM 194897, USNM 582122
MVZ 183047	MVZ 166708, MVZ 166709, MVZ 166710, MVZ 166711, AMNH 72112, AMNH 72128, AMNH 248283, FMNH 172378, FMNH 170696, USNM 194897, USNM 582122
MVZ 183048	MVZ 166708, MVZ 166709, MVZ 166710, MVZ 166711, AMNH 72112, AMNH 72128, AMNH 248283, FMNH 172378, FMNH 170696, USNM 194897, USNM 582122
AMNH 206097	FMNH 52524, USNM 507279, MVZ 172907, MVZ 172953, MVZ 171663, MVZ 171748, UF 27623, UF 27629, UF 27633, MVZ 171724, MVZ 174054
AMNH 206105	FMNH 52524, USNM 507279, MVZ 172907, MVZ 172953, MVZ 171663, MVZ 171748, UF 27623, UF 27629, UF 27633, MVZ 171724, MVZ 174054
AMNH 206118	FMNH 52524, USNM 507279, MVZ 172907, MVZ 172953, MVZ 171663, MVZ 171748, UF 27623, UF 27629, UF 27633, MVZ 171724, MVZ 174054
AMNH 206163	FMNH 52524, USNM 507279, MVZ 172907, MVZ 172953, MVZ 171663, MVZ 171748, UF 27623, UF 27629, UF 27633, MVZ 171724, MVZ 174054
USNM 184067	USNM 164387, USNM 164392, USNM 164454, FMNH 191597, FMNH 191598, FMNH 196686
MVZ 117690	USNM 164387, USNM 164392, USNM 164454, FMNH 191597, FMNH 191598, FMNH 196686
FMNH 191596	FMNH 191597, FMNH 191598, FMNH 196686
MVZ 196252	FMNH 167780, FMNH 167781, FMNH 167789
USNM 316662	USNM 316658, USNM 350037, USNM 350037
AMNH 84135	AMNH 58608, AMNH 58623, AMNH 84121
USNM 449246	USNM 328827, USNM 448974, USNM 578678
USNM 449253	USNM 448986, USNM 448987, USNM 449251
AMNH 44156	AMNH 44140, AMNH 44147, AMNH 44150
FMNH 50736	FMNH 134181, MVZ 186038, MVZ 186039
MVZ 154603	MVZ 115689, MVZ 115697
MVZ 154607	MVZ 115689, MVZ 115697
MVZ 159389	MVZ 115689, MVZ 115697
MVZ 162249	MVZ 115689, MVZ 115697
AMNH 83693	AMNH 83694, AMNH 83695
AMNH 83696	AMNH 83694, AMNH 83695
AMNH 219002	AMNH 219001, MVZ 149573, MVZ 149576
USNM 424172	USNM 424171, 424175
USNM 424173	USNM 424171, 424175
UF 29029	FMNH 87664, FMNH 87675, UF 28562, UF 28564
MVZ 34212	FMNH 87664, FMNH 87675
MVZ 34213	FMNH 87664, FMNH 87675
UF 15106	FMNH 87664, FMNH 87675, UF 28562, UF 28564
UF 14577	UF 28562, UF 28564

Table A.2—continued.

Target	Reference
UF 25903	UF 28562, UF 28564
FMNH 83032	FMNH 147940, FMNH 148163, FMNH 148170
FMNH 83034	FMNH 147940, FMNH 148163, FMNH 148170
FMNH 83036	FMNH 147940, FMNH 148163, FMNH 148170
UF 14613	FMNH 147940, FMNH 148163, FMNH 148170
USNM 162528	USNM 162529, USNM 162530, USNM 183754
FMNH 73916	USNM 299736
FMNH 73917	USNM 299736
FMNH 79469	USNM 299736
UF 27630	FMNH 28423, FMNH 46125, FMNH 50920
FMNH 5632	FMNH 151694, FMNH 151695, MVZ 221230
USNM 68609	USNM 68618, USNM 68619
USNM 68615	USNM 68618, USNM 68619
FMNH 32463	AMNH 160524
USNM 585169	USNM 584972, USNM 585164, USNM 585173
USNM 44626	USNM 44627, USNM 44634
USNM 44633	USNM 44627, USNM 44634
FMNH 136891	AMNH 210253, FMNH 87988, FMNH 88919
FMNH 55476	AMNH 210253, FMNH 87988, FMNH 88919
FMNH 93050	AMNH 210253, FMNH 87988, FMNH 88919
FMNH 118813	AMNH 210253, FMNH 87988, FMNH 88919
UF 13357	AMNH 210253, FMNH 87988, FMNH 88919
USNM 84522	USNM 545844, USNM 580207, USNM 580737
MVZ 119719	MVZ 127748, MVZ 119419
MVZ 129303	MVZ 127748, MVZ 119419
MVZ 196244	FMNH 165219, FMNH 165221, FMNH 165223
AMNH 194899	AMNH 194909
AMNH 194910	AMNH 194909
MVZ 129941	AMNH 194909
AMNH 119705	USNM 328796, USNM 328802, USNM 578717
MVZ 201154	MVZ 152171, MVZ 154620, MVZ 155837, MVZ 184955
FMNH 122710	USNM 584515, USNM 584516
FMNH 122711	USNM 584515, USNM 584516
AMNH 176249	AMNH 176250
AMNH 87095	AMNH 176250
AMNH 257134	AMNH 176250
AMNH 45439	AMNH 45438
USNM 172586	AMNH 45438
USNM 299098	AMNH 45438
MVZ 128854	UF 24163, UF 24166, UF 24167, UF 24407
MVZ 128855	UF 24163, UF 24166, UF 24167, UF 24407
MVZ 128857	UF 24163, UF 24166, UF 24167, UF 24407
MVZ 128863	UF 24163, UF 24166, UF 24167, UF 24407
FMNH 17280	FMNH 123809
FMNH 86192	FMNH 123809
UF 20537	FMNH 123809
MVZ 171513	MVZ 171511, MVZ 172656, MVZ 172657
FMNH 98584	MVZ 186495
FMNH 98585	MVZ 186495
FMNH 98587	MVZ 186495
AMNH 104199	AMNH 104200, AMNH 108447, AMNH 158203
FMNH 148174	FMNH 147947, FMNH 147950, FMNH 148175
USNM 172694	USNM 107726, MVZ 118306, USNM 181744, USNM 181750, USNM 182888, USNM 316997, USNM 317002, USNM 317006, USNM 317007, AMNH 162545, AMNH 162546, AMNH 219041
USNM 291766	MVZ 107726, MVZ 118306, USNM 181744, USNM 181750, USNM 182888, USNM 316997, USNM 317002, USNM 317006, USNM 317007, AMNH 162545, AMNH 162546, AMNH 219041
USNM 184114	MVZ 107726, MVZ 118306, USNM 181744, USNM 181750, USNM 182888, USNM 182889, USNM 316997, USNM 317002, USNM 317006, USNM 317007, AMNH 162545, AMNH 162546, AMNH 219041
USNM 184115	MVZ 107726, MVZ 118306, USNM 181744, USNM 181750, USNM 182888, USNM 316997, USNM 317002, USNM 317006, USNM 317007, AMNH 162545, AMNH 162546, AMNH 219041
USNM 259508	USNM 537875, USNM 537876, USNM 259515
USNM 589952	USNM 589943, USNM 589947, USNM 589948
USNM 585612	USNM 585614, USNM 585616
MVZ 155827	MVZ 138034, MVZ 145548, MVZ 135748, MVZ 135749, MVZ 135752, MVZ 135753, OMNH 30081, OMNH 30082, LCM 4037, LCM 4038, LCM 4057, LCM 4061, MVZ 174036, MVZ 174038, FMNH 52579, FMNH 107828, FMNH 107831, USNM 194576, LCM 3009, LCM 3021, LCM 3143
MVZ 155836	MVZ 138034, MVZ 145548, MVZ 135748, MVZ 135749, MVZ 135752, MVZ 135753, OMNH 30081, OMNH 30082, LCM 4037, LCM 4038, LCM 4057, LCM 4061, MVZ 174036, MVZ 174038, FMNH 52579, FMNH 107828, FMNH 107831, USNM 194576, LCM 3009, LCM 3021, LCM 3143
MVZ 158474	MVZ 138034, MVZ 145548, MVZ 135748, MVZ 135749, MVZ 135752, MVZ 135753, OMNH 30081, OMNH 30082, LCM 4037, LCM 4038, LCM 4057, LCM 4061, MVZ 174036, MVZ 174038, FMNH 52579, FMNH 107828, FMNH 107831, USNM 194576, LCM 3009, LCM 3021, LCM 3143
MVZ 158475	MVZ 138034, MVZ 145548, MVZ 135748, MVZ 135749, MVZ 135752, MVZ 135753, OMNH 30081, OMNH 30082, LCM 4037, LCM 4038, LCM 4057, LCM 4061, MVZ 174036, MVZ 174038, FMNH 52579, FMNH 107828, FMNH 107831, USNM 194576, LCM 3009, LCM 3021, LCM 3143
USNM 328795	USNM 328796, USNM 328802, USNM 578717
AMNH 152066	AMNH 152067, AMNH 152069
AMNH 152068	AMNH 152067, AMNH 152069
MVZ 196254	FMNH 147940, FMNH 148163, FMNH 148170
MVZ 196255	FMNH 147940, FMNH 148163, FMNH 148170
MVZ 196280	FMNH 147940, FMNH 148163, FMNH 148170
MVZ 196281	FMNH 147940, FMNH 148163, FMNH 148170
USNM 423204	USNM 343708, USNM 343711, USNM 423199
USNM 481465	USNM 481468
USNM 481516	USNM 481468
USNM 496858	USNM 481468
MVZ 155534	USNM 481468
MVZ 155535	USNM 481468
MVZ 155537	USNM 481468
MVZ 155539	USNM 481468
AMNH 225087	AMNH 225103, AMNH 225110, AMNH 225112
UF 28537	USNM 474185, USNM 474187, USNM 474208, USNM 474209, FMNH 32712, FMNH 32716
UF 28527	USNM 474185, USNM 474187, USNM 474208, USNM 474209, FMNH 32712, FMNH 32716

Table A.2—continued.

Target	Reference
MVZ 145685	FMNH 32712, FMNH 32716
USNM 141489	USNM 284344, USNM 284348
UF 3987	FMNH 63951, MVZ 102642, MVZ 102643
MVZ 117519	FMNH 147940, FMNH 148163, FMNH 148170
MVZ 117520	FMNH 147940, FMNH 148163, FMNH 148170
MVZ 117524	FMNH 147940, FMNH 148163, FMNH 148170
MVZ 123584	AMNH 160524
MVZ 123585	AMNH 160524
MVZ 174890	AMNH 160524
FMNH 103132	FMNH 103131, FMNH 103133, USNM 85655
FMNH 10745	FMNH 10743, USNM 295320
FMNH 10750	FMNH 10743, USNM 295320
MVZ 54425	AMNH 147362
MVZ 54426	AMNH 147362
MVZ 54427	AMNH 147362
USNM 358625	USNM 332964, USNM 332965, USNM 332967
UF 12732	FMNH 12649, FMNH 12653, FMNH 12664
USNM 150132	UF 3887, UF 3888, UF 3911
USNM 533774	FMNH 35292
FMNH 105714	FMNH 105715, MVZ 154455, MVZ 154456
FMNH 76796	FMNH 35292, FMNH 105715, MVZ 154455, MVZ 154456, AMNH 168548, MVZ 162508, UF 14562, UF 1840, UF 7588, MVZ 166472, MVZ 221556, USNM 398777, USNM 533851
FMNH 99769	FMNH 105715, MVZ 154455, MVZ 154456, AMNH 168548, MVZ 162508, UF 14562, UF 1840, UF 7588, MVZ 166472, MVZ 221556, USNM 398777, USNM 533851
FMNH 105731	FMNH 35292, FMNH 105715, MVZ 154455, MVZ 154456, AMNH 168548, MVZ 162508, UF 14562, UF 1840, UF 7588, MVZ 166472, MVZ 221556, USNM 398777, USNM 533851
MVZ 154450	FMNH 35292, FMNH 105715, MVZ 154455, MVZ 154456, AMNH 168548, MVZ 162508, UF 14562, UF 1840, UF 7588, MVZ 166472, MVZ 221556, USNM 398777, USNM 533851
MVZ 162503	AMNH 168548, MVZ 162508
MVZ 165138	AMNH 168548, MVZ 162508
UF 27595	UF 14562, UF 1840, UF 7588
MVZ 221555	MVZ 166472, MVZ 221556
USNM 355553	MVZ 166472, MVZ 221556
USNM 279167	USNM 398777, USNM 533851
USNM 533850	USNM 398777, USNM 533851
USNM 183604	USNM 183598
USNM 183608	USNM 183598
USNM 317996	USNM 183598
FMNH 49900	FMNH 49901
USNM 422538	USNM 422540, USNM 468440, USNM 468445
MVZ 153534	MVZ 153542, MVZ 153544
MVZ 153539	MVZ 153542, MVZ 153544
UF 6581	UF 6583, FMNH 26741
UF 30468	UF 6583, FMNH 26741
USNM 449167	USNM 449168, USNM 449172, USNM 449173
UF 14691	UF 166, UF 167, UF 12778
MVZ 171445	MVZ 171446, MVZ 171460, MVZ 173987
USNM 449239	AMNH 100679, MVZ 217006, USNM 449245
USNM 488957	USNM 292782, USNM 292790, USNM 488962
USNM 574372	USNM 574373
MVZ 182132	MVZ 115689, MVZ 115697
MVZ 124312	MVZ 124315
MVZ 124313	MVZ 124315
MVZ 124314	MVZ 124315
UF 7566	MVZ 98817, MVZ 98818, UF 7564, UF 7568, UF 7569
UF 112	UF 801, UF 2710, UF 12421
UF 635	FMNH 116919, FMNH 116920, FMNH 117010
USNM 374321	FMNH 87968
USNM 183631	USNM 297526, USNM 437349
USNM 220534	USNM 297526, USNM 437349
UF 6148	UF 6149, UF 6152
UF 28847	UF 6149, UF 6152
UF 25933	UF 27622, UF 27671
USNM 259583	UF 27622, UF 27671
UF 2415	UF 1793, UF 1795
UF 1791	UF 1793, UF 1795
UF 24175	FMNH 123450, FMNH 123451, UF 12613
UF 9869	UF 6901, UF 29867, UF 29868
USNM 437517	USNM 318084, USNM 382382, USNM 382383
USNM 340925	USNM 259555, USNM 381484
USNM 381486	USNM 259555, USNM 381484
FMNH 42043	FMNH 64565, FMNH 64567
UF 6910	FMNH 64565, FMNH 64567
AMNH 91602	AMNH 91601, MVZ 172660
MVZ 171520	AMNH 91601, MVZ 172660
USNM 484395	USNM 460550, USNM 460551, USNM 461881
MVZ 117756	AMNH 168509, AMNH 168510
MVZ 118405	AMNH 168509, AMNH 168510
UF 6221	UF 6121, UF 6224, UF 6225
USNM 569214	UF 24030, UF 24035, UF 24036, USNM 392010, UF 6121, UF 6224, UF 6225, USNM 53283, UF 9445, UF 9447, UF 9448, USNM 60100, USNM 69556, USNM 91566, UF 1968, UF 9303, USNM 157114, USNM 530841, UF 2802, UF 2803, UF 3637, USNM 314413, UF 23929, UF 23930, UF 23931, UF 786, UF 5167, UF 13035
USNM 81016	USNM 69556, USNM 91566
USNM 81017	USNM 69556, USNM 91566
UF 9298	UF 1968, UF 9303, USNM 157114
USNM 308898	UF 786, UF 5167, UF 13035
AMNH 165437	AMNH 165408, AMNH 165439
AMNH 165438	AMNH 165408, AMNH 165439
UF 22381	FMNH 147940, FMNH 148163, FMNH 148170
LCM 3047	LCM 4037, LCM 4038, LCM 4057, LCM 4061

Table A.2—continued.

Target	Reference
LCM 3338	LCM 4037, LCM 4038, LCM 4057, LCM 4061
LCM 3351	LCM 3009, LCM 3021, LCM 3143
AMNH 82454	MVZ 196286, MVZ 196287, MVZ 196289
AMNH 174334	AMNH 206579, AMNH 257138, USNM 547937
MVZ 129794	AMNH 104200, AMNH 108447, AMNH 158203
MVZ 129796	AMNH 104200, AMNH 108447, AMNH 158203
MVZ 129798	AMNH 104200, AMNH 108447, AMNH 158203
MVZ 133681	AMNH 65998, MVZ 134044, MVZ 134115
AMNH 262048	USNM 584586
USNM 390668	USNM 584586
USNM 584585	USNM 584586
MVZ 114757	MVZ 114758, MVZ 116193
UF 30104	UF 27816, UF 28982, USNM 321152
UF 2885	UF 27816, UF 28982, USNM 321152, USNM 277067, USNM 277303, USNM 290540, MVZ 133606, MVZ 133637, MVZ 133639, MVZ 133641, FMNH 171917, FMNH 171919, FMNH 171920, USNM 590331, USNM 357437, USNM 357439
UF 3945	UF 27816, UF 28982, USNM 321152, USNM 277067, USNM 277303, USNM 290540, MVZ 133606, MVZ 133637, MVZ 133639, MVZ 133641, FMNH 171917, FMNH 171919, FMNH 171920, USNM 590331, USNM 357437, USNM 357439
UF 12719	UF 27816, UF 28982, USNM 321152, USNM 277067, USNM 277303, USNM 290540, MVZ 133606, MVZ 133637, MVZ 133639, MVZ 133641, FMNH 171917, FMNH 171919, FMNH 171920, USNM 590331, USNM 357437, USNM 357439
UF 39452	UF 27816, UF 28982, USNM 321152, USNM 277067, USNM 277303, USNM 290540, MVZ 133606, MVZ 133637, MVZ 133639, MVZ 133641, FMNH 171917, FMNH 171919, FMNH 171920, USNM 590331, USNM 357437, USNM 357439
USNM 277304	USNM 277067, USNM 277303, USNM 290540
UF 465	UF 27816, UF 28982, USNM 321152, USNM 277067, USNM 277303, USNM 290540, MVZ 133606, MVZ 133637, MVZ 133639, MVZ 133641, FMNH 171917, FMNH 171919, FMNH 171920, USNM 590331, USNM 357437, USNM 357439
UF 468	UF 27816, UF 28982, USNM 321152, USNM 277067, USNM 277303, USNM 290540, MVZ 133606, MVZ 133637, MVZ 133639, MVZ 133641, FMNH 171917, FMNH 171919, FMNH 171920, USNM 590331, USNM 357437, USNM 357439
UF 1250	UF 27816, UF 28982, USNM 321152, USNM 277067, USNM 277303, USNM 290540, MVZ 133606, MVZ 133637, MVZ 133639, MVZ 133641, FMNH 171917, FMNH 171919, FMNH 171920, USNM 590331, USNM 357437, USNM 357439
USNM 356509	UF 27816, UF 28982, USNM 321152, USNM 277067, USNM 277303, USNM 290540, MVZ 133606, MVZ 133637, MVZ 133639, MVZ 133641, FMNH 171917, FMNH 171919, FMNH 171920, USNM 590331, USNM 357437, USNM 357439
USNM 357438	USNM 357431, USNM 357437, USNM 357437
MVZ 163411	MVZ 165853, MVZ 172218
MVZ 171163	MVZ 165853, MVZ 172218
MVZ 164897	MVZ 164892, MVZ 164894, MVZ 164898
FMNH 73418	FMNH 13115, USNM 70255, FMNH 54147
UF 6080	945, 94MVZ 115689, MVZ 11569747
MVZ 88820	MVZ 117468
MVZ 88823	MVZ 117468
MVZ 88824	MVZ 117468
MVZ 98811	MVZ 98798, MVZ 98808
MVZ 98814	MVZ 98798, MVZ 98808
MVZ 186543	MVZ 186544, FMNH 84849
MVZ 186548	MVZ 186544, FMNH 84849
AMNH 88875	AMNH 88865, AMNH 88868, AMNH 88871
USNM 573905	USNM 573911, USNM 573912
USNM 573906	USNM 573911, USNM 573912
AMNH 235431	MVZ 183265, MVZ 183269
MVZ 183267	MVZ 183268, MVZ 183269
AMNH 67522	MVZ 183166, MVZ 183167
MVZ 183168	MVZ 183166, MVZ 183167
MVZ 183169	MVZ 183166, MVZ 183167
FMNH 128560	UF 27712
FMNH 128561	UF 27712
UF 27717	UF 27712
FMNH 20042	FMNH 20040, FMNH 20045
USNM 442581	FMNH 20040, FMNH 20045
UF 143	UF 1584, UF 1588, UF 1589
FMNH 70535	FMNH 70534, MVZ 164891
FMNH 70536	FMNH 70534, MVZ 164891
FMNH 136919	FMNH 136920, FMNH 136922
USNM 115593	USNM 104838, USNM 113035
USNM 121764	USNM 104838, USNM 113035
UF 3839	UF 6436, UF 4946
UF 3841	UF 6436, UF 4946
MVZ 163068	MVZ 186544, FMNH 84849
MVZ 183904	MVZ 186544, FMNH 84849
MVZ 183907	MVZ 186544, FMNH 84849
MVZ 183908	MVZ 186544, FMNH 84849
USNM 144619	FMNH 148176, FMNH 148177
UF 30352	AMNH 240846, UF 30245, UF 30260, UF 30266
USNM 299721	USNM 165288, USNM 165289, USNM 299718
FMNH 26820	MVZ 183044
MVZ 183040	MVZ 183044
MVZ 183043	MVZ 183044
USNM 194898	FMNH 170696, USNM 194897, USNM 582122
AMNH 84761	FMNH 39131, FMNH 39131
AMNH 84769	FMNH 39131, FMNH 39131
USNM 438782	USNM 367020, USNM 367021, USNM 438783
MVZ 175372	MVZ 134112, MVZ 140440, MVZ 175371
FMNH 136942	MVZ 197566, MVZ 197567
USNM 45285	USNM 45287
UF 12731	AMNH 124327
UF 12734	AMNH 124327
UF 12741	AMNH 124327
USNM 183913	USNM 161804, USNM 183911, USNM 183912
MVZ 106227	MVZ 113383, UF 6574
UF 13359	MVZ 113383, UF 6574
USNM 578555	USNM 284323, USNM 284328, USNM 284336

Table A.3. List of specimens with extracted linear distances for chapter 6. See Table A.1 legend for more information.

Museum tag	
Anomaluromorphia	
Pedetidae	
<i>Pedetes capensis</i>	USNM 422522; FMNH 38263, 38231, 38261
Castorimorpha	
Geomysidae	
<i>Cratogeomys castanops</i>	AMNH 68767, 68766, 68768, 63812
<i>Thomomys umbrinus</i>	USNM 55913; UF 8238; FMNH 14058, 14059
Heteromyidae	
Dipodomysinae	
<i>Dipodomys agilis</i>	USNM 192339; UF 432, 3057, 3056
<i>Dipodomys californicus</i>	USNM 36389, 23545, 23543, 44152
<i>Dipodomys compactus</i>	USNM 43537, 43308, 42871, 100058
<i>Dipodomys deserti</i>	USNM 33926; AMNH 139598, 139597, 139600, 139599
<i>Dipodomys elator</i>	USNM 348461, 348460, 348459, 101124
<i>Dipodomys gravipes</i>	USNM 138910, 245885, 245884
<i>Dipodomys heermanni</i>	USNM 149736, 137911, 137918, 149735
<i>Dipodomys ingens</i>	USNM 128801, 214505, 128802, 214485
<i>Dipodomys merriami</i>	USNM 50007; AMNH 173786, 169577, 173787
<i>Dipodomys microps</i>	MVZ 73650, 73651, 73649, 73652
<i>Dipodomys nelsoni</i>	MVZ 76548, 76547; USNM 56195, 51068
<i>Dipodomys nitratoides</i>	USNM 54871, 149756, 214515, 149757
<i>Dipodomys ordii</i>	USNM 214113; UF 24179, 24180, 4673
<i>Dipodomys panamintinus</i>	USNM 41336; UF 3058, 3059, 3060
<i>Dipodomys phillipsii</i>	USNM 53324, 53331, 90803, 94622
<i>Dipodomys simulans</i>	USNM 555015, 555018, 139866, 531718
<i>Dipodomys spectabilis</i>	USNM 46288; UF 25951, 25952, 25953
<i>Dipodomys stephensi</i>	USNM 150613, 118393, 94042, 94043
<i>Dipodomys venustus venustus</i>	USNM 130113, 130114, 51847, 150940
<i>Dipodomys venustus elephantinus</i>	USNM 150948, 67151, 69448, 150962
<i>Microdipodops megacephalus</i>	MVZ 159877, 159878; USNM 54585, 54582
<i>Microdipodops pallidus</i>	USNM 246133, 246023, 246020, 246024
Heteromyinae	
<i>Heteromys anomalus</i>	USNM 540709; UF 13349, 13709, 23863
<i>Heteromys australis</i>	USNM 310391, 310402, 310393, 310394
<i>Heteromys catopterus</i>	USNM 517545, 370977, 405985, 517566
<i>Heteromys d. desmarestianus</i>	USNM 391895; UF 6822, 6823, 6824
<i>Heteromys d. goldmani</i>	USNM 275249, 275233, 275242, 77581
<i>Heteromys gaumeri</i>	USNM 108480, 108481, 108479, 108131
<i>Heteromys nelsoni</i>	USNM 77578; FMNH 41759, 41761, 41760
<i>Heteromys oasicus</i>	USNM 456324, 456327
<i>Heteromys teleus</i>	USNM 528573
<i>Liomys adspersus</i>	USNM 323676, 323674, 296299, 323672
<i>Liomys irroratus</i>	USNM 120169; UF 6202, 6203, 6206
<i>Liomys pictus</i>	USNM 126914; UF 6168, 6173, 6171
<i>Liomys salvini</i>	USNM 275285; UF 6161, 6164, 6165
Perognathinae	
<i>Chaetodipus arenarius</i>	USNM 531519, 531529, 146908, 531518
<i>Chaetodipus artus</i>	USNM 96303, 96304, 96301, 96302
<i>Chaetodipus baileyi</i>	USNM 49169; UF 3076; FMNH 52836, 52839
<i>Chaetodipus californicus</i>	USNM 55561; UF 3033; FMNH 10902, 10890
<i>Chaetodipus eremicus</i>	USNM 51096, 157404, 119104, 119781
<i>Chaetodipus fallax</i>	USNM 529907; UF 3044, 12761, 12760
<i>Chaetodipus formosus</i>	USNM 262926, 263160, 41957, 263139; AMNH 11850, 11837, 258740, 258738
<i>Chaetodipus goldmani</i>	USNM 96325, 96672, 96328, 96674
<i>Chaetodipus hispidus</i>	USNM 31559; UF 9633, 11944, 8672
<i>Chaetodipus intermedius</i>	USNM 532532; UF 12527, 12528, 7836
<i>Chaetodipus lineatus</i>	USNM 296791, 296790; FMNH 141795, 141796
<i>Chaetodipus nelsoni</i>	USNM 50210; FMNH 46911, 46910
<i>Chaetodipus penicillatus</i>	USNM 552796; UF 4681, 437, 4682
<i>Chaetodipus pernix</i>	USNM 96679, 96681, 95822, 96327
<i>Chaetodipus rufinoris</i>	USNM 145985, 146090, 14005, 140006
<i>Chaetodipus spinatus</i>	USNM 140038; UF 3041, 3042, 3043
<i>Perognathus alticola</i>	USNM 91561, 127813, 91562, 127811
<i>Perognathus amplus</i>	MVZ 47107, 47108, 47109, 47110
<i>Perognathus fasciatus</i>	USNM 168602, 179713, 202337, 179714
<i>Perognathus flavescens</i>	USNM 47378, 87901, 66537, 275699
<i>Perognathus flavus</i>	USNM 213440; UF 7833, 7834, 24183
<i>Perognathus inornatus</i>	USNM 41789, 93726, 41788, 149800
<i>Perognathus longimembris</i>	MVZ 55750, 60834, 55751, 55752
<i>Perognathus merriami</i>	USNM 48743, 48741, 93349, 48742
<i>Perognathus parvus</i>	USNM 55294; FMNH 11886, 11887, 11889

Table A.3—continued.

	Museum tag
Hystricomorpha	
Abrocomidae	
<i>Abrocoma bennettii</i>	USNM 391842; UF 23915; FMNH 23170, 23169
Bathyergidae	
<i>Bathyergus janetta</i>	USNM 469790, 469794, 469791, 469793
<i>Cryptomys hottentotus</i>	USNM 221431, 344826, 344869, 221431
Caviidae	
Caviinae	
<i>Microcavia australis</i>	USNM 84182; UF 27628, 27636, 27645
Dolichotinae	
<i>Dolichotis patagonum</i>	USNM 135946; UF 9949, 18999; FMNH 49212
<i>Dolichotis salinicola</i>	USNM 258569, 270234, 257010, 270306
Chinchillidae	
<i>Lagidium viscacia</i>	USNM 274565; UF 23901; FMNH 53673, 53672
<i>Lagostomus maximus</i>	USNM 114840; UF 14778; FMNH 54339, 53704
Ctenodactylidae	
<i>Ctenodactylus gundi</i>	MVZ 201015; USNM 475997, 475998, 476005
<i>Ctenodactylus vali</i>	USNM 302296
<i>Felovia vae</i>	USNM 401279, 401286, 402149, 402147
<i>Massoutiera mzabi</i>	USNM 482508, 482509, 482510; FMNH 48806
<i>Pectinator spekei</i>	FMNH 106442, 1438
Ctenomyidae	
<i>Ctenomys emilianus</i>	FMNH 29064
<i>Ctenomys latro</i>	USNM 236335, 236336; FMNH 29058, 41270
<i>Ctenomys mendocinus</i>	FMNH 46131, 46130, 46132, 46133
<i>Ctenomys occultus</i>	FMNH 41267, 41268
Hystricidae	
<i>Hystrix africaeaustralis</i>	USNM 368422, 469825, 221369, 470121
<i>Hystrix cristata</i>	USNM 162900; FMNH 57170, 89203, 41337
<i>Hystrix indica</i>	USNM 327158, 350765, 522678, 350763
Octodontidae	
<i>Octodon degus</i>	USNM 541816, 259581; UF 14997, 14998
<i>Octodon lunatus</i>	UF 23916; FMNH 23210, 23203, 23903
Petromuridae	
<i>Petromus typicus</i>	MVZ 117767; USNM 343968, 343962, 343963
Myodonta	
Dipodoidea	
Dipodidae	
Allactaginae	
<i>Allactaga balikunica</i>	FMNH 123651
<i>Allactaga bullata</i>	AMNH 58522, 58773, 84202, 46403
<i>Allactaga elater</i>	MVZ 192029; USNM 369890, 341604, 369889; AMNH 88749; FMNH 103865, 103867, 103868
<i>Allactaga euphratica</i>	USNM 327719, 327721, 327723, 327722
<i>Allactaga firozzi</i>	FMNH 112350, 112349, 112351
<i>Allactaga hotsoni</i>	MVZ 192030, 192031, 192034, 192033
<i>Allactaga major</i>	USNM 251639, 1445, 254957; AMNH 178795
<i>Allactaga severzovi</i>	AMNH 206589, 176269
<i>Allactaga sibirica</i>	USNM 155186, 155187, 155194, 155190
<i>Allactaga tetradactyla</i>	USNM 317092, 317093, 317088, 317089
<i>Allactaga williamsi</i>	USNM 327723, 327722; FMNH 82186, 82182
<i>Pygeretmus platyurus</i>	USNM 547939
<i>Pygeretmus pumilio</i>	USNM 1970, 1446, 192467, 122105
<i>Pygeretmus zhirkovi</i>	AMNH 98133, 174330, 176264
Cardiocrainiinae	
<i>Cardiocranus paradoxus</i>	USNM 199550; AMNH 84154
<i>Salpingotulus michaelis</i>	FMNH 99428, 106613
<i>Salpingotus crassicauda</i>	USNM 547940; FMNH 137435
Dipodinae	
<i>Dipus sagitta</i>	USNM 155096, 544449, 155095, 573127; AMNH 84135, 58608, 84121, 58623
<i>Eremodipus lichensteinii</i>	AMNH 174329
<i>Jaculus blanfordi</i>	MVZ 192035, 192036, 198826; USNM 354840, 354836
<i>Jaculus jaculus</i>	MVZ 34198, 107727, 34199, 34200
<i>Jaculus orientalis</i>	MVZ 32810, 183997; USNM 302289, 302290
<i>Paradipus ctenodactylus</i>	AMNH 174332
<i>Styloctenus telum</i>	MVZ 135291; USNM 547938, 4226; AMNH 174328
Sicistinae	
<i>Sicista betulina</i>	USNM 257391, 254986; AMNH 178814, 206586
<i>Sicista concolor</i>	USNM 173798, 173797; AMNH 37837; UF 26942, 26941
<i>Sicista napaea</i>	AMNH 206587
<i>Sicista subtilis</i>	USNM 122117, 122119; AMNH 178829, 206588
Zapodinae	
<i>Eozapus setchuanus</i>	USNM 240900, 240762; AMNH 113580; FMNH 36068
<i>Napaeozapus insignis</i>	MVZ 101049, 96835, 96883, 96887
<i>Zapus hudsonius</i>	MVZ 96834, 96880, 96881, 167703

Table A.3—continued.

	Museum tag
<i>Zapus princeps</i>	MVZ 84023, 84024, 84026, 84028; AMNH 124327; UF 12734, 12741, 12731
<i>Zapus trinotatus</i>	MVZ 99663, 99665, 99667, 99691
Muroidea	
Calomyscidae	
Calomyscinae	
<i>Calomyscus baluchi</i>	UF 28486, 28503, 28504, 28502
<i>Calomyscus bailwardi</i>	USNM 350196, 350198, 329048, 350200
Cricetidae	
Arvicolinae	
<i>Alticola strelzowi</i>	AMNH 178819; FMNH 34034; USNM 175208, 175222, 175199, 175200
<i>Arvicola amphibius</i>	FMNH 112222, 112223, 112224; UF 22400
<i>Chionomys nivalis</i>	MVZ 198808; USNM 369657, 104527, 105816
<i>Dicrostonyx groenlandicus</i>	UF 24163, 24407, 24167, 24116
<i>Ellobius talpinus</i>	MVZ 41292, 41294, 41291, 135298
<i>Eolagurus luteus</i>	AMNH 257136, 257135; FMNH 33720, 33721, 33722
<i>Eolagurus przewalskii</i>	USNM 547936; FMNH 33720, 33721, 33722
<i>Eothenomys custos</i>	AMNH 44140, 44150, 44156, 44147
<i>Lagurus lagurus</i>	AMNH 87095, 176250, 176249, 257134
<i>Lasiopodomys mandarinus</i>	AMNH 25438, 45439; USNM 172586, 299098
<i>Lemmus sibiricus</i>	MVZ 128863, 128857, 128855, 128854
<i>Microtus arvalis</i>	FMNH 103131, 103132, 103133; USNM 85655
<i>Microtus californicus</i>	FMNH 10743, 10745, 10750; USNM 41607
<i>Microtus chrotorrhinus</i>	AMNH 147362; MVZ 54425, 54427, 54426
<i>Microtus kikuchii</i>	USNM 358625, 332965, 332967, 332964
<i>Microtus montanus</i>	FMNH 12653, 12649, 12664; UF 12732
<i>Microtus pennsylvanicus</i>	UF 3887, 3888, 3911; USNM 150132
<i>Microtus richardsoni</i>	USNM 81384
<i>Myodes gapperi</i>	MVZ 56815, 56816, 56813, 56814
<i>Neodon irene</i>	USNM 449167, 449168, 449172, 449173
<i>Neofiber alleni</i>	UF 7418, 7421, 7445, 7440
<i>Ondatra zibethicus</i>	UF 1791, 1793, 1795, 2415
<i>Phenacomys intermedius</i>	USNM 557668, 174477, 557669, 174432
<i>Prometheomys schaposchnikowi</i>	AMNH 174334, 257138, 206579; USNM 547937
<i>Synaptomys cooperi</i>	UF 3839, 3841, 6436, 7946
Cricetinae	
<i>Allocricetus curtatus</i>	USNM 259524
<i>Allocricetus eversmanni</i>	AMNH 176255, 59753; FMNH 33959, 33964; MVZ 41233; USNM 259524
<i>Cricetus barabensis</i>	MVZ 227428, 125072, 125071, 125068
<i>Cricetus barabensis griseus</i>	FMNH 33980, 33981, 33982, 33985
<i>Cricetus longicaudatus</i>	MVZ 41235; USNM 172521, 576188, 449120
<i>Cricetus migratorius</i>	UF 14594, 27124, 27145, 27142; MVZ 41234, 191941; USNM 326786, 326787
<i>Cricetus cricetus</i>	AMNH 176483, 176484; MVZ, 41457, 129377
<i>Mesocricetus auratus</i>	FMNH 63951; MVZ 102642, 102643; UF 3987
<i>Phodopus campbelli</i>	USNM 259901; FMNH 33973, 33974, 33978
<i>Phodopus roborovskii</i>	USNM 155023, 155026, 155031, 155034
<i>Phodopus sungorus</i>	AMNH 206570; MVZ 174380, 41239, 174379
Neotominae	
<i>Habromys lepturus</i>	USNM 68615, 68618, 68609, 68619
<i>Hodomys allenii</i>	USNM 44633, 44634, 44626, 44627
<i>Isthomys pirrensis</i>	USNM 338302, 338269, 338306, 338270
<i>Megadontomys thomasi</i>	MVZ 113564, 113558, 113559, 113562
<i>Neotoma albigenula</i>	USNM 212131; UF 12618, 13245, 5386
<i>Neotoma bryanti</i>	MVZ 186295, 195326, 186296, 186297
<i>Neotoma cinerea</i>	UF 31327, 3166
<i>Neotoma devia</i>	USNM 215546, 226400, 202463, 226399
<i>Neotoma floridana</i>	UF 14691, 12778, 166, 167
<i>Neotoma goldmani</i>	MVZ 76946, 76947; USNM 116897, 116898
<i>Neotoma lepida</i>	USNM 398296; UF 458, 3164, 3163
<i>Neotoma mexicana</i>	USNM 127314; UF 6216, 7831, 5387
<i>Neotomodon alstoni</i>	MVZ 91979, 91978, 91986, 91984
<i>Ochrotomys nuttali</i>	UF 112, 12421, 2710, 801
<i>Onychomys leucogaster</i>	FMNH 123451, 123450; UF 24175, 12613, 941; USNM 273799
<i>Onychomys torridus</i>	MVZ 72814, 119666, 28081, 28077
<i>Osgoodomys banderanus</i>	USNM 45334, 45335, 45333, 33305
<i>Peromyscus aztecus</i>	USNM 392010; UF 24035, 24030, 24036
<i>Peromyscus boylii</i>	UF 6221, 6224, 6225, 6121; USNM 40514
<i>Peromyscus californicus</i>	USNM 569214
<i>Peromyscus crinitus</i>	USNM 53283; UF 3078, 5394, 5397
<i>Peromyscus eremicus</i>	UF 9445, 9447, 9448; USNM 60100
<i>Peromyscus fraterculus</i>	USNM 81017, 69556, 81016, 91566
<i>Peromyscus leucopus</i>	UF 9298, 9303, 1968; USNM 157114
<i>Peromyscus maniculatus</i>	UF 3637, 2802, 2803; USNM 530844
<i>Peromyscus merriami</i>	MVZ 85828, 85836, 85832, 85831
<i>Peromyscus mexicanus</i>	UF 23931, 23930, 23929; USNM 314413
<i>Peromyscus pectoralis</i>	MVZ 92138, 92135, 91786, 92140
<i>Peromyscus polionotus</i>	UF 13035, 5167, 786; USNM 308898

Table A.3—continued.

	Museum tag
<i>Reithrodontomys creper</i>	MVZ 164894, 164898, 164892, 164897
<i>Reithrodontomys fulvescens</i>	FMNH 73418, 13115, 54147; USNM 70255
<i>Reithrodontomys gracilis</i>	MVZ 98443, 98442; USNM 108143
<i>Reithrodontomys megalotis</i>	FMNH 12273, 12271, 12270; UF 6080, 6080, 6081, 6083; USNM 250559
<i>Scotinomys teguina</i>	FMNH 128560, 128561; UF 27717, 27712
<i>Xenomys nelsoni</i>	USNM 45287, 45285
<i>Baiomys musculus</i>	FMNH 54084, 54085, 54086; UF 6039
Sigmodontinae	
<i>Abrothrix andinus</i>	MVZ 115690, 115691, 115689, 115697
<i>Abrothrix longipilis</i>	MVZ 163783, 163784, 163782, 163783
<i>Aegialomys xanthaeolus</i>	FMNH 194444, 19445; USNM 304528, 551641
<i>Akodon aerosus</i>	FMNH 52529, 52524, 43232; USNM 507279
<i>Akodon boliviensis</i>	FMNH 107917; MVZ 172907, 172953; UF 9190
<i>Akodon inicatus</i>	MVZ 163790, 168995, 160118, 168996
<i>Akodon kofordi</i>	MVZ 171660, 171662, 171661, 171663
<i>Akodon lutescens</i>	USNM 259623
<i>Akodon minus</i>	MVZ 116109, 171748, 171751
<i>Akodon molinae</i>	USNM 331060
<i>Akodon spegazzinii</i>	UF 27623, 27625, 27629, 27633
<i>Akodon torques</i>	MVZ 171713, 171724, 174054; USNM 194638
<i>Andalgalomys pearsoni</i>	FMNH 164184, 164188, 157341; MVZ 145278
<i>Andinomys edax</i>	FMNH 162761; MVZ 120224, 120225, 141617
<i>Auliscomys sublimis</i>	MVZ 139474, 139475, 115912, 139477
<i>Brucepattersonius igniventris</i>	MVZ 191467, 183036, 191468, 183037
<i>Calomys callosus</i>	UF 27606, 27625, 27629, 27633; MVZ 145225, 145227, 145226, 145231
<i>Calomys lepidus</i>	MVZ 115752, 174016, 116018, 115754
<i>Calomys musculinus</i>	MVZ 66067, 119954, 151015, 163390
<i>Calomys venustus</i>	USNM 259264
<i>Cerradomys subflavus</i>	MVZ 197609, 197542, 1970610, 197541
<i>Chelemys macronyx</i>	MVZ 151013, 154583, 174384, 174382
<i>Chinchillula sahamae</i>	MVZ 116034, 172675, 116181, 174023
<i>Delomys dorsalis</i>	MVZ 183048, 183047, 183064, 183065
<i>Deltamys kempi</i>	AMNH 206118, 206105, 206163, 206097
<i>Eligmodontia moreni</i>	USNM 236312, 236313, 236311
<i>Eligmodontia morgani</i>	MVZ 182663, 182665, 182675, 182668
<i>Eligmodontia typus</i>	AMNH 262812; FMNH 124314, 124313, 124322; MVZ 169010, 174390, 174391; USNM 541732
<i>Euneomys chinchilloides</i>	FMNH 50736, 134181; MVZ 186039, 186038
<i>Geoxus valdivianus</i>	MVZ 162249, 159389, 154603, 154607
<i>Graomys edithae</i>	MVZ 162261
<i>Graomys griseoflavus</i>	FMNH 28423, 50920, 46125; MVZ 145252, 145254, 145255; UF 27630; USNM 390214
<i>Holochilus brasiliensis</i>	AMNH 210253; FMNH 136891, 87988, 88919
<i>Holochilus sciurus</i>	FMNH 55476, 118813, 93050; UF 13357
<i>Ichthyomys stolzmanni</i>	AMNH 10109
<i>Irenomys tarsalis</i>	MVZ 155837, 154620, 184955, 152171, 201154
<i>Juliomys pictipes</i>	MVZ 182079, 197565, 197563, 197564
<i>Kunisia tomentosus</i>	FMNH 122710, 122711; USNM 584515, 584516
<i>Lenoxus apicalis</i>	MVZ 172657, 171511, 172656, 171513
<i>Loxodontomys micropus</i>	MVZ 155836, 158475, 158474, 155827
<i>Melanomys caliginosus</i>	MVZ 164873, 164871, 164870, 124057
<i>Microromys minutus</i>	MVZ 115636, 171472, 173974, 166666
<i>Neacomys spinosus</i>	MVZ 136626, 136629, 136625, 136627
<i>Necromys amoenus</i>	MVZ 172884, 172886, 172881, 172885
<i>Nectomys apicalis</i>	MVZ 153544, 153542, 153534, 153539
<i>Nectomys squamipes</i>	FMNH 26741; UF 6581, 6583, 30468
<i>Neotomys ebriosus</i>	FMNH 75580; MVZ 114749, 114747, 172661
<i>Nephelomys keaysi</i>	MVZ 173987, 171460, 171445, 171446
<i>Nephelomys livipes</i>	FMNH 52703, 52702, 52705, 52708
<i>Notiomys edwardsii</i>	MVZ 182132
<i>Oecomys bicolor</i>	FMNH 117010, 116920, 116919; UF 635
<i>Oecomys concolor</i>	FMNH 87968; USNM 374321
<i>Oecomys superans</i>	MVZ 155007, 200944, 153524, 155008
<i>Oligoryzomys fulvescens</i>	UF 6148, 28847, 6149, 6152
<i>Oligoryzomys longicaudatus</i>	UF 25933, 27622, 27671; USNM 259583
<i>Oligoryzomys microtis</i>	FMNH 84349, 84350, 84351; USNM 584565
<i>Oryzomys couesi</i>	UF 9869, 29867, 29868, 6901
<i>Oryzomys palustris</i>	UF 23558, 23560, 23561; USNM 510842
<i>Oxymycterus hiska</i>	AMNH 91602, 91601; MVZ 172660, 171520
<i>Oxymycterus nasutus</i>	USNM 460550, 484395, 461881, 460551
<i>Phyllotis amicus</i>	MVZ 136282, 136283, 115806, 137624, 138034, 145548
<i>Phyllotis andium</i>	MVZ 135748, 135749, 135752, 135753
<i>Phyllotis caprinus</i>	OMNH 30081, 30082
<i>Phyllotis darwini</i>	LCM 3047, 3338, 4038, 4057, 4037, 4061
<i>Phyllotis gerbillus</i>	MVZ 138024, 138028, 135693, 135695
<i>Phyllotis magister</i>	MVZ 174036, 174038
<i>Phyllotis osilae</i>	FMNH 52579, 107828, 107831; USNM 194576
<i>Phyllotis xanthopygus</i>	LCM 3009, 3143, 3351, 3021

Table A.3—continued.

	Museum tag
<i>Pseudoryzomys simplex</i>	AMNH 262048; USNM 584585, 584586, 390668
<i>Punomys kofordi</i>	MVZ 1147557, 114758, 116193
<i>Reithrodon auritus auritus</i>	MVZ 163411, 172218, 171163, 165853
<i>Reithrodon auritus physodes</i>	UF 24357, 24358, 24359, 24360
<i>Rhagomys longilingua</i>	FMNH 170687
<i>Rheomys thomasi</i>	MVZ 98811, 98814, 98798, 98808
<i>Rhipidomys macconnelli</i>	MVZ 160085, 160088, 160082, 160086
<i>Rhipidomys nitela</i>	MVZ 197548, 197549, 197550, 197551
<i>Scapteromys tumidus</i>	AMNH 235431; MVZ 183268, 183267, 183269
<i>Scolomys melanops</i>	AMNH 67522
<i>Scolomys ucalayensis</i>	MVZ 183166, 183169, 183167, 183168
<i>Sigmodon alstoni</i>	FMNH 20040, 20042, 20045; USNM 442581
<i>Sigmodon arizonae</i>	MVZ 62573, 62576, 62574, 62575
<i>Sigmodon fulviventer</i>	MVZ 50867, 50866; USNM 20723, 247584
<i>Sigmodon hispidus</i>	UF 143, 1588, 1584, 1589
<i>Sigmodon ochrognathus</i>	MVZ 80495, 80499, 80493, 80494
<i>Sigmodontomys alfari</i>	FMNH 70536, 70535, 70534; MVZ 164891
<i>Sooretamys angouya ratticeps</i>	FMNH 136919, 136920, 136924
<i>Thaptomys nigrita</i>	FMNH 26820; MVZ 183043, 183040, 183044
<i>Thomasomys aureus</i>	MVZ 166710, 166708, 166709, 166711
<i>Thomasomys daphne</i>	AMNH 72128, 72112, 248283; FMNH 172378
<i>Thomasomys notatus</i>	FMNH 170696; USNM 582122, 194898, 194897
<i>Transandinomys talamancae</i>	FMNH 69207, 69211; MVZ 164879, 164878
<i>Wiedomys pyrrhorhinos</i>	FMNH 136942; MVZ 197566, 197567
<i>Zygodontomys brevicauda</i>	MVZ 106227, 113383; UF 13359, 6574
Tylomyinae	
<i>Nyctomys sumichrasti</i>	MVZ 98817, 98818; UF 7566, 7568, 7569, 7564
<i>Ototylomys phyllotis</i>	FMNH 42043, 64564, 64567; UF 6910
<i>Tylomys nudicaudus</i>	FMNH 64569; MVZ 131365, 131364, 223323
Muridae	
Deomyinae	
<i>Acomys cahirinus</i>	MVZ 107726, 118298, 118306, 1077262 118297, 1182982, 118320
<i>Acomys cinereaceus</i>	USNM 422402, 422404, 422401, 422419
<i>Acomys dimidiatus</i>	MVZ 34193
<i>Acomys percivali</i>	MVZ 186228, 186226, 186227, 186229
<i>Acomys ignitus</i>	USNM 181744, 182888, 181750, 182889
<i>Acomys russatus</i>	USNM 317002, 317007, 316997, 317006
<i>Acomys spinosissimus</i>	AMNH 162547, 162546, 219041, 162545
<i>Acomys wilsoni</i>	MVZ 186231, 186232, 186233, 191151
<i>Deomys ferrugineus</i>	FMNH 167789, 167781, 167780; MVZ 196252
<i>Lophuromys flavopunctatus</i>	USNM 259508, 537876, 259515, 537875
<i>Lophuromys zena</i>	USNM 589948, 589952, 589943, 589947
<i>Lophuromys sikapusi</i>	FMNH 81935, 81937, 81938; MVZ 196260
<i>Uranomys ruddi</i>	USNM 438783, 367021, 438782, 367020
Gerbillinae	
<i>Ammodillus imbellis</i>	FMNH 140092
<i>Brachionomys przewalskii</i>	USNM 102578
<i>Desmodilliscus braueri</i>	USNM 378287, 378289, 378290, 453904, 453899, 453893
<i>Desmodilllus auricularis</i>	MVZ 117381, 117379, 117371, 117372; AMNH 165455, 165453, 165451, 165456
<i>Dipodillus campestris</i>	USNM 401028, 401038, 401036, 401852
<i>Dipodillus dasypurus</i>	USNM 350041, 316662, 316658, 350037
<i>Dipodillus harwoodi</i>	USNM 162274, 162303, 162273, 162306
<i>Dipodillus lowei</i>	USNM 297499, 297498
<i>Dipodillus mackillagini</i>	USNM 316700
<i>Dipodillus magharebi</i>	USNM 472715, 472718, 472713, 472716, 472719, 472717
<i>Dipodillus simoni</i>	USNM 316687, 316699, 316683, 350045
<i>Dipodillus stigmonyx</i>	USNM 165286, 165283, 165284, 165285
<i>Gerbiliscus afra</i>	MVZ 117338, 117337, 117340, 117342
<i>Gerbiliscus boehmi</i>	USNM 162261, 162253, 162258, 162250
<i>Gerbiliscus brantsii brantsii</i>	USNM 295355, 295350, 462447, 295349
<i>Gerbiliscus brantsii humpatensis</i>	MVZ 88729, 88730
<i>Gerbiliscus brantsii perpallidus</i>	AMNH 83696, 83693, 83694, 83695
<i>Gerbiliscus guineae</i>	USNM 466209, 450763, 466212, 450765
<i>Gerbiliscus inclusus</i>	USNM 538396, 538397, 538395, 381480
<i>Gerbiliscus kempfi</i>	MVZ 196265, 196266, 196267; FMNH 25369
<i>Gerbiliscus leucogaster</i>	USNM 295398, 295400, 295394, 295395
<i>Gerbiliscus nigricaudus</i>	USNM 183938, 590061, 183933, 590058
<i>Gerbiliscus phillipsi</i>	USNM 344931, 344934; FMNH 28840, 28837
<i>Gerbiliscus robustus</i>	MVZ 186208, 186207, 186204, 186205
<i>Gerbiliscus validus</i>	MVZ 88727, 88732, 88717, 88720
<i>Gerbillurus paeba</i>	AMNH 219001, 219002; MVZ 149573, 149576
<i>Gerbillurus setzeri</i>	USNM 342232, 342260, 342229, 342233
<i>Gerbillurus tytonis</i>	USNM 379852, 379869, 342165, 379854
<i>Gerbillurus vallinus</i>	USNM 424171, 424172, 424173, 424175
<i>Gerbillus agag</i>	MVZ 1543290, 154330, 154326, 154332
<i>Gerbillus amoenus</i>	USNM 300231, 302217, 307626, 322544

Table A.3—continued.

	Museum tag
<i>Gerbillus andersoni</i>	MVZ 107721; USNM 316747, 283254, 300226
<i>Gerbillus aquilus</i>	USNM 328042, 369319, 328045, 369341
<i>Gerbillus cheesmani</i>	MVZ 191959, 191960; 29029, 29042
<i>Gerbillus famulus</i>	USNM 321586, 321664, 321587, 321663
<i>Gerbillus floweri</i>	USNM 316843, 316848, 316850, 316852
<i>Gerbillus garamantis</i>	FMNH 72828
<i>Gerbillus gerbillus</i>	MVZ 34214, 107722, 34212, 34213
<i>Gerbillus gleadowi</i>	USNM 353247, 353617, 353622, 369058
<i>Gerbillus henleyi</i>	MVZ 107720; USNM 472202, 472203, 472204
<i>Gerbillus hesperinus</i>	USNM 486006, 485964, 486005, 485970
<i>Gerbillus hoogstraali</i>	USNM 540028, 540038, 540037, 540034
<i>Gerbillus latastei</i>	USNM 321822, 321813, 321821, 321794
<i>Gerbillus mauritaniae</i>	USNM 401519, 401522, 401518, 401002
<i>Gerbillus mesopotamiae</i>	USNM 350442, 350444, 350443, 350450
<i>Gerbillus muriculus</i>	USNM 141503, 297485, 141504; FMNH 105600
<i>Gerbillus nanus</i>	MVZ 191952, 191953, 191955, 191958; UF 14577, 25903, 28564, 28562
<i>Gerbillus nigeriae</i>	USNM 573945, 573944
<i>Gerbillus occiduus</i>	USNM 540040
<i>Gerbillus perpallidus</i>	USNM 316820, 316823, 316819, 316822
<i>Gerbillus poecilops</i>	USNM 321575, 321584, 321577, 321579
<i>Gerbillus pulvinatus</i>	USNM 500939, 500943, 500940, 500942
<i>Gerbillus pusillus</i>	USNM 500947, 500946, 500945; FMNH 44419
<i>Gerbillus pyramidum</i>	MVZ 34208, 107723, 34210; AMNH 119507
<i>Gerbillus tarabuli</i>	USNM 302165, 302167, 302160, 302218
<i>Meriones crassus</i>	MVZ 191991; USNM 401159, 401161, 401157
<i>Meriones erythrourus</i>	FMNH 202109
<i>Meriones grandis</i>	USNM 473951, 483036, 473866, 474353
<i>Meriones hurrianae</i>	USNM 369162, 369163, 369161, 369510
<i>Meriones libycus</i>	MVZ 191968, 191972, 191962, 191963
<i>Meriones meridianus</i>	MVZ 41227, 41228; AMNH 59702, 59352
<i>Meriones persicus</i>	MVZ 198812, 198813, 198811, 198819
<i>Meriones rex</i>	USNM 321715; FMNH 77953, 77955, 77959
<i>Meriones shawi</i>	USNM 474209, 474187, 474208, 474185
<i>Meriones tamariscinus</i>	USNM 155457, 155459; AMNH 85369, 85377
<i>Meriones tristrami</i>	MVZ 183874; USNM 327436, 327438, 327437
<i>Meriones unguiculatus</i>	MVZ 41229; USNM 240765, 283918, 270551
<i>Meriones vinogradovi</i>	MVZ 183875; USNM 354663, 354662; FMNH 97405
<i>Pachyromys duprasi</i>	FMNH 74976, 89621, 80021, 80048; MVZ 34197; USNM 482421, 321829, 325567, 325569
<i>Psammomys obesus</i>	AMNH 203215; FMNH 78611, 91277, 91279; MVZ 183877; USNM 482457, 326018, 326025, 341974
<i>Rhombomys opimus</i>	AMNH 88865, 88868, 88871, 88875; MVZ 41226; USNM 341327, 341329, 341332, 341334
<i>Sekeetamys calurus</i>	FMNH 101021, 101025, 101024, 101033; USNM 321934, 321928, 321931, 321932
<i>Tater indica</i>	AMNH 240846; MVZ 192006, 192007, 192002, 192005; UF 30352, 30266, 30245, 30260
<i>Taterillus arenarius</i>	USNM 401124, 401978, 401117, 401980
<i>Taterillus congicus</i>	AMNH 50294, 50295, 50298, 50300
<i>Taterillus emini</i>	USNM 165288, 299721, 165289, 299718
<i>Taterillus gracilis</i>	USNM 403445, 438169, 403447, 438165
<i>Taterillus harringtoni</i>	USNM 483985, 483990, 483998, 483991
<i>Taterillus lacustris</i>	USNM 378930, 378929, 378925, 378923
<i>Taterillus pygargus</i>	USNM 376373, 380412, 376311, 380413
<i>Lophiomyinae</i>	
<i>Lophiomys imhausi</i>	USNM 291766, 172694, 184114, 184115
<i>Murinae</i>	
<i>Abeomelomys sevia</i>	AMNH 191963, 191965, 191966, 191964
<i>Aethomys chrysophilus</i>	MVZ 117532, 117534, 118188, 117531
<i>Aethomys namaquensis</i>	MVZ 117521, 117524, 117519, 117520
<i>Anisomys imitator</i>	AMNH 194893, 194894, 194892, 194891
<i>Apodemus agrarius</i>	MVZ 120896, 120898, 125183, 121103
<i>Apodemus mystacinus</i>	USNM 327654; MVZ 100019, 72459, 72461
<i>Apodemus semotus</i>	USNM 261057, 333017, 361053, 333014
<i>Apodemus speciosus</i>	MVZ 119797; USNM 299360
<i>Apodemus sylvaticus</i>	FMNH 74411, 74409, 74412; USNM 153235
<i>Apomys datae</i>	FMNH 188427, 188448, 188280; USNM 574889
<i>Apomys hylocoetes</i>	FMNH 147871, 147872; USNM 125243, 125244
<i>Archboldomys luzonensis</i>	USNM 573837, 573835, 573838, 573840
<i>Arvicathis neumanni</i>	FMNH 158037; MVZ 101023
<i>Arvicathis niloticus</i>	FMNH 105595, 105596, 105597; MVZ 154335
<i>Bandicota bengalensis</i>	MVZ 181303, 181305; UF 14630, 27590
<i>Batomys salomonensi</i>	FMNH 147940, 148163, 148170, 148172
<i>Berylmys bowersi</i>	MVZ 186483, 186484, 186482, 186490
<i>Bullimus bagobus</i>	USNM 462203, 459923, 462206, 458789
<i>Bunomys chrysocomus</i>	AMNH 224769, 224767; MVZ 225697, 225810
<i>Carpomys phaeurus</i>	FMNH 62291
<i>Chiromyscus chiropus</i>	AMNH 268333; FMNH 32010; USNM 321507, 308218
<i>Chiropodomys gliroides</i>	AMNH 106684, 106681, 106687; USNM 283681
<i>Chrotomys gonzalesi</i>	USNM 356290, 458955
<i>Colomys goslingi</i>	AMNH 55219, 55220; USNM 537872, 375903

Table A.3—continued.

	Museum tag
<i>Conilurus penicillatus</i>	AMNH 183587; FMNH 120704; USNM 141486, 141487
<i>Cremnomys cuthicus</i>	FMNH 35295, 82993, 82994, 82996
<i>Crunomys melanius</i>	FMNH 147106, 167889
<i>Dacnomys millardi</i>	FMNH 84892, 76519, 84881; MVZ 186519
<i>Dasyomys incomitus</i>	AMNH 118839, 118837, 118835; MVZ 88742
<i>Golunda ellioti</i>	FMNH 83032, 83034, 83036; UF 14613
<i>Grammomys dolichurus</i>	MVZ 117387, 117389, 117386, 118168
<i>Grammomys ibeanus</i>	USNM 183754, 162530, 162529, 162528
<i>Grammomys macmillani</i>	FMNH 73916, 73917, 79469; USNM 299736
<i>Hapalomys delacouri</i>	FMNH 32463
<i>Heimyscus fumosus</i>	USNM 585164, 584972, 585169, 585173
<i>Hybomys univittatus</i>	USNM 84522, 580737, 545844, 580207
<i>Hydromys chrysogaster</i>	MVZ 119719, 121748, 119419, 129303
<i>Hylomyscus parvus</i>	USNM 585202, 585208, 584752, 584754
<i>Hylomyscus stella</i>	FMNH 165219, 165221, 165223; MVZ 196244
<i>Hyomys goliath</i>	MVZ 129941; 194909, 194899, 194910
<i>Leggadina forresti</i>	USNM 284270; FMNH 120331, 120330
<i>Lemniscomys barbarus</i>	USNM 475121, 475161, 475122, 475165
<i>Lemniscomys striatus</i>	FMNH 17280, 86192, 123809; UF 20537
<i>Leopoldamys sabanus</i>	FMNH 98587, 98585, 98584; MVZ 186495
<i>Leptomyss elegans</i>	AMNH 158203, 104200, 108447, 104199
<i>Limnomyss sibuanus</i>	FMNH 148174, 147947, 147950, 148175
<i>Lorentzimys nouhuysi</i>	USNM 585614, 585616, 585612
<i>Macruromys major</i>	AMNH 152068, 152066, 152069, 152067
<i>Malacomys longipes</i>	MVZ 196255, 196280, 196254, 196279
<i>Margaretamyss elegans</i>	AMNH 223697, 223696, 225146, 223695
<i>Mastacomys fuscus</i>	USNM 574492
<i>Mastomys erythroleucus</i>	FMNH 42353, 42354; MVZ 196261, 196262
<i>Maxomys bartelsii</i>	USNM 481468, 481516, 481465, 496858
<i>Maxomys surifer</i>	MVZ 155535, 155537, 155534, 155539
<i>Melasmotherrix naso</i>	AMNH 225087, 225112, 225103, 225110
<i>Melomys cervinipes</i>	MVZ 134084, 134069, 126567, 126568
<i>Melomys rufescens</i>	FMNH 54064; USNM 295069
<i>Mesembriomys gouldii</i>	USNM 284348, 284344, 141489
<i>Micromys minutus</i>	AMNH 160524; MVZ 123584, 123585, 174890
<i>Millardia gleadowi</i>	USNM 354414, 413647, 369523, 354414
<i>Millardia kathleenae</i>	AMNH 163761; FMNH 82944
<i>Mus booduga</i>	FMNH 35292; USNM 369234, 533854, 533774, 533855
<i>Mus cervicolor</i>	FMNH 105715, 105714; MVZ 154456, 154455
<i>Mus cookii</i>	FMNH 105731, 76796, 99769; MVZ 154450
<i>Mus minutoides</i>	AMNH 168548; MVZ 162503, 162508, 165138, 18295, 117689, 117688; USNM 352800, 352806
<i>Mus musculus</i>	UF 27595, 14562, 1840, 7588; USNM 298998
<i>Mus pahari</i>	MVZ 166472, 221555, 221556; USNM 355553
<i>Mus saxicola</i>	USNM 556247, 556249, 556257, 556248
<i>Mus spretus</i>	MVZ 226632, 155909, 155911; USNM 486120
<i>Mus terricolus</i>	USNM 533850, 533851, 398777, 279167
<i>Myomys dybowskii</i>	USNM 317996, 183598, 183604, 183608
<i>Myomyscus brockmani</i>	USNM 183495, 259902, 183502, 162472
<i>Niviventer confucianus</i>	AMNH 58972; MVZ 174887, 174871, 174888
<i>Niviventer cremoniventer</i>	USNM 292782, 488957, 292790, 488962
<i>Niviventer excelsior</i>	USNM 574373, 574372
<i>Notomys alexis</i>	MVZ 134373; USNM 284363; AMNH 197502, 197504
<i>Notomys cervinus</i>	USNM 284352, 284359; AMNH 153491, 153492
<i>Notomys fuscus</i>	FMVZ 124313, 124312, 124314, 124315
<i>Oenomys hypoxanthus</i>	USNM 183631, 220534, 437349, 297526
<i>Otomys angoniensis</i>	USNM 437517, 382382, 318084, 382383
<i>Otomys denti</i>	USNM 381484, 381486, 259555, 340925
<i>Parotomys brantsii</i>	AMNH 168509, 168510; MVZ 117756, 118405
<i>Parotomys littledalei</i>	MVZ 81577; USNM 343927, 343936, 343923, 256963
<i>Paruromys dominator</i>	AMNH 225744, 225742; MVZ 225784, 225788
<i>Phloeomys cumingi</i>	UF 22381
<i>Pogonomys loriae</i>	USNM 357495, 357496
<i>Pogonomys macrourus</i>	MVZ 140443, 138620, 140447, 140450
<i>Praomys jacksoni</i>	AMNH 82454; MVZ 196286, 196289, 196287
<i>Praomys misomoei</i>	FMNH 149595, 149597, 149598, 149601
<i>Praomys tullbergi</i>	MVZ 133098, 133099; USNM 463056
<i>Pseudohydromys ellermani</i>	MVZ 129794, 129796, 129798
<i>Pseudomys australis</i>	AMNH 65998; MVZ 134044, 134115, 133681
<i>Pseudomys hermannsburgensis</i>	AMNH 197431, 197433, 220112, 220113
<i>Rattus exulans</i>	UF 27816, 28982, 30104; USNM 321152
<i>Rattus norvegicus</i>	UF 3945, 12719, 39452, 2885
<i>Rattus praetor</i>	USNM 277303, 290540, 277304, 277067
<i>Rattus rattus</i>	USNM 356509, 465, 1250, 468
<i>Rattus sordidus</i>	MVZ 133641, 133606, 133637, 133639
<i>Rattus tiomanicus</i>	FMNH 171919, 171920, 171917; USNM 590331
<i>Rattus verecundus</i>	USNM 357439, 357437, 357431, 357438

Table A.3—continued.

	Museum tag
<i>Rattus villosissimus</i>	AMNH 153476, 153495, 153475, 153477
<i>Rhabdomys pumilio</i>	MVZ 88824, 88823, 88820, 117468
<i>Rhynchomys isarogensis</i>	USNM 573906, 573905, 573912, 573911
<i>Stenocephalemys albipes</i>	USNM 515391, 516174, 516155, 516179
<i>Stochomys longicaudatus</i>	FMNH 29471, 29472, 74223; MVZ 196264
<i>Sundamys muelleri</i>	USNM 113035, 115593, 104838, 121764
<i>Tarsomys apoensis</i>	FMNH 148177, 148176; USNM 144619
<i>Uromys caudimaculatus</i>	MVZ 175371, 175372, 140440, 134112
<i>Vandeleuria oleracea</i>	AMNH 242257; USNM 279309, 277861, 279310
<i>Zelotomys hildegardeae</i>	USNM 183912, 183913, 181804, 183911
<i>Zelotomys woosnami</i>	USNM 428770, 428771, 428772, 470118
<i>Zyzomys argurus</i>	USNM 284323, 578555, 284328, 384336
Nesomyidae	
Cricetomyinae	
<i>Beamys hindei</i>	USNM 183107, 183109, 183103, 183108
<i>Cricetomys gambianus</i>	FMNH 128237; MVZ 196236, 196237; UF 29051
<i>Saccostomus campestris</i>	MVZ 118335, 118371, 118364, 118365
Delanymyinae	
<i>Delanymys brooksi</i>	AMNH 181210, 181208, 181209; FMNH 148417
Dendromurinae	
<i>Dendromus insignis</i>	USNM 164387, 184067, 164392, 164454
<i>Dendromus mesomelas</i>	MVZ 117690
<i>Dendromus nyasae</i>	FMNH 196686, 191596, 191597, 191598
<i>Malacothrix typica</i>	USNM 343711, 423199, 343708, 423204
<i>Steatomys krebsi</i>	FMNH 153193
<i>Steatomys parvus</i>	USNM 367225, 428962, 295978, 164468
Petromyscinae	
<i>Petromyscus collinus</i>	AMNH 165437, 165438, 165439, 165408; USNM 424617, 452334, 452406, 452433
Mystromyinae	
<i>Mystromys albicaudatus</i>	USNM 468440, 422538, 422540, 468445
Nesomyinae	
<i>Brachytarsomys albicauda</i>	AMNH 100692; MVZ 217015; USNM 449215, 449214
<i>Brachyuromys betsileoensis</i>	AMNH 100802; MVZ 216974; USNM 328818, 328815
<i>Eliurus minor</i>	USNM 448974, 578678, 328827, 449246
<i>Eliurus tanala</i>	USNM 448986, 449251, 448987, 449253
<i>Gymnuromys roberti</i>	FMNH 5632, 151694, 151695; MVZ 221230
<i>Hypogeomys antimena</i>	AMNH 119705
<i>Macrotarsomys bastardi</i>	USNM 328795, 328802, 328796, 578717
<i>Monticolomys koopmani</i>	AMNH 275217, 275214
<i>Nesomys rufus</i>	AMNH 100679; MVZ 217006; USNM 449239, 449245
<i>Voalavo gymno caudus</i>	FMNH 156162, 159648, 159725, 159727
Platacanthomyidae	
Platacanthomyinae	
<i>Typhlomys cinereus</i>	AMNH 84762, 84769, 84761; FMNH 39131
Spalacidae	
Myospalacinae	
<i>Eospalax fontanieri cansas</i>	FMNH 19070, 19069
<i>Myospalax aspalax</i>	FMNH 49900, 49901
Spalacinae	
<i>Spalax ehrenbergi</i>	FMNH 101009, 101010, 101014, 101011
Rhizomyinae	
<i>Cannomys badius</i>	FMNH 104207, 104211, 104212; MVZ 183902
<i>Rhizomys pruinosus</i>	FMNH 84849; MVZ 186543, 186544, 186548
Tachyoryctinae	
<i>Tachyoryctes splendens</i>	MVZ 163968, 183904, 183908, 183907
Sciromorpha	
Gliridae	
Leithiinae	
<i>Eliomys melanurus</i>	USNM 475706, 302274, 475705, 342024
<i>Eliomys querinus</i>	MVZ 154697; USNM 103031, 103032, 152768
Graphiurinae	
<i>Graphiurus ocularis</i>	AMNH 168333, 168332, 89052
Sciuridae	
Xerinae	
<i>Ammospermophilus harrisi</i>	USNM 33713; UF 2508; FMNH 14956, 4873
<i>Ammospermophilus interpres</i>	USNM 18154, 20077, 108389, 108928
<i>Ammospermophilus leucurus</i>	USNM 53221; UF 4744, 5383, 2494
<i>Ammospermophilus nelsoni</i>	USNM 31273, 129865, 54629, 127152
<i>Atlantoxerus getulus</i>	USNM 470900, 470895, 476815, 476821
<i>Spermophilus fulvus</i>	USNM 369544; AMNH 206566, 176239; FMNH 96891
<i>Spermophilus mexicanus</i>	USNM 33546, 34118, 33549, 34123
<i>Spermophilus mohavensis</i>	USNM 15975, 135838, 28740, 192753
<i>Spermophilus pygmaeus</i>	USNM 251636, 251637; AMNH 87089, 87090
<i>Spermophilus spilosoma</i>	USNM 247654, 35079, 35077, 350800
<i>Spermophilus tereticaudus</i>	USNM 96984, 33762, 138610, 33754

Table A.3—continued.

	Museum tag
<i>Spermophilus variegatus</i>	USNM 117529, 117602, 97156, 117604
<i>Xerus erythropus</i>	USNM 421581, 453006, 453008, 453009
<i>Xerus inauris</i>	USNM 368056, 368059, 259785, 368058
<i>Xerus princeps</i>	USNM 379848, 379847; AMNH 86479

Table A.4. List of specimens digitized in two dimensions for chapter 7. See Table A.1 legend for more information.

	Museum tag
Anomaluromorphia	
Pedetidae	
<i>Pedetes capensis</i>	USNM 422522; FMNH 38263, 38231, 38261
Castorimorpha	
Geomysidae	
<i>Cratogeomys castanops</i>	AMNH 68767, 68766, 68768, 63812
<i>Thomomys umbrinus</i>	USNM 55913; UF 8238; FMNH 14058, 14059
Heteromyidae	
Dipodomysinae	
<i>Dipodomys deserti</i>	USNM 33926; AMNH 139598, 139597, 139600, 139599
<i>Dipodomys gravipes</i>	USNM 138910, 245885, 245884
<i>Dipodomys heermanni</i>	USNM 149736, 137911, 137918, 149735
<i>Dipodomys merriami</i>	USNM 50007; AMNH 173786, 169577, 173787
<i>Dipodomys microps</i>	MVZ 73650, 73651, 73649, 73652
<i>Dipodomys nelsoni</i>	MVZ 76548, 76547; USNM 56195, 51068
<i>Dipodomys nitratoides</i>	USNM 54871, 149756, 214515, 149757
<i>Dipodomys ordii</i>	USNM 214113; UF 24179, 24180, 4673
<i>Dipodomys panamintinus</i>	USNM 41336; UF 3058, 3059, 3060
<i>Dipodomys phillipsii</i>	USNM 53324, 53331, 90803, 94622
<i>Dipodomys simulans</i>	USNM 555015, 555018, 139866, 531718
<i>Dipodomys spectabilis</i>	USNM 46288; UF 25951, 25952, 25953
<i>Microdipodops megacephalus</i>	MVZ 159877, 159878; USNM 54585, 54582
<i>Microdipodops pallidus</i>	USNM 246133, 246023, 246020, 246024
Perognathinae	
<i>Chaetodipus arenarius</i>	USNM 531519, 531529, 146908, 531518
<i>Chaetodipus artus</i>	USNM 96303, 96304, 96301, 96302
<i>Chaetodipus baileyi</i>	USNM 49169; UF 3076; FMNH 52836, 52839
<i>Chaetodipus californicus</i>	USNM 55561; UF 3033; FMNH 10902, 10890
<i>Chaetodipus eremicus</i>	USNM 51096, 157404, 119104, 119781
<i>Chaetodipus fallax</i>	USNM 529907; UF 3044, 12761, 12760
<i>Chaetodipus formosus</i>	USNM 262926, 263160, 41957, 263139; AMNH 11850, 11837, 258740, 258738
<i>Chaetodipus hispidus</i>	USNM 31559; UF 9633, 11944, 8672
<i>Chaetodipus intermedius</i>	USNM 532532; UF 12527, 12528, 7836
<i>Chaetodipus lineatus</i>	USNM 296791, 296790; FMNH 141795, 141796
<i>Chaetodipus nelsoni</i>	USNM 50210; FMNH 46911, 46910
<i>Chaetodipus penicillatus</i>	USNM 552796; UF 4681, 437, 4682
<i>Chaetodipus ruddinoris</i>	USNM 145985, 146090, 14005, 140006
<i>Chaetodipus spinatus</i>	USNM 140038; UF 3041, 3042, 3043
<i>Perognathus amplus</i>	MVZ 47107, 47108, 47109, 47110
<i>Perognathus flavescens</i>	USNM 47378, 87901, 66537, 275699
<i>Perognathus flavus</i>	USNM 213440; UF 7833, 7834, 24183
<i>Perognathus inornatus</i>	USNM 41789, 93726, 41788, 149800
<i>Perognathus longimembris</i>	MVZ 55750, 60834, 55751, 55752
<i>Perognathus merriami</i>	USNM 48743, 48741, 93349, 48742
<i>Perognathus parvus</i>	USNM 55294; FMNH 11886, 11887, 11889
Hyracidae	
Abrocomidae	
<i>Abrocoma bennettii</i>	USNM 391842; UF 23915; FMNH 23170, 23169
Bathyergidae	
<i>Bathyergus janetta</i>	USNM 469790, 469794, 469791, 469793
<i>Cryptomys hottentotus</i>	USNM 221431, 344826, 344869, 221431
Caviidae	
Caviinae	
<i>Microcavia australis</i>	USNM 84182; UF 27628, 27636, 27645
Dolichotinae	
<i>Dolichotis patagonum</i>	USNM 135946; UF 9949, 18999; FMNH 49212
<i>Dolichotis salinicola</i>	USNM 258569, 270234, 257010, 270306

Table A.4—continued.

	Museum tag
Chinchillidae	
<i>Lagidium viscacia</i>	USNM 274565; UF 23901; FMNH 53673, 53672
<i>Lagostomus maximus</i>	USNM 114840; UF 14778; FMNH 54339, 53704
Ctenodactylidae	
<i>Ctenodactylus gundi</i>	MVZ 201015; USNM 475997, 475998, 476005
<i>Ctenodactylus vali</i>	USNM 302296
<i>Felovia vae</i>	USNM 401279, 401286, 402149, 402147
<i>Massoutiera mzabi</i>	USNM 482508, 482509, 482510; FMNH 48806
<i>Pectinator spekei</i>	FMNH 106442, 1438
Ctenomyidae	
<i>Ctenomys emilianus</i>	FMNH 29064
<i>Ctenomys latro</i>	USNM 236335, 236336; FMNH 29058, 41270
<i>Ctenomys mendocinus</i>	FMNH 46131, 46130, 46132, 46133
<i>Ctenomys occultus</i>	FMNH 41267, 41268
Hystricidae	
<i>Hystrix africaeaustralis</i>	USNM 368422, 469825, 221369, 470121
<i>Hystrix cristata</i>	USNM 162900; FMNH 57170, 89203, 41337
<i>Hystrix indica</i>	USNM 327158, 350765, 522678, 350763
Octodontidae	
<i>Octodon degus</i>	USNM 541816, 259581; UF 14997, 14998
<i>Octodon lunatus</i>	UF 23916; FMNH 23210, 23203, 23903
Petromuridae	
<i>Petromus typicus</i>	MVZ 117767; USNM 343968, 343962, 343963
Myodonta	
Dipodoidea	
Dipodidae	
Allactaginae	
<i>Allactaga balikunica</i>	FMNH 123651
<i>Allactaga bullata</i>	AMNH 58522, 58773, 84202, 46403
<i>Allactaga elater</i>	MVZ 192029; USNM 369890, 341604, 369889; AMNH 88749; FMNH 103865, 103867, 103868
<i>Allactaga euphratica</i>	USNM 327719, 327721, 327723, 327722; FMNH 82186, 82182
<i>Allactaga firozzi</i>	FMNH 112349, 112350, 112351
<i>Allactaga major</i>	USNM 251639, 1445, 254957; AMNH 178795
<i>Allactaga severtzovi</i>	AMNH 206589, 176269
<i>Allactaga sibirica</i>	USNM 155186, 155187, 155194, 155190
<i>Allactaga tetradactyla</i>	USNM 317092, 317093, 317088, 317089
<i>Pygeretmus platyurus</i>	USNM 547939
<i>Pygeretmus pumilio</i>	USNM 1970, 1446, 192467, 122105
<i>Pygeretmus zhitkovi</i>	AMNH 98133, 174330, 176264
Cardioceraniinae	
<i>Cardiocranus paradoxus</i>	USNM 199550; AMNH 84154
<i>Salpingotus crassicauda</i>	USNM 547940; FMNH 137435
<i>Salpingotus michaelsi</i>	FMNH 106613, 99428
Dipodinae	
<i>Dipus sagitta</i>	USNM 155096, 544449, 155095, 573127; AMNH 84135, 58608, 84121, 58623
<i>Eremodipus lichtensteinii</i>	AMNH 174329
<i>Jaculus blanfordi</i>	MVZ 192035, 192036, 198826; USNM 354840, 354836
<i>Jaculus jaculus</i>	MVZ 34198, 107727, 34199, 34200
<i>Jaculus orientalis</i>	MVZ 32810, 183997; USNM 302289, 302290
<i>Paradipus ctenodactylus</i>	AMNH 174332
<i>Styloctopus telum</i>	MVZ 135291; USNM 547938, 4226; AMNH 174328
Muroidea	
Calomyscidae	
<i>Calomyscus bailwardi</i>	USNM 329048, 350196, 350198, 350200
Cricetidae	
Arvicolinae	
<i>Alticola strelzowi</i>	AMNH 178819; FMNH 34034; USNM 175208, 175222, 175199, 175200
<i>Ellobius talpinus</i>	MVZ 41292, 41294, 41291, 135298
<i>Eolagurus luteus</i>	AMNH 257136, 257135; FMNH 33720, 33721, 33722
<i>Eolagurus przewalskii</i>	USNM 547936; FMNH 33720, 33721, 33722
<i>Microtus californicus</i>	FMNH 10743, 10745, 10750; USNM 41607
Cricetinae	
<i>Allocricetus eversmanni</i>	AMNH 176255, 59753; FMNH 33959, 33964; MVZ 41233; USNM 259524
<i>Cricetus barabensis</i>	MVZ 227428, 125072, 125071, 125068; FMNH 33980, 33981, 33982, 33985
<i>Cricetus longicaudatus</i>	MVZ 41235; USNM 172521, 576188, 449120
<i>Cricetus migratorius</i>	UF 14594, 27124, 27145, 27142; MVZ 41234, 191941; USNM 326786, 326787
<i>Phodopus campbelli</i>	USNM 259901; FMNH 33973, 33974, 33978
<i>Phodopus roborowskii</i>	USNM 155023, 155026, 155031, 155034
<i>Phodopus sungorus</i>	AMNH 206570; MVZ 174380, 41239, 174379
Neotominae	
<i>Neotoma albigenula</i>	USNM 212131; UF 12618, 13245, 5386
<i>Neotoma cinerea</i>	UF 31327, 3166
<i>Neotoma devia</i>	USNM 215546, 226400, 202463, 226399
<i>Neotoma goldmani</i>	MVZ 76946, 76947; USNM 116897, 116898
<i>Neotoma lepida</i>	USNM 398296; UF 458, 3164, 3163

Table A.4—continued.

	Museum tag
<i>Neotoma mexicana</i>	USNM 127314; UF 6216, 7831, 5387
<i>Onychomys leucogaster</i>	FNMH 123451, 123450; UF 24175, 12613, 941; USNM 273799
<i>Onychomys torridus</i>	MVZ 72814, 119666, 28081, 28077
<i>Peromyscus boylii</i>	UF 6221, 6224, 6225, 6121; USNM 40514
<i>Peromyscus crinitus</i>	USNM 53283; UF 3078, 5394, 5397
<i>Peromyscus eremicus</i>	UF 9445, 9447, 9448; USNM 60100
<i>Peromyscus fraterculus</i>	USNM 81017, 69556, 81016, 91566
<i>Peromyscus leucopus</i>	UF 9298, 9303, 1968; USNM 157114
<i>Peromyscus maniculatus</i>	UF 3637, 2802, 2803; USNM 530844
<i>Peromyscus merriami</i>	MVZ 85828, 85836, 85832, 85831
<i>Peromyscus pectoralis</i>	MVZ 92138, 92135, 91786, 92140
<i>Reithrodontomys fulvescens</i>	FNMH 73418, 13115, 54147; USNM 70255
<i>Reithrodontomys megalotis</i>	FNMH 12273, 12271, 12270; UF 6080, 6080, 6081, 6083; USNM 250559
Sigmodontinae	
<i>Aegialomys xanthalaelous</i>	FNMH 194444, 19445; USNM 304528, 551641
<i>Akodon iniscatus</i>	MVZ 163790, 168995, 160118, 168996
<i>Akodon molinae</i>	USNM 331060
<i>Calomys callosus</i>	UF 27606, 27625, 27629, 27633; MVZ 145225, 145227, 145226, 145231
<i>Calomys musculinus</i>	MVZ 66067, 119954, 151015, 163390
<i>Eligmodontia moreni</i>	USNM 236312, 236313, 236311
<i>Eligmodontia morgani</i>	MVZ 182663, 182665, 182675, 182668
<i>Eligmodontia typus</i>	AMNH 262812; FNMH 124314, 124313, 124322; MVZ 169010, 174390, 174391; USNM 541732
<i>Graomys edithae</i>	MVZ 162261
<i>Graomys griseoflavus</i>	FNMH 28423, 50920, 46125; MVZ 145252, 145254, 145255; UF 27630; USNM 390214
<i>Phyllotis amicus</i>	MVZ 136282, 136283, 115806, 137624, 138034, 145548
<i>Phyllotis darwini</i>	LCM 3047, 3338, 4038, 4057, 4037, 4061
<i>Phyllotis gerbillus</i>	MVZ 138024, 138028, 135693, 135695
<i>Phyllotis xanthopygus</i>	LCM 3009, 3143, 3351, 3021
<i>Reithrodon auritus</i>	MVZ 163411, 172218, 171163, 165853; UF 24357, 24358, 24359, 24360
<i>Sigmodon arizonae</i>	MVZ 62573, 62576, 62574, 62575
<i>Sigmodon fulviventer</i>	MVZ 50867, 50866; USNM 20723, 247584
<i>Sigmodon hispidus</i>	UF 143, 1588, 1584, 1589
<i>Sigmodon ochrognathus</i>	MVZ 80495, 80499, 80493, 80494
Muridae	
Deomyinae	
<i>Acomys cahirinus</i>	MVZ 107726, 118298, 118306, 1077262 118297, 1182982, 118320
<i>Acomys cineraceus</i>	USNM 422402, 422404, 422401, 422419
<i>Acomys russatus</i>	USNM 317002, 317007, 316997, 317006
Gerbillinae	
<i>Ammodillus imbellis</i>	FNMH 140092
<i>Brachionomys przewalskii</i>	USNM 102578
<i>Desmodilliscus braueri</i>	USNM 378287, 378289, 378290, 453904, 453899, 453893
<i>Desmodilliscus auricularis</i>	MVZ 117381, 117379, 117371, 117372; AMNH 165455, 165453, 165451, 165456
<i>Dipodillus campestris</i>	USNM 401028, 401038, 401036, 401852
<i>Dipodillus dasyurus</i>	USNM 350041, 316662, 316658, 350037
<i>Dipodillus mackilligini</i>	USNM 316700
<i>Dipodillus simoni</i>	USNM 316687, 316699, 316683, 350045
<i>Gerbilliscus afra</i>	MVZ 117338, 117337, 117340, 117342
<i>Gerbilliscus brantsii</i>	AMNH 83696, 83693, 83694, 83695; MVZ 88729, 88730; USNM 295355, 295350, 462447, 295349
<i>Gerbilliscus leucogaster</i>	USNM 295398, 295400, 295394, 295395
<i>Gerbillurus paeba</i>	AMNH 219001, 219002; MVZ 149573, 149576
<i>Gerbillurus setzeri</i>	USNM 342232, 342260, 342229, 342233
<i>Gerbillurus tytonis</i>	USNM 379852, 379869, 342165, 379854
<i>Gerbillurus vallinus</i>	USNM 424171, 424172, 424173, 424175
<i>Gerbillus agag</i>	MVZ 1543290, 154330, 154326, 154332
<i>Gerbillus amoenus</i>	USNM 300231, 302217, 307626, 322544
<i>Gerbillus andersoni</i>	MVZ 107721; USNM 316747, 283254, 300226
<i>Gerbillus aquilus</i>	USNM 328042, 328045, 369319, 369341
<i>Gerbillus cheesmani</i>	MVZ 191959, 191960; 29029, 29042
<i>Gerbillus famulus</i>	USNM 321586, 321664, 321587, 321663
<i>Gerbillus floweri</i>	USNM 316843, 316848, 316850, 316852
<i>Gerbillus gerbillus</i>	MVZ 34214, 107722, 34212, 34213
<i>Gerbillus gleadowi</i>	USNM 353247, 353617, 353622, 369058
<i>Gerbillus henleyi</i>	MVZ 107720; USNM 472202, 472203, 472204
<i>Gerbillus hoogstraali</i>	USNM 540028, 540038, 540037, 540034
<i>Gerbillus latastei</i>	USNM 321822, 321813, 321821, 321794
<i>Gerbillus mauritaniae</i>	USNM 401519, 401522, 401518, 401002
<i>Gerbillus mesopotamiae</i>	USNM 350442, 350444, 350443, 350450
<i>Gerbillus nanus</i>	MVZ 191952, 191953, 191955, 191958; UF 14577, 25903, 28564, 28562
<i>Gerbillus nigeriae</i>	USNM 573945, 573944
<i>Gerbillus perpallidus</i>	USNM 316820, 316823, 316819, 316822
<i>Gerbillus poecilops</i>	USNM 321575, 321584, 321577, 321579
<i>Gerbillus pusillus</i>	USNM 500947, 500946, 500945; FNMH 44419
<i>Gerbillus pyramidum</i>	MVZ 34208, 107723, 34210; AMNH 119507
<i>Gerbillus tarabuli</i>	USNM 302165, 302167, 302160, 302218
<i>Meriones crassus</i>	MVZ 191991; USNM 401159, 401161, 401157

Table A.4—continued.

	Museum tag
<i>Meriones erythrourus</i>	FMNH 202109
<i>Meriones grandis</i>	USNM 473951, 483036, 473866, 474353
<i>Meriones hurrianae</i>	USNM 369162, 369163, 369161, 369510
<i>Meriones libycus</i>	MVZ 191968, 191972, 191962, 191963
<i>Meriones meridianus</i>	MVZ 41227, 41228; AMNH 59702, 59352
<i>Meriones persicus</i>	MVZ 198812, 198813, 198811, 198819
<i>Meriones rex</i>	USNM 321715; FMNH 77953, 77955, 77959
<i>Meriones shawi</i>	USNM 474209, 474187, 474208, 474185
<i>Meriones tamariscinus</i>	USNM 155457, 155459; AMNH 85369, 85377
<i>Meriones unguiculatus</i>	MVZ 41229; USNM 240765, 283918, 270551
<i>Pachyuromys duprasi</i>	FMNH 74976, 89621, 80021, 80048; MVZ 34197; USNM 482421, 321829, 325567, 325569
<i>Psammomys obesus</i>	AMNH 203215; FMNH 78611, 91277, 91279; MVZ 183877; USNM 482457, 326018, 326025, 341974
<i>Rhomomys opimus</i>	AMNH 88865, 88868, 88871, 88875; MVZ 41226; USNM 341327, 341329, 341332, 341334
<i>Sekeetamys calurus</i>	FMNH 101021, 101024, 101025, 101033; USNM 321928, 321931, 321932, 321934
<i>Tatera indica</i>	AMNH 240846; MVZ 192006, 192007, 192002, 192005; UF 30352, 30266, 30245, 30260
<i>Taterillus emini</i>	USNM 165288, 299721, 165289, 299718
<i>Taterillus harringtoni</i>	USNM 483985, 483990, 483998, 483991
Murinae	
<i>Aethomys chrysophilus</i>	MVZ 117532, 117534, 118188, 117531
<i>Aethomys namaquensis</i>	MVZ 117521, 117524, 117519, 117520
<i>Cremnomys cutchicus</i>	FMNH 35295, 82993, 82994, 82996
<i>Leggadina forresti</i>	USNM 284270; FMNH 120331, 120330
<i>Millardia gleadowi</i>	USNM 354414, 413647, 369523, 354414
<i>Mus booduga</i>	FMNH 35292; USNM 369234, 533854, 533774, 533855
<i>Mus minutoides</i>	AMNH 168548; MVZ 162503, 162508, 165138, 18295, 117689, 117688; USNM 352800, 352806
<i>Mus musculus</i>	UF 27595, 14562, 1840, 7588; USNM 298998
<i>Mus saxicola</i>	USNM 556247, 556249, 556257, 556248
<i>Mus spretus</i>	MVZ 226632, 155909, 155911; USNM 486120
<i>Notomys alexis</i>	MVZ 134373; USNM 284363; AMNH 197502, 197504
<i>Notomys cervinus</i>	USNM 284352, 284359; AMNH 153491, 153492
<i>Notomys fuscus</i>	MVZ 124313, 124312, 124314, 124315
<i>Parotomys brantsii</i>	AMNH 168509, 168510; MVZ 117756, 118405
<i>Parotomys littledalei</i>	MVZ 81577; USNM 343927, 343936, 343923, 256963
<i>Pseudomys australis</i>	AMNH 65998; MVZ 134044, 134115, 133681
<i>Pseudomys hermannsburgensis</i>	AMNH 197431, 197433, 220112, 220113
<i>Rattus villosissimus</i>	AMNH 153476, 153495, 153475, 153477
<i>Rhabdomys pumilio</i>	MVZ 88824, 88823, 88820, 117468
<i>Zelotomys woosnami</i>	USNM 428770, 428771, 428772, 470118
<i>Zyzomys argurus</i>	USNM 284323, 578555, 284328, 384336
Nesomyidae	
Cricetomyinae	
<i>Saccostomus campestris</i>	MVZ 118335, 118371, 118364, 118365
Dendromurinae	
<i>Dendromus nyasae</i>	FMNH 196686, 191596, 191597, 191598
<i>Malacothrix typica</i>	USNM 343711, 423199, 343708, 423204
Petromyscinae	
<i>Petromyscus collinus</i>	AMNH 165437, 165438, 165439, 165408; USNM 424617, 452334, 452406, 452433
Spalacidae	
Spalacinae	
<i>Spalax ehrenbergi</i>	FMNH 101009, 101010, 101014, 101011
Sciuromorpha	
Gliridae	
Leithiinae	
<i>Eliomys melanurus</i>	USNM 475706, 302274, 475705, 342024
<i>Eliomys quercinus</i>	MVZ 154697; USNM 103031, 103032, 152768
Graphiurinae	
<i>Graphiurus ocularis</i>	AMNH 168333, 168332, 89052
Sciuridae	
Xerinae	
<i>Ammospermophilus harrisii</i>	USNM 33713; UF 2508; FMNH 14956, 4873
<i>Ammospermophilus interpres</i>	USNM 18154, 20077, 108389, 108928
<i>Ammospermophilus leucurus</i>	USNM 53221; UF 4744, 5383, 2494
<i>Ammospermophilus nelsoni</i>	USNM 31273, 129865, 54629, 127152
<i>Atlantoxerus getulus</i>	USNM 470900, 470895, 476815, 476821
<i>Spermophilus fulvus</i>	USNM 369544; AMNH 206566, 176239; FMNH 96891
<i>Spermophilus mexicanus</i>	USNM 33546, 34118, 33549, 34123
<i>Spermophilus mohavensis</i>	USNM 15975, 135838, 28740, 192753
<i>Spermophilus pygmaeus</i>	USNM 251636, 251637; AMNH 87089, 87090
<i>Spermophilus spilosoma</i>	USNM 247654, 35079, 35077, 350800
<i>Spermophilus tereticaudus</i>	USNM 96984, 33762, 138610, 33754
<i>Spermophilus variegatus</i>	USNM 117529, 117602, 97156, 117604
<i>Xerus erythropus</i>	USNM 421581, 453006, 453008, 453009
<i>Xerus inauris</i>	USNM 368056, 368059, 259785, 368058
<i>Xerus princeps</i>	USNM 379848, 379847; AMNH 86479

Table A.5. List of reference and target specimens used in the missing data estimation procedure for chapter 7. See Table A.1 legend for more information.

Target	Reference
Dorsal cranium	
AMNH 46403	AMNH 58773, AMNH 84202
AMNH 58522	AMNH 58773, AMNH 84202
AMNH 84154	FMNH 137435, USNM 547940
UF 3076	FMNH 52836, FMNH 52839, USNM 49169
UF 11944	UF 8672, UF 9633, USNM 31559
MVZ 41235	USNM 172521, USNM 449120, USNM 576188
USNM 302296	MVZ 201015, USNM 475997, USNM 475998, USNM 476005
FMNH 29064	FMNH 29058, FMNH 41270, USNM 236335, USNM 236336, FMNH 46130, FMNH 46131, FMNH 46132, FMNH 46133, FMNH 41267, FMNH 41268
UF 24179	UF 4673, UF 24180, USNM 214113
USNM 541732	AMNH 262812, FMNH 124313, FMNH 124314, USNM 103031, USNM 103032, USNM 152768, MVZ 41291
MVZ 34208	AMNH 119507, MVZ 34210, MVZ 107723
FMNH 48806	USNM 482508, USNM 482509, USNM 482510
MVZ 41227	AMNH 59352, AMNH 59702, MVZ 41228
UF 27628	UF 27645, USNM 84182
UF 27636	UF 27645, USNM 84182
MVZ 117688	AMNH 168548, MVZ 118295, MVZ 162503, MVZ 162508, MVZ 165138, USNM 352800, USNM 352806
MVZ 117689	AMNH 168548, MVZ 118295, MVZ 162503, MVZ 162508, MVZ 165138, USNM 352800, USNM 352806
UF 23916	FMNH 23203, FMNH 23210, FMNH 23903
USNM 1970	USNM 1446, USNM 192467
USNM 122105	USNM 1446, USNM 192467
UF 24357	UF 24358, UF 24359
UF 24360	UF 24358, UF 24359
UF 6083	FMNH 12270, FMNH 12271, FMNH 12273, UF 6080, UF 6081, USNM 250559
MVZ 41226	AMNH 88865, AMNH 88868, AMNH 88871, AMNH 88875, USNM 341327, USNM 341329, USNM 341332, USNM 341334
USNM 135838	USNM 15975, USNM 28740, USNM 192753
USNM 251637	AMNH 87089, AMNH 87090, USNM 251636
MVZ 135291	AMNH 174328, USNM 4226, USNM 547938
Lateral mandible	
USNM 251639	AMNH 178795, USNM 1445, USNM 254957
FMNH 140092	All complete Gerbillinae
UF 2508	FMNH 4873, FMNH 14956, USNM 33713
USNM 476821	USNM 470895, USNM 470900, USNM 476815
UF 3076	FMNH 52836, FMNH 52839, USNM 49169
UF 12761	UF 3044, UF 12760, USNM 529907
AMNH 11837	AMNH 258738, AMNH 258740, USNM 41957, USNM 262926, USNM 263139, USNM 263160
AMNH 11850	AMNH 258738, AMNH 258740, USNM 41957, USNM 262926, USNM 263139, USNM 263160
FMNH 82996	FMNH 35295, FMNH 82993, FMNH 82994
USNM 576188	MVZ 41235, USNM 172521, USNM 449120
FMNH 41270	FMNH 29058, USNM 236335, USNM 236336
USNM 316658	USNM 316662, USNM 350037, USNM 350041
USNM 54871	USNM 149756, USNM 149757, USNM 214515, USNM 1497562
UF 9949	FMNH 49212, USNM 135946
UF 18999	FMNH 49212, USNM 135946
AMNH 174329	All complete Dipodinae
USNM 353247	USNM 353617, USNM 353622, USNM 369058
MVZ 107727	MVZ 34198, MVZ 34199, MVZ 34200
UF 23901	FMNH 53672, FMNH 53673, USNM 274565
UF 14778	FMNH 53704, FMNH 54339, USNM 114840
FMNH 48806	USNM 482508, USNM 482509, USNM 482510
USNM 401161	MVZ 191991, USNM 401157, USNM 401159
USNM 413647	USNM 354414, USNM 369523, USNM 3544142
MVZ 117689	AMNH 168548, MVZ 117688, MVZ 118295, MVZ 162503, MVZ 162508, MVZ 165138
USNM 352800	AMNH 168548, MVZ 117688, MVZ 118295, MVZ 162503, MVZ 162508, MVZ 165138
USNM 352806	AMNH 168548, MVZ 117688, MVZ 118295, MVZ 162503, MVZ 162508, MVZ 165138
UF 1840	UF 7588
UF 5386	USNM 212131
UF 12618	USNM 212131
UF 13245	USNM 212131
USNM 202463	USNM 215546
USNM 226399	USNM 215546
USNM 226400	USNM 215546
MVZ 124314	MVZ 124313, MVZ 124315
MVZ 34197	FMNH 74976, FMNH 80021, FMNH 80048, FMNH 89621, USNM 321829, USNM 325567, USNM 325569, USNM 482421
USNM 47378	USNM 66537, USNM 87901, USNM 275699
AMNH 165437	AMNH 165408, AMNH 165438, AMNH 165439, USNM 424617, USNM 452334, USNM 452406, USNM 452433
MVZ 133681	AMNH 65998, AMNH 659982, MVZ 134115
UF 24358	UF 24357
UF 24359	UF 24357
UF 24360	UF 24357
UF 6081	FMNH 12270, FMNH 12271, FMNH 12273, UF 6080, UF 6083, USNM 250559
USNM 15975	USNM 28740, USNM 35838, USNM 192753
AMNH 87090	AMNH 87089, USNM 251636, USNM 251637
USNM 117604	USNM 97156, USNM 117529, USNM 117602
MVZ 135291	AMNH 174328, USNM 4226, USNM 547938
FMNH 14059	FMNH 14058, UF 8238, USNM 55913
Lateral cranium	
FMNH 23169	All complete Hystricomorpha
FMNH 23170	All complete Hystricomorpha
UF 23915	All complete Hystricomorpha
USNM 391842	All complete Hystricomorpha
AMNH 58522	AMNH 46403, AMNH 84202
AMNH 58773	AMNH 46403, AMNH 84202
MVZ 192029	FMNH 103867, FMNH 103868, USNM 341604, AMNH 88749

Table A.5—continued.

Target	Reference
USNM 369889	FMNH 103867, FMNH 103868, USNM 341604, AMNH 88749
USNM 369890	FMNH 103867, FMNH 103868, USNM 341604, AMNH 88749
USNM 3277232	FMNH 82182, USNM 327719, USNM 327721, USNM 327722, USNM 327723
AMNH 178795	USNM 254957
USNM 1445	USNM 254957
USNM 251639	USNM 254957
AMNH 206589	AMNH 176269
USNM 3170932	USNM 317088, USNM 317089, USNM 317092, USNM 317093, USNM 3170892
FMNH 4873	UF 2508
FMNH 14956	UF 2508
USNM 33713	UF 2508
AMNH 84154	All complete Dipodidae
USNM 531519	USNM 146908, USNM 531518, USNM 531529
UF 3076	FMNH 52836, FMNH 52839
USNM 49169	FMNH 52836, FMNH 52839
UF 3033	FMNH 10890, FMNH 10902, USNM 55561
USNM 51096	USNM 119104, USNM 119781, USNM 157404
UF 3044	UF 12761, USNM 529907
UF 12760	UF 12761, USNM 529907
AMNH 258738	AMNH 11837, AMNH 11850, AMNH 258740, USNM 41957, USNM 262926, USNM 263139, USNM 263160
UF 8672	USNM 31559
UF 9633	USNM 31559
UF 11944	USNM 31559
UF 7836	UF 12527, USNM 532532
UF 12528	UF 12527, USNM 532532
FMNH 141796	FMNH 141795, USNM 296790, USNM 296791
FMNH 46911	FMNH 46910, USNM 50210
UF 437	UF 4681, UF 4682, USNM 552796
USNM 140006	USNM 140005, USNM 145985, USNM 146090
UF 3041	USNM 140038
UF 3042	USNM 140038
UF 3043	USNM 140038
AMNH 68767	AMNH 63812, AMNH 68766, AMNH 68768
MVZ 41235	USNM 172521, USNM 449120, USNM 576188
MVZ 41234	MVZ 191941, UF 27124, UF 27142, UF 27145, USNM 326786, USNM 326787
MVZ 201015	USNM 475998, USNM 476005
USNM 475997	USNM 475998, USNM 476005
USNM 302296	USNM 475998, USNM 476005, FMNH 29058, FMNH 41270, USNM 236335, USNM 236336, FMNH 46130, FMNH 46131, FMNH 46132, FMNH 46133, FMNH 41267, FMNH 41268
FMNH 29064	USNM 475998, USNM 476005, FMNH 29058, FMNH 41270, USNM 236335, USNM 236336, FMNH 46130, FMNH 46131, FMNH 46132, FMNH 46133, FMNH 41267, FMNH 41268
AMNH 165456	AMNH 165451, AMNH 165453, AMNH 165455, MVZ 117371, MVZ 117372, MVZ 117379, MVZ 117381
USNM 316699	USNM 316683, USNM 316687, USNM 350045
AMNH 139597	AMNH 139598, AMNH 139599, AMNH 139600, USNM 33926
USNM 149735	USNM 137911, USNM 137918
UF 24179	UF 4673, UF 24180, USNM 214113
UF 3058	UF 3060, USNM 41336
UF 3059	UF 3060, USNM 41336
UF 9949	FMNH 49212
UF 18999	FMNH 49212
USNM 135946	FMNH 49212
USNM 257010	FMNH 49212
USNM 258569	FMNH 49212
USNM 270234	FMNH 49212
USNM 270306	FMNH 49212
USNM 541732	AMNH 262812, FMNH 124313, FMNH 124314, FMNH 124322, MVZ 169010, MVZ 174390, MVZ 174391
AMNH 257135	AMNH 257136, FMNH 33721, FMNH 33722
FMNH 33720	AMNH 257136, FMNH 33721, FMNH 33722
USNM 462447	USNM 295349, USNM 295350, USNM 295355, MVZ 88729, MVZ 88730
USNM 342260	USNM 342229, USNM 342232, USNM 342233
MVZ 34212	FMNH 87664, FMNH 87675, MVZ 34214, MVZ 107722
MVZ 34213	FMNH 87664, FMNH 87675, MVZ 34214, MVZ 107722
USNM 573944	All complete <i>Gerbillus</i>
USNM 573945	All complete <i>Gerbillus</i>
USNM 469825	USNM 368422, USNM 382480, USNM 470121
MVZ 34198	MVZ 34200, MVZ 107727
MVZ 34199	MVZ 34200, MVZ 107727
MVZ 41227	AMNH 59352, AMNH 59702, MVZ 41228
MVZ 117520	MVZ 117519, MVZ 117524
UF 27628	USNM 84182
UF 27636	USNM 84182
UF 27645	USNM 84182
USNM 413647	USNM 354414, USNM 369523, USNM 3544142
MVZ 117688	AMNH 168548, MVZ 118295, MVZ 162503, MVZ 162508, MVZ 165138, USNM 352800, USNM 352806
MVZ 117689	AMNH 168548, MVZ 118295, MVZ 162503, MVZ 162508, MVZ 165138, USNM 352800, USNM 352806
MVZ 155909	MVZ 155911, MVZ 226632, USNM 486120
UF 5837	UF 6216, UF 7831, USNM 127314
UF 14997	UF 14998, USNM 259581, USNM 541816
UF 23916	FMNH 23203, FMNH 23210, FMNH 23903
FMNH 74976	FMNH 80021, FMNH 80048, FMNH 89621, MVZ 34197, USNM 321829, USNM 325567, USNM 325569, USNM 482421
UF 7834	UF 7833, UF 24183, USNM 213440
MVZ 117767	USNM 343962, USNM 343963, USNM 343968
USNM 1970	USNM 1446
USNM 122105	USNM 1446
USNM 192467	USNM 1446
UF 24357	UF 24358
UF 24359	UF 24358
UF 24360	UF 24358
AMNH 88875	AMNH 88865, AMNH 88868, AMNH 88871, USNM 341327, USNM 341329

Table A.5—continued.

Target	Reference
MVZ 41226	AMNH 88865, AMNH 88868, AMNH 88871, USNM 341327, USNM 341329
USNM 341332	AMNH 88865, AMNH 88868, AMNH 88871, USNM 341327, USNM 341329
USNM 341334	AMNH 88865, AMNH 88868, AMNH 88871, USNM 341327, USNM 341329
MVZ 50867	MVZ 50866, USNM 20723, USNM 247584
FMNH 96891	AMNH 176239, AMNH 206566
USNM 369544	AMNH 176239, AMNH 206566
MVZ 135291	AMNH 174328, USNM 547938
USNM 4226	AMNH 174328, USNM 547938
USNM 299721	USNM 165288, USNM 165289, USNM 299718
USNM 483991	USNM 483985, USNM 483990, USNM 483998
USNM 428771	USNM 428770, USNM 428772, USNM 470118
USNM 529907	UF 12761
USNM 317089	USNM 317088, USNM 317092, USNM 317093, USNM 317092
USNM 2214312	USNM 221431, USNM 344826, USNM 344869
AMNH 11837	AMNH 11850, AMNH 258740, USNM 41957, USNM 262926, USNM 263139, USNM 263160
USNM 316843	USNM 316848, USNM 316850, USNM 316852
Occlusal mandible	
FMNH 23169	USNM 391842
FMNH 23170	USNM 391842
UF 23915	USNM 391842
AMNH 46403	All complete <i>Allactaga</i>
AMNH 58522	All complete <i>Allactaga</i>
AMNH 58773	All complete <i>Allactaga</i>
AMNH 84202	All complete <i>Allactaga</i>
AMNH 88749	FMNH 103865, FMNH 103867, FMNH 103868, MVZ 192029, USNM 341604, USNM 369889, USNM 369890
FMNH 82186	FMNH 82182, USNM 327719, USNM 327721, USNM 327722, USNM 327723, USNM 327723
AMNH 178795	USNM 251639, USNM 254957
USNM 1445	USNM 251639, USNM 254957
AMNH 176269	All complete <i>Allactaga</i>
AMNH 206589	All complete <i>Allactaga</i>
USNM 155190	All complete <i>Allactaga</i>
USNM 155194	All complete <i>Allactaga</i>
USNM 3170892	USNM 317088, USNM 317089, USNM 317092, USNM 317093, USNM 3170932
FMNH 4873	USNM 33713
FMNH 14956	USNM 33713
UF 2508	USNM 33713
USNM 20077	USNM 18154
USNM 108389	USNM 18154
USNM 108928	USNM 18154
UF 2494	USNM 53221
UF 4744	USNM 53221
UF 5383	USNM 53221
USNM 127152	USNM 31273, USNM 54629
USNM 129865	USNM 31273, USNM 54629
USNM 476815	USNM 470895, USNM 470900
USNM 476821	USNM 470895, USNM 470900
UF 3076	FMNH 52836, FMNH 52839, USNM 49169
UF 12761	UF 3044, UF 12760, USNM 529907
AMNH 63812	USNM 55913
AMNH 68766	USNM 55913
AMNH 68767	USNM 55913
AMNH 68768	USNM 55913
USNM 344826	USNM 221431
USNM 344869	USNM 221431
USNM 2214312	USNM 221431
USNM 475997	MVZ 201015
USNM 475998	MVZ 201015
USNM 476005	MVZ 201015
FMNH 29064	USNM 236335, USNM 236336
FMNH 29058	USNM 236335, USNM 236336
FMNH 41270	USNM 236335, USNM 236336
FMNH 46130	USNM 236335, USNM 236336
FMNH 46131	USNM 236335, USNM 236336
FMNH 46132	USNM 236335, USNM 236336
FMNH 46133	USNM 236335, USNM 236336
FMNH 46127	USNM 236335, USNM 236336
FMNH 41268	USNM 236335, USNM 236336
AMNH 165451	AMNH 165453, AMNH 165455, MVZ 117371, MVZ 117372, MVZ 117379, MVZ 117381
AMNH 165456	AMNH 165453, AMNH 165455, MVZ 117371, MVZ 117372, MVZ 117379, MVZ 117381
AMNH 139597	USNM 33926
AMNH 139598	USNM 33926
AMNH 139599	USNM 33926
AMNH 139600	USNM 33926
USNM 51068	MVZ 76547, MVZ 76548
USNM 56195	MVZ 76547, MVZ 76548
UF 3059	UF 3058, UF 3060, USNM 41336
UF 25951	USNM 46288
UF 25952	USNM 46288
UF 25953	USNM 46288
USNM 573127	USNM 155095, USNM 155096, USNM 544449
AMNH 58608	USNM 155095, USNM 155096, USNM 544449
AMNH 58623	USNM 155095, USNM 155096, USNM 544449
AMNH 84121	USNM 155095, USNM 155096, USNM 544449
AMNH 84135	USNM 155095, USNM 155096, USNM 544449
UF 9949	MVN 49212, USNM 135946
UF 18999	MVN 49212, USNM 135946
USNM 270306	USNM 257010, USNM 258569, USNM 270234
AMNH 257136	AMNH 257135, FMNH 33720, FMNH 33721, FMNH 33722

Table A.5—continued.

Target	Reference
AMNH 174329	All complete Dipodinae
USNM 402147	USNM 401279, USNM 401286
USNM 402149	USNM 401279, USNM 401286
AMNH 219001	AMNH 219002, MVZ 149573, MVZ 149576
MVZ 34208	AMNH 119507, MVZ 34210, MVZ 107723
AMNH 168333	AMNH 89052, AMNH 168332
FMNH 57170	FMNH 41337, FMNH 89203, USNM 162900
MVZ 107727	MVZ 34198, MVZ 34199, MVZ 34200
USNM 302290	MVZ 32810, MVZ 183997, USNM 302289
FMNH 53672	USNM 274565
FMNH 53673	USNM 274565
UF 23901	USNM 274565
FMNH 53704	USNM 114840
FMNH 54339	USNM 114840
UF 14778	USNM 114840
FMNH 48806	USNM 482508, USNM 482509
USNM 482510	USNM 482508, USNM 482509
FMNH 202109	MVZ 191962, MVZ 191963, MVZ 191968, MVZ 191972
FMNH 77953	USNM 321715
FMNH 77955	USNM 321715
FMNH 77959	USNM 321715
USNM 474185	USNM 474187, USNM 474208, USNM 474209
AMNH 85369	USNM 155457, USNM 155459
AMNH 85377	USNM 155457, USNM 155459
UF 27628	UF 27636, USNM 84182
UF 27645	UF 27636, USNM 84182
UF 5386	USNM 212131
UF 12618	USNM 212131
UF 13245	USNM 212131
UF 3166	USNM 212131, USNM 202463, USNM 215546, USNM 226399, USNM 226400, MVZ 76946, MVZ 76947, USNM 398296, USNM 127314
UF 31327	USNM 212131, USNM 202463, USNM 215546, USNM 226399, USNM 226400, MVZ 76946, MVZ 76947, USNM 398296, USNM 127314
USNM 116897	MVZ 76946, MVZ 76947
USNM 116898	MVZ 76946, MVZ 76947
UF 458	USNM 398296
UF 3163	USNM 398296
UF 3164	USNM 398296
UF 5837	USNM 127314
UF 6216	USNM 127314
UF 7831	USNM 127314
FMNH 23203	UF 23916
FMNH 23210	UF 23916
FMNH 23903	UF 23916
FMNH 74976	FMNH 80021, MVZ 34197, USNM 321829, USNM 325569, USNM 482421
FMNH 80048	FMNH 80021, MVZ 34197, USNM 321829, USNM 325569, USNM 482421
FMNH 89621	FMNH 80021, MVZ 34197, USNM 321829, USNM 325569, USNM 482421
USNM 325567	FMNH 80021, MVZ 34197, USNM 321829, USNM 325569, USNM 482421
AMNH 168509	MVZ 117756, MVZ 118405
AMNH 168510	MVZ 117756, MVZ 118405
USNM 256963	MVZ 81577, USNM 343923, USNM 343936
USNM 343927	MVZ 81577, USNM 343923, USNM 343936
FMNH 1438	MVZ 201015, USNM 302296, USNM 401279, USNM 401286, USNM 482508, USNM 482509
FMNH 106442	MVZ 201015, USNM 302296, USNM 401279, USNM 401286, USNM 482508, USNM 482509
FMNH 38231	USNM 422522
FMNH 38261	USNM 422522
FMNH 38263	USNM 422522
USNM 343962	MVZ 117767
USNM 343963	MVZ 117767
USNM 343968	MVZ 117767
LCM 4037	LCM 4038, LCM 4057, LCM 4061
AMNH 203215	MVZ 183877, USNM 341974, USNM 482457
FMNH 78611	MVZ 183877, USNM 341974, USNM 482457
FMNH 91277	MVZ 183877, USNM 341974, USNM 482457
FMNH 91279	MVZ 183877, USNM 341974, USNM 482457
USNM 326018	MVZ 183877, USNM 341974, USNM 482457
USNM 326025	MVZ 183877, USNM 341974, USNM 482457
AMNH 153475	AMNH 153476, AMNH 153477
AMNH 153495	AMNH 153476, AMNH 153477
UF 24358	UF 24357, UF 24359
UF 24360	UF 24357, UF 24359
AMNH 88865	MVZ 41226, USNM 341327, USNM 341329, USNM 341332, USNM 341334
AMNH 88868	MVZ 41226, USNM 341327, USNM 341329, USNM 341332, USNM 341334
AMNH 88871	MVZ 41226, USNM 341327, USNM 341329, USNM 341332, USNM 341334
AMNH 88875	MVZ 41226, USNM 341327, USNM 341329, USNM 341332, USNM 341334
UF 1584	MVZ 62573, MVZ 62574, MVZ 62575, MVZ 62576, MVZ 50866, MVZ 50867, USNM 20723, USNM 247584, MVZ 80493, MVZ 80494, MVZ 80495, MVZ 80499
UF 1588	MVZ 62573, MVZ 62574, MVZ 62575, MVZ 62576, MVZ 50866, MVZ 50867, USNM 20723, USNM 247584, MVZ 80493, MVZ 80494, MVZ 80495, MVZ 80499
UF 1589	MVZ 62573, MVZ 62574, MVZ 62575, MVZ 62576, MVZ 50866, MVZ 50867, USNM 20723, USNM 247584, MVZ 80493, MVZ 80494, MVZ 80495, MVZ 80499
FMNH 101009	FMNH 101014
FMNH 101010	FMNH 101014
FMNH 101011	FMNH 101014
AMNH 176239	USNM 369544
AMNH 206566	USNM 369544
FMNH 96891	USNM 369544
USNM 3549	USNM 33546, USNM 34118
USNM 34123	USNM 33546, USNM 34118
USNM 135838	USNM 15975, USNM 28740
USNM 192753	USNM 15975, USNM 28740

Table A.5—continued.

Target	Reference
AMNH 87089	USNM 251636
AMNH 87090	USNM 251636
USNM 251637	USNM 251636
USNM 35077	USNM 247654
USNM 35079	USNM 247654
USNM 35080	USNM 247654
USNM 33754	USNM 138610
USNM 33762	USNM 138610
USNM 96984	USNM 138610
USNM 117529	USNM 97156
USNM 117602	USNM 97156
USNM 117604	USNM 97156
AMNH 174328	MVZ 135291, USNM 4226, USNM 547938
AMNH 204846	MVZ 192002, MVZ 192005, MVZ 192006, MVZ 192007, UF 30266
UF 30245	MVZ 192002, MVZ 192005, MVZ 192006, MVZ 192007, UF 30266
UF 30260	MVZ 192002, MVZ 192005, MVZ 192006, MVZ 192007, UF 30266
USNM 299721	USNM 165288, USNM 165289, USNM 299718
FMNH 14058	USNM 55913
FMNH 14059	USNM 55913
UF 8238	USNM 55913
USNM 453006	USNM 421581
USNM 453008	USNM 421581
USNM 453009	USNM 421581
USNM 368056	USNM 259785
USNM 368058	USNM 259785
USNM 368059	USNM 259785
AMNH 86479	USNM 379847, USNM 379848
Ventral cranium	
UF 23915	FMNH 23169, FMNH 23170, USNM 391842
MVZ 107726	MVZ 118297, MVZ 118298, MVZ 118306, MVZ 118320, MVZ 1182982
MVZ 107726	MVZ 118297, MVZ 118298, MVZ 118306, MVZ 118320, MVZ 1182982
USNM 551641	FMNH 19444, FMNH 19445, USNM 304528
USNM 3277232	FMNH 82182, FMNH 82186, USNM 327719, USNM 327721, USNM 327722, USNM 327722, USNM 327723
AMNH 59753	FMNH 33959, FMNH 33964, USNM 259524, USNM 259524
FMNH 14956	FMNH 4873, UF 2508, USNM 33713
MVZ 41235	USNM 172521, USNM 449120, USNM 576188
USNM 302296	MVZ 201015, USNM 475997, USNM 475998, USNM 476005
FMNH 29064	FMNH 29058, FMNH 41270, USNM 236335, USNM 236336, FMNH 46130, FMNH 46131, FMNH 46133, FMNH 41267, FMNH 41268
FMNH 46132	FMNH 46130, FMNH 46131, FMNH 46133
USNM 453893	USNM 378287, USNM 378289, USNM 378290, USNM 453893
USNM 453904	USNM 378287, USNM 378289, USNM 378290, USNM 453893
MVZ 73651	MVZ 73649, MVZ 73650, MVZ 73652
USNM 541732	AMNH 262812, FMNH 124313, FMNH 124314, FMNH 124322, MVZ 169010, MVZ 174390, MVZ 174391
MVZ 41291	MVZ 41292, MVZ 41294, MVZ 135298
FMNH 33720	AMNH 257135, AMNH 257136, FMNH 33721, FMNH 33722
USNM 424173	USNM 424171, USNM 424172, USNM 424175
MVZ 34214	FMNH 87664, FMNH 87675, MVZ 34212, MVZ 34213, MVZ 107722
USNM 540034	USNM 540028, USNM 540037, USNM 540038
USNM 573944	All complete <i>Gerbillus</i>
USNM 573945	All complete <i>Gerbillus</i>
MVZ 34210	AMNH 119507, MVZ 34208, MVZ 107723
FMNH 120331	FMNH 120330, USNM 284270
MVZ 41227	AMNH 59352, AMNH 59702
MVZ 41228	AMNH 59352, AMNH 59702
USNM 155457	AMNH 85369, AMNH 85377, USNM 155459
MVZ 117520	MVZ 117519, MVZ 117524
MVZ 117688	AMNH 168548, MVZ 118295, MVZ 162503, MVZ 162508, MVZ 165138, USNM 352800, USNM 352806
MVZ 117689	AMNH 168548, MVZ 118295, MVZ 162503, MVZ 162508, MVZ 165138, USNM 352800, USNM 352806
MVZ 155909	MVZ 155911, MVZ 226632, USNM 486120
UF 23916	FMNH 23203, FMNH 23210, FMNH 23903
USNM 1970	USNM 1446
USNM 122105	USNM 1446
USNM 192467	USNM 1446
UF 24357	UF 24358
UF 24359	UF 24358
UF 24360	UF 24358
MVZ 41226	AMNH 88865, AMNH 88868, AMNH 88871, AMNH 88875, USNM 341327, USNM 341329, USNM 341332, USNM 341334
AMNH 176239	AMNH 206566, FMNH 96891
USNM 369544	AMNH 206566, FMNH 96891
USNM 4226	AMNH 174328, MVZ 135291, USNM 547938
FMNH 14059	FMNH 14058, UF 8238, USNM 55913
USNM 428771	USNM 428770, USNM 428772, USNM 470118

Table A.6. List of specimens digitized in two dimensions using the semilandmark approach for chapter 8. See Table A.1 legend for more information.

Museum tag	
Cricetidae	
Arvicolinae	
<i>Microtus chrotorrhinus</i>	AMNH 147362; MVZ 54425, 54427, 54426
<i>Ondatra zibethicus</i>	UF 1791, 1793, 1795, 2415
Cricetinae	
<i>Cricetus cricetus</i>	AMNH 176483, 176484; MVZ, 41457, 129377
Sigmodontinae	
<i>Phyllotis xanthopygus</i>	LCM 3009, 3143, 3351, 3021
<i>Rheomys thomasi</i>	MVZ 98811, 98814, 98798, 98808
<i>Sigmodon hispidus</i>	UF 143, 1588, 1584, 1589
Muridae	
Deomyinae	
<i>Acomys cahirinus</i>	MVZ 107726, 118298, 118306, 1077262, 118297, 1182982, 118320
<i>Acomys cinereus</i>	USNM 422402, 422404, 422401, 422419
<i>Acomys dimidiatus</i>	MVZ 34193
<i>Acomys percivali</i>	MVZ 186228, 186226, 186227, 186229
<i>Acomys ignitus</i>	USNM 181744, 182888, 181750, 182889
<i>Acomys russatus</i>	USNM 317002, 317007, 316997, 317006
<i>Acomys spinosissimus</i>	AMNH 162547, 162546, 219041, 162545
<i>Acomys wilsoni</i>	MVZ 186231, 186232, 186233, 191151
<i>Deomys ferrugineus</i>	FMNH 167789, 167781, 167780; MVZ 196252
<i>Lophuromys flavopunctatus</i>	USNM 259508, 537876, 259515, 537875
<i>Lophuromys zena</i>	USNM 589948, 589952, 589943, 589947
<i>Lophuromys sikapusi</i>	FMNH 81935, 81937, 81938; MVZ 196260
<i>Uranomys ruddi</i>	USNM 438783, 367021, 438782, 367020
Gerbillinae	
<i>Ammodillus imbellis</i>	FMNH 140092
<i>Brachionus przewalskii</i>	USNM 102578
<i>Desmodillus braueri</i>	USNM 378287, 378289, 378290, 453904, 453899, 453893
<i>Desmodillus auricularis</i>	MVZ 117381, 117379, 117371, 117372; AMNH 165455, 165453, 165451, 165456
<i>Dipodillus campestris</i>	USNM 401028, 401038, 401036, 401852
<i>Dipodillus dasyurus</i>	USNM 350041, 316662, 316658, 350037
<i>Dipodillus harwoodi</i>	USNM 162274, 162303, 162273, 162306
<i>Dipodillus lowei</i>	USNM 297499, 297498
<i>Dipodillus mackilligini</i>	USNM 316700
<i>Dipodillus maghrebi</i>	USNM 472715, 472718, 472713, 472716, 472719, 472717
<i>Dipodillus simoni</i>	USNM 316687, 316699, 316683, 350045
<i>Dipodillus stigmonyx</i>	USNM 165286, 165283, 165284, 165285
<i>Gerbilliscus afra</i>	MVZ 117338, 117337, 117340, 117342
<i>Gerbilliscus boehmi</i>	USNM 162261, 162253, 162258, 162250
<i>Gerbilliscus brantsii</i>	AMNH 83696, 83693, 83694, 83695; MVZ 88729, 88730; USNM 295355, 295350, 462447, 295349
<i>Gerbilliscus guineae</i>	USNM 466209, 450763, 466212, 450765
<i>Gerbilliscus inclusus</i>	USNM 538396, 538397, 538395, 381480
<i>Gerbilliscus kempti</i>	MVZ 196265, 196266, 196267; FMNH 25369
<i>Gerbilliscus leucogaster</i>	USNM 295398, 295400, 295394, 295395
<i>Gerbilliscus nigricaudus</i>	USNM 183938, 590061, 183933, 590058
<i>Gerbilliscus phillippi</i>	USNM 344931, 344934; FMNH 28840, 28837
<i>Gerbilliscus robustus</i>	MVZ 186208, 186207, 186204, 186205
<i>Gerbilliscus validus</i>	MVZ 88727, 88732, 88717, 88720
<i>Gerbillurus paeba</i>	AMNH 219001, 219002; MVZ 149573, 149576
<i>Gerbillurus setzeri</i>	USNM 342232, 342260, 342229, 342233
<i>Gerbillurus tytonis</i>	USNM 379852, 379869, 342165, 379854
<i>Gerbillurus vallinus</i>	USNM 424171, 424172, 424173, 424175
<i>Gerbillus agag</i>	MVZ 1543290, 154330, 154326, 154332
<i>Gerbillus amoenus</i>	USNM 300231, 302217, 307626, 322544
<i>Gerbillus andersoni</i>	MVZ 107721; USNM 316747, 283254, 300226
<i>Gerbillus aquilus</i>	USNM 328042, 369319, 328045, 369341
<i>Gerbillus cheesmani</i>	MVZ 191959, 191960; 29029, 29042
<i>Gerbillus famulus</i>	USNM 321586, 321664, 321587, 321663
<i>Gerbillus floweri</i>	USNM 316843, 316848, 316850, 316852
<i>Gerbillus garamantis</i>	FMNH 72828
<i>Gerbillus gerbillus</i>	MVZ 34214, 107722, 34212, 34213
<i>Gerbillus gleadowi</i>	USNM 353247, 353617, 353622, 369058
<i>Gerbillus henleyi</i>	MVZ 107720; USNM 472202, 472203, 472204
<i>Gerbillus hesperinus</i>	USNM 486006, 485964, 486005, 485970
<i>Gerbillus hoogstraali</i>	USNM 540028, 540038, 540037, 540034
<i>Gerbillus latastei</i>	USNM 321822, 321813, 321821, 321794
<i>Gerbillus mauritaniae</i>	USNM 401519, 401522, 401518, 401002
<i>Gerbillus mesopotamiae</i>	USNM 350442, 350444, 350443, 350450
<i>Gerbillus muriculus</i>	USNM 141503, 297485, 141504; FMNH 105600
<i>Gerbillus nanus</i>	MVZ 191952, 191953, 191955, 191958; UF 14577, 25903, 28564, 28562
<i>Gerbillus nigeriae</i>	USNM 573945, 573944
<i>Gerbillus occiduus</i>	USNM 540040

Table A.6—continued.

	Museum tag
<i>Gerbillus perpallidus</i>	USNM 316820, 316823, 316819, 316822
<i>Gerbillus poecilops</i>	USNM 321575, 321584, 321577, 321579
<i>Gerbillus pulvinatus</i>	USNM 500939, 500943, 500940, 500942
<i>Gerbillus pusillus</i>	USNM 500947, 500946, 500945; FMNH 44419
<i>Gerbillus pyramidatus</i>	MVZ 34208, 107723, 34210; AMNH 119507
<i>Gerbillus tarabuli</i>	USNM 302165, 302167, 302160, 302218
<i>Meriones crassus</i>	MVZ 191991; USNM 401159, 401161, 401157
<i>Meriones erythrourus</i>	FMNH 202109
<i>Meriones grandis</i>	USNM 473951, 483036, 473866, 474353
<i>Meriones hurrianae</i>	USNM 369162, 369163, 369161, 369510
<i>Meriones libycus</i>	MVZ 191968, 191972, 191962, 191963
<i>Meriones meridianus</i>	MVZ 41227, 41228; AMNH 59702, 59352
<i>Meriones persicus</i>	MVZ 198812, 198813, 198811, 198819
<i>Meriones rex</i>	USNM 321715; FMNH 77953, 77955, 77959
<i>Meriones shawi</i>	USNM 474209, 474187, 474208, 474185
<i>Meriones tamariscinus</i>	USNM 155457, 155459; AMNH 85369, 85377
<i>Meriones tristrami</i>	MVZ 183874; USNM 327436, 327438, 327437
<i>Meriones unguiculatus</i>	MVZ 41229; USNM 240765, 283918, 270551
<i>Meriones vinogradovi</i>	MVZ 183875; USNM 354663, 354662; FMNH 97405
<i>Pachyuromys duprasi</i>	FMNH 74976, 89621, 80021, 80048; MVZ 34197; USNM 482421, 321829, 325567, 325569
<i>Psammomys obesus</i>	AMNH 203215; FMNH 78611, 91277, 91279; MVZ 183877; USNM 482457, 326018, 326025, 341974
<i>Rhomomys optimus</i>	AMNH 88865, 88868, 88871, 88875; MVZ 41226; USNM 341327, 341329, 341332, 341334
<i>Sekeetamys calurus</i>	FMNH 101021, 101025, 101024, 101033; USNM 321934, 321928, 321931, 321932
<i>Tatera indica</i>	AMNH 240846; MVZ 192006, 192007, 192002, 192005; UF 30352, 30266, 30245, 30260
<i>Taterillus arenarius</i>	USNM 401124, 401978, 401117, 401980
<i>Taterillus congicus</i>	AMNH 50294, 50295, 50298, 50300
<i>Taterillus emini</i>	USNM 165288, 299721, 165289, 299718
<i>Taterillus gracilis</i>	USNM 403445, 438169, 403447, 438165
<i>Taterillus harringtoni</i>	USNM 483985, 483990, 483998, 483991
<i>Taterillus lacustris</i>	USNM 378930, 378929, 378925, 378923
<i>Taterillus pygargus</i>	USNM 376373, 380412, 376311, 380413
<i>Lophiomyinae</i>	
<i>Lophiomys imhausi</i>	USNM 291766, 172694, 184114, 184115
<i>Murinae</i>	
<i>Apodemus agrarius</i>	MVZ 120896, 120898, 125183, 121103
<i>Mus pahari</i>	MVZ 166472, 221555, 221556; USNM 355553
<i>Phloeomys cumingi</i>	UF 22381
<i>Rattus tiomanicus</i>	FMNH 171919, 171920, 171917; USNM 590331

APPENDIX B

SUPPORTING MATERIAL FOR CHAPTER 3

Table B.1. Ecomorphological data for muroid rodents used in phenotypic evolution analyses. Values are based on averages of all the data included in the listed references. Mass is in grams; HBL= head-body length in millimeters; TL= tail length in millimeters; HFL= hindfoot length in millimeters; EL= ear length in millimeters; Elev= elevation above sea level in meters. Missing data are designated with (-).

	Mass	HBL	TL	HFL	EL	Elev	References
<i>Abeomelomys sevia</i>	56.5	127.5	173.0	24.8	18.2	2277.0	23, 86, 87, 215
<i>Abrothrix andinus</i>	24.7	95.0	59.0	20.6	14.4	3986.5	23, 33, 81, 220
<i>Abrothrix jelskii</i>	34.5	96.9	79.6	23.1	18.6	3546.0	23, 81, 232, 259, 318
<i>Abrothrix longipilis</i>	36.8	141.1	79.1	23.9	18.0	456.5	23, 34, 232, 321
<i>Acomys ignitus</i>	24.4	92.9	77.1	15.9	15.9	685.3	23, 71, 249, 262, 278
<i>Acomys russatus</i>	49.8	111.1	69.6	19.8	19.8	1547.7	111, 170, 217, 255, 257, 259
<i>Aegialomys xanthalous</i>	80.3	105.0	158.0	30.0	23.5	910.7	23, 81, 215, 333
<i>Aethomys namaquensis</i>	51.7	107.5	151.8	25.3	19.6	1095.5	23, 63, 180, 243, 259, 263, 275
<i>Akodon aterios baliolus</i>	60.0	106.6	83.1	24.4	-	2924.0	23, 81, 187
<i>Akodon boliviensis</i>	27.7	108.8	75.2	21.6	15.4	4065.6	23, 81, 232, 259, 318
<i>Akodon kojordi</i>	29.5	96.3	77.6	22.5	15.3	2854.2	23, 81, 187, 318
<i>Akodon lutescens</i>	20.8	89.0	63.4	19.2	14.1	4232.0	23, 81, 232, 318
<i>Akodon mimus</i>	24.0	98.4	96.0	24.2	18.1	2609.8	23, 81, 187, 211, 318
<i>Akodon torques</i>	39.0	102.0	94.0	22.3	17.0	3001.5	23, 81, 187, 288, 332
<i>Andalgalomys pearsoni</i>	25.4	96.3	107.8	24.2	18.5	437.5	23, 76, 81, 187, 232
<i>Andinomys edax</i>	69.7	141.6	59.2	27.8	25.1	3712.0	23, 81, 187, 215, 232, 318
<i>Anisomys imitator</i>	494.0	264.6	321.2	61.1	22.2	1852.0	23, 86, 87, 166, 215
<i>Apodemus agrarius</i>	21.9	96.3	72.9	19.4	12.1	919.5	23, 29, 58, 84, 151, 171, 295
<i>Apodemus mystacinus</i>	38.3	114.6	121.9	26.4	21.1	1190.3	7, 23, 29, 56, 84, 111, 112
<i>Apodemus semotus</i>	26.3	116.8	121.9	26.4	25.3	2257.1	23, 169, 272, 330
<i>Apodemus speciosus</i>	33.8	111.2	100.5	24.0	15.7	976.0	148, 149, 171, 272, 273
<i>Apodemus sylvaticus</i>	24.3	96.5	92.2	22.0	17.0	2860.0	23, 29, 58, 111, 112, 159, 203, 244, 272, 295
<i>Apomys datae</i>	106.0	150.7	135.8	35.8	21.0	1659.3	58, 124, 259, 318
<i>Apomys hylocoetes</i>	45.1	112.5	134.3	30.3	20.0	2143.2	58, 127, 197, 259
<i>Archboldomys luzonensis</i>	37.1	89.3	70.0	27.5	16.5	2200.0	131, 208, 215, 318
<i>Arvicathis neumanni</i>	85.0	146.0	100.5	27.5	10.3	779.5	23, 30, 189, 190, 215, 278
<i>Arvicathis niloticus</i>	108.1	158.8	130.5	31.0	20.0	1105.0	104, 115, 217, 292, 318
<i>Arvicola terrestris</i>	163.4	173.8	89.0	27.0	10.5	366.6	23, 29, 84, 193, 295, 309
<i>Auliscomys sublimis</i>	38.5	110.7	52.5	22.9	21.4	4497.3	23, 81, 215, 232, 259, 318
<i>Baiomys musculus</i>	9.7	72.5	48.5	15.0	12.0	1666.7	39, 46, 236, 238
<i>Bandicota bengalensis</i>	244.3	195.0	151.5	34.8	22.0	1354.3	17, 23, 58, 84, 89, 226
<i>Batomys granti</i>	179.3	202.0	149.0	36.3	21.2	1942.0	23, 58, 131, 215, 318
<i>Beamys hindei</i>	93.6	158.5	127.5	23.0	22.0	1018.7	23, 141, 159, 215, 215, 266, 285
<i>Berylmus bowersi</i>	406.7	266.3	278.3	58.8	32.0	1092.9	23, 58, 89, 118
<i>Brachytarsomys albicauda</i>	206.7	220.0	221.0	34.0	14.0	915.7	23, 92, 93, 215
<i>Brachyuromys betsileoensis</i>	107.5	151.5	93.5	31.0	20.5	1837.0	23, 92, 93
<i>Brucopattersonius igniventris</i>	32.0	119.0	96.0	24.7	16.7	783.0	23, 186
<i>Bullimus bagobus</i>	450.8	278.3	183.7	53.5	28.0	786.4	19, 58, 130, 195, 215, 241
<i>Bunomys chrysocomus</i>	100.8	160.0	141.0	34.8	22.7	1166.3	23, 58, 259, 318
<i>Calomys callosus</i>	33.6	96.3	83.9	21.3	18.6	1150.0	23, 75, 81, 232, 259
<i>Calomys lepidus</i>	26.6	85.0	43.3	18.0	-	3821.3	23, 78, 81, 232, 259
<i>Calomys venustus</i>	49.8	103.5	85.4	23.4	-	831.3	23, 34, 48, 221, 228
<i>Calomyscus baluchi</i>	20.4	174.3	89.8	20.9	17.4	625.3	84, 204, 214, 244, 264
<i>Calomyscus sp</i>	20.6	79.5	87.0	22.3	18.2	1518.0	23, 84, 96, 215, 244, 310
<i>Cannomys badius</i>	597.3	206.2	63.8	32.5	9.0	2129.3	21, 23, 58, 84, 89, 191, 215
<i>Carpomys phaeurus</i>	123.0	177.8	164.3	31.5	19.0	2192.0	58, 122, 215, 280
<i>Cerradomys subflavus</i>	83.0	157.8	184.4	34.5	21.5	612.0	23, 81, 187, 225, 232
<i>Chelemys macroonyx</i>	70.5	128.9	53.0	25.2	14.6	731.0	23, 34, 187, 232
<i>Chinchillula sahamae</i>	152.2	158.0	104.0	34.8	36.0	4125.0	77, 81, 187, 215, 232, 318
<i>Chionomys nivalis</i>	46.5	135.8	62.5	21.1	14.4	1750.3	23, 84, 162, 179, 202
<i>Chironomys chiropus</i>	77.8	148.0	218.8	28.0	19.5	599.3	15, 23, 89, 215, 259
<i>Chiropodomys gliroides</i>	24.1	89.2	126.7	18.5	16.0	1323.3	23, 58, 84, 89, 198, 224, 262
<i>Chiruromys vates</i>	46.0	110.0	162.5	24.3	17.0	1000.0	23, 86, 87
<i>Chromotomys gonzalezi</i>	133.4	168.5	94.0	36.5	21.5	1528.3	23, 131, 240
<i>Clethrionomys gapperi</i>	23.8	97.3	38.7	18.3	13.7	2758.7	23, 24, 52, 147, 152, 194, 259
<i>Colomys goslingi</i>	60.5	122.4	160.0	37.9	17.8	1733.3	143, 153, 157, 159, 215, 278
<i>Conilurus penicillatus</i>	183.4	188.5	183.0	48.0	22.0	65.7	23, 86, 136, 166, 269
<i>Crateromys heaneyi</i>	124.0	279.5	320.0	63.5	22.0	549.0	49, 126, 215, 318
<i>Cricetomys gambianus</i>	1338.1	322.5	413.0	70.8	40.6	1607.7	23, 115, 160, 243, 263, 266, 303
<i>Cricetulus griseus</i>	35.0	93.0	28.0	-	-	1773.3	23, 199, 293
<i>Cricetulus migratorius</i>	35.1	96.9	24.9	13.3	18.0	2401.7	23, 29, 58, 112, 171, 203, 295
<i>Cricetus cricetus</i>	381.4	253.8	46.5	37.5	-	277.0	23, 29, 84, 119, 163, 179, 295
<i>Crunomys melanius</i>	54.5	110.0	80.8	26.0	15.0	817.0	58, 123, 215, 259, 283
<i>Dacromys millardi</i>	168.3	198.6	254.3	44.8	30.0	967.5	23, 89, 210, 215, 318
<i>Dasyomys incomitus</i>	135.3	154.3	144.8	33.8	20.9	1089.5	23, 115, 243, 263, 275, 318
<i>Delanymys brooksi</i>	5.6	55.8	97.0	-	-	2644.0	23, 156, 159, 215, 318
<i>Delomys dorsalis</i>	67.5	125.0	129.0	32.0	20.0	1300.5	23, 31, 81, 259
<i>Dendromus insignis</i>	13.5	84.5	99.0	20.0	13.0	3692.3	23, 262, 318
<i>Dendromus mesomelas</i>	11.1	75.8	103.7	19.1	13.8	1276.7	23, 243, 263, 266, 275
<i>Dendromus nyasae</i>	13.0	84.5	99.0	20.0	13.0	2679.0	23, 207, 287
<i>Deomys ferrugineus</i>	57.3	130.4	178.3	33.6	23.2	792.0	23, 64, 159, 215, 251, 278

Table B.1-continued.

	Mass	HBL	TL	HFL	EL	Elev	References
<i>Desmodillus auricularis</i>	56.6	113.3	89.9	25.0	11.7	1074.0	23, 73, 159, 215, 243, 259, 263
<i>Diplothrix legata</i>	1000.0	275.0	285.0	-	-	401.0	150, 215, 325
<i>Dipodillus dasyurus</i>	23.7	86.0	108.8	22.4	13.1	1228.6	9, 111, 117, 154, 230, 262
<i>Eluris minor</i>	35.8	112.5	130.0	-	-	900.3	23, 92, 93
<i>Eluris tanala</i>	85.0	150.3	178.0	31.0	24.0	1110.8	23, 92, 93
<i>Euneomys chinchilloides</i>	83.5	135.2	80.3	29.4	25.5	1224.3	23, 32, 232, 259
<i>Geoxus valdivianus</i>	30.2	100.8	43.1	11.5	25.5	1272.5	23, 215, 232, 259
<i>Gerbillurus paeba</i>	27.1	94.7	110.0	25.0	16.1	632.5	23, 72, 149, 243, 259, 263, 305
<i>Gerbillurus vallinus</i>	36.1	93.7	109.7	29.5	14.3	740.0	72, 107, 243, 259, 263
<i>Gerbillus gerbillus</i>	26.0	85.0	120.0	26.0	14.0	573.3	23, 58, 112, 217, 259, 329
<i>Gerbilus nanus</i>	26.9	61.2	94.2	16.6	7.3	520.3	23, 58, 112, 259, 278
<i>Golunda elliotti</i>	63.4	128.4	83.7	25.9	16.1	844.3	205, 212, 215, 226, 244, 272
<i>Grammomys dolichurus</i>	37.2	115.3	169.2	23.5	17.2	1169.0	23, 64, 243, 263, 275
<i>Grammomys ibeanus</i>	43.7	120.4	182.6	22.5	20.0	2004.0	23, 70, 139, 218, 266
<i>Grammomys macmillani</i>	42.0	105.7	165.0	23.0	16.0	1150.0	23, 266, 318, 323
<i>Graomys centralis</i>	80.0	130.0	156.0	29.0	26.0	818.0	23, 85, 279, 318
<i>Graomys griseoflavus</i>	65.4	134.0	146.4	29.2	23.5	741.3	23, 34, 81, 232, 259
<i>Gymnomyzys roberti</i>	111.6	156.3	173.1	35.3	20.7	956.8	23, 92, 93, 215
<i>Habromys lepturus</i>	85.0	124.0	114.0	29.0	-	2188.0	4, 23, 39, 103, 318
<i>Heimyscus fumosus</i>	14.3	76.8	104.5	17.5	14.4	380.3	105, 215, 278, 324
<i>Hodomys allenii</i>	367.8	241.0	211.5	46.0	29.0	646.0	23, 215, 259, 318
<i>Holochilus sciurus</i>	212.1	174.4	175.7	42.1	22.0	162.7	23, 27, 80, 81, 232
<i>Hybomys univittatus</i>	50.4	121.4	103.3	27.9	15.5	1389.0	23, 64, 158, 278, 302
<i>Hydromys chrysogaster</i>	451.8	281.8	259.3	61.9	17.3	841.7	23, 62, 86, 87, 166, 269
<i>Hylomys parvus</i>	13.4	60.0	95.0	14.0	14.0	325.5	23, 37, 45, 262, 278
<i>Hylomys stellata</i>	19.8	91.5	130.5	18.0	18.0	1973.5	23, 115, 254, 259, 286
<i>Hyomys goliath</i>	822.5	324.5	312.0	59.4	24.8	2140.3	23, 86, 87
<i>Hypogeomys antimena</i>	1197.1	325.0	228.2	73.2	57.7	125.7	23, 79, 84, 93, 215, 265
<i>Irenomys tarsalis</i>	45.8	117.1	162.7	21.7	46.3	616.9	23, 215, 232, 259
<i>Isthomys pirrensis</i>	121.0	164.5	195.3	35.4	28.5	657.3	12, 80, 135, 238, 259, 318
<i>Juliomys pictipes</i>	22.9	89.4	95.4	21.0	13.5	1350.0	23, 81, 94, 187, 232
<i>Kunsta tomentosus</i>	115.6	278.5	150.0	43.0	33.0	182.3	23, 81, 187
<i>Lasiodipodomys mandarinus</i>	39.1	115.0	28.0	-	-	1900.0	28, 108, 318
<i>Leggadina forresti</i>	20.0	104.0	72.0	19.0	15.0	120.5	23, 35, 166, 269
<i>Lemmus sibiricus</i>	64.2	128.3	18.9	21.0	8.8	1742.7	23, 194, 259, 267, 317
<i>Lemniscomys barbarus</i>	35.1	100.8	122.5	24.5	15.3	583.7	23, 64, 67, 115, 139, 296
<i>Lemniscomys striatus</i>	40.8	114.3	132.8	27.1	15.0	1411.9	64, 115, 139, 172, 278, 298
<i>Lenoxus apicalis</i>	53.6	160.0	170.0	-	20.0	1984.0	23, 81, 187, 215, 318
<i>Leopardomys sabanus</i>	347.8	234.5	350.1	46.7	27.4	1650.0	58, 89, 118, 181, 224, 326
<i>Leporillus conditor</i>	350.0	197.0	178.0	44.0	43.0	62.5	23, 35, 166, 269, 318
<i>Leptomys elegans</i>	87.4	151.8	147.6	38.5	20.9	968.7	23, 86, 87, 166, 215
<i>Limnomys sibuanus</i>	64.3	127.0	156.5	29.5	21.0	2270.7	128, 196, 215, 242, 318
<i>Lophiomys imhausi</i>	755.0	307.5	177.5	42.0	20.0	2200.3	156, 159, 215, 227, 247, 256
<i>Lophuromys flavopunctatus</i>	66.7	119.3	73.5	21.0	17.8	3188.5	23, 156, 159, 278, 308, 318
<i>Lophuromys sikapusi</i>	73.2	138.5	71.3	22.3	16.0	572.0	23, 64, 115, 277, 278, 278
<i>Lophuromys zena</i>	42.3	113.0	59.5	20.0	18.0	2685.0	23, 278
<i>Lorentzimys nouhuysi</i>	15.5	74.2	112.4	18.6	16.3	1399.0	23, 86, 87, 166, 215
<i>Loxodontomys micropus</i>	72.9	131.4	96.6	29.0	20.1	1168.2	23, 34, 81, 81, 187, 215, 232
<i>Macrotarsomys bastardi</i>	28.0	90.4	121.9	25.0	22.2	645.3	92, 93, 100, 146
<i>Macrouromys major</i>	350.0	240.8	327.5	52.7	16.9	1481.7	23, 35, 86, 87, 215
<i>Malacomys longipes</i>	96.9	156.7	177.7	39.7	25.7	1164.5	23, 64, 158, 278, 300
<i>Malacothrix typica</i>	15.5	74.3	35.8	18.2	18.8	840.0	54, 243, 259, 263, 315, 318
<i>Mallomys rothschildi</i>	1158.3	380.0	379.7	65.1	26.6	1866.7	23, 86, 87, 166
<i>Mammelomys lanosus</i>	116.5	162.3	123.7	36.6	19.6	2218.7	23, 86, 87, 166
<i>Margaretomys elegans</i>	121.0	180.0	259.8	36.5	-	2007.0	23, 58, 215, 259
<i>Mastacomys fuscus</i>	125.0	161.7	108.3	30.0	96.0	1442.0	23, 35, 116, 166, 200, 215
<i>Mastomys erythroleucus</i>	49.8	118.0	107.7	23.0	16.7	1001.5	10, 106, 259, 278
<i>Mastomys hildebrandti</i>	50.7	122.5	119.0	24.0	16.0	1330.3	23, 259, 260, 278
<i>Maxomys bartelsii</i>	102.0	152.5	152.5	33.5	-	730.5	23, 58, 259
<i>Maxomys surifer</i>	158.4	182.5	181.3	41.0	25.0	671.6	20, 23, 58, 89, 258, 259, 326
<i>Mayeromys ellermani</i>	22.5	92.5	99.5	19.9	10.5	1868.0	23, 86, 87, 215
<i>Megadontomys thomasi</i>	110.9	162.0	188.0	34.0	-	3033.3	3, 23, 119, 179, 201, 259
<i>Melanomys caliginosus</i>	52.4	122.0	95.3	26.0	16.3	727.0	23, 80, 81, 213, 238, 259
<i>Melasmothrix naso</i>	47.5	118.0	88.8	27.5	-	1553.5	23, 58, 215, 259, 318
<i>Melomys cervinipes</i>	85.8	140.0	146.7	28.7	19.0	609.0	23, 35, 166, 269, 311
<i>Melomys rufescens</i>	67.9	136.3	137.0	27.2	13.8	1766.7	23, 86, 87, 88, 166
<i>Meriones shawi</i>	116.4	196.6	125.0	33.3	18.0	332.3	25, 137, 217, 278
<i>Meriones unguiculatus</i>	57.1	115.0	108.7	28.0	13.5	1618.4	23, 51, 84, 110, 312
<i>Mesembriomys gouldii</i>	718.3	295.0	330.0	-	-	280.0	23, 35, 215, 269, 320
<i>Mesocricetus auratus</i>	111.7	148.6	116.3	28.2	18.0	359.5	23, 84, 278, 295, 328
<i>Micromys minutus</i>	6.7	67.0	64.9	14.5	9.0	800.3	16, 23, 29, 84, 89, 119, 179, 215, 295
<i>Microromys minutus</i>	15.1	75.3	116.8	23.0	15.0	2570.3	23, 81, 81, 187, 318
<i>Microtus arvalis</i>	26.9	108.8	36.0	16.7	11.1	900.3	8, 23, 26, 84, 144, 179, 203, 295
<i>Microtus californicus</i>	53.1	120.0	53.3	24.5	18.0	60.0	23, 82, 152, 194, 259
<i>Microtus chrotorrhinus</i>	38.4	109.0	52.0	20.0	15.0	1320.9	23, 147, 152, 259
<i>Microtus guentheri</i>	44.3	116.0	30.8	19.9	13.0	2461.5	23, 112, 185, 295, 327
<i>Microtus kikuchii</i>	46.6	125.0	82.5	21.5	-	2641.3	23, 58, 207
<i>Microtus montanus</i>	44.1	117.5	45.3	19.4	13.8	2088.1	23, 24, 90, 152, 194, 259
<i>Microtus pennsylvanicus</i>	45.1	122.5	46.8	21.0	14.0	878.9	23, 147, 152, 194, 259
<i>Microtus richardsoni</i>	74.8	172.0	61.2	24.5	13.9	2034.9	23, 23, 152, 194, 322
<i>Millardia kathleenae</i>	93.0	147.5	138.4	27.5	21.5	70.5	14, 58, 89, 259, 318
<i>Monticolomys koopmani</i>	23.4	92.5	129.5	24.0	17.5	1716.7	44, 92, 93, 99, 101
<i>Mus booduga</i>	13.6	75.5	55.3	15.6	16.8	2565.3	22, 58, 89, 216, 259
<i>Mus cervicolor</i>	15.6	81.6	67.0	16.8	14.6	1587.8	18, 58, 89, 216, 259
<i>Mus cookii</i>	21.6	89.7	85.0	19.0	15.0	352.5	23, 58, 89, 216, 259, 318
<i>Mus musculus</i>	15.2	81.4	80.1	17.8	13.7	1688.1	23, 52, 80, 81, 115, 156, 159, 161, 215, 238, 269, 295
<i>Mus pahari</i>	23.6	90.0	85.0	20.3	-	745.0	19, 23, 58, 89, 259
<i>Mus terricolor</i>	8.3	68.0	64.0	15.0	11.5	2283.4	23, 216, 262
<i>Myomys dybowskii</i>	110.0	198.4	139.8	34.6	18.3	1646.5	64, 68, 159, 215, 278

Table B.1-continued.

	Mass	HBL	TL	HFL	EL	Elev	References
<i>Myomyscus brockmani</i>	29.5	90.0	123.5	22.0	-	953.3	278, 284, 301
<i>Myospalax aspalax</i>	304.5	216.8	47.5	37.0	5.0	1411.5	23, 290
<i>Mystromys albicaudatus</i>	90.7	148.2	66.2	24.7	26.0	1724.0	55, 74, 159, 215, 243, 263, 278
<i>Nanospalax ehrenbergi</i>	159.1	193.7	0.1	25.1	0.1	514.5	23, 60, 112, 159, 213, 253, 259
<i>Neacomys minutus</i>	13.5	70.6	77.1	20.8	12.3	185.5	23, 81, 187, 223, 318
<i>Neacomys spinosus</i>	23.3	78.5	90.5	24.5	15.5	693.0	23, 81, 318
<i>Necromys aemonus</i>	29.0	96.0	66.5	21.0	11.5	3715.5	23, 81, 259, 318
<i>Nectomys apicalis</i>	290.0	216.4	234.3	51.7	16.9	766.5	23, 83, 97, 134
<i>Nectomys squamipes</i>	255.0	184.0	213.7	50.4	22.4	671.2	23, 80, 81, 215, 232, 259
<i>Neodon irene</i>	49.1	112.2	38.4	18.3	14.5	3116.3	2, 29, 215, 231, 261, 318
<i>Neotoma bryanti</i>	193.3	209.0	168.0	38.0	31.3	1039.0	6, 23
<i>Neotoma cinera</i>	300.2	220.7	166.6	39.8	33.1	2235.3	23, 24, 24, 39, 152, 192
<i>Neotoma devia</i>	130.0	161.3	128.5	30.0	29.5	1008.0	23, 39, 152, 233, 318
<i>Neotoma floridana</i>	270.7	222.5	155.8	41.0	25.5	926.8	23, 147, 152, 259
<i>Neotomodon alstoni</i>	40.0	115.0	92.5	25.7	21.0	3166.0	23, 39, 215, 316, 318
<i>Neotomys ebriosus</i>	65.1	127.4	74.5	23.0	18.4	3631.3	23, 81, 187, 215, 232, 306
<i>Nephelomys keyssi</i>	58.3	156.7	175.3	34.7	21.0	1864.5	23, 81, 187, 331
<i>Nephelomys livipes</i>	60.5	145.0	53.0	33.0	23.0	2073.5	23, 81, 187, 318
<i>Nesomys rufus</i>	156.3	175.3	157.0	47.0	23.0	1380.3	23, 92, 93
<i>Niviventer confucianus</i>	32.5	147.5	187.3	30.0	21.5	2162.0	23, 58, 89, 182, 259
<i>Niviventer cremoriventer</i>	73.1	147.5	180.6	24.8	18.0	1332.8	58, 84, 89, 224, 245, 258
<i>Niviventer culteratus</i>	103.0	160.0	160.0	-	-	1663.0	1, 23, 36, 318
<i>Niviventer excelsior</i>	102.0	152.5	202.1	32.0	24.5	1815.0	23, 58, 259, 318
<i>Notiomys edwardsii</i>	21.5	84.9	40.5	19.0	7.4	872.0	23, 187, 232
<i>Notomys fuscus</i>	35.0	106.5	121.5	33.3	26.0	150.5	23, 35, 166, 269
<i>Nyctomyssumichrasti</i>	50.3	119.0	125.8	24.5	18.0	905.5	23, 39, 80, 142, 215, 238, 246
<i>Ochrotomys nutalli</i>	21.1	83.3	75.5	18.5	15.5	348.3	23, 147, 152, 215, 259, 315
<i>Oecomys bicolor</i>	33.3	101.2	112.0	22.5	14.5	576.0	23, 81, 238, 259, 318
<i>Oecomys concolor</i>	62.6	134.8	160.7	28.0	18.5	1281.5	23, 80, 81, 232, 259
<i>Oecomys superans</i>	73.4	146.3	176.3	30.7	17.0	453.5	23, 81, 164, 187, 318
<i>Oenomys hypoxanthus</i>	87.0	158.8	171.3	32.0	19.5	2202.0	23, 69, 156, 159, 215, 229
<i>Oligoryzomys fulvescens</i>	13.1	78.6	100.3	21.0	14.0	1681.0	23, 80, 81, 238, 259, 313
<i>Oligoryzomys longicaudatus</i>	26.3	95.2	127.3	27.0	15.5	1554.0	23, 34, 81, 187
<i>Oligoryzomys micrurus</i>	19.8	82.0	105.6	23.7	14.0	750.4	23, 81, 232, 259, 318
<i>Ondatra zibethicus</i>	1162.4	306.6	234.1	75.4	22.0	1692.5	23, 24, 52, 86, 147, 194, 215, 259, 295
<i>Onychomys leucogaster</i>	36.6	112.5	42.5	21.0	15.5	1517.0	23, 147, 152, 259
<i>Oryzomys couesi</i>	65.9	96.4	132.5	30.1	15.6	1022.0	23, 80, 152, 178, 238, 259
<i>Oryzomys palustris</i>	57.7	115.0	111.7	31.0	14.0	10.5	23, 147, 152, 259
<i>Osgoodomys banderanus</i>	50.0	110.0	119.5	-	-	924.2	23, 39, 47, 215
<i>Otomys angoniensis</i>	107.6	220.0	79.0	25.5	19.5	1633.3	23, 263, 275, 318
<i>Otomys denti</i>	160.0	162.5	104.5	28.8	23.5	2258.5	23, 64, 278, 282
<i>Ototylomys phyllotis</i>	79.3	143.3	143.3	26.5	23.5	964.5	23, 215, 235, 238, 322
<i>Oxymycterus hiskia</i>	68.0	100.0	77.0	25.0	16.0	2174.0	23, 81, 187, 318
<i>Oxymycterus nasutus</i>	68.0	135.0	85.0	25.0	17.0	301.3	23, 61, 81, 187
<i>Parahydromys asper</i>	540.0	225.0	254.3	53.1	14.5	2001.0	23, 86, 87, 166, 215
<i>Paramelomys levipes</i>	88.4	144.0	137.7	34.4	18.4	708.3	23, 86, 166, 207
<i>Parotomys brantsii</i>	129.2	157.5	97.7	30.7	19.0	465.7	23, 53, 243, 259, 263, 315
<i>Paruromys dominator</i>	283.9	223.5	263.0	51.9	29.7	615.0	23, 215, 318
<i>Peromyscus aztecus</i>	43.3	117.5	124.0	24.5	19.5	2417.0	23, 39, 238, 318
<i>Peromyscus boylii</i>	24.8	100.5	102.3	22.5	20.5	1579.5	23, 152, 175, 238, 259, 315
<i>Peromyscus californicus</i>	35.9	97.1	121.2	24.5	23.1	976.3	23, 152, 177, 180, 259, 291, 315
<i>Peromyscus crinitus</i>	17.5	77.4	96.5	20.2	19.2	1368.7	23, 152, 259, 315
<i>Peromyscus eremicus</i>	25.8	88.3	100.1	19.7	18.2	867.7	23, 152, 176, 259, 315
<i>Peromyscus fraterculus</i>	22.6	84.3	106.3	19.3	-	677.5	23, 43, 259, 315, 318
<i>Peromyscus leucopus</i>	22.0	95.2	78.8	21.0	16.3	910.1	23, 52, 95, 147, 152, 238, 259
<i>Peromyscus mexicanus</i>	41.7	126.3	126.3	27.3	23.2	1526.5	23, 80, 234, 238, 259
<i>Peromyscus polionotus</i>	13.0	84.8	48.3	16.8	14.1	1.7	23, 114, 140, 152, 259, 314, 315
<i>Petromyscus monticolarus</i>	21.7	93.5	74.6	18.8	16.8	1440.5	23, 24, 147, 152, 259, 315
<i>Phenacomys intermedius</i>	31.0	109.3	32.3	18.0	14.0	2069.0	23, 24, 147, 152, 174, 194, 215, 259
<i>Phloeomys sp</i>	1815.4	446.7	313.8	70.0	25.4	967.0	40, 125, 131, 138
<i>Phodopus sungorus</i>	30.2	93.3	9.5	14.3	13.5	1225.3	23, 215, 315
<i>Phyllotis andium</i>	38.3	108.5	106.5	26.5	23.0	2636.5	23, 81, 259, 318
<i>Phyllotis osilae</i>	53.0	115.5	121.6	25.2	21.4	3191.0	23, 81, 187, 232, 318
<i>Phyllotis xanthopygus</i>	53.1	127.5	147.5	28.0	23.0	2162.3	23, 34, 81, 259, 318
<i>Pogonomys loriae</i>	94.1	151.0	219.3	26.6	14.9	2003.0	23, 84, 86, 87, 166
<i>Pogonomys macrourus</i>	47.4	120.5	157.0	20.9	13.2	622.0	23, 86, 87, 269
<i>Praomys degraaffi</i>	39.1	110.4	135.6	25.8	85.5	2363.8	23, 304
<i>Praomys jacksoni</i>	40.8	120.0	142.5	22.3	20.0	2258.5	23, 64, 115, 156, 159, 304, 319
<i>Praomys missonnei</i>	40.0	114.0	136.0	22.8	15.6	975.0	23, 65, 278, 299
<i>Praomys tulbergi</i>	33.6	109.0	132.0	25.0	16.0	719.5	23, 115, 259, 278, 297
<i>Prometheomys schaposchnikowi</i>	70.0	142.4	51.1	25.4	14.8	2093.7	42, 57, 109, 215, 318
<i>Pseudomys australis</i>	65.0	134.0	83.0	25.0	-	97.0	23, 35, 166, 269
<i>Pseudoryzomys simplex</i>	51.2	117.0	124.7	31.0	17.0	119.0	23, 81, 215, 259
<i>Punomys kofordi</i>	82.0	134.1	69.2	27.2	24.7	3994.0	23, 81, 219, 318
<i>Rattus exulans</i>	75.2	135.8	150.9	26.1	17.3	733.3	23, 58, 89, 118, 155, 166, 224, 269, 326
<i>Rattus gilwensis</i>	75.0	170.8	134.2	30.0	-	2885.0	86, 133, 168, 215, 274
<i>Rattus leucopus</i>	210.8	201.3	176.3	38.8	20.2	442.0	23, 86, 87, 166, 269
<i>Rattus norvegicus</i>	340.8	213.5	177.0	39.0	17.5	304.8	23, 35, 80, 81, 238, 269, 295
<i>Rattus novaeguineae</i>	134.7	172.8	162.0	30.8	20.8	908.2	23, 86, 87, 274
<i>Rattus praetor</i>	198.7	196.7	166.3	35.5	18.2	972.3	23, 86, 87, 88, 166
<i>Rattus rattus</i>	180.4	180.8	196.6	36.1	22.7	1251.7	23, 52, 80, 81, 238, 269, 295
<i>Rattus sordidus</i>	172.3	169.0	128.0	30.6	-	227.0	23, 86, 166, 269, 315
<i>Rattus tiomanicus</i>	127.4	161.3	173.1	31.5	-	16.5	23, 58, 84, 89, 224, 258, 326
<i>Rattus verecundus</i>	84.0	157.7	160.7	32.8	18.4	971.7	23, 86, 166, 207
<i>Rattus villosissimus</i>	192.3	158.0	145.5	32.0	20.0	324.5	23, 136, 166, 269
<i>Reithrodontomys auritus</i>	74.8	147.5	84.5	32.0	21.0	1635.0	23, 32, 91, 259
<i>Reithrodontomys creper</i>	23.3	97.0	132.1	23.0	16.4	2666.7	23, 80, 238, 289, 294
<i>Reithrodontomys fulvescens</i>	13.1	69.5	97.8	18.5	14.0	445.5	23, 152, 238, 259, 318

Table B.1-continued.

	Mass	HBL	TL	HFL	EL	Elev	References
<i>Reithrodontomys gracilis</i>	12.1	73.5	101.5	18.5	14.0	952.5	23, 237, 238, 238, 259
<i>Reithrodontomys megalotis</i>	10.6	73.8	67.2	16.3	11.3	2333.0	23, 52, 147, 152, 173, 259, 315
<i>Rhabdomys pumilio</i>	39.6	115.8	115.2	24.0	14.1	865.0	23, 111, 159, 184, 215, 243, 263, 275
<i>Rheomys thomasi</i>	31.3	114.0	121.0	31.0	10.0	966.0	23, 39, 238, 318
<i>Rhipidomys macconnelli</i>	41.6	109.0	141.9	26.7	-	1850.5	23, 80, 81, 187, 318
<i>Rhipidomys masticalis</i>	88.7	70.0	156.4	27.3	19.1	743.6	23, 80, 81, 259
<i>Rhizomys pruinosus</i>	2225.0	307.5	111.3	52.5	21.5	2120.0	23, 58, 89, 188, 203
<i>Rhynchosomys isarogensis</i>	122.5	187.0	105.0	37.0	-	1637.0	23, 58, 131, 215, 318
<i>Saccostomus campestris</i>	53.2	128.8	51.2	20.0	16.8	1061.0	23, 59, 64, 113, 243, 263
<i>Scapteromys tumidus</i>	148.2	175.7	149.6	37.5	22.9	88.0	23, 81, 187, 215, 232
<i>Scolomys juriaense</i>	23.3	85.0	65.3	19.5	14.5	260.5	23, 81, 187, 215, 318
<i>Scotinomys teguina</i>	11.6	76.0	54.0	17.3	14.3	1750.0	23, 80, 238, 259, 315
<i>Signodon alstoni</i>	64.9	145.0	107.0	30.0	21.0	534.5	23, 80, 81, 222, 259
<i>Signodon arizonae</i>	178.0	154.0	120.5	33.5	21.5	1048.0	64, 115, 239, 252, 278
<i>Signodon hispidus</i>	103.5	125.1	113.6	31.9	18.1	1039.7	23, 52, 80, 81, 147, 152, 238, 259, 315
<i>Signomystomys alfari</i>	74.7	136.5	168.7	35.8	19.3	112.0	23, 81, 215, 238, 262, 318
<i>Solomys salebrus</i>	397.0	276.5	244.0	-	-	441.7	23, 88, 167, 215
<i>Sooretamys raticeps</i>	141.2	181.0	209.6	38.0	24.5	694.0	23, 81, 187, 232
<i>Steatomys krebsi</i>	20.7	89.5	50.5	17.0	16.5	887.3	23, 184, 243, 263
<i>Steatomys parvus</i>	15.7	74.5	39.0	15.0	12.0	1048.0	23, 80, 81, 147, 152, 318
<i>Stenocephalemys albipes</i>	49.8	115.0	137.0	27.0	22.0	2050.0	50, 165, 262, 318
<i>Stochomys longicaudatus</i>	76.0	145.1	211.5	29.3	18.7	775.8	23, 64, 115, 159, 179, 215, 278
<i>Sundamys muelleri</i>	244.4	243.8	303.7	47.0	23.5	692.5	23, 58, 84, 89, 224, 258
<i>Synaptomys cooperi</i>	33.6	106.0	20.0	21.0	11.5	495.5	23, 147, 152, 259
<i>Tachyoryctes splendens</i>	201.6	201.1	73.1	29.8	8.7	2212.3	156, 159, 191, 215, 248, 278, 318
<i>Tapecomyia wolffsohni</i>	56.5	124.0	136.0	28.0	24.5	2381.3	13, 23, 66, 268
<i>Tarsomys apoensis</i>	76.7	145.5	141.3	31.5	20.5	2002.7	129, 132, 209, 215, 318
<i>Tatera robusta</i>	92.7	137.7	169.0	34.0	19.0	745.3	23, 121, 250, 259, 292
<i>Taterillus emini</i>	52.0	144.5	140.7	27.5	15.0	1025.0	23, 64, 120, 278
<i>Thaptomys nigrita</i>	20.4	93.6	47.5	18.4	12.3	895.2	23, 81, 187, 232
<i>Thomasomys aureus</i>	88.0	155.0	210.5	36.7	22.6	1940.1	23, 80, 81, 259, 318
<i>Thomasomys cinereiventer</i>	77.0	145.0	154.6	35.0	13.0	3029.5	23, 80, 81, 187, 318
<i>Thomasomys notatus</i>	77.0	95.0	117.5	26.0	17.5	2310.5	23, 81, 187, 318
<i>Tokudaiya osimensis</i>	117.8	151.0	114.3	30.7	22.2	250.5	145, 271
<i>Transandinomys talamancae</i>	58.7	127.6	126.5	29.6	20.2	682.3	11, 23, 80, 81, 187, 238
<i>Tylomys nudicaudus</i>	213.0	224.0	228.5	42.0	26.5	1585.5	23, 238, 259, 307
<i>Tylomys watsoni</i>	242.0	224.5	190.8	36.8	24.0	145.5	23, 80, 215, 238, 262, 318
<i>Typhlomys cinereus</i>	24.6	81.7	100.9	19.5	-	1006.7	23, 58, 183, 215, 262
<i>Uranomys ruddi</i>	40.4	107.5	64.9	17.0	13.3	997.0	23, 64, 115, 215, 278, 318
<i>Uromys caudimaculatus</i>	622.3	267.7	304.0	54.8	25.0	918.3	23, 86, 87, 136, 269
<i>Vandeleuria oleracea</i>	13.3	75.0	111.3	17.8	13.0	1400.0	58, 89, 206, 215, 259
<i>Voadavlo gymnocoelius</i>	22.1	88.5	115.0	19.5	15.5	1526.7	93, 98, 102
<i>Wiedomys pyrrhorhinos</i>	46.7	114.0	182.5	-	-	378.7	23, 81, 187, 215
<i>Xenomys nelsoni</i>	130.0	161.0	156.5	-	-	300.3	5, 39, 215, 318
<i>Xeromys myoides</i>	45.7	117.3	115.3	40.0	20.0	7.0	23, 35, 166, 215, 215, 269, 318
<i>Zelotomys hildegardeae</i>	60.0	110.0	100.4	22.3	17.0	1299.3	23, 64, 139, 156, 159, 278, 281
<i>Zygodontomys brevicauda</i>	60.8	127.7	94.6	26.3	15.8	447.6	23, 80, 81, 238, 259
<i>Zyzomys argurus</i>	36.0	85.0	103.0	20.0	18.0	105.7	23, 166, 269, 318

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Table B.2. Full model parameters of the censored rate test for primary continental colonizations. Significant fit of the 2-rate parameter model over the 1-rate parameter model is based on a $\Delta \text{AICc} > 4$ units. σ^2 = evolution rate; Anc = ML ancestral state value; -Ln = negative log likelihood; Tail length= relative tail length; Proportions= relative appendage proportions based on PPCA.

	1-rate			2-rate									Model	Rate Shift		
	σ^2	AICc	-LnL	Foreground			Background			AICc	-LnL	$\Delta \sigma^2$ (F-B)	ΔAICc			
				Anc	σ^2	-LnL	Anc	σ^2	-LnL							
Africa																
Mass	0.02345	239.72	116.86	1.77487	0.02005	12.97	1.91628	0.02373	103.75	241.57	116.72	-0.00368	-1.77	1-rate	n.s.	
Proportions 1	0.00375	-258.65	-132.33	-0.44935	0.00267	-10.09	-0.00919	0.00385	-122.85	-257.72	-132.94	-0.00118	-0.84	1-rate	n.s.	
Proportions 2	0.00213	-408.92	-207.46	0.11089	0.00086	-22.55	-0.00629	0.00224	-188.49	-413.94	-211.05	-0.00138	5.11	2-rate	slowdown	
Tail length	0.01263	55.91	24.96	0.84972	0.01131	6.38	0.74572	0.01274	18.50	57.90	24.88	-0.00143	-1.91	1-rate	n.s.	
Elevation	0.20158	878.70	436.35	1.44860	0.26239	42.54	1.21622	0.19647	393.33	879.88	435.87	0.06592	-1.09	1-rate	n.s.	
Madagascar																
Mass	0.02346	236.61	115.31	2.00850	0.02510	6.69	1.89288	0.02340	108.61	238.72	115.29	0.00170	-2.03	1-rate	n.s.	
Proportions 1	0.00374	-262.58	-134.29	-0.63278	0.00084	-8.63	0.01380	0.00384	-128.93	-266.96	-137.56	-0.00300	4.48	2-rate	slowdown	
Proportions 2	0.00213	-412.20	-209.10	0.06924	0.00134	-6.53	0.00476	0.00215	-202.99	-410.89	-209.52	-0.00081	-1.22	1-rate	n.s.	
Tail length	0.01262	52.57	23.28	1.05248	0.00371	-2.87	0.72865	0.01293	23.52	49.45	20.65	-0.00922	3.21	2-rate	n.s.	
Elevation	0.20182	875.84	434.92	1.06978	0.04972	10.10	1.27602	0.20712	421.53	871.41	431.64	-0.15740	4.52	2-rate	slowdown	
North America																
Mass	0.02350	237.71	115.86	1.77339	0.01755	8.80	1.91248	0.02422	106.38	238.49	115.18	-0.00667	-0.69	1-rate	n.s.	
Proportions 1	0.00372	-263.20	-134.60	-0.58649	0.00235	-18.53	0.01529	0.00388	-117.40	-263.71	-135.93	-0.00153	0.60	2-rate	n.s.	
Proportions 2	0.00213	-411.43	-208.71	0.10561	0.00035	-44.43	0.00170	0.00233	-178.04	-436.77	-222.46	-0.00198	25.43	2-rate	slowdown	
Tail length	0.01260	52.68	23.34	0.94249	0.00888	-2.10	0.72617	0.01305	24.48	52.90	22.38	-0.00417	-0.14	1-rate	n.s.	
Elevation	0.20181	876.39	435.20	1.03372	0.16258	44.42	1.27361	0.20655	390.40	877.76	434.81	-0.04397	-1.29	1-rate	n.s.	
South America																
Mass	0.02345	237.35	115.68	1.78682	0.01503	-0.38	1.91000	0.02605	112.40	232.19	112.02	-0.01102	5.25	2-rate	slowdown	
Proportions 1	0.00374	-261.53	-133.77	-0.52755	0.00441	-38.69	0.00026	0.00353	-95.71	-260.63	-134.39	0.00088	-0.81	1-rate	n.s.	
Proportions 2	0.00212	-411.92	-208.96	0.14969	0.00229	-59.58	-0.00236	0.00207	-149.51	-410.03	-209.09	0.00023	-1.79	1-rate	n.s.	
Tail length	0.01266	54.22	24.11	0.88513	0.02023	10.02	0.73995	0.01033	7.36	42.91	17.38	0.00990	11.40	2-rate	speedup	
Elevation	0.20160	876.28	435.14	1.90738	0.32326	107.02	1.24098	0.16408	321.28	864.73	428.30	0.15918	11.64	2-rate	speedup	
Sahul																
Mass	0.02339	235.23	114.61	2.11678	0.06787	22.14	1.90863	0.01876	77.72	207.87	99.86	0.04911	27.45	2-rate	speedup	
Proportions 1	0.00374	-262.72	-134.36	-0.65257	0.00142	-27.58	0.00054	0.00399	-111.35	-269.72	-138.94	-0.00256	7.09	2-rate	slowdown	
Proportions 2	0.00212	-413.89	-209.94	-0.00826	0.00632	-8.96	0.00057	0.00168	-215.12	-440.00	-224.08	0.00464	26.20	2-rate	speedup	
Tail length	0.01257	50.83	22.41	1.18077	0.01018	-4.42	0.73703	0.01282	26.52	52.33	22.10	-0.00264	-1.42	1-rate	n.s.	
Elevation	0.20185	875.30	434.65	1.38341	0.15732	33.91	1.25711	0.20649	400.30	876.57	434.22	-0.04917	-1.18	1-rate	n.s.	
Southeast Asia																
Mass	0.02322	237.23	115.62	2.13605	0.02374	10.50	1.89768	0.02317	105.11	239.36	115.61	0.00057	-2.05	1-rate	n.s.	
Proportions 1	0.00367	-264.01	-135.00	-0.63199	0.00336	-13.11	0.00322	0.00370	-121.94	-261.95	-135.05	-0.00034	-1.97	1-rate	n.s.	
Proportions 2	0.00213	-408.75	-207.37	0.03054	0.00076	-30.26	0.00130	0.00226	-181.81	-415.98	-212.07	-0.00150	7.33	2-rate	slowdown	
Tail length	0.01253	53.92	23.96	0.99110	0.01084	-0.48	0.73899	0.01270	24.29	55.75	23.81	-0.00187	-1.75	1-rate	n.s.	
Elevation	0.20156	879.02	436.51	1.09469	0.10761	31.66	1.25718	0.21134	402.43	876.32	434.09	-0.10373	2.77	2-rate	n.s.	

Table B.3. Full model parameters of the censored rate test for nodes with increased phylogenetic diversification. See Table B.2 legend for more information.

	1-rate			2-rate									Model	Rate Shift		
	σ^2	AICc	-lnL	Foreground			Background			AICc	-lnL	$\Delta \sigma^2$ (F-B)	Δ AICc			
				Anc	σ^2	-lnL	Anc	σ^2	-lnL							
Node D1																
Mass	0.02350	236.55	115.27	1.84328	0.02375	108.46	1.87397	0.01437	6.39	237.84	114.85	0.00938	-1.21	1-rate	n.s.	
Proportions 1	0.00372	-264.45	-135.23	-0.48651	0.00333	-149.87	0.19760	0.01817	5.82	-279.95	-144.05	-0.01484	15.59	2-rate	slowdown	
Proportions 2	0.00213	-412.59	-209.30	0.10065	0.00215	-205.84	-0.04267	0.00104	-4.18	-411.88	-210.02	0.00111	-0.62	1-rate	n.s.	
Tail length	0.01263	52.08	23.04	0.86243	0.01246	15.28	0.66313	0.01854	7.41	53.52	22.69	-0.00608	-1.36	1-rate	n.s.	
Elevation	0.20188	875.33	434.67	1.31250	0.20618	420.75	1.21241	0.04657	11.09	871.83	431.85	0.15961	3.59	2-rate	n.s.	
Node D2																
Mass	0.02287	229.18	111.59	2.04728	0.03792	-1.35	1.91007	0.02223	111.97	229.37	110.62	0.01569	-0.11	1-rate	n.s.	
Proportions 1	0.00375	-261.70	-133.85	-0.60346	0.00395	-10.74	0.00006	0.00374	-123.12	-259.56	-133.86	0.00021	-2.05	1-rate	n.s.	
Proportions 2	0.00213	-411.89	-208.94	0.03867	0.00106	-16.67	0.00003	0.00216	-193.18	-411.53	-209.84	-0.00111	-0.26	1-rate	n.s.	
Tail length	0.01262	52.53	23.26	1.01924	0.01342	-7.59	0.73798	0.01258	30.84	54.64	23.25	0.00084	-2.03	1-rate	n.s.	
Elevation	0.20162	875.67	434.83	1.08205	0.68926	16.05	1.25637	0.18109	410.86	861.95	426.90	0.50817	13.80	2-rate	n.s.	
Node D3																
Mass	0.02345	235.70	114.85	1.71827	0.01470	-2.30	1.91288	0.02620	113.10	229.73	110.80	-0.01150	6.05	2-rate	slowdown	
Proportions 1	0.00375	-262.36	-134.18	-0.52965	0.00440	-40.47	0.00053	0.00354	-94.32	-261.41	-134.78	0.00086	-0.85	1-rate	n.s.	
Proportions 2	0.00212	-413.34	-209.67	0.11716	0.00219	-63.12	0.00119	0.00210	-146.58	-411.23	-209.69	0.00010	-2.01	1-rate	n.s.	
Tail length	0.01262	51.55	22.77	0.92400	0.02090	10.18	0.73608	0.01002	4.42	37.33	14.60	0.01088	14.30	2-rate	speedup	
Elevation	0.20124	874.10	434.05	1.52813	0.31515	106.51	1.26762	0.16545	321.33	863.83	427.85	0.14970	10.35	2-rate	speedup	
Node D4																
Mass	0.02350	236.55	115.28	1.96035	0.03254	56.58	1.90436	0.01754	51.72	224.74	108.30	0.01500	11.89	2-rate	speedup	
Proportions 1	0.00374	-262.89	-134.44	-0.61159	0.00294	-71.30	0.01517	0.00426	-65.22	-264.88	-136.52	-0.00131	2.09	2-rate	n.s.	
Proportions 2	0.00213	-412.61	-209.30	0.03410	0.00302	-69.93	0.00362	0.00155	-146.68	-425.07	-216.61	0.00148	12.55	2-rate	speedup	
Tail length	0.01262	52.08	23.04	0.98753	0.01067	-9.19	0.72769	0.01391	31.01	51.76	21.81	-0.00324	0.40	2-rate	n.s.	
Elevation	0.20188	875.35	434.67	1.23607	0.16195	151.27	1.26051	0.22820	281.37	873.42	432.64	-0.06625	2.01	2-rate	n.s.	
Node D5																
Mass	0.02349	236.97	115.49	1.65302	0.00532	-5.03	1.91006	0.02399	117.63	233.35	112.61	-0.01867	3.70	2-rate	n.s.	
Proportions 1	0.00375	-261.98	-133.99	-0.19599	0.00182	-8.41	0.00008	0.00381	-126.33	-261.32	-134.74	-0.00199	-0.57	1-rate	n.s.	
Proportions 2	0.00213	-412.73	-209.37	0.16872	0.00063	-12.10	-0.00008	0.00217	-199.07	-414.18	-211.17	-0.00153	1.54	2-rate	n.s.	
Tail length	0.01263	52.60	23.30	0.44121	0.00343	-6.78	0.73786	0.01288	27.75	50.08	20.97	-0.00945	2.60	2-rate	n.s.	
Elevation	0.20168	875.58	434.79	1.64020	0.27232	10.72	1.25714	0.19972	423.87	877.31	434.58	0.07260	-1.64	1-rate	n.s.	
Node D6																
Mass	0.02345	236.25	115.13	2.10271	0.04012	7.62	1.90876	0.02165	104.57	232.51	112.19	0.01847	3.82	2-rate	n.s.	
Proportions 1	0.00374	-262.96	-134.48	-0.71708	0.00417	-18.48	0.00088	0.00370	-116.07	-260.95	-134.55	0.00047	-1.91	1-rate	n.s.	
Proportions 2	0.00213	-412.37	-209.19	0.03844	0.00110	-33.14	0.00016	0.00222	-178.11	-414.35	-211.25	-0.00112	2.07	2-rate	n.s.	
Tail length	0.01263	52.38	23.19	1.07128	0.01390	-7.76	0.73751	0.01249	30.87	54.37	23.12	0.00141	-1.90	1-rate	n.s.	
Elevation	0.20181	875.55	434.77	1.28509	0.32409	37.91	1.25508	0.18857	394.65	873.25	432.55	0.13551	2.38	2-rate	n.s.	
Node D7																
Mass	0.02347	236.49	115.25	1.67382	0.02459	0.82	1.90967	0.02345	114.42	238.62	115.24	0.00114	-2.05	1-rate	n.s.	
Proportions 1	0.00373	-263.49	-134.75	-0.65109	0.00073	-6.52	0.00037	0.00377	-129.90	-264.68	-136.42	-0.00305	1.28	2-rate	n.s.	
Proportions 2	0.00213	-412.14	-209.07	0.15395	0.00003	-12.77	0.00002	0.00216	-202.75	-422.89	-215.52	-0.00213	10.83	2-rate	slowdown	
Tail length	0.01262	52.14	23.07	0.99584	0.00818	-2.48	0.73782	0.01271	25.30	53.78	22.82	-0.00453	-1.56	1-rate	n.s.	
Elevation	0.20059	873.70	433.85	2.30346	0.15485	6.34	1.25486	0.20153	427.42	875.65	433.76	-0.04668	-1.87	1-rate	n.s.	

Table B.3-continued.

	1-rate			2-rate									Prefered Model	Rate Shift		
	σ^2	AICc	-lnL	Foreground			Background			AICc	-lnL	$\Delta \sigma^2$ (F-B)	Δ AICc			
				Anc	σ^2	-lnL	Anc	σ^2	-lnL							
Node D8																
Mass	0.02348	236.20	115.10	1.76555	0.02362	109.05	2.08570	0.01659	5.89	238.01	114.94	0.00703	-1.73	1-rate	n.s.	
Proportions 1	0.00361	-273.01	-139.51	-0.50816	0.00330	-151.25	0.63993	0.01943	4.50	-285.34	-146.75	-0.01613	12.42	2-rate	slowdown	
Proportions 2	0.00212	-413.89	-209.94	0.10393	0.00214	-207.77	-0.13078	0.00115	-2.57	-412.52	-210.33	0.00099	-1.28	1-rate	n.s.	
Tail length	0.01262	51.82	22.91	0.85396	0.01282	20.09	0.58727	0.00311	0.87	50.04	20.95	0.00970	1.86	2-rate	n.s.	
Elevation	0.20188	875.23	434.61	1.27724	0.20581	424.03	1.26973	0.01130	4.74	865.68	428.77	0.19451	9.63	2-rate	speedup	
Node D9																
Mass	0.02350	236.19	115.10	1.78584	0.01482	-1.38	1.91005	0.02628	112.45	230.28	111.07	-0.01145	5.99	2-rate	slowdown	
Proportions 1	0.00375	-262.46	-134.23	-0.52706	0.00434	-40.95	0.00082	0.00356	-93.78	-261.31	-134.73	0.00078	-1.06	1-rate	n.s.	
Proportions 2	0.00212	-413.38	-209.69	0.14943	0.00224	-62.76	-0.00160	0.00208	-147.00	-411.35	-209.75	0.00016	-1.93	1-rate	n.s.	
Tail length	0.01263	51.89	22.95	0.88524	0.02071	10.66	0.73742	0.01005	4.33	38.12	14.99	0.01066	13.86	2-rate	speedup	
Elevation	0.20157	874.50	434.25	1.90654	0.32099	109.33	1.24486	0.16336	318.03	862.84	427.35	0.15763	11.74	2-rate	speedup	

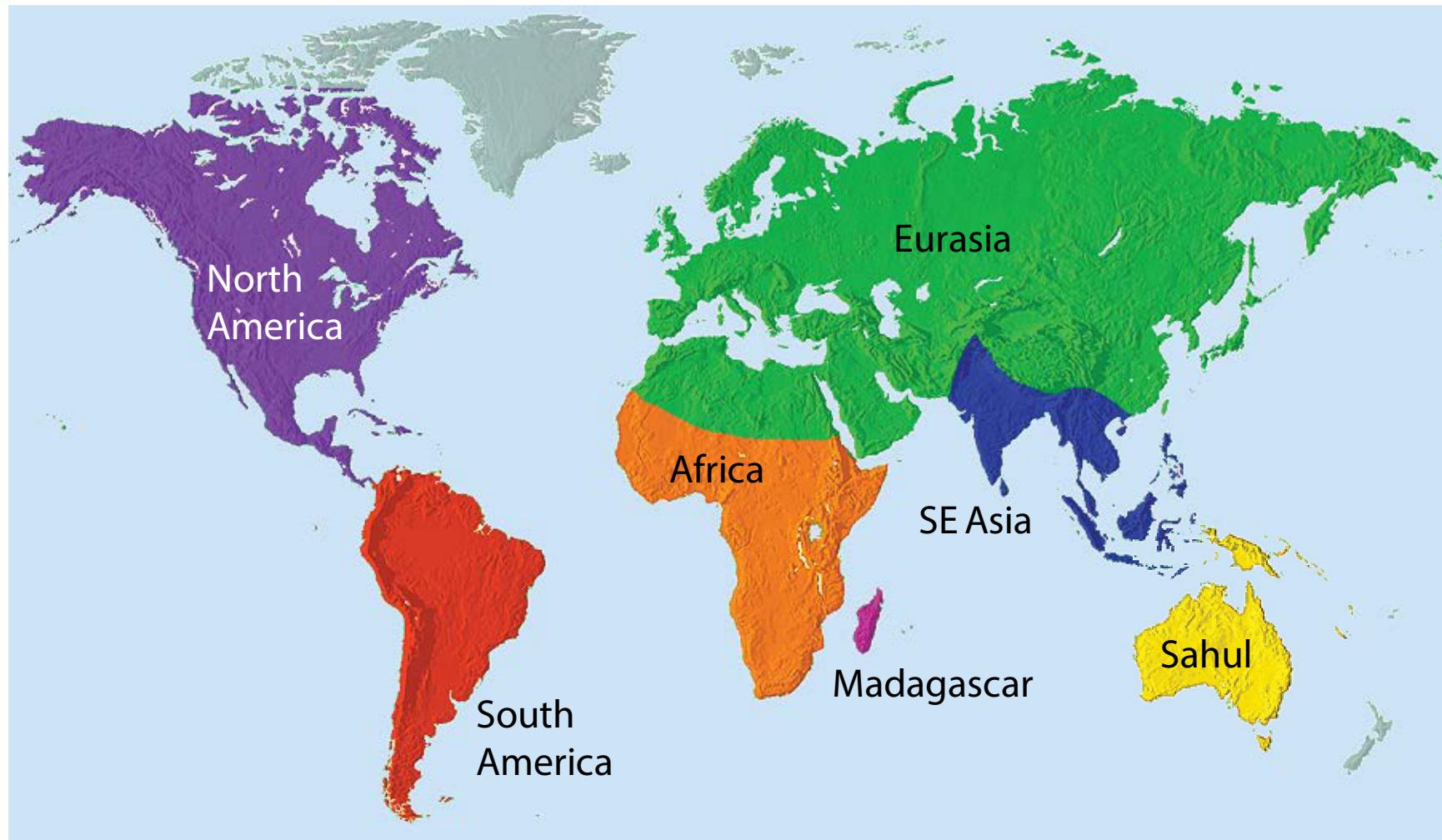


Figure B.1. Biogeographic regions used by Schenk et al. (2013) in ancestral-state estimations of primary continental colonizations. Figure from Schenk et al. (2013): Figure S1, available at <http://datadryad.org/resource/doi:10.5061/dryad.dc34q> [CC-BY].

APPENDIX C

SUPPORTING MATERIAL FOR CHAPTER 4

Table C.1. Ecological data for muroid rodents used in trait dependent diversification analyses. GC= general diet (F= faunivore, O= omnivore, H= herbivore); SC= specific diet (C= carnivore, I= insectivore, G= generalist herbivore, S= specialist herbivore); NS= nesting site (A= arboreal, F= fossorial, T= terrestrial); PA= period of activity (D= diurnal, N= nocturnal, O= other). See Table 4.2 for more information. Missing data are designated with (-).

	GC	SC	Diet description	NS	PA	References
<i>Abeomelomys sevia</i>	-	-	-	A	-	Flannery 1990; Nowak 1999
<i>Abrothrix andinus</i>	O	O	Consumes both animal material and plant material and diet varies seasonally	F	D	Eisenberg and Redford 2000
<i>Abrothrix jelskii</i>	O	O	Based on the contents of seven stomachs: 19% grass, 42% forbs, 4% seeds, and 35% insects	-	D	Eisenberg and Redford 2000
<i>Abrothrix longipilis</i>	O	O	Frugivorous, granivorous, insectivorous, and omnivorous; stomach content included berries, seeds, fern spores, insects, fungi, worms and slugs	F	O	Redford and Eisenberg 1992; Eisenberg and Redford 2000; Ricardo et al. 2003
<i>Acomys ignitus</i>	O	O	Consumes seeds, leaves, dry plant matter, invertebrates, and organic debris	-	-	Kingdon 1997
<i>Acomys russatus</i>	O	O	Consumes salty plants and land snails	T	N	Lee et al. 1998; Fishman 2000
<i>Aegialomys xanthaeolus</i>	H	S	Based on stomach content: 96.46 % was plants, 83.2% of which were fibrous portions of plants; fungal and animal material compose 3.6 % of stomach content	T	N	Guablocle et al. 2002; Zeballos and Weksler 2008
<i>Aethomys namaquensis</i>	H	G	Content of six stomachs: 60% foliage, 40% seeds; 89.9% of fecal content is herbage, 2.1% seeds, and 8% insects	A	N	Smithers 1983; Kerley et al. 1990; Korn 1992; Denys 1994; Monadjem 1997
<i>Akodon aerosus baliolus</i>	O	O	Feeds on insects, seeds, and vegetation	F	D	Dunnum et al. 2008c
<i>Akodon boliviensis</i>	F	I	Diet consists mostly of invertebrates, especially cleoptera larvae; based on the content of 26 stomachs: 8% grass, 6% forbes, 8% seeds, 78% insects	F	D	Eisenberg and Redford 2000
<i>Akodon kofordi</i>	-	-	-	T	-	Dunnum et al. 2008
<i>Akodon lutescens</i>	-	-	-	-	-	-
<i>Akodon mimus</i>	O	O	Omnivore that feeds on invertebrates	-	-	Dunnum et al. 2008
<i>Akodon torques</i>	F	I	Insectivorous, mostly consumes arthropod larvae	-	-	Kelt et al. 2007
<i>Andalgalomys pearsoni</i>	O	O	Feeds mostly on plants with a small amount of arthropods	-	-	MacDonald 2001
<i>Andinomys edax</i>	H	G	Diet includes green plants	T	N	Redford and Eisenberg 1992; Nowak 1999; Eisenberg and Redford 2000; Dunnum et al. 2008
<i>Anisomys imitator</i>	H	G	Based on stomach content, diet consists of hard shelled nuts, soft white pulp, and vegetable matter	T	-	Menziez and Dennis 1979; Flannery 1990
<i>Apodemus agrarius</i>	O	O	Diet consists of roots, grains, seeds, berries, nuts, insect larvae, mollusks, small vertebrates, and green plants	F	O	Bjarvall and Ullstrom 1986; Nowak Paradiso 1983; Hutchins et al. 2003
<i>Apodemus mystacinus</i>	O	O	Diet consists of grains, pine seeds, acorns, carob pods, snails, and insects	-	N	Qumsieh 1996
<i>Apodemus semotus</i>	O	O	Omnivorous, stomach content includes leaves, fruit, fungi, seeds, and animals remains	T	-	Lin and Shiraishi 1992
<i>Apodemus speciosus</i>	O	O	Stomach content includes: 45% seeds and 45% insects	T	-	Ota 1984; Kaneko and Ishii 2008
<i>Apodemus sylvaticus</i>	O	O	Based on content of 140 stomachs: 99.3% contained seeds; however, some studies show that the animal is omnivorous consuming insects, invertebrates, seeds, fruits, and fungi	F	N	Van Den Brink 1968; Bjarvall and Ullstrom 1986; Canova and Fasola 1991; Zubaid and Gorman 1991; Kingdon 1997; Abt and Bock 1998; Khammes and Aulagnier 2007
<i>Apomys datae</i>	O	O	Diet includes insects such as earthworms and seeds [diet for Apomys camiguinensis]	-	N	Heaney and Tabaranza 2006
<i>Apomys hylocoetes</i>	O	O	Feeds on seeds and invertebrates	-	N	Mearns 1905
<i>Archboldomys luzonensis</i>	F	I	Stomach content includes insects such as earthworms and other invertebrates	T	D	Musser 1982; Rickart and Heaney 1991; Nowak 1999; Samuels 2009
<i>Arvicathis neumanni</i>	H	G	Consumes seeds, leaves, and grass	-	D	Kingdon 1997; Nowak 1999
<i>Arvicathis niloticus</i>	H	G	Diet includes seeds, leaves, and grass	T	O	Delany 1975; Hutchins et al. 2003
<i>Arvicola terrestris</i>	O	O	Diet consists mostly of plants with some animal matter	F	O	Van Den Brink 1968; Flannery 1990; Samuels 2009
<i>Auliscomys sublimis</i>	H	G	Granivorous and frugivorous with green plant material [Auliscomys boliviensis]	F	N	Eisenberg 1992; Nowak 1999
<i>Baiomys musculus</i>	O	O	Stomach content: 50% insects, 25% seeds (such as Solanaceae), 25% green plant material	F	D	Reid 1997
<i>Bandicota bengalensis</i>	O	O	Content of 50 stomachs consists mostly of sugarcane and wheat with few insects	F	N	Smiet et al. 1980; Ismail 1987; Hussain 1989; Butt 1990; Francis 2008
<i>Batomys granti</i>	H	G	Diet consists of seeds and leaves	-	N	Thomas 1895; Nowak 1999
<i>Beamys hindei</i>	H	G	Consumes mostly seeds and fruit with limited animal matter	F	N	Kingdon 1974; 1997
<i>Berylmyns bowersi</i>	H	G	Diet consists mostly of fruits with few insects and snails	F	N	Archer 1999; Francis 2008
<i>Brachytarsomys albicauda</i>	H	G	Consumes fruit and seeds	A	N	Nowak 1999; Garbutt 2007
<i>Brachytarsomys betsileensis</i>	-	-	-	F	O	Garbutt 2007
<i>Brucepattersonius igniventris</i>	F	I	Stomach content analysis indicates that it feeds mainly on arthropods [Brucepattersonius soricinus]	-	-	Pinotti et al. 2011
<i>Bullimus bagobus</i>	H	G	Feeds on plant material	F	N	Mearns 1905; Nowak 1999
<i>Bunomys chrysocomus</i>	F	C	Feeds primarily on small vertebrates including frogs and lizards as well as some fruit and earthworms	T	-	Musser et al. 2008

Table C.1—continued.

	GC	SC	Diet description	NS	PA	References
<i>Calomys callosus</i>	O	O	Consumes fruits and animals	T	N	Kay and Madden 1997; Nowak 1999; Eisenberg and Redford 2000; Williams and Kay 2001
<i>Calomys lepidus</i>	-	-	-	-	-	-
<i>Calomys venustus</i>	O	O	Stomach content and cafeteria tests indicate that it is omnivorous although it becomes folivorous in spring and fall and granivorous in the summer	-	-	Castellarini et al. 1998
<i>Calomyscus baluchi</i>	O	O	Diet includes seeds, flowers, leaves, and animal matter	F	N	Nowak 1999
<i>Calomyscus sp</i>	-	-	-	-	-	-
<i>Cannomys badius</i>	H	S	Diet includes shrubs, grass, cereals, roots, seeds, and fruit	F	N	Nowak 1999; Francis 2008; Samuels 2009
<i>Carpomys phaeurus</i>	H	G	Granivorous	A	N	Thomas 1888; Rabor 1952; Nowak 1999
<i>Cerradomys subflavus</i>	H	G	Stomach content includes herbaceous vegetation and fruit	-	-	Eisenberg and Redford 2000
<i>Chelemys macrouryx</i>	O	O	Stomach content includes grass, seeds, fruit, fungi, arthropods, and earthworms	F	O	Redford and Eisenberg 1992; Ricardo et al. 2003
<i>Chinchillula sahamae</i>	H	G	Herbivorous; stomach content includes leaves, seeds, and few insects	T	N	Nowak 1999; Eisenberg and Redford 2000; Dunnum et al. 2008
<i>Chionomys nivalis</i>	H	S	Herbivorous; content of 32 stomachs: 94% green vegetable matter (e.g. grass, shrubs, and berries) and 6% insects	F	O	Kryštufek and Amori 2008; Metcheva et al. 2008
<i>Chromomys chiropus</i>	-	-	-	A	N	Nowak 1999
<i>Chiropodomys gliroides</i>	H	S	Herbivorous; consumes roots, grains, and fruits	A	N	Nowak 1999; Lunde et al. 2008
<i>Chiruromys vates</i>	H	-	Largely herbivorous diet	A	-	Nowak 1999; Smales 2011
<i>Chrotomys gonzalezi</i>	F	I	Stomach content and feeding trials indicated the consumption of arthropods including earthworms, insects, and other invertebrates	F	O	Rickart and Heaney 1991
<i>Clethrionomys gapperi</i>	O	O	Diet includes green foliage, seeds, fungi, herbage, berries, bark, nuts, berries, shrubs, roots, insects, and invertebrates	F	N	Cockrum 1982; Armstrong 1987; Jones and Birney 1988
<i>Colomys gosling</i>	F	C	Diet includes invertebrates such as aquatic insects, worms, slugs, crustaceans, small vertebrates, and occasionally consumes vegetable matter	F	N	Kingdon 1974; Delany 1975; Kingdon 1997; Michaux et al. 2007; Samuels 2009
<i>Conilurus penicillatus</i>	H	G	Herbivorous; fecal content includes 68% seeds, 21%, leaves, 8% stem, 2% insects	A	N	Flannery 1990; 1995; Firth et al. 2005
<i>Crateromys heaneyi</i>	H	G	Diet includes bananas, guavas, corn, and leaves	A	N	Gonzales and Kennedy 1996; Nowak 1999
<i>Cricetomys gambianus</i>	O	O	Omnivorous, stomach content consist mostly of vegetable matter with few insects including termites	T	N	Smithers 1983
<i>Cricetus griseus</i>	H	-	Diet includes shoots, millet seeds, soybeans, peas, grains, and legumes [Genus: Cricetus]	F	N	Nowak 1999
<i>Cricetomys migratorius</i>	H	S	Mainly herbivorous, diet includes roots, shoots, and seeds, and with occasional insects and consumes frogs and jerboas in captivity	F	N	Van Den Brink 1968; Nowak 1999; Kryštufek et al. 2008
<i>Cricetus cricetus</i>	O	O	Consumes corn, maize, fodder, beets, potatoes, fruit, vegetables, insects, and small animals	F	N	Van Den Brink 1968; Bjarvall and Ullstrom 1986
<i>Crinomys melanopus</i>	F	I	Diet includes insects and other arthropods	T	D	Thomas 1907; Nowak 1999
<i>Dactomys millardi</i>	-	-	-	T	N	Francis 2008
<i>Dasyomys incomitus</i>	O	O	Diet includes stems, fruit of semi-aquatic grasses, and reeds, stomach contain insect remains	T	D	Smithers 1983
<i>Delanymys brooksi</i>	H	G	Diet includes mostly mainly sedge seeds, with some grass and fruit	T	N	Kingdon 1997; Nowak 1999
<i>Delomys dorsalis</i>	O	O	Omnivorous, they feed on fruits, invertebrates, and other plant material	-	N	Emmons 1997; Vieira et al. 2006
<i>Dendromus insignis</i>	O	O	Omnivorous and/or insectivorous, stomach content includes seeds, berries, and arthropods also consumes grass	A	O	Kingdon 1997; Kingdon et al. 2013
<i>Dendromus mesomelas</i>	O	O	Stomach content consists of grass seeds and insects	A	N	Smithers 1983; Cameron 1996
<i>Dendromus nyasae</i>	O	O	Omnivorous or insectivorous, content of 5 stomachs include both seeds and insects, other stomachs contain only insects	A	-	Kingdon et al. 2013
<i>Deomys ferrugineus</i>	F	I	Diet includes insects, crustaceans, slugs, and occasionally vegetable matter and fallen fruits	T	N	Kingdon 1974; 1997
<i>Desmodillus auricularis</i>	O	O	Diet consists of seeds, grass, shrubs, grain, insects, locusts, and grasshoppers	T	N	Roberts 1951; Kingdon 1997; Nowak 1999; Samuels 2009
<i>Diplothrix legata</i>	-	-	-	-	-	-
<i>Dipodillus dasyurus</i>	H	G	Consumes seeds, succulent plants, and occasionally insects	F	N	Harrison 1956; Qumsiyeh 1996
<i>Elurillus minor</i>	H	G	Feeds on coconut, seeds, and grains	A	O	Goodman and Benstead 2003; Garbutt 2007
<i>Elurillus tanala</i>	-	-	-	A	-	Garbutt 2007
<i>Euneomys chinchilloides</i>	H	G	Herbivorous	F	-	Redford and Eisenberg 1992
<i>Geoxus valdivianus</i>	F	I	Stomach contains earthworms, grubs, slugs, beetle larvae, and other arthropods	F	O	Nowak 1999
<i>Gerbillurus paeba</i>	O	O	Diet consists seeds, grass, stems, and arthropods, based on information from stomach content, roughly equal amount of animal and vegetable matter consumed varying depending on location	F	N	Roberts 1951; Perrin et al. 1999
<i>Gerbillurus vallinus</i>	O	O	Diet includes seeds and insects	F	N	Roberts 1951; Smithers 1983; Kingdon 1997
<i>Gerbillus gerbillus</i>	H	G	Consumes mostly seeds with some leaves, buds, and fruit	F	N	Yunker and Guirguis 1969; Osborn and Helmy 1980
<i>Gerbillus nanus</i>	H	G	Granivorous	F	N	Kam et al. 2010; Azizi et al. 2011; Kam et al. 2011
<i>Golunda ellioti</i>	H	S	Consumes roots, stems, grass, and buds	T	D	Nowak 1999
<i>Grammomys dolichurus</i>	H	G	Consumes mostly fruits, stems, nuts, flowers with some invertebrates and insects, a study of the contents of 20 stomachs indicated that its diet consisted of 90% green vegetable matter	A	N	Kingdon 1974; Smithers 1983; Cameron 1996; Wirminghaus and Perrin 1992; Kingdon et al. 2013
<i>Grammomys ibeanus</i>	H	G	Consumes mostly fruits, seeds, stems, and other vegetable matter and on occasion insects [Genus: Grammomys]	A	N	Kingdon 1997
<i>Grammomys macmillani</i>	H	G	Consumes mostly fruits, seeds, stems, and other vegetable matter and on occasion insects [Genus: Grammomys]	A	N	Kingdon 1997; Dieterlen 2008
<i>Graomys centralis</i>	-	-	-	-	-	-
<i>Graomys griseoflavus</i>	H	G	Herbivorous	A	-	Eisenberg and Redford 2000
<i>Gymnuromys roberti</i>	H	G	Feeds on seeds and fruit	F	N	Nowak 1999; Garbutt 2007
<i>Habromys lepturus</i>	-	-	-	-	-	-
<i>Heimyscus fumosus</i>	-	-	-	-	-	-
<i>Hodomys allenii</i>	O	O	Feeds on seeds and land crabs	F	-	Genoways and Birney 1974
<i>Holochilus sciurus</i>	O	O	Feeds on stems, seeds, and snails	T	N	Eisenberg and Redford 2000; Barreto and García-Rangel 2005

Table C.1—continued.

	GC	SC	Diet description	NS	PA	References
<i>Hybomys univittatus</i>	O	O	Content of 31 stomachs includes fruit, stems, shoots, roots, leaves, and insects such as ants and termites	T	D	Delany and Neal 1966; Kingdon 1974; Delany 1975; Kingdon 1984
<i>Hydromys chrysogaster</i>	F	C	Based on stomach and caecum contents as well as observations, it feeds on large aquatic insects, fish, crayfish, mussels, frogs, lizards, small mammals, carrion, birds, spiders, frogs, tortoise, eggs, and some plant material	F	N	Woollard et al. 1978; Strahan 1983; Flannery 1990; Nowak 1999; Hutchins 2003
<i>Hylomyscus parvus</i>	O	O	Feeds on fruits, seeds, and insects	A	-	Kingdon 1997; Kingdon et al. 2013
<i>Hylomyscus stella</i>	O	O	Omnivore	A	N	Happold 1987; Chapman and Chapman 1999; Kingdon et al. 2013
<i>Hyomys goliath</i>	H	G	Feeds on shoots, palms, and nuts	F	-	Menzies and Dennis 1979; Flannery 1990
<i>Hypogeomys antimena</i>	O	O	Feeds on fruit, leaves, seeds, roots, and invertebrates (in captivity)	F	N	Nowak 1999; Garbutt 2007
<i>Irenomys tarsalis</i>	H	G	Feeds on fruits, seeds, and green vegetation	T	N	Redford and Eisenberg 1992; Nowak 1999; Eisenberg and Redford 2000
<i>Isthmomyss pirrensis</i>	-	-	-	F	N	Reid 1997
<i>Juliomys pictipes</i>	-	-	-	A	N	Eisenberg and Redford 2000; Geise and Pardinas 2008; Oliveira-Santos et al. 2008
<i>Kunisia tomentosus</i>	H	G	Consumes leaves and seeds	F	N	Kay and Madden 1997; Eisenberg and Redford 2000; Williams and Kay 2001
<i>Lasiopodomys mandarinus</i>	H	S	Feeds on roots and sometimes green plants and herbs	F	-	Nowak 1999
<i>Leggadina forresti</i>	O	O	Omnivore	F	N	Dickman 1993; Murray et al. 1999
<i>Lemmus sibiricus</i>	H	S	Feeds on sedges, grass, moss, shrubs, and leaves	F	-	Barkley et al. 1980; Batzli 1993; Wilson and Ruff 1999; Tsytulina et al. 2008
<i>Lemniscomys barbarus</i>	O	O	Feeds on leaves, roots, fruit, seeds, stems, and insects	F	D	Shortridge 1934; Smithers 1983; Kingdon 1984; Stoetzel et al. 2011
<i>Lemniscomys striatus</i>	O	O	Omnivore	F	D	Delany 1975; Happold 1987; Cameron 1996; Hoffmann and Klings 2001
<i>Lenoxus apicalis</i>	-	-	-	-	-	-
<i>Leopoldamys sabanus</i>	O	O	Feeds on insects, snails, fruit, and other vegetable matter	T	N	Delany and Neal 1966; Lim 1970; Francis 2008
<i>Leporillus conditor</i>	H	S	Feeds on green plant material	F	N	Watts and Eves 1976; Copley 1999
<i>Leptomyss elegans</i>	F	C	Feeds on insects and invertebrates	T	-	Flannery 1990; 1995; Nowak 1999
<i>Limnomys sibianus</i>	H	G	Consumes fruit, seeds, and infrequently on invertebrates	A	N	Mearns 1904; Nowak 1999
<i>Lophiomys imhausi</i>	O	O	Feeds on leaves, shoots, fruits, shoots, and insects	T	N	Kingdon 1997; Nowak 1999
<i>Lophuromys flavopunctatus</i>	O	O	Omnivorous and feeds on invertebrates such as ants as well as carrion and plant material	T	D	Cameron 1996; Kingdon 1997; Dieterlen 2008
<i>Lophuromys sikapusi</i>	O	O	Both insectivorous and omnivorous and feeds on invertebrates such as ants as well as carrion and plant material	T	O	Kingdon 1997; Boitani 2008
<i>Lophuromys zena</i>	O	O	Omnivorous and feeds on invertebrates such as ants as well as carrion and plant material	T	O	Kingdon 1997; Dieterlen 2008
<i>Lorentzimys nouhuysi</i>	O	O	Omnivorous, consumes plants, fungi, and insects	A	N	Flannery 1990; 1995; Nowak 1999; Sillito 2013
<i>Loxodontomys micropus</i>	H	G	Content of stomach include: green vegetation, fungi, blossoms, grass, seeds, and fruit	T	N	Nowak 1999; Eisenberg and Redford 2000
<i>Macrotarsomys bastardi</i>	H	S	Feeds on seeds, fruits, roots, and stems	F	N	Garbutt 2007
<i>Macruromys major</i>	-	-	-	F	N	Nowak 1999; Helgen et al. 2008
<i>Malacomys longipes</i>	O	O	Content of 30 stomachs comprise animal and vegetable matter in roughly equal proportions and include fruits, seeds, nuts, roots, termites, crickets, slugs, snails, caterpillars, crabs, and toads	T	N	Kingdon 1984; Happold 1987
<i>Malacothrix typica</i>	H	G	Diet includes seeds and green plant parts	F	N	Smithers 1983; Kingdon 1997
<i>Mallomys rothschildi</i>	H	G	Consumes shoots of bamboo and wild ginger as well as leaves	A	N	Menzies and Dennis 1979; Flannery 1990; 1995; Helgen and Opiang 2011; Sillito 2013
<i>Mammelomys lanosus</i>	-	-	-	-	-	-
<i>Margaretamyss elegans</i>	F	I	Insectivore	A	-	Musser 1982; Nowak 1999
<i>Mastacomys fuscus</i>	H	S	Consumes grass, leaves, shrubs, seeds, fungi, and bark	-	N	Bubela et al. 1991; Dyck and Strahan 2006
<i>Mastomys erythroleucus</i>	O	O	Content of 41 stomachs includes grass, shoots, seeds, grass, and fruits, wild herbs, and arthropods	F	-	Logan et al. 1993; Gebreslassie et al. 2004
<i>Mastomys hildebrandti</i>	O	O	Consumes fruits, seeds, and invertebrates	F	N	Cameron 1996; Kingdon 1997; Morris 2009
<i>Maxomys bartelsii</i>	-	-	-	-	-	-
<i>Maxomys surifer</i>	O	O	Feeds on roots, fallen fruit, insects, and small vertebrates	T	N	Francis 2008; Smith and Xie 2008
<i>Mayeromys ellermani</i>	F	I	Insectivorous-carnivore	-	N	Flannery 1995; Wilson and Reeder 2005; Wolff and Sherman 2008
<i>Megadontomys thomasi</i>	H	G	Berries	-	-	Nowak 1999
<i>Melanomys caliginosus</i>	O	O	Omnivorous, consumes insects, fruit, seeds, and shoots	T	D	Reid 1997; Eisenberg and Redford 2000
<i>Melasmotherix naso</i>	F	I	Mainly consumes invertebrates including earthworms and insect larvae	T	D	Landry 1970; Musser 1982; Nowak 1999
<i>Melomys cervinipes</i>	H	G	Green leaves with smaller amount of fruit	A	N	Wood 1971; Freeland 1972; Fimbel et al. 2011
<i>Melomys rufescens</i>	H	G	>90% of diet consists of fruit	A	-	McPhee 1988; Flannery 1990
<i>Meriones shawi</i>	H	G	Diet consists of seeds, grains, stems, leaves, and bulbs	F	N	Greaves 1989; Engeman et al. 1997; Kingdon 1997
<i>Meriones unguiculatus</i>	H	G	Feeds primarily on seeds with some fruits, grass, and stems	F	O	Chen 2001; Wang et al. 2003; Batsaikhan and Tsytulina 2008
<i>Mesembriomys gouldii</i>	H	G	Based on fecal samples, large seeds and fruit are a large portion of their diet, it also consumes some insects, grass, and invertebrates	A	N	Friend 1987; Nowak 1999
<i>Mesocricetus auratus</i>	O	O	Omnivorous, consumes seeds, nuts, and insects such as ants, flies, cockroaches, and wasps	F	N	Qumsiyeh 1996; Burnie and Wilson 2005; Yigit and Kryštufek 2008
<i>Micromys minutus</i>	O	O	Omnivorous, fecal content includes seeds and fruit; in addition it consumes fungus, moss, roots, buds, invertebrates, green vegetation, and eggs	T	O	Van Den Brink 1968; Bjärwall and Ullström 1986; Dickman 1986; Nowak 1999; Hutchins et al. 2003; Francis 2008
<i>Microryzomys minutus</i>	H	G	Feeds on seeds and other vegetation	A	-	Pascual 1994; Eisenberg and Redford 2000; Gómez-Laverde and Delgado 2008
<i>Microtus arvalis</i>	H	S	Mainly consumes green parts of grass and herbaceous plants	T	N	Van Den Brink 1968; Amori et al. 2008
<i>Microtus californicus</i>	H	S	Herbivorous, most diet consists of grass and roots with a few sedges, fruits, and forbs	F	D	Ingles 1965; Burt and Grossenheimer 1980; Peronne 2002
<i>Microtus chrotorrhinus</i>	H	S	Feeds on stems, leaves, shrubs, forbs, berries, grass, mushrooms, roots, fungi, and foliage; rarely eats insects	F	O	Jones and Birney 1988; Linzey et al. 2008
<i>Microtus guentheri</i>	H	S	Stomach contents in the field included plant material and seeds, in captivity they preferred to eat fresh plants	F	N	Van Den Brink 1968; Colak et al. 1998

Table C.1—continued.

	GC	SC	Diet description	NS	PA	References
<i>Microtus kikuchii</i>	H	S	(grass) over seeds	F	-	Yeh et al. 2012
<i>Microtus montanus</i>	H	S	Herbivorous, consumes leaves and its major food source is the Yushan cane (woody bamboo)	T	N	Armstrong 1987
<i>Microtus pennsylvanicus</i>	H	S	Most of diet consists of grass and abrasive foliage supplemented with a variety of other plants	T	O	Jones and Birney 1988
<i>Microtus richardsoni</i>	H	S	Diet consists mostly of vegetable matter including grass, roots, and seeds	F	O	Ludwig 1984; Young 1999
<i>Millardia kathleneae</i>	H	G	Diet consists mostly of leaves and stems of forbs, grass, sedges, and willows as well as some seeds and insects	F	N	Nowak 1999; Francis 2008
<i>Monticolomys koopmani</i>	H	G	Grain, seeds, and swamp vegetation	A	N	Carleton and Goodman 1996; Goodman et al. 1999; 2003; Garbutt 2007
<i>Mus booduga</i>	O	O	Consumes fruits and seeds	F	N	Kingdon 1997; Singh et al. 2009
<i>Mus cervicolor</i>	O	O	Omnivorous	T	N	Francis 2008
<i>Mus cookii</i>	O	O	Feeds on seeds and insects	-	N	Kingdon 1997; Francis 2008
<i>Mus musculus</i>	O	O	Omnivorous	T	N	Watts and Braithwaite 1978; Canova and Fasola 1993; Reid 1997; Nowak 1999; Eisenberg and Redford 2000; Hutchins et al. 2003
<i>Mus pahari</i>	O	O	Consumes leaves, stems, seeds, roots, insects, and grains	T	N	Kingdon 1997; Francis 2008; Smith et al. 2010
<i>Mus terricolor</i>	O	O	Omnivorous	F	N	Kingdon 1997; Basu et al. 2012
<i>Myomys dybowskii</i>	H	S	Herbivorous and consumes grass stems and leaves	T	D	Nowak 1999; Kingdon et al. 2013
<i>Myomyscus brockmani</i>	O	O	Seeds and insects [Myomyscus verreauxii]	T	N	Skinner and Chimimba 2005; Kingdon et al. 2013
<i>Myospalax aspalax</i>	H	S	Mostly consumes roots in addition to wheatgrass, dandelion, bluegrass, and wormwood	F	O	Bannikov 1953; Timin et al. 2002; Poor 2005
<i>Myospalax albicaudatus</i>	O	O	Feeds on seeds, insects, and green vegetable matter	F	N	Smithers 1983; Kingdon 1997; Nowak 1999; Coetze and Monadjem 2008
<i>Nanospalax ehrenbergi</i>	H	S	Eats roots, bulbs, tubers, rhizomes, grass, seeds, and rarely insects	F	N	Kingdon 1997; Nowak 1999
<i>Neacomys minutus</i>	-	-	-	-	-	-
<i>Neacomys spinosus</i>	O	O	Feeds on seeds, insects, and fruit	A	N	Allen 1916; Eisenberg and Redford 1999; Patton et al. 2008
<i>Necromys amoenus</i>	H	G	Granivorous [Necromys obscurus and Necromys lasiurus]	F	O	Raval 2004; Vadell et al. 2011
<i>Nectomys apicalis</i>	O	O	Diet includes arthropods, crabs, and other invertebrates as well as some fruit and fungi	T	N	Emmons and Feer 1997
<i>Nectomys squamipes</i>	O	O	Omnivorous consuming both animal and plant matter including fruits, fungi, seeds, invertebrates, and vertebrates	T	N	Eisenberg 1989; Kay and Madden 1997; Nowak 1999; Williams and Kay 2001; Eisenberg and Redford 2000
<i>Neodon irene</i>	H	-	Herbivorous [Neodon juldaschi]	T	D	Molur 2008
<i>Neotoma bryanti</i>	H	G	Mostly creosote bush	T	N	Alvarez-Castañeda and Yensen 1999; Kohl et al. 2011
<i>Neotoma cinerea</i>	H	G	Generalist herbivore that consumes a variety of plant matter	T	N	Armstrong 1987; Topping et al. 1999; Samuels 2009
<i>Neotoma devia</i>	H	G	Prefers cholla cactus, Mormon tea, wolfberry, creosote bush, and mesquite	T	N	Burt and Grossenheimer 1980; Feldhamer et al. 2003; Reid 2006
<i>Neotoma floridana</i>	H	G	Consumes leaves, seeds, and fruit	A	N	Palmer 1957; Jones and Birney 1988
<i>Neotomodon alstoni</i>	O	O	Omnivore, consumes insects such as monarch butterflies and vegetation including seeds	F	N	Glendinning and Brower 1990; Nowak 1999; Huereca 2002
<i>Neotomys eriosus</i>	H	-	Herbivorous	T	N	Nowak 1999; Eisenberg and Redford 2000
<i>Nephelomys keaysi</i>	O	O	Omnivorous [Nephelomys albicularis, Nephelomys caracolus, and Nephelomys meridensis]	T	N	Aguilera et al. 2008a; 2008b; Reid et al. 2008
<i>Nephelomys livipes</i>	O	O	Omnivorous [Nephelomys albicularis, Nephelomys caracolus, and Nephelomys meridensis]	T	N	Aguilera et al. 2008a; 2008b; Reid et al. 2008
<i>Nesomys rufus</i>	H	G	Mainly consumes seeds and fruits	F	D	Garbutt 2007
<i>Niviventer confucianus</i>	H	G	Granivorous	-	N	Francis 2008; Huaiqiang et al. 2012
<i>Niviventer cremoriventer</i>	O	O	Omnivorous, feeds on fruits, seeds, and insects	T	N	Wells and Bagchi 2005; Francis 2008; Wells et al. 2009
<i>Niviventer culteratus</i>	-	-	-	-	-	-
<i>Niviventer excelsior</i>	-	-	-	-	-	-
<i>Notomys edwardsii</i>	F	I	Insectivorous but sometimes consumes plant material	F	-	Pearson 1984; Redford and Eisenberg 1992
<i>Notomys fuscus</i>	H	G	Diet consists of seeds, berries, leaves, green plants, and occasionally insects	F	N	Honaki 1982; Grizzimek 1990; Nowak 1991; Moseby and Menhorst 2008
<i>Nyctomyssumichrasti</i>	H	G	Mainly herbivorous and feeds on seeds, fruit, figs, avocados, borage, also feeds on small amounts of insects including moths	A	N	Eisenberg 1989; Reid 1997; Nowak 1999; Hunt et al. 2004
<i>Ochrotomys nutalli</i>	O	O	Consumes seeds and invertebrates	A	N	Jones and Birney 1988; Nowak 1999; Linzey and Hammerson 2008
<i>Oecomys bicolor</i>	H	G	Consumes unripe fruits and seeds	A	N	Eisenberg and Redford 2000; Lobova et al. 2003; Reid 2009; Castellanos and Stevenson 2011
<i>Oecomys concolor</i>	H	-	Herbivore	A	-	Eisenberg and Redford 2000; Schloss et al. 2012
<i>Oecomys superans</i>	-	-	-	A	N	Weksler and Tirira 2008
<i>Oenomys hypoxanthus</i>	O	O	Omnivorous, consumes green vegetation, insects, millets, and other crops	A	N	Kingdon 1974; Delany 1975; Happold 1987; Cameron 1996; Nowak 1999
<i>Oligoryzomys fulvescens</i>	O	O	Diet consists mostly of seeds with few insects	T	N	Reid 1997; Eisenberg and Redford 2000
<i>Oligoryzomys longicaudatus</i>	O	O	Granivorous and feeds on flowers, pollen, foliage, also consumes some arthropods and insects	A	O	Eisenberg and Redford 2000; Ricardo et al. 2003
<i>Oligoryzomys microtis</i>	O	O	Consumes seeds, fruits, and insects	T	N	Nowak 1999
<i>Ondatra zibethicus</i>	O	O	Consumes shoots and roots of: grasses, sedges, bulrushes, horsetails, cattails, water lilies, and forbs as well as crabs, snails, crayfish, mussels, fish, frogs, salamanders, and carrion	F	N	Cockrum 1982; Armstrong 1987; Jones and Birney 1988; Flannery 1990; Nowak 1999
<i>Onychomys leucogaster</i>	F	C	Carnivorous with up to 80% of diet composed of animal matter including insects, invertebrates, carrion, vertebrates, as well as small amounts of forbes, grasses, sedges, seeds, and grains	F	N	Jones and Birney 1988; Samuels 2009
<i>Oryzomys couesi</i>	O	O	Consumes green plant material, seeds, and insects including ants, beetles and caterpillars	T	N	Eisenberg 1989; Reid 1997; Linzey et al. 2008
<i>Oryzomys palustris</i>	O	O	Omnivorous and consumes seeds, green vegetation, fungi, invertebrates, fish, birds, eggs, turtles, carrion, and insects	T	N	Negus et al. 1961; Sharp 1967; Kincaid and Cameron 1982; Jones and Birney 1988; Kays and Wilson 2002
<i>Osgoodomys banderanus</i>	O	O	Consumes seeds, fruits, and insects	A	N	Fa and Morales 1991; Nowak 1999
<i>Otomys anchietae</i>	H	S	Based on stomach content it is a herbivore that consumes grass, seeds, and plant material; it also consumes shoots of reed and thistle	T	D	Smithers 1983
<i>Otomys angoniensis</i>	H	S	Herbivorous and consumes succulent stems and rhizomes of grass and fine reeds	T	D	Smithers 1983; Korn 1992

Table C.1—continued.

	GC	SC	Diet description	NS	PA	References
<i>Ototomys denti</i>	H	S	Consumes grass, reed, herbs, bark, and occasionally roots and seeds	-	-	Kingdon 1997
<i>Ototylomys phyllotis</i>	H	G	Consumes fruits, leaves, madders, and seeds	A	N	Reid 1997; Nowak 1999
<i>Oxymycterus hiska</i>	F	I	Most diet consists of insects and other invertebrates	F	O	Dunnum et al. 2008b
<i>Oxymycterus nasutus</i>	F	I	Insectivore	-	D	Delia and Teta 2008
<i>Parahydromys asper</i>	F	I	Mainly consumes insects and other invertebrates, based on stomach content, it consumes a great amount of earthworms	F	-	Menzies and Dennis 1979; Flannery 1990; Nowak 1999; Leary et al. 2008
<i>Paramelomys levipes</i>	H	-	Stomach content includes vegetable matter	-	-	Flannery 1990
<i>Paratomys brantsii</i>	H	G	Generalist herbivore that consumes a variety of plant species such as winter annuals and succulent perennials feeding on their stems and leaves	F	D	Smithers 1983; du Plessis et al. 1991; Jackson 1998; Jackson and Spinks 1998; Coetze 2008
<i>Paruromys dominator</i>	H	G	Herbivorous and frugivorous	F	-	Nowak 1999; Musser and Durden 2002
<i>Peromyscus aztecus</i>	O	O	Insectivorous and consumes ants, weevils, crickets, and beetles; also consumes few seeds and plant material; also described as omnivorous with diet varying depending on location and time from feeding on plant matter to animal matter	F	N	Reid 1997; Vazquez et al. 2001; Krueger 2004
<i>Peromyscus boylii</i>	O	O	Omnivorous, feeding on acorns, conifer seeds, berries, fungi, fruit, cactus, however, the content of 11 stomachs contained: 91% arthropods including beetles, crickets, ants, caterpillars, and spiders, and 6% seeds, and 3% green plant material	T	N	Jameson 1952; Smartt 1978; Reid 1997
<i>Peromyscus californicus</i>	O	O	Diet includes fruits, seeds, shrubs, and a small amount of arthropods	A	N	Meserve 1976; Jess 2000
<i>Peromyscus crinitus</i>	O	O	Diet includes green vegetation, insects, fruits, leaves, and seeds	A	N	Merriam 1891; Matthews 1971; Nowak and Paradiso 1983
<i>Peromyscus eremicus</i>	O	O	Omnivorous, consuming fruits, seeds, insects, leaves, and green vegetation	A	N	Parker 1990; Caire 1999; Myers 2008
<i>Peromyscus fraterculus</i>	O	O	Diet includes seeds, insects, flowers, and fruit	F	N	Veal and Caire 1979; Timm et al. 2008
<i>Peromyscus leucopus</i>	O	O	Omnivorous and consumes berries and other fruits, seeds, buds, worms, insects and other invertebrates, and acorns and other nuts	T	N	Cockrum 1982; Jones and Birney 1988; Reid 1997
<i>Peromyscus mexicanus</i>	O	O	Omnivorous, feeding on both seeds and invertebrates, however, based on the content of 27 stomachs there is a greater preference for arthropods: 67% arthropods including spiders, ants, crickets, and beetles, 23% seeds, and 10% green plant material; also consumes fruit	T	N	Eisenberg 1989; Reid 1997; Trujano-Alvarez and Alvarez-Castañeda 2010
<i>Peromyscus polionotus</i>	O	O	Carnivorous and omnivorous with most of the diet composed of seeds in addition to insects such as beetles, leaf hoppers, true bugs, and ants, as well as vertebrates	F	N	Gentry and Smith 1968; Smith 1971; Moyers 1996; Whitaker and Hamilton 1998; Weigl 2005 Reid 2009
<i>Petromyscus monticularius</i>	O	O	Omnivorous, consumes seeds, fungi, berries, other fruits, lesser amount of green herbage, insects, invertebrates, and grains	A	N	Armstrong 1987; Jones and Birney 1988; Nowak 1999
<i>Phenacomys intermedius</i>	H	S	Diet includes bark, buds, heaths, forbs, berries, seeds, herbs, fungi, and shrubs	F	N	Armstrong 1987; Jones and Birney 1988; Nowak 1999
<i>Phloeomys sp</i>	H	S	Herbivorous, and consumes bark, wood, young vegetation, and roots, wood; in captivity eats birds, mammals, and fish [Phloeomys cumingi]	T	N	Heaney et al. 1991; Nowak 1999; Samuels 2009
<i>Phodopus sungorus</i>	O	O	Feeds on seeds, insects, and larvae	F	O	Mattke 2002; Tsytulsina 2008
<i>Phyllotis andium</i>	O	O	Omnivorous	-	N	Zeballos and Vivar 2008
<i>Phyllotis osilae</i>	O	O	The content of 11 stomachs contained: 31% grass, 22% forbes, 26% seeds, 20% insects	-	N	Eisenberg and Redford 2000
<i>Phyllotis xanthopygus</i>	O	O	Frugivore, granivore, herbivore, but insect consumption observed sometimes; Phyllotis x. rupestris is omnivorous that feeds on seeds, insects and grass	T	N	Kramer et al. 1999; Lagos and Bozinovic 1999; Ricardo et al. 2003
<i>Pogonomys loriae</i>	H	G	Based on stomach content, it consumes a variety of vegetable matter including flowers and pollen	F	-	Menzies and Dennis 1979; Flannery 1990
<i>Pogonomys macrourus</i>	H	G	>90% of diet consists of fruit	F	N	McPhee 1988; Flannery 1990; 1995
<i>Praomys degraaffi</i>	O	O	Omnivorous, consumes invertebrates, fruits, seeds and leaves	T	N	Kingdon 1997; Kingdon et al. 2013
<i>Praomys jacksoni</i>	O	O	Omnivorous, consumes plant matter and invertebrates	T	N	Delany 1975; Cameron 1996; Chapman and Chapman 1999
<i>Praomys missonnei</i>	O	O	Omnivorous, consumes invertebrates, fruits, seeds and leaves	T	N	Van der Straeten et al. 1987; Kingdon 1997; Kingdon et al. 2013
<i>Praomys tullbergi</i>	O	O	Omnivorous, consumes invertebrates, fruits, seeds and leaves	T	N	Kingdon 1997; Yeboah 1998; Angelici and Luiselli 2005
<i>Prometheomys schaposchnikowi</i>	H	S	Feeds on green part of plants and roots	F	-	Nowak 1999
<i>Pseudomys australis</i>	H	G	Herbivorous and consumes mostly seeds and some green plant material and a few insects	F	N	Clark and Reserve 1991; Moseby and Kemper 2008
<i>Pseudoryzomys simplex</i>	-	-	-	T	-	Nowak 1999
<i>Punomys kofordi</i>	H	G	Diet consists mostly herbs	-	-	Nowak 1999
<i>Rattus exulans</i>	O	O	Feeds on seeds, insects, snails, bark, seedlings, lepidopteran larvae, centipedes, spiders, earthworms, ants, beetles, weevils, cicadas, snails, lizards, birds, flowers, fruits, stems, leaves, and roots	T	N	King 1990; Francis 2008
<i>Rattus giluvensis</i>	-	-	-	F	N	Leary et al. 2008; Helgen and Opiang 2011
<i>Rattus leucopus</i>	O	O	Omnivorous, consumes nuts, fruits and insects	F	N	Strahan 1983; Flannery 1990; Leung and Leung 1999
<i>Rattus norvegicus</i>	O	O	Omnivorous and a dietary generalist	F	N	Reid 1997; Eisenberg and Redford 2000; Galef and Whiskin 2005
<i>Rattus novaeguineae</i>	-	-	-	T	-	Flannery 1990
<i>Rattus praetor</i>	-	-	-	F	-	Flannery 1990
<i>Rattus rattus</i>	O	O	Omnivorous, consumes foliage, seeds, arthropods, grass, insects, fungi, birds, grain, and fruit	A	N	Watts and Braithwaite 1978; Cockrum 1982; Monadjem 1997; Eisenberg and Redford 2000; Gillespie 2004
<i>Rattus sordidus</i>	O	O	Consumes mostly grass with small amounts of invertebrates and seeds	F	N	Johnson and Kerle 1991; Flannery 1990; Jarman et al. 2003
<i>Rattus tiomanicus</i>	O	O	Consumes a wide range of plant and animal matter including fruits	A	N	Francis 2008
<i>Rattus verecundus</i>	O	O	Stomach content includes insects and seeds	T	N	Flannery 1990; Sillitoe 2013
<i>Rattus villosissimus</i>	O	O	Mostly herbivorous but sometimes carnivorous	F	N	Predavec and Dickman 1994; Van Dyck 2008; Woinarski and Aplin 2008
<i>Reithrodont auritus</i>	H	S	Stomach content is mostly grass	F	O	Gallari 2001
<i>Reithrodontomys creper</i>	-	-	-	O	N	Reid 1997; Timm and Reid 2008

Table C.1—continued.

	GC	SC	Diet description	NS	PA	References
<i>Reithrodontomys fulvescens</i>	O	O	Based on fecal and stomach content it mostly consumes invertebrates with some fruit; it also consumes seeds, insects, and shoots of grasses and sedges	T	N	Stephensogn et al. 1963; Gaertner 1968; Kincaid and Cameron 1982; Reid 1997
<i>Reithrodontomys gracilis</i>	O	O	Consumes insects and seeds	T	N	Reid 1997
<i>Reithrodontomys megalotis</i>	H	G	Mainly granivorous, but also consumes green vegetation and insects	T	N	Cockrum 1982; Jones and Birney 1988; Cody and Smallwood 1996
<i>Rhabdomys pumilio</i>	O	O	Omnivorous, data from stomach content indicates the consumption of invertebrates, foliage, seeds and is known to eat berries cultivated grains, snails, insects eggs, stems, and leaves	T	D	Smithers 1971; Delany 1975; Smithers 1983; Kerley et al. 1990; Skinner 1990; Korn 1992; Wirminghaus and Perrin 1992; Cameron 1996; Kingdon 1997; Monadjem 1997; Nowak 1999
<i>Rheomys thomasi</i>	F	C	Feeds on insects, birds, salamanders, mammals including other Rheomys, stoneflies, mayfly larvae, and beetles	-	-	Stirtton 1944; Hooper 1968; Reid 1997
<i>Rhipidomys macconnelli</i>	-	-	-	A	N	Aguilera and Rivas 2008
<i>Rhipidomys masticalis</i>	O	O	Diet consists of fruits, seeds, leaves, fungi, and adult insects	A	N	Eisenberg and Redford 2000
<i>Rhizomys pratinosus</i>	H	S	Staple food sources include roots and stems of various species, analyses of stomach contents indicate no consumption of leaves or seeds	F	N	Xu 1984; Francis 2008
<i>Rhynchomys isarogensis</i>	F	I	Based on stomach content and feeding trials, it mainly consumes invertebrates and almost exclusively earthworms	-	N	Rickart and Heaney 1991; Nowak 1999
<i>Saccostomus campestris</i>	H	G	Feeds on seeds and fruits of many species	F	N	Smithers 1983
<i>Scapteromys tumidus</i>	F	I	Insectivorous and based on stomach content, arthropods make up 85% of diet mostly consisting of beetles and earthworms; includes small amount of plant material such as grass seeds in diet	T	O	Nowak 1999; Eisenberg and Redford 1999; 2000; Bonaventura 2001
<i>Scolomys juraeense</i>	O	O	Based on stomach content, it consumes seeds, spiders, and insects	-	N	Emmons and Feer 1997; Nowak 1999
<i>Scotinomys teguina</i>	F	I	Insects make up 80% of diet, especially adult beetles; consumes seeds and fruit on occasion	T	D	Eisenberg 1989; Reid 1997
<i>Sigmodon alstoni</i>	O	O	Diet consists of forbs, green plants, seeds, and insects	T	D	Eisenberg and Redford 2000; Patton et al. 2008
<i>Sigmodon arizonae</i>	O	O	Omnivorous, however, mainly consumes grass and some insects and carrion	T	O	Mearns 1890; Porter 2004; Samuels 2009
<i>Sigmodon hispidus</i>	O	O	Omnivorous, fecal and stomach content includes: invertebrates, fruit, green plant material, seeds, insects, bird eggs, stems, grass, stalks, weeds, grains, vertebrates, forbs, seeds, and insects	T	O	Gaertner 1968; Flehartey et al. 1969; Baker 1971; Cockrum 1982; Kincaid and Cameron 1982; Jones and Birney 1988; Reid 1997; Eisenberg and Redford 2000
<i>Sigmodontomys alfaroi</i>	H	G	Consumes seeds and vegetation	T	N	Reid 1997; Eisenberg and Redford 2000; Anderson et al. 2008
<i>Solomys salebrosum</i>	H	G	Consumes nuts and coccinoids	A	-	Nowak 1999
<i>Sooretamys rattiiceps</i>	H	G	Frugivore and granivore	A	-	Melo et al. 2013
<i>Steatomys krebsi</i>	O	O	Granivorous but also consumes insects and bulbs	T	N	Smithers 1983; Stuart and Stuart 2001
<i>Steatomys parvus</i>	O	O	Diet includes seeds, bulbs, roots, insects, and grass	T	N	Kingdon 1997; Skinner and Chimimba 2005
<i>Stenocerealemys albipes</i>	O	O	Omnivorous	T	N	Kingdon 1997; Kingdon et al. 2013
<i>Stochomys longicaudatus</i>	O	O	Omnivorous, consumes fruits, green vegetation, seeds, and insects	T	N	Delany 1975; Happold 1987; Kingdon 1997; Purvis 1997; Nowak 1999; Kingdon et al. 2013
<i>Sundamys muelleri</i>	O	O	Omnivorous	T	N	Archer 1999; Francis 2008
<i>Synaptomys cooperi</i>	H	S	Consumes plant material including leaves, sedges, grass, twigs, fruit, rootlets, fungi, mosses, ferns, and bark	T	O	Jones and Birney 1988; Linzey and Hammerson 2008
<i>Tachyoryctes splendens</i>	H	S	Specialist herbivore that feeds on grass, legumes, roots, rhizomes, tuber bulbs, and corn	F	D	Fiedler 1994; Nowak 1999; Samuels 2009
<i>Tapecomys wolffsohni</i>	-	-	-	-	-	-
<i>Tarsomys apoenensis</i>	F	I	Mainly consumes invertebrates	-	-	Nowak 1999
<i>Tatera robusta</i>	O	O	Diet includes seeds, stems, roots, grass, bulbs, leaves, fruits, insects, and other arthropods	F	N	Senzata 1984; Oguge 1995; Kingdon 1997
<i>Taterillus emini</i>	O	O	Feeds on a variety of plants and insects	F	N	Kingdon 1997; Kingdon et al. 2013
<i>Thaptomys nigrita</i>	F	I	Insectivore	T	N	Eisenberg and Redford 2000; Patton et al. 2008
<i>Thomasomys aureus</i>	H	G	Consumes fruits	T	-	Eisenberg 1989; Eisenberg and Redford 2000
<i>Thomasomys cinereiventer</i>	-	-	-	-	-	-
<i>Thomasomys notatus</i>	H	G	Stomach content had >89% plant material	A	-	Huiman and Carolina 2008
<i>Tokudaiia osimensis</i>	O	O	Omnivorous	A	-	Sugimura et al. 2004; Abe 2005
<i>Transandinomys talamancae</i>	O	O	Feeds on seeds, fruit, and insects in both adult and larval form	T	N	Reid 1997; Anderson et al. 2008
<i>Tylomys nudicaudatus</i>	H	S	Stomach content includes vegetation resembling lichen or bark	A	N	Reid 1997; Vázquez et al. 2008
<i>Tylomys watsoni</i>	H	S	Diet includes fruits, leaves, seeds, lichens, and bark	A	N	Goodwin 1946; Emmons 1990; Reid 1997; Ellis 1999
<i>Typhlomys cinereus</i>	H	G	Consumes leaves, stems, fruits, and seeds	T	N	Smith and Xie 2008; Smith et al. 2010
<i>Uromomys ruddi</i>	F	I	Stomach content includes adult insect remains of dipterous larvae and ant pupae with few seeds	F	N	Smithers 1983; Nowak 1999
<i>Uromys caudimaculatus</i>	O	O	Omnivorous, consumes fruits, seeds, fungi, bark, insects, small reptiles, amphibians, and bird eggs	T	N	Menzies and Dennis 1979; Strahan 1983; Flannery 1990; 1995; Beletsky 2007
<i>Vandeleuria oleracea</i>	H	G	Consumes shoots, buds, fruits, and leaves	A	N	Negi 1993; Molur et al. 2008
<i>Voalavo gymnocephalus</i>	H	G	Eats fruits and seeds	T	N	Goodman et al. 2003; Garbutt 2007
<i>Wiedomys pyrrhorhinus</i>	O	O	Granivorous and insectivorous, consuming beetles, moths, and native seeds	T	-	Nowak 1999; Eisenberg and Redford 2000
<i>Xenomys nelsoni</i>	H	G	The content of 11 stomachs contained finely ground green plant material and a young female had a leaf in her mouth	A	N	Nowak 1999; Ceballos et al. 2002; Álvarez-Castañeda et al. 2008
<i>Xeromys myoides</i>	F	C	Carnivorous, feeds on aquatic invertebrates and fishes as well as some vegetable matter, insects, lizards, and crabs	T	N	Hume et al. 1989; Nowak 1999; Winter et al. 2008
<i>Zelotomys hildegardae</i>	F	I	Mainly consumes invertebrates and some seeds	T	N	Hollister 1919; Kingdon 1997; Kingdon et al. 2013
<i>Zygodontomys brevicauda</i>	O	O	Consumes insects, seeds, fruits, and green vegetation	T	N	Reid 1997; Eisenberg and Redford 2000
<i>Zyzomys argurus</i>	O	O	Omnivorous, fecal content of 23 individual is composed mostly of plant matter and some insects	T	N	Dyck and Strahan 2006; Cronin 2008

Table C.1—continued.

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Table C.1—continued.

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Table C.2. Comparison of fit between the unpartitioned, linear 1-rate mode and four, partitioned, 2-rate models of correlation between speciation rates and continuous ecomorphological data. The nodes refer to clades with exceptional shifts in diversification rates as in Figure 4.1. Fg= foreground, or the clade undergoing the shift in diversification rate; Bg= background, or the tree excluding the foreground group. ΔAIC indicates the fit of the best model (italicized) relative to the null (1-rate, linear) model. Complete parameters for the four 2-rate models are indicated in Tables C.3, C.4, C.5, and C.6. Models that failed to converge are designated with (-).

	AIC					
	1-rate (linear)	2-rate				
		Bg flat, fg flat	Bg linear, fg flat	Bg flat, fg linear	Bg linear, fg linear	ΔAIC
Mass						
Node D1	1205.2	<i>1182.9</i>	1184.7	1184.8	1186.6	22.3
Node D2	1205.2	-	-	-	-	-
Node D3	1205.2	1179.5	<i>1178.5</i>	1181.2	1180.2	26.7
Node D4	1205.2	1195.3	1180.8	1193.7	<i>1180.1</i>	25.1
Node D5	1205.2	-	-	-	-	-
Node D6	1205.2	1190.5	<i>1168.3</i>	1191.5	1169.4	36.9
Node D7	1205.2	1216.8	<i>1207.7</i>	1218.7	1209.6	-2.5
Node D8	1205.2	<i>1190.5</i>	1192.1	1191.9	1193.1	13.3
Node D9	1205.2	1183.6	<i>1182.5</i>	1184.3	1183	22.7.3
Proportions 2						
Node D1	465.66	438.54	438.74	<i>427.84</i>	428.74	37.8
Node D2	465.66	-	-	-	-	-
Node D3	465.66	-	-	-	-	-
Node D4	465.66	-	-	-	-	-
Node D5	465.66	473.85	<i>464.45</i>	475.84	466.47	1.2
Node D6	465.66	-	-	-	-	-
Node D7	465.66	471.22	<i>464.7</i>	472.79	466.26	1.0
Node D8	465.66	<i>453.22</i>	455.01	<i>435.71</i>	437.47	30.0
Node D9	465.66	-	-	-	-	-
Tail length						
Node D1	1003.25	998.74	1000.22	<i>990.56</i>	992.37	12.7
Node D2	1003.25	-	-	-	-	-
Node D3	1003.25	995.16	976.92	997.15	978.92	26.3
Node D4	1003.25	1010.9	<i>1002.36</i>	1012.64	1003.49	0.9
Node D5	1003.25	-	-	-	-	-
Node D6	1003.25	1006.19	982.58	1005.93	982.57	20.7
Node D7	1003.25	1032.42	<i>1006.73</i>	1034.27	1008.59	-3.5
Node D8	1003.25	1006.18	1007.78	<i>994.96</i>	996.83	8.3
Node D9	1003.25	999.21	981.02	1001.18	982.95	22.2
Elevation						
Node D1	5923.6	5936.1	5938.1	<i>5907.1</i>	5916	16.5
Node D2	5923.6	-	-	-	-	-
Node D3	5923.6	5932.7	<i>5912.1</i>	5934.4	5913.4	11.5
Node D4	5923.6	-	-	-	-	-
Node D5	5923.6	-	-	-	-	-
Node D6	5923.6	-	-	-	-	-
Node D7	5923.6	-	-	-	-	-
Node D8	5923.6	-	-	-	-	-
Node D9	5923.6	-	-	-	-	-

Table C.3. ML parameter estimates for the partitioned, 2-rate, analyses with a flat function for both the background and the foreground, for the correlation between diversification rates and continuous ecomorphological data. λ = speciation rate; μ = extinction rate; σ_2 = diffusion coefficient, or BM evolution rate which is shared by both the background and the foreground groups. The best fit model parameters for each trait are italicized. Models that failed to converge are designated with (-). See Table C.2 legend for more information.

	Flat background		Flat foreground		
	λ	μ	λ	μ	σ_2
Mass					
Node D1	0.23853	0.22926	<i>0.01438</i>	0.35753	<i>0.17030</i>
Node D2	-	-	-	-	-
Node D3	0.37030	0.24329	0.01440	0.38604	0.00002
Node D4	0.39122	0.27778	0.01439	0.30086	0.01635
Node D5	-	-	-	-	-
Node D6	0.35598	0.20920	0.01439	0.60456	0.00001
Node D7	0.41970	0.27820	0.01437	0.32035	0.00002
Node D8	<i>0.21838</i>	<i>0.21404</i>	<i>0.01439</i>	<i>0.37102</i>	<i>0.19438</i>
Node D9	0.37314	0.24660	0.01440	0.37471	0.00026
Proportions 2					
Node D1	0.15954	0.08322	0.00138	0.32545	0.11045
Node D2	-	-	-	-	-
Node D3	-	-	-	-	-
Node D4	-	-	-	-	-
Node D5	0.38015	0.22927	0.00139	0.12261	0.00002
Node D6	-	-	-	-	-
Node D7	0.37277	0.22570	0.00138	0.46643	0.00002
Node D8	0.33700	0.33853	0.00138	0.34741	0.16932
Node D9	-	-	-	-	-
Tail length					
Node D1	0.29377	0.28957	0.00805	0.37087	0.18779
Node D2	-	-	-	-	-
Node D3	0.37066	0.24405	0.00805	0.38646	0.00000
Node D4	0.40271	0.29122	0.00803	0.30710	0.02518
Node D5	-	-	-	-	-
Node D6	0.35592	0.20910	0.00806	0.60391	0.00010
Node D7	0.42347	0.28285	0.00805	0.32079	0.00003
Node D8	0.21960	0.21527	0.00805	0.37129	0.19419
Node D9	0.37233	0.24570	0.00805	0.37213	0.00002
Elevation					
Node D1	0.23098	0.22084	0.35646	0.16899	134130.9
Node D2	-	-	-	-	-
Node D3	0.36993	0.24315	0.38571	0.00000	134130.6
Node D4	-	-	-	-	-
Node D5	-	-	-	-	-
Node D6	-	-	-	-	-
Node D7	-	-	-	-	-
Node D8	-	-	-	-	-
Node D9	-	-	-	-	-

Table C.4. ML parameter estimates for the partitioned, 2-rate, analyses with a linear function for the background and a flat function for the foreground, for the correlation between diversification rates and continuous ecomorphological data. λ_m = slope of speciation function; all other parameters are described in Table C.3. See Table C.2 legend for more information.

	Linear background			Flat foreground		
	λ	λ_m	μ	λ	μ	σ_2
Mass						
Node D1	0.19059	0.01069	0.19912	0.35619	0.16864	0.01438
Node D2	-	-	-	-	-	-
<i>Node D3</i>	0.49765	-0.08217	0.20294	0.38587	0.00000	0.01474
Node D4	0.55030	-0.14138	0.12379	0.31399	0.03542	0.01479
Node D5	-	-	-	-	-	-
<i>Node D6</i>	0.54933	-0.15343	0.06237	0.60433	0.00002	0.01537
<i>Node D7</i>	0.58535	-0.11807	0.19447	0.32036	0.00000	0.01502
Node D8	0.12005	0.02355	0.15443	0.37004	0.19288	0.01437
<i>Node D9</i>	0.50000	-0.07817	0.21527	0.37261	0.00001	0.01467
Proportions 2						
Node D1	0.12792	0.13008	0.05020	0.32683	0.11250	0.00138
Node D2	-	-	-	-	-	-
Node D3	-	-	-	-	-	-
Node D4	-	-	-	-	-	-
<i>Node D5</i>	0.29127	0.43520	0.15257	0.12242	0.00000	0.00144
Node D6	-	-	-	-	-	-
<i>Node D7</i>	0.28355	0.39635	0.14730	0.46670	0.00000	0.00143
Node D8	0.33568	-0.02960	0.33904	0.33122	0.14799	0.00139
Node D9	-	-	-	-	-	-
Tail length						
Node D1	0.23117	-0.01946	0.20624	0.35651	0.16901	0.00804
Node D2	-	-	-	-	-	-
<i>Node D3</i>	0.14732	0.16877	0.12267	0.38608	0.00000	0.00821
<i>Node D4</i>	0.20881	0.15168	0.18261	0.30759	0.02568	0.00818
Node D5	-	-	-	-	-	-
Node D6	0.11613	0.18826	0.08306	0.60418	0.00002	0.00840
<i>Node D7</i>	0.15541	0.19539	0.13176	0.32079	0.00048	0.00841
Node D8	0.22915	-0.02257	0.20905	0.37156	0.19488	0.00803
Node D9	0.14718	0.16949	0.12322	0.37213	0.00002	0.00827
Elevation						
Node D1	0.21831	0.00000	0.20853	0.35686	0.16943	134130.9
Node D2	-	-	-	-	-	-
<i>Node D3</i>	0.14920	0.00007	0.01593	0.38590	0.00000	134155.3
Node D4	-	-	-	-	-	-
Node D5	-	-	-	-	-	-
Node D6	-	-	-	-	-	-
Node D7	-	-	-	-	-	-
Node D8	-	-	-	-	-	-
Node D9	-	-	-	-	-	-

Table C.5. ML parameter estimates for the partitioned, 2-rate, analyses with a flat function for the background and a linear function for the foreground, for the correlation between diversification rates and continuous ecomorphological data. See Table C.3 for more information.

	Flat background		Linear foreground			
	λ	μ	λ	λ_m	μ	σ_2
Mass						
Node D1	0.22948	0.21914	0.30114	0.02982	0.16560	0.01438
Node D2	-	-	-	-	-	-
Node D3	0.37029	0.24351	0.57330	-0.10897	0.00003	0.01439
Node D4	0.40276	0.29111	0.05214	0.12998	0.00002	0.01449
Node D5	-	-	-	-	-	-
Node D6	0.35600	0.20914	-0.41285	0.47588	0.00000	0.01441
Node D7	0.41767	0.27579	0.54524	-0.13733	0.00000	0.01438
Node D8	0.21899	0.21453	0.23064	0.07449	0.17928	0.01459
Node D9	0.37298	0.24638	0.76652	-0.22634	0.00001	0.01441
Proportions 2						
Node D1	0.15933	0.08284	0.37277	-0.79214	0.00000	0.00149
Node D2	-	-	-	-	-	-
Node D3	-	-	-	-	-	-
Node D4	-	-	-	-	-	-
Node D5	0.38096	0.23015	0.12260	-0.00126	0.00000	0.00139
Node D6	-	-	-	-	-	-
Node D7	0.37075	0.22322	0.30488	1.11920	0.00001	0.00138
Node D8	0.33330	0.33477	0.35539	-0.76543	0.00008	0.00148
Node D9	-	-	-	-	-	-
Tail length						
Node D1	0.23066	0.22044	0.16712	0.17382	0.11440	0.00829
Node D2	-	-	-	-	-	-
Node D3	0.37066	0.24405	0.39319	-0.00804	0.00001	0.00804
Node D4	0.40290	0.29119	0.19881	0.10221	0.01992	0.00808
Node D5	-	-	-	-	-	-
Node D6	0.35587	0.20896	1.44697	-0.75471	0.00001	0.00806
Node D7	0.41802	0.27631	0.05371	0.26938	0.00000	0.00804
Node D8	0.21969	0.21531	0.14688	0.19661	0.11508	0.00839
Node D9	0.37300	0.24636	0.34067	0.03267	0.00000	0.00805
Elevation						
Node D1	0.23148	0.22135	0.15088	0.00010	0.00003	141658.4
Node D2	-	-	-	-	-	-
Node D3	0.37094	0.24434	0.36378	0.00002	0.00139	134130.7
Node D4	-	-	-	-	-	-
Node D5	-	-	-	-	-	-
Node D6	-	-	-	-	-	-
Node D7	-	-	-	-	-	-
Node D8	-	-	-	-	-	-
Node D9	-	-	-	-	-	-

Table C.6. ML parameter estimates for the partitioned, 2-rate, analyses with a linear function for both the background and the foreground, for the correlation between diversification rates and continuous ecomorphological data. See Table C.3 for more information.

	Linear background			Linear foreground			
	λ	λ_m	μ	λ	λ_m	μ	σ_2
Mass							
Node D1	0.21021	0.00729	0.21267	0.30114	0.03046	0.16699	0.01441
Node D2	-	-	-	-	-	-	-
Node D3	0.50205	-0.08421	0.20289	0.57328	-0.10897	0.00003	0.01467
<i>Node D4</i>	<i>0.55435</i>	<i>-0.14772</i>	<i>0.11103</i>	<i>0.07793</i>	<i>0.11568</i>	<i>0.00008</i>	<i>0.01493</i>
Node D5	-	-	-	-	-	-	-
Node D6	0.55142	-0.15187	0.07017	-0.41334	0.47588	0.00000	0.01532
Node D7	0.58904	-0.11959	0.19482	0.54615	-0.13746	0.00001	0.01497
Node D8	0.11304	0.02651	0.15024	0.23065	0.07356	0.17681	0.01457
Node D9	0.49616	-0.07652	0.21541	0.76662	-0.22634	0.00001	0.01473
Proportions 2							
Node D1	0.12757	0.10623	0.05039	0.37282	-0.79397	0.00001	0.00149
Node D2	-	-	-	-	-	-	-
Node D3	-	-	-	-	-	-	-
Node D4	-	-	-	-	-	-	-
Node D5	0.29461	0.43148	0.15645	0.10614	0.10506	0.00004	0.00144
Node D6	-	-	-	-	-	-	-
Node D7	0.28406	0.39603	0.14782	0.30552	1.12122	0.00000	0.00143
Node D8	0.33321	-0.04435	0.33520	0.35557	-0.76542	0.00005	0.00149
Node D9	-	-	-	-	-	-	-
Tail length							
Node D1	0.23028	-0.01593	0.20913	0.15914	0.17818	0.10830	0.00831
Node D2	-	-	-	-	-	-	-
Node D3	0.14782	0.16857	0.12338	0.39306	-0.00717	0.00002	0.00822
Node D4	0.20798	0.15281	0.18200	0.12759	0.17514	0.02038	0.00825
Node D5	-	-	-	-	-	-	-
<i>Node D6</i>	<i>0.10431</i>	<i>0.19123</i>	<i>0.07000</i>	<i>1.40070</i>	<i>-0.71294</i>	<i>0.00001</i>	<i>0.00843</i>
Node D7	0.15974	0.19206	0.13483	0.05386	0.27014	0.00008	0.00835
Node D8	0.21667	-0.01354	0.20406	0.14693	0.19654	0.11510	0.00837
Node D9	0.14684	0.17019	0.12320	0.34067	0.03286	0.00000	0.00822
Elevation							
Node D1	0.21750	0.00000	0.20885	0.23530	0.00008	0.09978	139347.8
Node D2	-	-	-	-	-	-	-
Node D3	0.14920	0.00007	0.01593	0.36378	0.00001	0.00046	137747.7
Node D4	-	-	-	-	-	-	-
Node D5	-	-	-	-	-	-	-
Node D6	-	-	-	-	-	-	-
Node D7	-	-	-	-	-	-	-
Node D8	-	-	-	-	-	-	-
Node D9	-	-	-	-	-	-	-

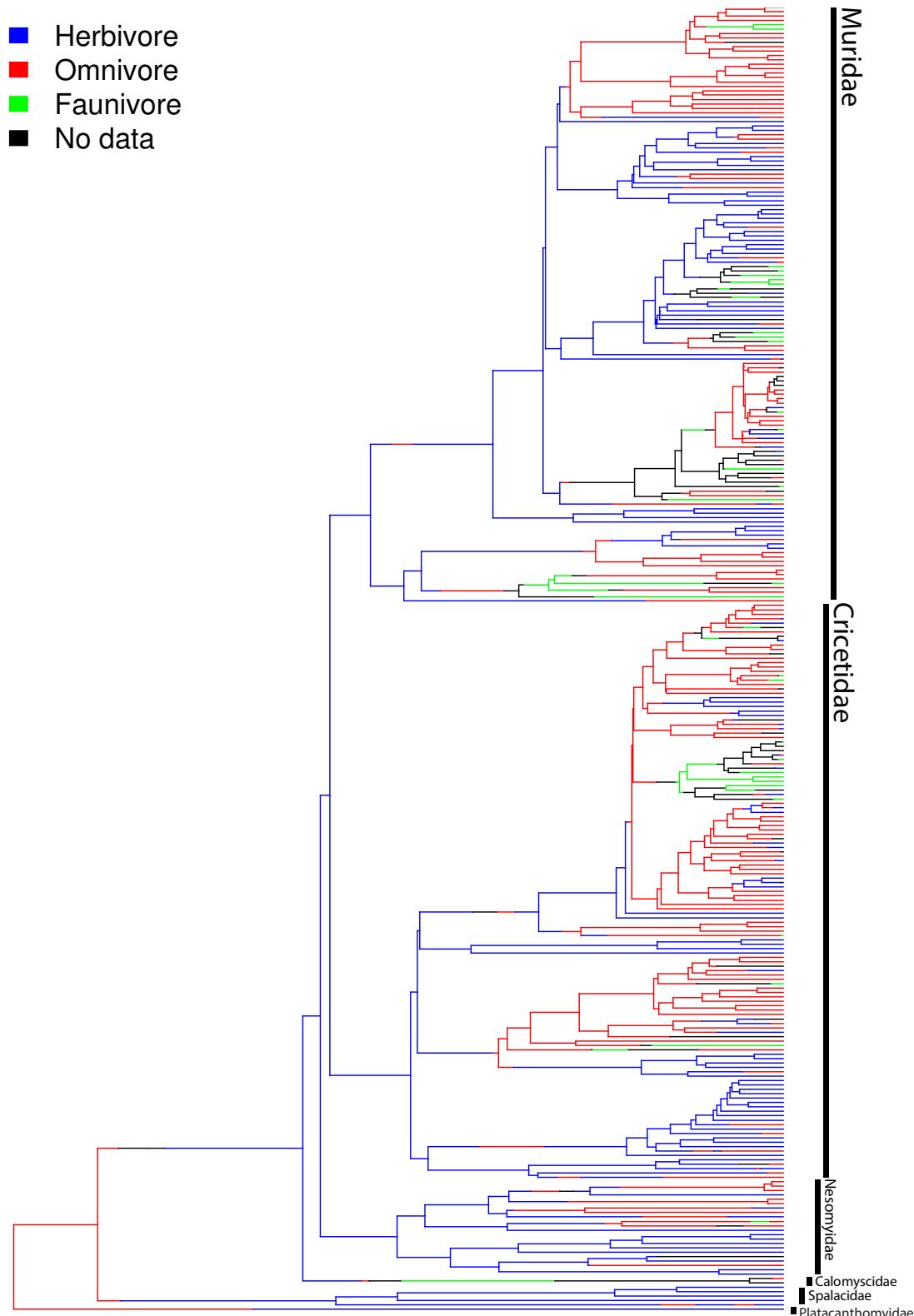


Figure C.1. Stochastic character map of the three dietary categories in muroids. Observed data are indicated on the tips, and branches indicate one of many possible stochastic character map histories estimated using the symmetrical model in the *Phytools* library (Revell 2012) in R. Unlike trait diversification analyses, for illustration purposes, missing data are not pruned here.

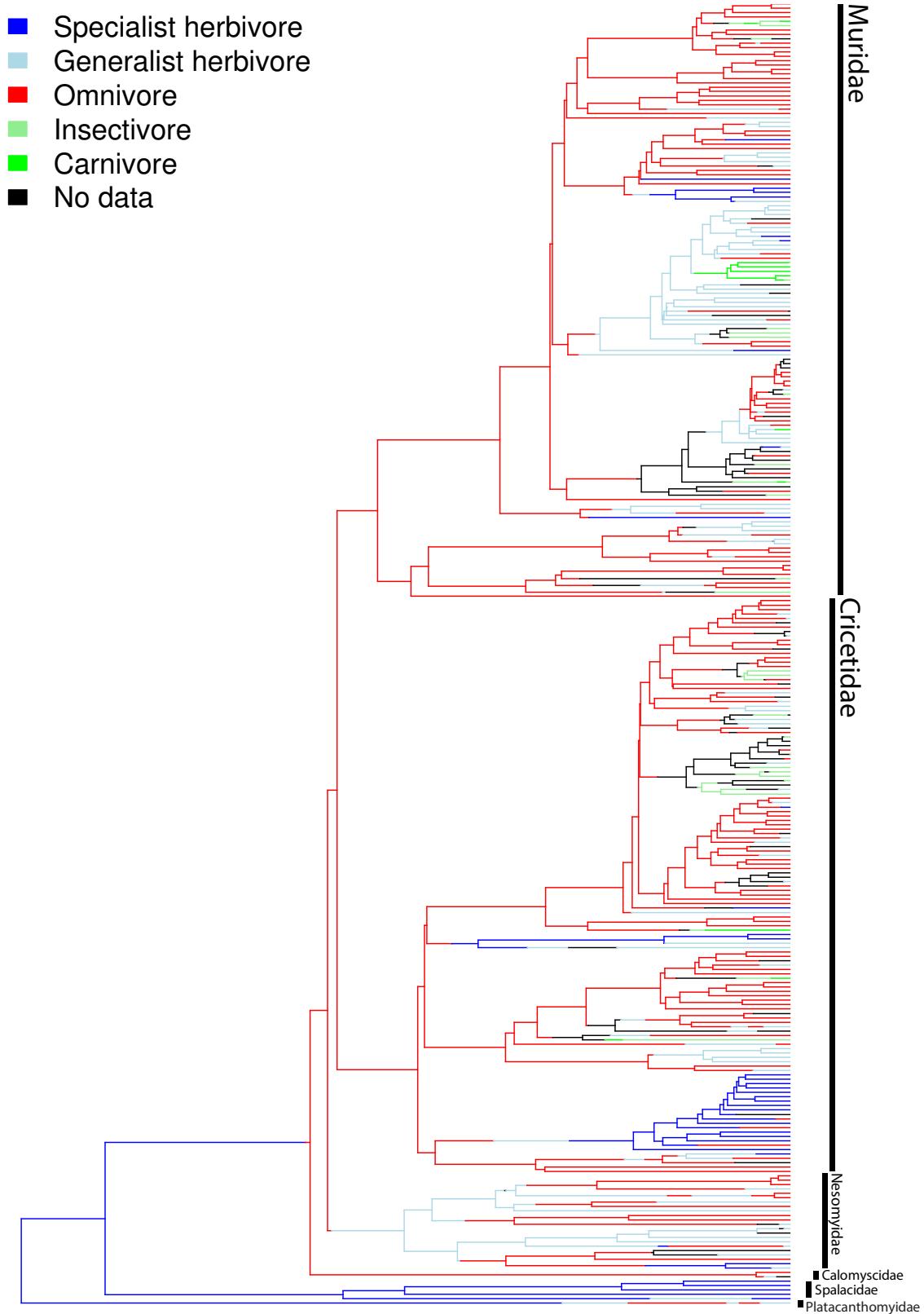


Figure C.2. Stochastic character map of the five dietary categories in muroids. See Figure C.1 legend for more information.

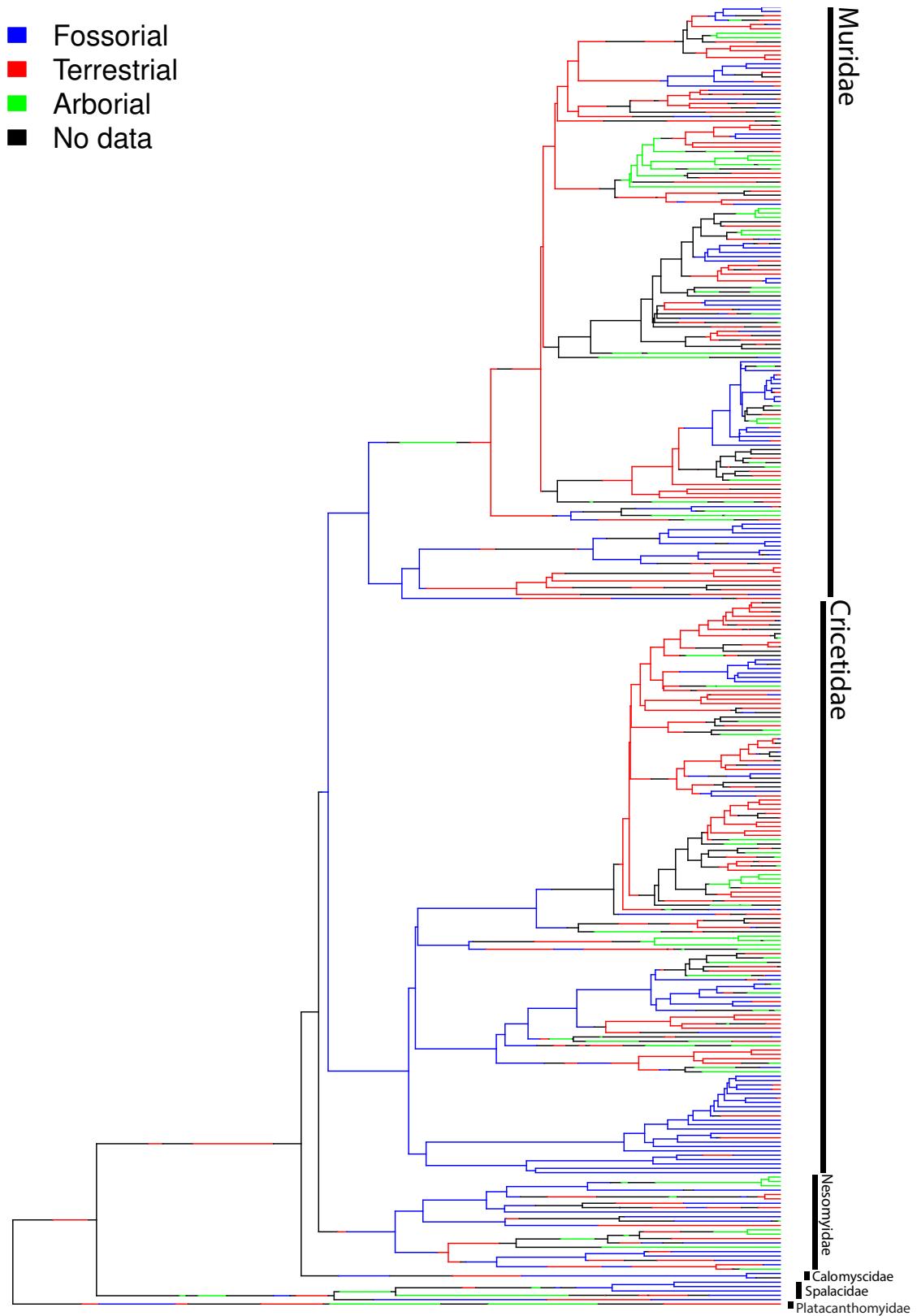


Figure C.3. Stochastic character map of the three nesting sites in muroids. See Figure C.1 legend for more information.

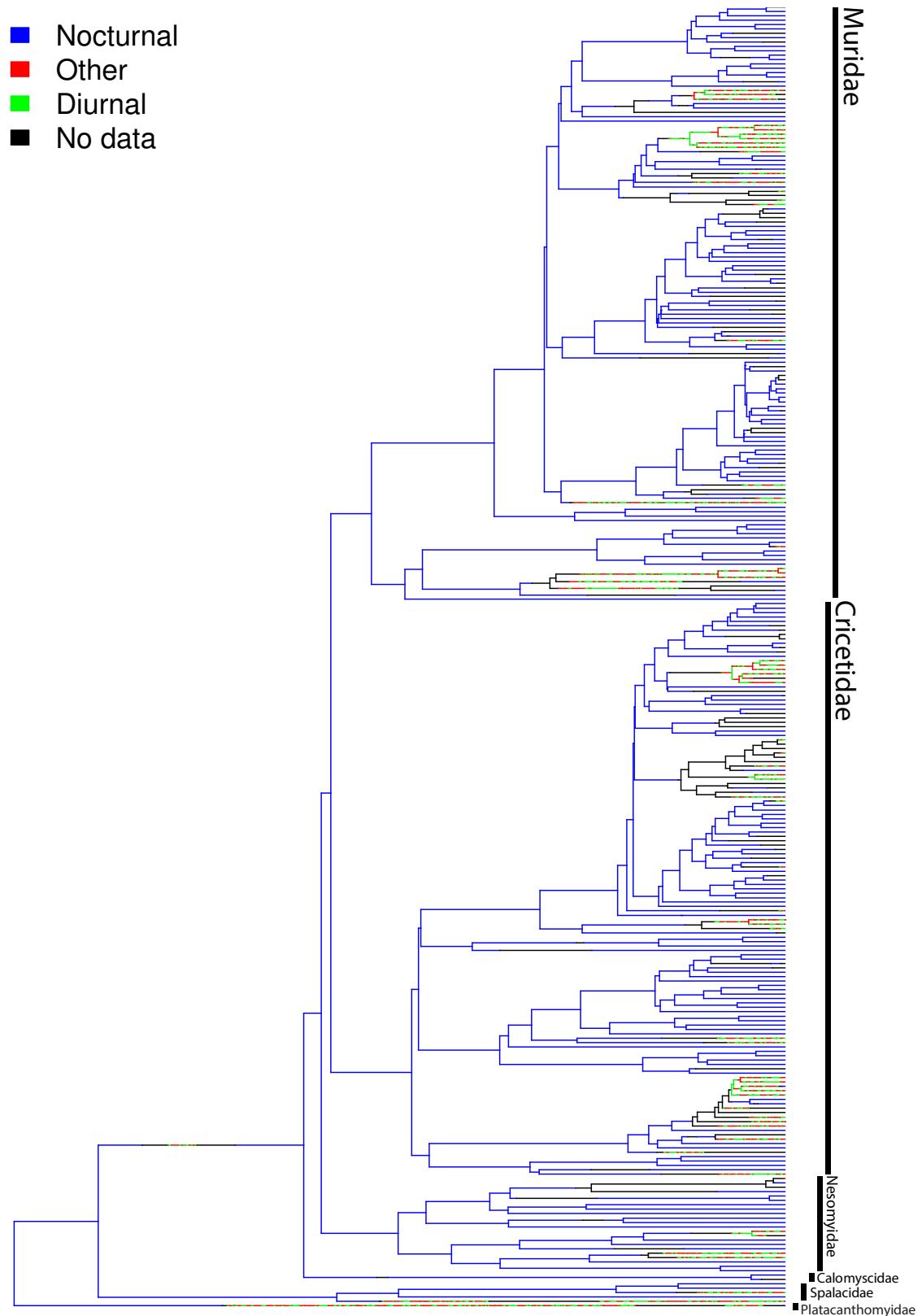


Figure C.4. Stochastic character map of the three activity periods in muroids. See Figure C.1 legend for more information

APPENDIX D

SUPPORTING MATERIAL FOR CHAPTER 5

Table D.1. Genera in clades used in diversity vs. morphological variance regressions.

<u>Acomys clade</u>
all <i>Acomys</i> excluding <i>A. spinosissimus</i> , <i>A. subspinosus</i>
<u>Apodemus clade</u>
all <i>Apodemus</i> excluding <i>A. mystacinus</i> , <i>A. sylvaticus</i>
<u>Arvicolinae clade I</u>
<i>Synaptomys</i> , <i>Lemmus</i> , <i>Phenacomys</i> , <i>Dicrostonyx</i>
<u>Arvicolinae clade II</u>
<i>Eothenomys</i> , <i>Alticola</i> , <i>Myodes</i> , <i>Lagurus</i> , <i>Arvicola</i> , <i>Chionomys</i> , <i>Lasiopodomys</i> , <i>Neodon</i> , <i>Microtus</i>
<u>Cricetinae clade</u>
<i>Cricetus</i> , <i>Allocricetus</i>
<u>Dendromurinae clade</u>
<i>Dendromus</i> , <i>Malacothrix</i>
<u>Deomyinae clade</u>
<i>Lophuromys</i> , <i>Deomys</i>
<u>Dipodidae clade</u>
all Dipodidae excluding <i>Sicista</i>
<u>Gerbillinae clade I</u>
<i>Desmodillus</i> , <i>Gerbilliscus</i> , <i>Gerbillurus</i>
<u>Gerbillinae clade II</u>
<i>Psammomys</i> , <i>Meriones</i> , <i>Rhombomys</i> , <i>Taterillus</i> , <i>Sekeetamys</i> , <i>Gerbillus</i> , <i>Dipodillus</i>
<u>Gerbillinae clade III</u>
<i>Gerbilliscus</i> and <i>Gerbillurus</i> excluding <i>G. robustus</i>
<u>Gerbillinae clade IV</u>
<i>Psammomys</i> , <i>Meriones</i> , <i>Rhombomys</i>
<u>Gerbillinae clade V</u>
<i>Sekeetamys</i> , <i>Gerbillus</i> , <i>Dipodillus</i>
<u>Murinae clade I</u>
<i>Batomys</i> , <i>Carpomys</i> , <i>Phloemys</i>
<u>Murinae clade II</u>
all Murinae excluding <i>Batomys</i> , <i>Carpomys</i> , <i>Phloemys</i>
<u>Murinae clade III</u>
<i>Crunomys</i> , <i>Maxomys</i> , <i>Melasmotherrix</i> , <i>Margaretamys</i> , <i>Chiromyscus</i> , <i>Dacnomys</i> , <i>Leopoldamys</i> , <i>Niviventer</i> , <i>Berylmys</i> , <i>Paruromys</i> , <i>Bunomys</i> , <i>Sundamys</i> , <i>Bullimus</i> , <i>Bandicota</i> , <i>Rattus</i> , <i>Tarsomys</i> , <i>Limnomys</i>
<u>Murinae clade IV</u>
<i>Apomys</i> , <i>Archboldomys</i> , <i>Rhynchomys</i> , <i>Chrotomys</i> , <i>Anisomys</i> , <i>Lorentzimys</i> , <i>Macruromys</i> , <i>Hyomys</i> , <i>Pogonomys</i> , <i>Abeomelomys</i> , <i>Leptomys</i> , <i>Hydromys</i> , <i>Pseudohydromys</i> , <i>Zyzomys</i> , <i>Leggadina</i> , <i>Notomys</i> , <i>Pseudomys</i> , <i>Mastacomys</i> , <i>Conilurus</i> , <i>Mesembriomys</i> , <i>Uromys</i> , <i>Melomys</i>

Table D.1-continued.

<u>Murinae clade V</u>
<i>Otomys, Parotomys, Oenomys, Golunda, Stochomys, Hybomys, Micaelamys, Aethomys, Grammomys, Dasymys, Mylomys, Rhabdomys, Arvicanthis, Lemniscomys</i>
<u>Murinae clade VI</u>
<i>Myomyscus, Stenocephalemys, Heimyscus, Hylomyscus, Mastomys, Colomys, Zelotomys, Praomys</i>
<u>Murinae clade VII</u>
<i>Crunomys, Maxomys</i>
<u>Murinae clade VIII</u>
<i>Margaretamys, Chiromyscus, Dacnomys, Leopoldamys, Niviventer, Berylmys, Paruromys, Bunomys, Sundamys, Bullimus, Bandicota, Rattus, Tarsomys, Limnomyss</i>
<u>Murinae clade IX</u>
<i>Apomys, Archboldomys, Rhynchomys, Chrotomys</i>
<u>Murinae clade X</u>
<i>Hyomys, Pogonomys</i>
<u>Murinae clade XI</u>
<i>Leptomys, Hydromys, Pseudohydromys, Zyzomys, Leggadina, Notomys, Pseudomys, Mastacomys, Conilurus, Mesembriomys, Uromys, Melomys</i>
<u>Murinae clade XII</u>
<i>Otomys, Parotomys</i>
<u>Murinae clade XIII</u>
<i>Aethomys, Grammomys</i>
<u>Murinae clade XIV</u>
<i>Mylomys, Rhabdomys, Arvicanthis, Lemniscomys</i>
<u>Mus clade</u>
all <i>Mus</i> excluding <i>M. pahari</i> , <i>M. minutoides</i>
<u>Neotominae clade I</u>
<i>Xenomys, Hodomys, Neotoma</i>
<u>Neotominae clade II</u>
<i>Isthmomys, Reithrodontomys, Onychomys, Megadontomys, Peromyscus, Neotomodon, Habromys, Osgoodomys</i>
<u>Neotominae clade III</u>
<i>Megadontomys, Peromyscus, Neotomodon, Habromys, Osgoodomys</i>
<u>Nesomyidae clade I</u>
all Nesomyidae excluding Nesomyinae
<u>Nesomyidae clade II</u>
<i>Delanymys, Mystromys, Petromyscus</i>
<u>Nesomyinae clade I</u>
<i>Macrotarsomys, Monticolomys, Hypogeomys, Nesomys, Brachyuromys</i>
<u>Nesomyinae clade II</u>
<i>Brachytarsomys, Gymnuromys, Voalavo, Eliurus</i>
<u>Nesomyinae clade III</u>
<i>Hypogeomys, Nesomys, Brachyuromys</i>

Table D.1-continued.

Nesomyinae clade IV
<i>Gymnuromys, Voalavo, Eliurus</i>
Nesomyinae clade V
<i>Voalavo, Eliurus</i>
Sigmodontinae clade I
<i>Ichthyomys, Rheomys, Sigmodon</i>
Sigmodontinae clade II
<i>Rhagomys, Rhipidomys, Thomasomys</i>
Sigmodontinae clade III
<i>Zygodontomys, Scolomys, Nephelomys, Transandinomys, Oecomys, Microryzomys, Neacomys, Oligoryzomys, Cerradomys, Sooretamys, Pseudoryzomys, Holochilus, Nectomys, Oryzomys, Melanomys, Sigmodontomys, Aegialomys</i>
Sigmodontinae clade IV
<i>Kunsia, Scapteromys, Lenoxus, Brucepattersonius, Oxymycterus, Thaptomys, Necromys, Deltamys, Akodon</i>
Sigmodontinae clade V
<i>Andinomys, Punomys, Euneomys, Neotomys, Irenomys, Wiedomys, Juliomys, Abrothrix, Geoxus, Notiomys, Chelemys, Delomys, Calomys, Graomys, Eligmodontia, Andalgalomys, Loxodontomys, Auliscomys, Phyllotis</i>
Sigmodontinae clade VI
<i>Nephelomys, Transandinomys, Oecomys</i>
Sigmodontinae clade VII
<i>Microryzomys, Neacomys, Oligoryzomys</i>
Sigmodontinae clade VIII
<i>Cerradomys, Sooretamys, Pseudoryzomys, Holochilus, Nectomys, Oryzomys, Melanomys, Sigmodontomys, Aegialomys</i>
Sigmodontinae clade IX
<i>Kunsia, Scapteromys, Lenoxus, Brucepattersonius</i>
Sigmodontinae clade X
<i>Thaptomys, Necromys, Deltamys, Akodon</i>
Sigmodontinae clade XI
<i>Euneomys, Neotomys, Irenomys</i>
Sigmodontinae clade XII
<i>Abrothrix, Geoxus, Notiomys, Chelemys</i>
Sigmodontinae clade XIII
<i>Eligmodontia, Andalgalomys, Loxodontomys, Auliscomys, Phyllotis</i>
Spalacidae clade
<i>Tachyoryctes, Rhizomys, Cannomys</i>
Tylomyinae clade
<i>Ototylomys, Tylomys</i>

Table D.2. Loadings onto the first 15 relative warp axes for the relative warp analysis conducted on the procrustes coordinates of the 34 cranial landmarks.

	RW1	RW2	RW3	RW4	RW5	RW6	RW7	RW8	RW9	RW10	RW11	RW12	RW13	RW14	RW15
Procrustes coordinate 1	0.100	0.124	0.008	-0.035	0.090	-0.100	0.078	-0.013	0.075	-0.011	0.042	-0.043	0.020	-0.040	0.098
Procrustes coordinate 2	-0.041	-0.206	-0.041	0.061	-0.222	0.023	0.099	0.024	0.112	-0.038	-0.043	0.077	-0.022	0.046	-0.037
Procrustes coordinate 3	0.159	0.009	0.102	0.096	0.008	0.189	0.091	0.161	-0.075	-0.062	-0.053	0.043	-0.033	-0.265	-0.071
Procrustes coordinate 4	-0.080	-0.172	0.052	-0.081	0.189	0.074	0.166	-0.060	0.113	0.077	-0.137	0.032	0.056	0.155	-0.257
Procrustes coordinate 5	0.012	-0.095	-0.037	0.004	-0.295	-0.067	0.061	0.070	0.071	-0.083	0.053	0.090	-0.017	-0.033	0.087
Procrustes coordinate 6	-0.042	0.086	0.222	0.087	-0.194	0.069	-0.114	0.102	-0.011	-0.112	0.073	-0.107	-0.133	-0.309	0.165
Procrustes coordinate 7	-0.048	0.087	-0.024	0.056	0.072	-0.032	0.025	-0.005	0.118	-0.017	-0.017	0.048	-0.073	-0.018	-0.065
Procrustes coordinate 8	-0.076	0.132	-0.014	-0.042	-0.008	-0.062	0.048	0.008	0.055	0.014	-0.008	0.065	0.025	0.000	-0.016
Procrustes coordinate 9	-0.046	-0.110	-0.003	-0.047	-0.065	-0.026	0.043	-0.031	0.037	-0.037	0.034	0.064	0.017	0.033	0.001
Procrustes coordinate 10	0.031	0.035	0.049	0.076	0.155	-0.259	0.277	0.049	0.155	-0.030	-0.181	-0.151	-0.149	-0.034	0.027
Procrustes coordinate 11	-0.113	0.065	-0.002	0.004	-0.012	0.039	0.073	0.049	-0.056	-0.036	0.099	0.005	-0.080	0.029	0.027
Procrustes coordinate 12	0.069	0.159	0.020	0.108	0.098	0.192	-0.082	0.108	0.125	0.068	-0.107	0.295	0.008	0.089	-0.076
Procrustes coordinate 13	0.001	0.027	0.003	0.062	0.115	-0.144	0.159	0.024	0.124	-0.027	-0.136	-0.123	-0.096	-0.035	0.002
Procrustes coordinate 14	-0.138	0.126	0.024	-0.005	-0.021	-0.064	0.080	0.008	-0.001	-0.074	0.010	-0.005	0.004	0.046	0.076
Procrustes coordinate 15	-0.156	0.033	0.107	0.137	0.030	-0.080	0.001	0.026	0.019	-0.084	-0.075	0.018	0.003	0.180	0.207
Procrustes coordinate 16	-0.050	0.054	-0.070	0.015	0.028	0.067	-0.097	-0.055	0.081	-0.021	-0.001	-0.039	0.022	-0.011	0.031
Procrustes coordinate 17	0.011	0.110	0.018	-0.028	0.113	-0.032	-0.059	-0.021	-0.011	0.070	-0.025	0.011	0.026	0.022	0.014
Procrustes coordinate 18	-0.085	-0.085	-0.070	-0.073	-0.100	-0.029	0.202	0.002	0.097	-0.048	0.080	0.116	0.004	0.034	-0.101
Procrustes coordinate 19	-0.020	0.105	-0.111	-0.045	-0.050	0.135	-0.162	-0.086	0.068	0.011	0.033	-0.063	0.113	0.022	0.064
Procrustes coordinate 20	0.087	0.011	0.124	0.068	0.176	-0.070	-0.093	0.009	-0.157	0.051	0.027	-0.007	0.028	0.087	-0.087
Procrustes coordinate 21	0.193	0.081	-0.177	-0.058	0.003	-0.023	0.152	-0.033	0.122	-0.081	0.044	0.042	-0.035	0.013	-0.004
Procrustes coordinate 22	-0.010	0.010	-0.006	0.020	0.041	0.071	-0.141	-0.017	-0.019	0.045	0.037	0.033	0.002	0.058	-0.047
Procrustes coordinate 23	-0.127	0.077	0.043	0.100	0.044	-0.094	-0.027	0.038	0.034	-0.010	-0.108	0.093	0.019	-0.121	0.028
Procrustes coordinate 24	-0.115	0.067	-0.133	0.031	-0.170	0.046	0.039	-0.114	0.186	-0.053	0.070	0.074	0.014	0.116	-0.114
Procrustes coordinate 25	0.028	0.147	-0.081	-0.046	-0.059	0.091	-0.115	-0.069	0.085	0.007	-0.009	-0.075	0.131	-0.077	0.137
Procrustes coordinate 26	0.095	-0.163	-0.142	0.226	0.025	-0.148	-0.213	-0.104	-0.044	-0.098	-0.008	-0.175	-0.099	0.257	0.029
Procrustes coordinate 27	0.295	0.023	-0.208	0.111	0.072	-0.165	0.029	-0.041	-0.065	-0.140	0.148	0.003	-0.156	0.188	-0.015
Procrustes coordinate 28	0.067	0.140	-0.062	-0.028	-0.007	-0.007	-0.054	-0.047	0.054	0.010	-0.008	-0.076	0.089	-0.023	0.140
Procrustes coordinate 29	0.012	-0.171	-0.032	0.106	-0.098	0.064	0.034	0.061	-0.012	-0.036	0.054	-0.050	0.003	-0.042	-0.131
Procrustes coordinate 30	0.273	0.091	-0.050	-0.003	0.072	0.105	0.108	0.079	-0.072	-0.028	0.173	-0.116	0.028	-0.252	-0.136
Procrustes coordinate 31	-0.169	-0.009	0.055	0.052	-0.263	0.027	0.037	0.277	-0.309	-0.005	-0.061	-0.096	-0.129	-0.072	-0.260
Procrustes coordinate 32	0.036	-0.270	-0.114	0.107	0.110	0.039	-0.152	-0.228	0.202	-0.102	0.054	-0.009	0.059	-0.062	0.115
Procrustes coordinate 33	0.047	0.008	-0.181	0.036	-0.124	0.030	-0.031	0.018	-0.197	0.002	-0.048	-0.088	-0.105	-0.142	-0.141
Procrustes coordinate 34	0.040	-0.160	0.047	-0.028	0.010	0.026	-0.013	0.037	-0.163	-0.060	0.222	0.066	-0.052	0.023	0.090
Procrustes coordinate 35	0.035	-0.114	-0.111	-0.041	0.069	0.060	0.039	0.074	-0.135	0.108	-0.241	0.129	0.080	-0.147	0.155
Procrustes coordinate 36	-0.088	0.052	-0.108	0.064	-0.151	0.121	-0.082	0.002	-0.129	0.056	-0.187	0.055	0.110	0.197	0.072
Procrustes coordinate 37	0.115	-0.165	-0.047	-0.130	0.146	0.116	-0.012	0.022	-0.204	0.026	0.092	0.135	-0.020	0.000	0.084
Procrustes coordinate 38	0.060	-0.038	-0.093	-0.111	0.154	0.156	0.012	0.020	-0.012	0.119	-0.212	0.179	0.032	-0.154	0.013
Procrustes coordinate 39	-0.067	0.003	-0.075	0.026	-0.160	0.133	-0.027	0.010	-0.098	0.082	-0.121	0.054	0.081	0.211	0.083
Procrustes coordinate 40	0.083	0.045	0.055	-0.077	-0.012	-0.096	0.017	0.105	-0.088	-0.099	0.060	0.262	0.027	0.089	-0.064
Procrustes coordinate 41	0.163	0.022	0.028	0.204	-0.194	-0.041	0.066	-0.069	0.102	0.379	0.214	-0.119	0.242	-0.032	-0.019
Procrustes coordinate 42	0.059	-0.029	0.163	0.034	-0.089	-0.082	0.158	-0.207	-0.005	0.641	0.016	-0.053	-0.279	-0.004	0.166
Procrustes coordinate 43	-0.023	0.031	0.025	-0.104	-0.013	0.031	-0.087	-0.052	-0.118	0.062	0.024	-0.013	0.065	-0.013	0.083
Procrustes coordinate 44	0.105	-0.046	-0.045	0.167	0.007	0.112	-0.102	-0.033	0.127	-0.065	-0.255	0.001	-0.022	-0.171	-0.013
Procrustes coordinate 45	-0.155	0.123	-0.195	-0.028	0.100	0.186	0.228	0.116	0.031	-0.007	0.092	-0.077	-0.051	0.026	0.236
Procrustes coordinate 46	0.045	0.082	0.012	-0.057	0.035	-0.044	0.005	0.029	-0.010	0.036	0.032	-0.019	0.046	-0.038	0.115
Procrustes coordinate 47	0.058	-0.079	-0.117	-0.014	-0.165	-0.077	0.029	-0.025	0.098	-0.063	-0.069	-0.024	-0.080	-0.038	0.084
Procrustes coordinate 48	0.109	0.061	0.265	-0.068	-0.049	0.211	0.048	0.011	0.098	-0.043	-0.273	-0.082	0.195	0.217	-0.150
Procrustes coordinate 49	0.012	0.059	0.005	0.033	-0.023	-0.064	0.039	0.027	0.050	0.067	0.022	0.195	0.030	0.071	0.157
Procrustes coordinate 50	0.083	-0.085	-0.084	-0.143	-0.143	-0.035	0.088	0.001	0.032	-0.063	0.011	-0.044	0.113	-0.097	-0.022
Procrustes coordinate 51	0.060	0.070	0.252	-0.037	-0.093	-0.110	-0.100	-0.004	-0.037	-0.042	-0.160	0.007	-0.105	0.153	0.100
Procrustes coordinate 52	-0.015	-0.020	-0.016	0.014	0.077	0.052	0.052	-0.025	0.055	0.118	0.005	0.075	-0.011	-0.037	-0.049
Procrustes coordinate 53	0.023	-0.107	-0.119	-0.073	-0.217	-0.072	0.070	0.020	0.064	-0.048	-0.086	0.044	-0.010	0.011	0.029
Procrustes coordinate 54	-0.006	-0.019	0.360	-0.217	-0.036	0.163	-0.150	-0.191	0.306	-0.192	0.292	0.007	-0.097	-0.096	-0.015
Procrustes coordinate 55	0.006	-0.006	-0.041	-0.048	-0.098	0.023	-0.084	-0.018	-0.041	0.015	-0.001	-0.074	0.044	-0.044	0.038
Procrustes coordinate 56	0.082	0.037	0.025	0.008	0.056	0.018	-0.129	-0.091	0.044	0.005	-0.042	0.128	-0.039	-0.052	-0.062
Procrustes coordinate 57	-0.076	0.081	0.154	0.057	0.133	0.276	0.238	0.153	0.065	-0.080	0.023	-0.179	-0.051	0.048	0.225
Procrustes coordinate 58	-0.029	-0.024	-0.008	0.152	-0.078	0.067	0.009	0.030	0.072	0.085	0.096	0.137	-0.028	-0.043	-0.039
Procrustes coordinate 59	0.135	0.024	0.055	-0.201	-0.007	-0.055	0.068	0.060	-0.079	-0.071	0.023	0.044	0.249	-0.025	0.114
Procrustes coordinate 60	0.042	0.048	-0.078	-0.408	-0.059	-0.160	-0.092	-0.164	-0.044	-0.012	-0.171	-0.044	-0.245	-0.046	-0.106
Procrustes coordinate 61	0.018	-0.028	0.014	0.145	-0.071	0.053	-0.034	-0.007	0.025	0.061	0.108	0.025	0.050	-0.012	0.079
Procrustes coordinate 62	0.115	0.045	0.068	-0.097	0.010	-0.003	0.006	0.030	-0.098	-0.019	0.114	-0.002	-0.004	0.064	0.142
Procrustes coordinate 63	0.050	0.028	-0.079	-0.043	-0.116	-0.068	-0.115	-0.011	0.024	-0.148	-0.051	-0.070	-0.102	-0.104	-0.069
Procrustes coordinate 64	0.011	-0.071	0.104	-0.008	0.032	0.042	0.098	-0.010	0.032	0.015	0.084	0.009	0.007	0.059	-0.123
Procrustes coordinate 65	0.073	0.007	0.057	-0.096	-0.079	0.083	0.069	0.016	0.026	0.004	0.078	-0.117	0.114	0.194	-0.096
Procrust															

Table D.2-continued.

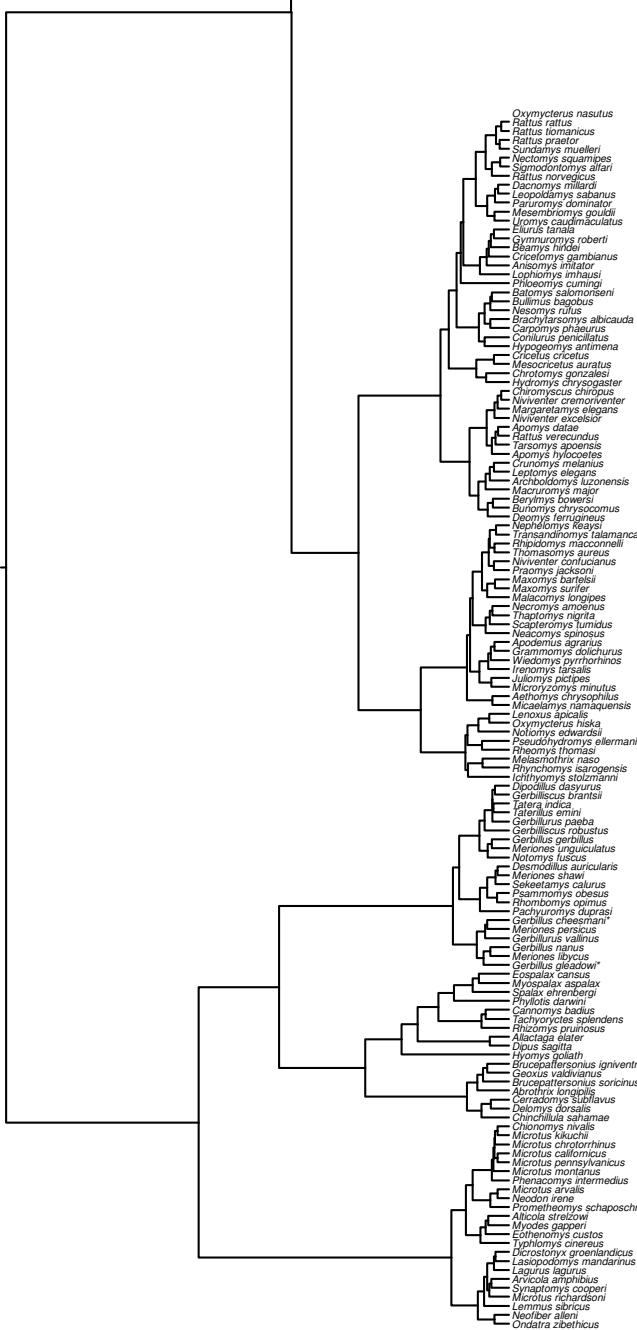
	RW1	RW2	RW3	RW4	RW5	RW6	RW7	RW8	RW9	RW10	RW11	RW12	RW13	RW14	RW15
Procrustes coordinate 88	-0.033	-0.030	0.034	-0.065	0.005	-0.082	0.068	0.011	0.030	-0.091	-0.025	-0.165	0.091	-0.001	-0.141
Procrustes coordinate 89	-0.106	0.071	-0.006	-0.103	0.066	0.012	0.043	0.010	0.012	0.010	-0.022	-0.070	0.051	0.070	-0.168
Procrustes coordinate 90	-0.117	-0.210	0.026	-0.028	0.097	-0.022	0.018	-0.051	-0.135	0.005	-0.017	0.080	0.002	-0.045	0.148
Procrustes coordinate 91	-0.089	-0.031	0.028	0.047	0.011	-0.123	0.046	0.020	-0.017	-0.022	0.009	0.052	-0.027	-0.004	-0.006
Procrustes coordinate 92	-0.023	0.072	-0.038	-0.136	0.021	0.028	0.026	-0.003	0.007	0.080	0.015	0.136	-0.028	-0.011	0.049
Procrustes coordinate 93	0.103	-0.332	0.063	-0.144	0.125	0.106	0.093	-0.021	-0.153	-0.071	0.030	-0.196	0.068	0.212	0.106
Procrustes coordinate 94	-0.023	0.035	-0.010	0.073	0.048	0.030	0.049	-0.134	0.062	-0.066	-0.040	-0.016	-0.063	0.026	-0.029
Procrustes coordinate 95	-0.102	0.096	0.021	-0.084	0.017	-0.081	-0.036	0.120	0.104	0.038	0.031	-0.038	0.036	-0.011	-0.033
Procrustes coordinate 96	-0.067	-0.213	-0.101	-0.170	0.140	-0.154	-0.389	0.637	0.328	0.248	0.097	-0.119	-0.037	0.046	-0.009
Procrustes coordinate 97	-0.061	-0.002	0.026	-0.095	-0.030	0.082	-0.120	-0.065	-0.098	0.037	0.055	-0.010	0.061	0.040	0.012
Procrustes coordinate 98	0.114	-0.035	0.051	0.081	0.111	0.104	-0.089	-0.049	0.012	-0.035	-0.043	-0.009	-0.142	-0.065	0.007
Procrustes coordinate 99	0.068	0.078	-0.156	0.143	0.059	0.082	-0.072	-0.026	0.003	-0.013	0.066	-0.043	0.013	0.005	-0.179
Procrustes coordinate 100	-0.050	-0.029	-0.028	-0.012	-0.050	0.058	-0.098	-0.052	-0.022	-0.018	-0.079	-0.077	0.007	-0.057	0.065
Procrustes coordinate 101	0.018	0.036	0.084	0.024	0.131	0.014	-0.019	-0.006	-0.089	0.016	-0.026	-0.113	-0.064	-0.018	0.028
Procrustes coordinate 102	-0.074	0.112	-0.101	0.065	0.007	-0.249	-0.050	-0.042	-0.152	-0.016	0.091	-0.103	0.237	-0.053	0.003

Table D.3. Loadings onto the first 15 principal component axes for the principal component analysis on the 39 log transformed linear distances. See chapter 2 for a description of acronyms.

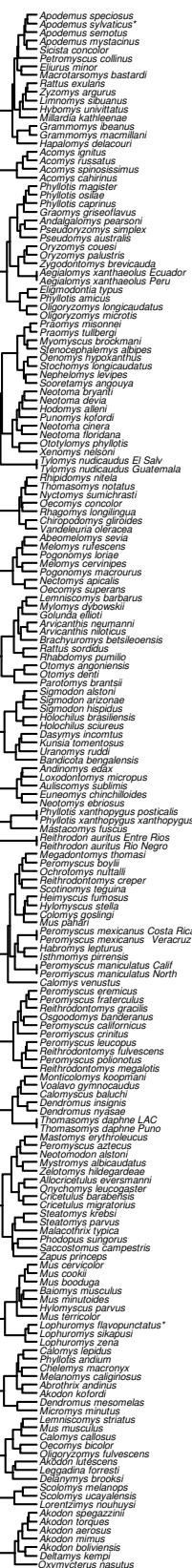
	PC1	PC2	PC3	PC4	PC5	PC6	PC7	PC8	PC9	PC10	PC11	PC12	PC13	PC14	PC15
BR-PT	-0.085	0.217	0.087	-0.232	0.229	-0.028	0.292	-0.215	0.172	-0.089	0.032	-0.225	0.470	-0.243	-0.151
BR-APT	-0.139	-0.037	0.065	-0.019	-0.010	0.088	0.105	0.089	0.058	-0.039	-0.131	-0.169	0.072	-0.040	-0.021
PT-APT	-0.158	-0.082	0.023	0.065	-0.060	0.095	0.002	0.192	-0.098	-0.014	-0.173	-0.109	0.064	-0.047	-0.070
PT-BA	-0.150	0.024	-0.001	0.029	-0.024	0.045	0.026	0.066	-0.108	0.035	-0.024	-0.021	0.027	-0.085	0.007
PT-DM	-0.149	0.008	-0.030	0.129	-0.044	0.085	-0.096	0.128	-0.331	0.046	-0.075	-0.005	0.198	-0.137	0.187
PIP-APT	-0.153	0.186	-0.038	-0.042	0.109	-0.404	-0.282	0.103	-0.026	-0.070	0.022	-0.195	0.102	0.004	0.134
LD-AS	-0.078	0.182	-0.028	-0.081	0.223	0.204	0.170	0.478	0.163	-0.113	0.417	0.238	0.132	-0.031	0.021
BR-LD	-0.139	0.187	-0.129	-0.049	-0.027	0.117	0.106	0.089	0.036	0.120	0.000	-0.183	-0.192	-0.050	0.184
OP-LD	-0.164	-0.231	0.480	-0.050	0.216	-0.280	0.321	0.121	-0.357	-0.092	0.008	0.283	-0.119	-0.109	0.096
PT-AS	-0.144	0.088	-0.059	0.097	0.038	0.057	-0.030	0.126	-0.260	0.198	0.039	-0.031	0.154	-0.170	0.110
PJ-AS	-0.171	-0.101	0.157	-0.076	-0.217	-0.035	0.213	-0.251	0.053	-0.098	-0.402	-0.153	0.053	0.035	0.129
BA-OP	-0.082	0.039	0.023	-0.004	-0.007	0.094	0.026	-0.043	0.213	0.017	0.004	-0.180	0.194	0.140	0.089
BA-DM	-0.141	-0.052	0.037	-0.021	-0.124	0.057	0.076	0.040	0.160	-0.068	-0.016	0.047	-0.058	0.199	0.019
IDR-ANS	-0.171	0.092	0.066	-0.027	0.154	-0.022	0.197	0.062	-0.057	-0.118	0.104	-0.199	-0.496	-0.053	-0.323
NA-PIP	-0.174	-0.067	-0.013	0.021	-0.148	0.005	0.066	-0.112	0.034	0.025	0.014	-0.047	-0.060	-0.151	-0.161
ANS-DZ	-0.167	0.152	0.081	0.103	0.034	0.004	0.063	-0.042	0.153	0.062	-0.075	0.088	0.006	0.065	-0.037
IDR-MPM	-0.177	0.013	0.045	-0.022	-0.087	0.022	0.052	-0.009	0.085	0.041	-0.081	0.003	-0.236	-0.158	0.173
MPM-DZ	-0.182	0.061	0.050	0.207	-0.038	-0.019	-0.051	-0.085	0.093	0.035	0.025	0.147	0.078	0.135	-0.193
MPM-VZ	-0.191	-0.011	-0.048	0.168	0.080	-0.014	-0.028	-0.079	0.125	0.191	-0.047	0.209	0.054	0.027	-0.080
MPM-MT	-0.185	-0.029	-0.067	0.122	-0.045	-0.067	-0.054	-0.068	-0.036	0.217	0.136	0.111	0.047	0.005	-0.053
DZ-VZ	-0.220	-0.575	-0.506	-0.348	0.424	0.083	-0.006	-0.102	-0.016	0.006	-0.044	0.006	-0.013	0.052	0.060
VZ-MT	-0.184	-0.085	-0.046	0.150	-0.103	0.072	-0.228	-0.076	0.078	-0.021	0.160	0.054	-0.118	-0.068	-0.203
MT-PIP	-0.155	-0.028	-0.161	-0.124	-0.208	-0.661	0.030	0.314	0.128	-0.020	0.009	-0.091	0.025	0.298	-0.004
DM-VTZ	-0.143	-0.021	-0.041	0.293	-0.042	0.105	0.156	-0.299	-0.330	-0.327	0.391	-0.230	0.073	0.356	0.278
VTZ-SPF	-0.179	-0.139	0.047	0.020	-0.187	0.047	-0.157	0.082	0.206	-0.277	-0.043	0.094	0.058	-0.392	0.246
VZ-VTZ	-0.150	0.037	0.306	-0.684	-0.308	0.193	-0.258	-0.056	-0.197	0.209	0.225	0.016	0.045	0.150	-0.036
VZ-SPF	-0.192	-0.112	0.025	-0.035	-0.133	0.033	-0.134	-0.009	0.231	-0.472	0.252	-0.005	0.013	-0.068	-0.125
PT-VTZ	-0.160	-0.091	0.037	0.098	-0.082	0.118	-0.119	0.252	-0.104	-0.175	-0.209	-0.037	0.151	-0.065	-0.074
PT-SPF	-0.151	-0.062	0.074	0.099	0.087	0.233	-0.086	0.274	-0.142	0.012	-0.219	-0.222	0.062	0.311	-0.436
IDR-PIP	-0.179	-0.005	0.012	0.020	-0.059	0.007	0.013	-0.118	0.073	0.083	-0.024	0.128	-0.082	-0.013	0.001
ANS-VZ	-0.178	0.057	0.002	0.064	0.086	0.014	0.059	-0.038	0.137	0.127	-0.098	0.104	-0.011	0.020	0.021
APT-BA	-0.142	0.037	0.039	-0.003	-0.025	-0.008	0.146	-0.135	0.006	0.012	0.079	0.090	-0.062	0.184	-0.026
NA-BR	-0.144	0.060	-0.003	0.009	0.066	-0.171	0.085	-0.217	-0.071	0.172	0.103	-0.074	0.117	-0.233	-0.288
ANS-NA	-0.165	0.123	0.120	-0.025	0.184	0.103	0.052	0.013	0.157	0.047	-0.176	0.285	0.162	0.358	0.218
MPI-BR	-0.130	0.054	0.050	0.027	0.063	0.126	0.076	0.156	0.191	0.286	0.091	-0.415	-0.263	-0.036	0.301
MPI-LD	-0.148	0.481	-0.489	-0.198	-0.183	0.053	0.166	-0.033	-0.275	-0.223	-0.212	0.231	-0.107	-0.034	-0.045
AFM-LIS	-0.176	0.015	0.008	0.058	-0.050	0.041	-0.086	-0.100	0.064	0.092	0.038	0.195	-0.175	-0.024	0.065
AFM-PTM	-0.186	-0.090	-0.128	0.120	-0.121	-0.131	-0.001	-0.009	-0.088	0.290	0.226	-0.030	0.181	-0.091	0.009
APT-PTM	-0.161	0.273	0.147	-0.020	0.451	-0.085	-0.528	-0.195	-0.062	-0.163	-0.108	-0.061	-0.141	0.002	0.084

a)

To Fig. D.1b

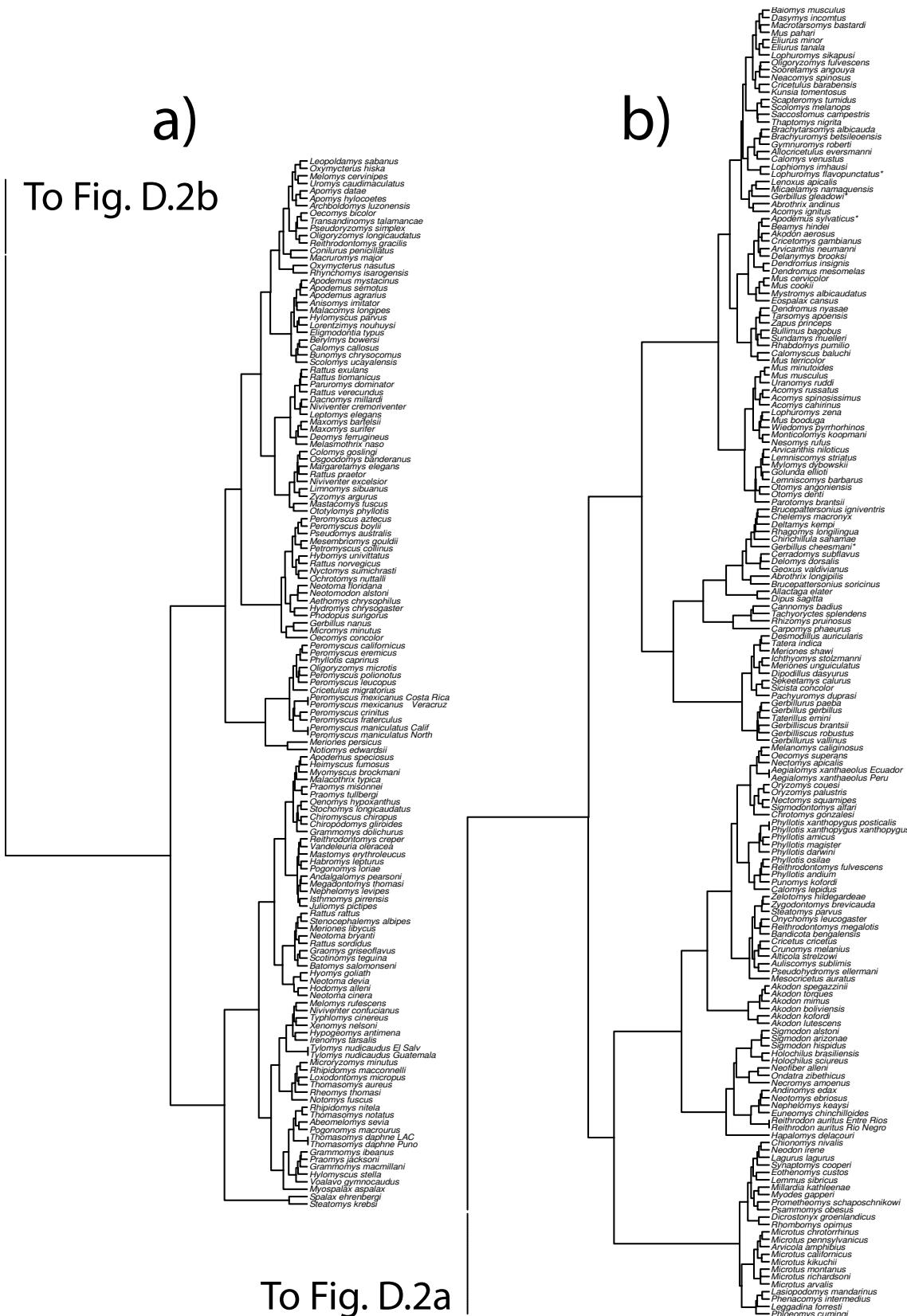


b)



To Fig. D.1a

Figure D.1. PrC 1-102 dendrogram based on squared Euclidean distance between species. Dendrogram uses Ward's hierarchical cluster analysis method.



To Fig. D.2a

Figure D.2. PC 2-39 dendrogram based on squared Euclidean distance between species. Dendrogram uses Ward's hierarchical cluster analysis method.

APPENDIX E

SUPPORTING MATERIAL FOR CHAPTER 6

Table E.1. Average of the raw bioclimatic variables encountered by species within their range. Variables and units are described in Table E.2.

	BIO1	BIO9	BIO12	BIO17	AI
<u>Anomaluromorphia</u>					
Pedetidae					
<i>Pedetes capensis</i>	20.37	15.76	694.51	8.53	13.42
<u>Castorimorpha</u>					
Geomysidae					
<i>Cratogeomys castanops</i>	17.00	10.09	367.12	29.02	15.47
<i>Thomomys umbrinus</i>	17.67	16.76	681.11	27.00	18.36
Heteromyidae					
Dipodomysinae					
<i>Dipodomys agilis</i>	13.93	20.68	444.60	10.65	11.37
<i>Dipodomys californicus</i>	11.04	18.97	860.50	32.05	27.09
<i>Dipodomys compactus</i>	21.82	15.21	645.07	96.24	33.04
<i>Dipodomys deserti</i>	17.84	21.09	173.60	15.84	6.17
<i>Dipodomys elator</i>	17.23	6.16	695.06	91.62	46.77
<i>Dipodomys gravipes</i>	18.42	20.79	176.95	3.16	3.73
<i>Dipodomys heermanni</i>	15.60	22.96	404.96	5.08	8.84
<i>Dipodomys ingens</i>	16.25	24.47	269.45	3.33	5.71
<i>Dipodomys merriami</i>	17.94	17.09	333.31	24.89	11.48
<i>Dipodomys microps</i>	9.71	13.90	245.41	41.19	16.56
<i>Dipodomys nelsoni</i>	18.99	15.35	324.27	22.77	10.98
<i>Dipodomys nitratoides</i>	16.99	25.44	228.19	3.05	4.74
<i>Dipodomys ordii</i>	11.18	6.62	391.56	40.38	23.82
<i>Dipodomys panamintinus</i>	10.72	18.05	349.77	27.97	14.42
<i>Dipodomys phillipsii</i>	16.60	14.81	634.42	25.94	18.20
<i>Dipodomys simulans</i>	17.58	20.69	266.04	7.93	6.37
<i>Dipodomys spectabilis</i>	15.00	13.07	338.21	27.41	13.89
<i>Dipodomys stephensi</i>	16.96	23.42	360.16	12.07	8.85
<i>Dipodomys venustus venustus</i>	13.72	18.40	540.76	6.27	12.72
<i>Dipodomys venustus elephantinus</i>	13.90	19.83	498.00	7.00	11.82
<i>Microdipodops megacephalus</i>	7.98	13.54	271.95	46.10	19.31
<i>Microdipodops pallidus</i>	9.89	10.99	171.83	33.15	13.79
Heteromyinae					
<i>Heteromys anomalus</i>	25.39	25.18	1540.91	108.83	40.33
<i>Heteromys australis</i>	21.13	21.20	3266.05	497.74	148.18
<i>Heteromys catopterius</i>	20.23	19.60	979.00	78.00	32.00
<i>Heteromys d. desmarestianus</i>	23.52	23.22	2072.50	140.11	56.22
<i>Heteromys d. goldmani</i>	20.08	18.64	1894.24	35.67	38.96
<i>Heteromys gaumeri</i>	25.73	25.08	1245.88	103.12	35.07
<i>Heteromys nelsoni</i>	13.57	11.87	1699.22	34.61	45.54
<i>Heteromys oasicus</i>	26.39	25.50	562.50	54.50	16.94
<i>Heteromys teleus</i>	23.76	23.08	1799.00	83.95	41.87
<i>Liomys adspersus</i>	25.71	26.00	2472.16	72.31	46.67
<i>Liomys irroratus</i>	19.25	16.97	807.48	41.62	23.06
<i>Liomys pictus</i>	22.78	22.22	1117.46	33.24	23.23

Table E.1—continued.

	BIO1	BIO9	BIO12	BIO17	AI
<i>Liomys salvini</i>	23.59	23.11	1709.44	45.71	33.73
Perognathinae					
<i>Chaetodipus arenarius</i>	19.95	20.58	121.99	2.24	2.48
<i>Chaetodipus artus</i>	23.00	22.55	784.46	23.57	16.23
<i>Chaetodipus baileyi</i>	20.09	22.14	320.58	17.60	8.61
<i>Chaetodipus californicus</i>	14.49	20.40	487.31	10.21	11.96
<i>Chaetodipus eremicus</i>	17.76	14.04	332.55	24.19	12.03
<i>Chaetodipus fallax</i>	17.54	20.75	258.55	7.32	6.12
<i>Chaetodipus formosus</i>	13.47	16.87	217.07	29.37	11.18
<i>Chaetodipus goldmani</i>	23.10	22.67	526.89	19.29	11.50
<i>Chaetodipus hispidus</i>	14.70	6.94	562.23	61.32	33.10
<i>Chaetodipus intermedius</i>	16.31	16.07	302.10	23.95	11.25
<i>Chaetodipus lineatus</i>	17.64	16.14	392.97	32.45	14.56
<i>Chaetodipus nelsoni</i>	18.31	14.30	398.94	26.16	13.50
<i>Chaetodipus penicillatus</i>	19.33	21.96	287.40	17.79	8.24
<i>Chaetodipus pernix</i>	23.91	23.29	709.51	17.93	13.69
<i>Chaetodipus rудinoris</i>	19.97	20.90	157.30	4.03	3.41
<i>Chaetodipus spinatus</i>	20.40	21.73	160.75	4.57	3.51
<i>Perognathus alticolus</i>	12.08	20.34	416.78	10.17	11.45
<i>Perognathus amplus</i>	18.91	21.88	277.26	19.97	8.55
<i>Perognathus fasciatus</i>	5.56	-7.09	383.65	38.94	92.56
<i>Perognathus flavescens</i>	10.56	0.14	507.91	45.05	39.01
<i>Perognathus flavus</i>	13.68	9.20	422.33	32.85	19.18
<i>Perognathus inornatus</i>	15.92	23.82	364.84	5.63	8.04
<i>Perognathus longimembris</i>	12.82	17.56	237.67	27.81	11.26
<i>Perognathus merriami</i>	18.64	10.60	539.00	62.88	27.73
<i>Perognathus parvus</i>	7.93	12.76	327.92	49.02	22.07
Hystricomorpha					
Ctenodactylomorphi					
Ctenodactylidae					
<i>Ctenodactylus gundi</i>	18.93	28.08	157.16	10.77	4.41
<i>Ctenodactylus vali</i>	20.23	30.07	119.96	6.85	3.01
<i>Felovia vae</i>	28.87	26.61	213.20	0.75	2.87
<i>Massoutiera mzabi</i>	23.81	25.05	33.22	2.08	0.85
<i>Pectinator spekei</i>	25.84	24.86	188.60	10.70	4.47
Hystricognathi					
Abrocomidae					
<i>Abrocoma bennettii</i>	10.11	13.89	322.78	9.49	10.41
Bathyergidae					
<i>Bathyergus janetta</i>	17.18	19.60	112.04	8.90	3.86
<i>Cryptomys hottentotus</i>	16.62	12.77	578.02	43.79	22.39
Caviidae					
Caviinae					
<i>Microcavia australis</i>	12.39	10.62	314.39	35.63	17.39
Dolichotinae					
<i>Dolichotis patagonum</i>	13.13	11.34	267.67	32.19	14.84
<i>Dolichotis salinicola</i>	22.00	16.97	647.13	35.68	18.05
Chinchillidae					
<i>Lagidium viscacia</i>	9.03	7.05	369.36	19.33	16.51
<i>Lagostomus maximus</i>	17.94	12.22	680.82	66.59	30.17
Ctenomyidae					
<i>Ctenomys emilianus</i>	9.19	15.58	468.70	43.32	22.37

Table E.1—continued.

	BIO1	BIO9	BIO12	BIO17	AI
<i>Ctenomys latro</i>	19.09	14.44	618.29	11.01	13.33
<i>Ctenomys mendocinus</i>	15.76	8.72	392.07	32.05	17.88
<i>Ctenomys occultus</i>	20.02	14.21	902.52	82.31	35.43
Hystricidae					
<i>Hystrix africaeaustralis</i>	20.94	17.58	809.19	17.41	16.86
<i>Hystrix cristata</i>	23.18	23.66	1091.45	43.82	24.26
<i>Hystrix indica</i>	19.00	23.31	504.94	15.34	11.47
Octodontidae					
<i>Octodon degus</i>	13.49	17.71	342.74	6.06	8.61
<i>Octodon lunatus</i>	14.43	18.62	369.32	6.14	8.85
Petromuridae					
<i>Petromus typicus</i>	19.43	15.87	220.64	4.27	4.74
Myodonta					
Dipodoidea					
Dipodidae					
Allactaginae					
<i>Allactaga balikunica</i>	5.33	-9.57	83.41	2.91	43.21
<i>Allactaga bullata</i>	4.24	-11.40	125.56	4.11	-13.15
<i>Allactaga elater</i>	12.04	18.39	184.90	16.48	7.68
<i>Allactaga euphratica williamsi</i>	20.33	30.67	180.04	0.23	3.00
<i>Allactaga firouzi</i>	11.48	21.74	197.40	3.00	5.16
<i>Allactaga hotsoni</i>	20.84	28.06	98.19	2.17	1.93
<i>Allactaga major</i>	5.25	-3.48	356.05	58.17	65.16
<i>Allactaga severzovi</i>	12.00	23.85	159.31	12.74	5.88
<i>Allactaga sibirica</i>	3.59	-7.41	225.54	15.46	44.12
<i>Allactaga tetradactyla</i>	19.46	24.74	133.39	0.34	2.32
<i>Pygeretmus platyurus</i>	6.83	8.69	188.93	33.34	16.32
<i>Pygeretmus pumilio</i>	7.62	4.44	204.61	26.44	16.79
<i>Pygeretmus zhikovii</i>	7.29	17.83	261.17	39.93	16.16
Cardiocrainiinae					
<i>Cardiocranus paradoxus</i>	3.26	-12.30	160.59	6.97	-12.14
<i>Salpingotulus michaelis</i>	20.03	25.07	158.03	4.04	3.32
<i>Salpingotus crassicauda</i>	4.90	-10.57	133.58	7.96	-78.75
Dipodinae					
<i>Dipus sagitta</i>	8.65	1.16	132.03	7.62	7.64
<i>Eremodipus lichtensteinii</i>	13.32	25.83	141.65	9.00	4.54
<i>Jaculus blanfordi</i>	18.51	27.97	137.51	2.79	2.85
<i>Jaculus jaculus</i>	23.14	26.63	82.39	2.62	1.67
<i>Jaculus orientalis</i>	16.27	24.13	376.07	25.47	11.64
<i>Paradipus ctenodactylus</i>	14.50	27.17	132.36	5.75	3.63
<i>Stylopodus telum</i>	7.55	7.48	206.52	34.63	17.77
Sicistinae					
<i>Sicista betulina</i>	0.45	-11.88	556.04	76.12	-215.83
<i>Sicista concolor</i>	5.18	-4.02	541.23	18.78	36.66
<i>Sicista napaea</i>	0.40	-13.56	531.27	62.69	-80.08
<i>Sicista subtilis</i>	4.55	-7.64	371.44	60.50	166.49
Zapodinae					
<i>Eozapus setchuanus</i>	2.01	-7.12	634.55	13.71	54.97
<i>Napaeozapus insignis</i>	3.42	-6.21	949.51	173.25	309.50
<i>Zapus hudsonius</i>	2.12	-7.52	701.58	109.85	294.54
<i>Zapus princeps</i>	3.20	0.29	530.39	75.41	64.05
<i>Zapus trinotatus</i>	8.41	14.95	1685.75	117.46	74.03

Table E.1—continued.

	BIO1	BIO9	BIO12	BIO17	AI
Muroidea					
Calomyscidae					
Calomyscinae					
<i>Calomyscus baluchi</i>	13.32	23.91	250.47	2.90	5.88
<i>Calomyscus bailwardi</i>	12.13	17.07	397.66	19.00	13.20
Cricetidae					
Arvicolinae					
<i>Alticola strelzowi</i>	-0.05	-14.74	308.66	37.74	-32.25
<i>Arvicola amphibius</i>	8.97	7.57	815.80	161.25	76.58
<i>Chionomys nivalis</i>	7.93	11.25	768.53	120.88	55.56
<i>Dicrostonyx groenlandicus</i>	-13.54	-25.05	228.77	29.09	-43.89
<i>Ellobius talpinus</i>	6.71	-0.07	288.64	45.98	36.42
<i>Eolagurus luteus</i>	4.01	-12.43	185.86	15.12	-30.65
<i>Eolagurus przewalskii</i>	3.86	-10.94	106.84	3.41	-17.79
<i>Eothenomys custos</i>	8.89	2.35	911.84	22.66	35.15
<i>Lagurus lagurus</i>	3.65	-7.24	338.02	50.14	121.52
<i>Lasiopodomys mandarinus</i>	8.14	-6.82	594.91	24.05	61.82
<i>Lemmus sibiricus</i>	-11.89	-25.54	308.79	42.78	-98.03
<i>Microtus arvalis</i>	5.48	-3.77	592.26	96.82	112.34
<i>Microtus californicus</i>	13.62	20.41	658.59	18.17	17.53
<i>Microtus chrotorrhinus</i>	2.49	-6.66	983.91	182.59	367.53
<i>Microtus kikuchii</i>	10.10	7.43	3454.53	250.19	172.06
<i>Microtus montanus</i>	6.05	8.47	436.00	61.89	33.69
<i>Microtus pennsylvanicus</i>	5.18	-2.71	732.96	121.56	124.22
<i>Microtus richardsoni</i>	3.88	6.40	652.84	96.24	58.72
<i>Myodes gapperi</i>	0.83	-8.64	653.97	100.80	473.46
<i>Neodon irene</i>	2.38	-6.14	661.28	14.93	49.91
<i>Neofiber alleni</i>	21.70	17.61	1317.57	178.43	59.56
<i>Ondatra zibethicus</i>	1.98	-5.83	640.43	97.96	167.77
<i>Phenacomys intermedius</i>	4.93	6.35	674.57	94.71	57.34
<i>Prometheomys schaposchnikowi</i>	2.30	-6.00	967.49	143.34	254.10
<i>Synaptomys cooperi</i>	6.41	-4.15	936.08	158.94	191.51
Cricetinae					
<i>Allocricetus curtatus</i>	0.73	-16.38	207.98	6.19	3.87
<i>Allocricetus eversmanni</i>	3.88	-7.88	290.27	47.21	144.32
<i>Cricetus barabensis barabensis</i>	2.34	-14.47	429.78	21.67	-11.67
<i>Cricetus barabensis griseus</i>	2.34	-14.47	429.78	21.67	-11.67
<i>Cricetus longicaudatus</i>	1.63	-13.50	330.44	10.43	-3.69
<i>Cricetus migratorius</i>	7.86	6.58	348.22	40.69	24.48
<i>Cricetus cricetus</i>	4.84	-5.16	459.01	72.57	105.35
<i>Mesocricetus auratus</i>	17.17	27.59	349.23	2.36	6.80
<i>Phodopus campbelli</i>	1.32	-15.62	255.70	8.58	2.13
<i>Phodopus roborovskii</i>	4.50	-10.43	185.17	6.60	-85.82
<i>Phodopus sungorus</i>	1.84	-13.80	356.97	47.17	-59.49
Neotominae					
<i>Baiomys musculus</i>	21.96	21.01	1336.86	36.09	27.90
<i>Habromys lepturus</i>	13.00	12.57	1798.00	103.40	66.58
<i>Hodomys alleni</i>	22.36	21.50	1072.37	18.75	20.14
<i>Isthmomys pirrensis</i>	24.45	24.66	2758.97	147.79	65.63
<i>Megadontomys thomasi</i>	16.75	17.13	1642.29	34.71	38.37
<i>Neotoma albigena</i>	16.22	17.45	361.96	26.68	12.73
<i>Neotoma bryanti</i>	18.98	21.00	84.25	1.85	1.81
<i>Neotoma cinerea</i>	3.54	2.02	554.79	75.79	58.34

Table E.1—continued.

	BIO1	BIO9	BIO12	BIO17	AI
<i>Neotoma devia</i>	17.78	20.88	223.48	20.78	8.06
<i>Neotoma floridana</i>	15.77	12.94	1151.77	206.78	76.43
<i>Neotoma goldmani</i>	18.75	16.37	359.98	23.98	11.72
<i>Neotoma lepida</i>	12.83	16.55	252.00	30.50	12.41
<i>Neotoma mexicana</i>	16.02	14.20	597.70	33.93	19.90
<i>Neotomodon alstoni</i>	13.12	11.52	959.36	37.63	31.24
<i>Ochrotomys nutalli</i>	15.87	15.47	1284.59	248.87	83.46
<i>Onychomys leucogaster</i>	9.15	2.07	428.58	47.24	34.68
<i>Onychomys torridus</i>	16.58	19.64	305.16	24.01	10.60
<i>Osgoodomys banderanus</i>	22.71	22.16	1119.30	17.08	20.29
<i>Peromyscus aztecus</i>	19.99	18.58	1494.48	67.41	39.06
<i>Peromyscus boylii</i>	11.27	8.80	401.16	41.25	22.59
<i>Peromyscus californicus</i>	14.35	19.83	446.35	11.14	11.41
<i>Peromyscus crinitus</i>	10.69	14.55	257.00	39.32	15.82
<i>Peromyscus eremicus</i>	18.59	17.43	356.13	23.24	11.31
<i>Peromyscus fraterculus</i>	18.83	20.74	200.71	6.19	4.69
<i>Peromyscus leucopus</i>	12.31	4.66	834.08	128.59	71.34
<i>Peromyscus maniculatus</i>	5.33	-1.52	662.63	95.27	89.05
<i>Peromyscus merriami</i>	22.04	23.07	398.58	13.83	8.73
<i>Peromyscus mexicanus</i>	22.49	21.51	1834.06	114.30	49.99
<i>Peromyscus pectoralis</i>	18.79	14.01	515.67	42.65	19.61
<i>Peromyscus polionotus</i>	17.78	17.86	1335.08	244.54	76.69
<i>Reithrodontomys creper</i>	17.20	16.93	2973.63	226.47	105.13
<i>Reithrodontomys fulvescens</i>	18.79	15.63	875.41	93.01	36.98
<i>Reithrodontomys gracilis</i>	24.73	24.14	1626.04	94.33	39.99
<i>Reithrodontomys megalotis</i>	11.21	7.09	515.60	47.54	28.84
<i>Scotinomys teguina</i>	20.59	19.85	1810.27	102.10	50.12
<i>Xenomys nelsoni</i>	25.79	24.35	982.16	11.77	15.78
Sigmodontinae					
<i>Abrothrix andinus</i>	6.55	4.40	286.73	9.78	12.74
<i>Abrothrix longipilis</i>	8.13	11.62	626.34	73.72	37.73
<i>Aegialomys xanthaeolus</i>	18.41	17.49	559.39	27.42	15.83
<i>Akodon aerosus</i>	19.86	18.99	1884.46	263.46	86.08
<i>Akodon boliviensis</i>	9.00	6.03	595.78	17.82	22.35
<i>Akodon iniscatus</i>	11.14	12.82	236.95	36.99	15.33
<i>Akodon kofordi</i>	15.07	13.11	1898.81	187.87	86.65
<i>Akodon lutescens</i>	12.33	8.56	606.70	19.12	19.76
<i>Akodon mimus</i>	10.50	8.17	818.26	38.07	32.53
<i>Akodon molinae</i>	14.67	9.53	374.42	47.71	22.25
<i>Akodon spegazzinii</i>	14.21	9.09	380.80	12.16	11.69
<i>Akodon torques</i>	15.70	14.44	1267.27	101.58	49.60
<i>Andalgalomys pearsoni</i>	24.68	21.26	683.60	44.61	18.42
<i>Andinomys edax</i>	11.02	6.90	387.23	7.79	11.98
<i>Auliscomys sublimis</i>	6.65	3.53	388.39	9.42	15.84
<i>Brucepattersonius igniventris</i>	19.22	15.62	1340.65	182.98	65.79
<i>Brucepattersonius soricinus</i>	20.01	16.52	1577.39	193.74	70.11
<i>Calomys callosus</i>	23.81	21.55	1177.49	69.43	30.62
<i>Calomys lepidus</i>	7.67	4.69	448.90	13.27	18.13
<i>Calomys musculinus</i>	15.12	11.56	512.72	48.23	23.63
<i>Calomys venustus</i>	16.91	10.49	766.38	47.07	28.02
<i>Cerradomys subflavus</i>	23.34	22.11	983.76	48.56	23.82
<i>Chelemys macronyx</i>	7.69	12.41	864.57	91.40	48.91
<i>Chinchillula sahamae</i>	5.52	2.78	588.33	14.59	25.81

Table E.1—continued.

	BIO1	BIO9	BIO12	BIO17	AI
<i>Delomys dorsalis</i>	17.76	15.01	1654.65	291.13	99.63
<i>Deltamys kempfi</i>	17.42	18.14	1217.94	262.00	78.07
<i>Eligmodontia moreni</i>	17.77	10.60	258.45	11.46	7.99
<i>Eligmodontia morgani</i>	7.49	10.54	305.93	44.72	21.81
<i>Eligmodontia typus</i>	12.18	11.09	280.70	37.46	16.99
<i>Euneomys chinchilloides</i>	4.90	3.92	641.68	133.96	79.26
<i>Geoxus valdivianus</i>	8.27	12.53	1274.21	144.90	73.47
<i>Graomys edithae</i>	12.76	6.27	341.50	13.77	12.58
<i>Graomys griseoflavus</i>	17.77	13.88	545.28	43.05	20.63
<i>Holochilus brasiliensis</i>	19.97	17.01	1227.87	168.03	57.81
<i>Holochilus sciurus</i>	25.68	25.42	2015.25	173.42	57.62
<i>Ichthyomys stolzmanni</i>	15.40	14.76	2068.15	309.29	115.65
<i>Irenomys tarsalis</i>	7.93	12.22	1659.57	210.25	103.05
<i>Juliomys pictipes</i>	18.92	16.02	1494.26	195.33	70.88
<i>Kunsia tomentosus</i>	24.32	22.90	1563.17	55.78	32.95
<i>Lenoxus apicalis</i>	17.92	16.25	1675.25	144.14	62.95
<i>Loxodontomys micropus</i>	7.60	11.85	809.77	94.68	49.00
<i>Melanomys caliginosus</i>	22.69	22.67	2535.25	271.20	88.59
<i>Microryzomys minutus</i>	16.45	15.72	1584.92	187.85	73.79
<i>Neacomys spinosus</i>	24.40	23.58	2020.41	211.27	67.12
<i>Necromys amoenus</i>	7.84	5.20	667.72	19.65	26.46
<i>Nectomys apicalis</i>	25.74	25.14	2316.25	309.77	85.30
<i>Nectomys squamipes</i>	21.59	19.61	1270.55	133.30	47.12
<i>Neotomys ebriosus</i>	7.17	4.36	409.81	12.74	17.26
<i>Nephelomys keaysi</i>	17.27	15.38	1753.54	172.66	72.96
<i>Nephelomys livipes</i>	15.19	13.22	1331.60	109.72	54.79
<i>Notiomys edwardsii</i>	8.31	11.60	221.57	34.70	15.69
<i>Oecomys bicolor</i>	25.47	25.13	2125.18	198.00	63.78
<i>Oecomys concolor</i>	25.83	25.68	2204.31	215.27	66.96
<i>Oecomys superans</i>	25.51	25.13	2475.40	358.57	96.09
<i>Oligoryzomys fulvescens</i>	24.72	24.59	1970.08	176.53	58.99
<i>Oligoryzomys longicaudatus</i>	9.58	11.35	1189.26	188.37	83.32
<i>Oligoryzomys microtis</i>	25.52	24.71	2037.99	152.39	55.03
<i>Oryzomys couesi</i>	23.41	22.44	1606.31	96.37	41.86
<i>Oryzomys palustris</i>	16.80	16.16	1281.67	241.74	79.36
<i>Oxymycterus hiska</i>	18.42	16.45	1469.96	112.54	51.39
<i>Oxymycterus nasutus</i>	18.16	17.20	1554.84	327.40	99.82
<i>Phyllotis amicus</i>	19.29	18.31	61.23	0.71	1.20
<i>Phyllotis andium</i>	13.24	12.36	793.97	64.46	34.38
<i>Phyllotis caprinus</i>	12.74	8.05	394.77	5.88	10.63
<i>Phyllotis darwini</i>	13.39	17.46	405.41	12.68	11.44
<i>Phyllotis gerbillus</i>	22.94	21.29	56.83	0.03	0.87
<i>Phyllotis magister</i>	7.86	5.92	313.27	4.17	10.34
<i>Phyllotis osilae</i>	8.66	5.34	427.13	12.15	16.20
<i>Phyllotis xanthopygus</i>	8.15	8.28	330.31	24.70	17.20
<i>Pseudoryzomys simplex</i>	23.93	21.97	1290.69	56.18	29.57
<i>Punomys kofordi</i>	4.04	1.28	742.02	26.98	40.78
<i>Reithrodon auritus auritus</i>	11.22	10.35	400.65	61.84	27.67
<i>Reithrodon auritus physodes</i>	5.55	10.35	584.00	81.00	42.66
<i>Rhagomys longilingua</i>	18.72	17.19	2011.27	226.46	84.99
<i>Rheomys thomasi</i>	21.81	20.94	2037.28	53.51	42.40
<i>Rhipidomys macconnelli</i>	23.62	23.61	2573.30	303.51	92.44
<i>Rhipidomys nitela</i>	25.81	26.31	2316.77	241.21	72.20

Table E.1—continued.

	BIO1	BIO9	BIO12	BIO17	AI
<i>Scapteromys tumidus</i>	17.50	16.87	1295.04	274.75	84.89
<i>Scolomys melanops</i>	24.44	24.65	3028.23	613.48	150.20
<i>Scolomys ucayalensis</i>	25.95	25.56	2693.92	471.50	117.02
<i>Sigmodon alstoni</i>	26.32	26.70	1885.10	122.83	46.03
<i>Sigmodon arizonae</i>	19.79	20.55	586.94	26.90	15.13
<i>Sigmodon fulviventer</i>	16.48	15.30	472.06	21.97	14.12
<i>Sigmodon hispidus</i>	16.52	11.93	963.35	160.31	62.03
<i>Sigmodon ochrognathus</i>	16.93	15.20	410.96	23.48	13.22
<i>Sigmodontomys alfari</i>	24.76	24.72	2877.64	318.40	96.41
<i>Sooretamys angouya ratticeps</i>	20.56	17.86	1411.33	196.67	65.45
<i>Thaptomys nigrita</i>	20.02	17.74	1407.86	212.44	69.39
<i>Thomasomys aureus</i>	14.54	13.48	1544.77	173.92	75.93
<i>Thomasomys daphne</i>	17.36	15.45	1821.20	176.71	74.95
<i>Thomasomys notatus</i>	15.15	13.82	1237.83	99.31	49.63
<i>Transandinomys talamancae</i>	25.05	24.89	2447.98	254.66	78.72
<i>Wiedomys pyrrhorhinos</i>	23.54	22.61	764.30	31.05	17.11
<i>Zygodontomys brevicauda</i>	26.03	26.27	2072.55	161.19	55.43
Tylomyinae					
<i>Nyctomys sumichrasti</i>	23.80	23.44	2009.03	111.00	49.63
<i>Ototylomys phyllotis</i>	24.53	24.19	1788.69	117.65	46.55
<i>Tylomys nudicaudus</i>	23.18	22.60	1794.77	98.18	45.12
Muridae					
Deomyinae					
<i>Acomys cahirinus</i>	23.19	22.13	46.18	1.80	1.03
<i>Acomys cineraceus</i>	25.51	24.49	758.79	20.17	14.19
<i>Acomys dimidiatus</i>	23.81	27.77	118.24	4.07	2.40
<i>Acomys ignitus</i>	23.71	22.31	721.29	44.92	19.04
<i>Acomys percivali</i>	24.95	25.23	597.48	45.31	16.27
<i>Acomys russatus</i>	22.75	25.65	105.49	5.83	2.59
<i>Acomys spinosissimus</i>	21.90	18.60	863.30	13.74	16.41
<i>Acomys wilsoni</i>	24.66	23.91	584.21	26.12	13.05
<i>Deomys ferrugineus</i>	23.89	23.40	1738.34	148.42	52.31
<i>Lophuromys flavopunctatus</i>	22.85	22.38	1548.56	145.15	50.46
<i>Lophuromys zena</i>	15.71	15.60	955.83	111.33	44.68
<i>Lophuromys sikapusi</i>	24.42	24.16	1656.52	107.60	42.96
<i>Uranomys ruddi</i>	24.93	24.24	1199.21	32.86	22.93
Gerbillinae					
<i>Ammodillus imbellis</i>	26.55	25.72	195.70	2.95	3.17
<i>Brachionomys przewalskii</i>	7.89	-3.67	65.03	2.17	3.88
<i>Desmodillus braueri</i>	28.00	24.45	200.55	0.14	2.66
<i>Desmodillus auricularis</i>	18.90	14.02	325.30	13.01	8.88
<i>Dipodillus campestris</i>	18.47	25.17	250.26	15.86	7.10
<i>Dipodillus dasyurus</i>	22.41	29.05	126.50	2.55	2.34
<i>Dipodillus harwoodi</i>	20.15	18.72	796.65	38.71	21.30
<i>Dipodillus lowei</i>	20.53	17.85	575.43	0.63	9.56
<i>Dipodillus mackillagini</i>	25.47	20.18	33.31	0.43	0.56
<i>Dipodillus magharebi</i>	17.17	24.26	531.91	14.47	12.32
<i>Dipodillus simoni</i>	17.49	25.51	235.06	19.43	7.56
<i>Dipodillus stigmonyx</i>	28.72	25.76	242.47	0.00	3.13
<i>Gerbilliscus afra</i>	16.64	20.73	355.56	44.83	15.43
<i>Gerbilliscus boehmi</i>	21.15	18.85	1101.83	12.92	20.37
<i>Gerbilliscus brantsii brantsii</i>	19.47	13.76	513.26	13.62	12.15
<i>Gerbilliscus brantsii humpatensis</i>	18.51	16.42	1292.00	2.00	23.11

Table E.1—continued.

	BIO1	BIO9	BIO12	BIO17	AI
<i>Gerbilliscus brantsii perpallidus</i>	19.47	13.76	513.26	13.62	12.15
<i>Gerbilliscus guineae</i>	26.77	26.02	1275.15	15.04	19.84
<i>Gerbilliscus inclusus</i>	23.71	21.56	1101.55	29.06	21.86
<i>Gerbilliscus kempfi</i>	25.71	25.29	1249.08	45.13	25.16
<i>Gerbilliscus leucogaster</i>	21.38	17.75	838.89	10.56	15.65
<i>Gerbilliscus nigricaudus</i>	25.24	24.38	512.66	30.17	12.54
<i>Gerbilliscus phillipsi</i>	23.73	22.71	540.52	47.61	16.75
<i>Gerbilliscus robustus</i>	25.43	24.05	619.68	17.70	11.86
<i>Gerbilliscus validus</i>	23.26	21.54	1093.29	22.04	20.63
<i>Gerbillurus paeba</i>	19.34	14.69	338.42	12.47	8.80
<i>Gerbillurus setzeri</i>	18.77	16.70	46.90	0.09	0.84
<i>Gerbillurus tytonis</i>	16.75	14.80	44.90	3.08	1.58
<i>Gerbillurus vallinus</i>	18.65	14.27	159.88	9.38	5.11
<i>Gerbillus agag</i>	28.14	24.94	312.67	0.00	4.10
<i>Gerbillus amoenus</i>	21.58	21.75	16.28	0.10	0.28
<i>Gerbillus andersoni</i>	19.69	25.31	126.38	0.38	2.19
<i>Gerbillus aquilus</i>	20.23	29.90	93.19	1.20	1.72
<i>Gerbillus cheesmani</i>	24.66	30.59	91.40	1.67	1.57
<i>Gerbillus famulus</i>	24.57	22.27	240.86	13.43	5.98
<i>Gerbillus floweri</i>	19.82	25.65	40.81	0.01	0.69
<i>Gerbillus garamantis</i>	24.36	32.65	16.00	1.00	0.37
<i>Gerbillus gerbillus</i>	24.59	23.83	47.77	0.85	0.84
<i>Gerbillus gleadowi</i>	26.49	21.36	269.94	5.29	4.71
<i>Gerbillus henleyi</i>	24.09	25.98	143.65	3.90	2.76
<i>Gerbillus hesperinus</i>	17.20	19.99	295.38	3.92	6.21
<i>Gerbillus hoogstraali</i>	18.70	23.70	230.07	2.80	4.51
<i>Gerbillus latastei</i>	19.84	27.24	127.30	2.15	2.48
<i>Gerbillus mauritaniae</i>	28.21	24.83	245.01	0.02	3.21
<i>Gerbillus mesopotamiae</i>	22.97	33.72	174.49	0.05	2.65
<i>Gerbillus muriculus</i>	24.76	20.77	218.09	0.00	3.14
<i>Gerbillus nanus</i>	24.46	26.96	106.05	2.51	1.95
<i>Gerbillus nigeriae</i>	25.99	25.24	75.07	0.27	1.09
<i>Gerbillus occiduus</i>	19.62	21.91	86.04	1.29	1.70
<i>Gerbillus perpallidus</i>	19.86	25.52	63.05	0.00	1.06
<i>Gerbillus poecilops</i>	28.34	29.27	157.91	17.51	4.74
<i>Gerbillus pulvinatus</i>	26.91	27.32	508.30	60.04	16.54
<i>Gerbillus pusillus</i>	25.02	24.05	520.51	21.07	11.14
<i>Gerbillus pyramidum</i>	25.94	22.02	76.29	0.04	1.07
<i>Gerbillus tarabuli</i>	25.02	25.70	62.45	1.39	1.13
<i>Meriones crassus</i>	21.75	28.07	84.25	1.95	1.63
<i>Meriones erythrourus</i>	13.24	24.07	257.00	11.00	7.47
<i>Meriones grandis</i>	16.34	24.45	368.10	23.55	11.09
<i>Meriones hurrianae</i>	26.36	22.40	266.02	5.78	4.73
<i>Meriones libycus</i>	16.64	24.96	179.53	8.84	4.89
<i>Meriones meridianus</i>	7.40	2.79	217.01	14.40	13.00
<i>Meriones persicus</i>	15.08	24.64	240.40	8.35	6.24
<i>Meriones rex</i>	22.33	22.83	196.62	13.79	5.56
<i>Meriones shawi</i>	17.48	25.30	291.73	19.33	8.59
<i>Meriones tamariscinus</i>	7.37	4.70	202.41	24.15	15.68
<i>Meriones tristrami</i>	12.84	21.52	449.35	23.64	14.34
<i>Meriones unguiculatus</i>	1.09	-15.30	315.61	12.09	0.55
<i>Meriones vinogradovi</i>	12.06	22.29	416.56	15.98	12.41
<i>Pachyuromys duprasi</i>	18.75	27.40	201.57	14.01	5.75

Table E.1—continued.

	BIO1	BIO9	BIO12	BIO17	AI
<i>Psammomys obesus</i>	21.43	27.90	112.66	5.52	2.67
<i>Rhombomys opimus</i>	9.62	8.84	154.40	9.35	6.91
<i>Sekeetamys calurus</i>	21.10	24.32	34.62	0.07	0.57
<i>Tatera indica</i>	23.94	24.71	688.03	16.04	12.91
<i>Taterillus arenarius</i>	28.84	25.80	164.73	0.48	2.20
<i>Taterillus congicus</i>	25.57	25.06	1307.90	41.73	25.52
<i>Taterillus emini</i>	24.81	23.98	788.07	34.83	17.47
<i>Taterillus gracilis</i>	27.30	25.81	829.45	9.06	12.64
<i>Taterillus harringtoni</i>	23.16	23.22	670.86	41.36	17.58
<i>Taterillus lacustris</i>	27.20	25.30	482.53	0.00	6.49
<i>Taterillus pygargus</i>	27.95	25.89	425.68	0.22	5.64
Lophiomysinae					
<i>Lophiomys imhausi</i>	22.38	20.84	604.94	41.79	17.47
Murinae					
<i>Abeomelomys sevia</i>	16.48	15.75	2509.20	373.78	134.48
<i>Aethomys chrysophilus</i>	21.76	17.98	745.68	11.76	14.26
<i>Aethomys namaquensis</i>	19.32	14.79	476.37	18.42	12.58
<i>Anisomys imitator</i>	18.02	17.53	3163.05	606.35	188.58
<i>Apodemus agrarius</i>	5.46	-6.06	628.83	71.91	129.78
<i>Apodemus mystacinus</i>	11.16	19.39	625.69	49.32	24.85
<i>Apodemus semotus</i>	19.68	16.56	2469.35	179.36	82.12
<i>Apodemus speciosus</i>	10.48	2.30	1686.94	231.78	154.20
<i>Apodemus sylvaticus</i>	9.31	7.03	751.18	126.32	63.95
<i>Apomys datae</i>	21.30	20.21	2985.20	186.78	84.79
<i>Apomys hylocoetes</i>	20.50	20.43	2754.84	420.93	128.15
<i>Archboldomys luzonensis</i>	20.60	20.25	3170.00	317.00	114.67
<i>Arvicanthis neumanni</i>	24.09	22.82	541.61	17.88	11.21
<i>Arvicanthis niloticus</i>	25.55	24.00	738.16	20.12	13.93
<i>Bandicota bengalensis</i>	24.71	21.92	1278.08	36.85	25.34
<i>Batomys salomonensi</i>	24.51	24.53	2636.03	394.57	106.77
<i>Berylmys bowersi</i>	19.85	14.42	1590.19	93.06	49.50
<i>Bullimus bagobus</i>	25.22	25.31	2663.22	402.93	106.27
<i>Bunomys chrysocomus</i>	23.87	23.87	2149.66	326.99	89.66
<i>Carpomys phaeurus</i>	19.05	17.99	3151.20	217.86	100.94
<i>Chiromyscus chiropus</i>	22.26	18.78	1661.13	47.46	35.64
<i>Chiropodomys gliroides</i>	22.43	19.06	1996.10	124.60	56.50
<i>Chrotomys gonzalesi</i>	21.19	20.82	3069.00	304.50	108.49
<i>Colomys goslingi</i>	22.94	23.05	1518.97	151.18	50.50
<i>Conilurus penicillatus</i>	27.09	23.60	1194.83	7.15	17.38
<i>Cremnomys cutchicus</i>	26.30	23.10	539.67	6.03	8.53
<i>Crunomys melanius</i>	24.36	24.26	2223.22	337.49	91.47
<i>Dacnomys millardi</i>	17.09	12.06	1655.83	55.70	45.71
<i>Dasymys incomitus</i>	22.32	20.65	1222.51	72.34	33.07
<i>Golunda ellioti</i>	25.68	23.50	984.95	22.51	17.84
<i>Grammomys dolichurus</i>	21.70	19.60	1023.46	32.00	22.63
<i>Grammomys ibeanus</i>	19.46	18.27	990.58	47.45	26.89
<i>Grammomys macmillani</i>	24.88	25.02	1146.32	37.19	22.81
<i>Hapalomys delacourii</i>	20.63	15.45	1538.78	71.64	42.01
<i>Heimyscus fumosus</i>	24.22	23.85	1735.48	152.97	52.47
<i>Hybomys univittatus</i>	24.24	23.81	1766.76	165.43	55.16
<i>Hydromys chrysogaster</i>	21.46	18.88	1080.33	144.24	47.13
<i>Hylomyscus parvus</i>	24.02	23.96	1651.41	129.24	47.11
<i>Hylomyscus stella</i>	23.99	23.90	1769.51	196.63	60.83

Table E.1—continued.

	BIO1	BIO9	BIO12	BIO17	AI
<i>Hyomys goliath</i>	18.61	17.75	2773.08	438.13	143.22
<i>Leggadina forresti</i>	22.51	16.65	294.68	28.28	10.90
<i>Lemniscomys barbarus</i>	16.84	23.95	509.15	19.04	12.85
<i>Lemniscomys striatus</i>	24.15	23.82	1411.28	58.94	31.12
<i>Leopoldamys sabanus</i>	24.91	23.54	2327.88	276.22	82.75
<i>Leptomysh elegans</i>	23.80	23.37	2947.56	504.25	134.28
<i>Limnomys sibuanus</i>	20.26	20.37	2696.23	419.49	127.45
<i>Lorentzimys nouhuysi</i>	20.98	20.44	3178.84	577.51	165.13
<i>Macruromys major</i>	19.06	18.37	3109.00	562.15	172.36
<i>Malacomys longipes</i>	24.25	24.09	1836.13	160.87	55.12
<i>Margaretamys elegans</i>	18.36	18.21	2202.87	295.56	101.69
<i>Mastacomys fuscus</i>	10.04	14.59	1518.02	238.87	96.15
<i>Mastomys erythroleucus</i>	26.27	25.30	1050.13	32.73	20.04
<i>Maxomys bartelsii</i>	20.10	19.61	3039.36	330.33	117.42
<i>Maxomys surifer</i>	25.32	24.11	2291.24	250.90	76.57
<i>Melasmotherix naso</i>	18.37	18.22	2200.52	295.50	101.59
<i>Melomys cervinipes</i>	19.89	15.73	1180.08	116.19	46.83
<i>Melomys rufescens</i>	24.84	24.44	3044.66	546.75	138.94
<i>Mesembriomys gouldii</i>	25.11	22.49	1314.06	27.51	23.79
<i>Micromys minutus</i>	4.67	-6.74	675.23	74.65	160.55
<i>Millardia gleadowi</i>	26.73	21.81	260.97	4.15	4.33
<i>Millardia kathleenae</i>	26.57	23.62	855.12	8.69	13.24
<i>Mus booduga</i>	25.70	23.03	1081.74	22.71	19.28
<i>Mus cervicolor</i>	22.04	18.35	2127.53	121.03	58.82
<i>Mus cookii</i>	21.29	16.69	1859.89	41.41	39.03
<i>Mus minutoides</i>	21.84	20.17	1035.60	55.51	27.30
<i>Mus musculus</i>	15.53	15.35	658.05	92.89	34.87
<i>Mus pahari</i>	19.43	14.15	1589.54	47.85	38.89
<i>Mus saxicola</i>	24.89	22.72	1000.58	21.07	18.20
<i>Mus spretus</i>	15.07	21.77	517.99	44.76	18.78
<i>Mus terricolor</i>	25.71	23.14	1003.66	19.89	17.65
<i>Mylomys dybowskii</i>	23.74	23.91	1436.64	88.77	37.00
<i>Myomyscus brockmani</i>	23.66	23.13	1014.95	50.68	24.25
<i>Niviventer confucianus</i>	13.37	3.97	1044.90	65.41	50.45
<i>Niviventer cremoriventer</i>	25.74	25.72	2805.75	450.51	114.94
<i>Niviventer excelsior</i>	8.32	1.57	922.13	27.72	39.55
<i>Notomys alexis</i>	22.46	18.93	250.04	23.45	8.72
<i>Notomys cervinus</i>	23.35	17.48	203.00	23.31	8.13
<i>Notomys fuscus</i>	21.84	15.46	172.63	26.98	9.07
<i>Oenomys hypoxanthus</i>	23.90	23.46	1570.82	117.20	44.19
<i>Otomys angoniensis</i>	18.99	15.12	889.40	26.40	21.65
<i>Otomys denti</i>	19.35	19.13	1365.57	157.86	55.78
<i>Parotomys brantsii</i>	17.67	13.19	249.75	19.83	9.64
<i>Parotomys littledalei</i>	17.79	14.02	178.03	12.73	6.38
<i>Paruromys dominator</i>	23.87	23.87	2149.66	326.99	89.66
<i>Phloeomys cumingi</i>	26.22	26.02	2815.08	294.55	87.93
<i>Pogonomys loriae</i>	20.06	19.50	3222.03	575.63	170.67
<i>Pogonomys macrourus</i>	21.74	21.14	2900.10	496.49	141.35
<i>Praomys jacksoni</i>	23.78	23.08	1577.17	118.94	44.92
<i>Praomys misonnei</i>	23.96	23.87	1820.59	276.13	75.72
<i>Praomys tullbergi</i>	25.88	26.16	1856.28	97.78	42.09
<i>Pseudohydromys ellermani</i>	18.13	17.60	3202.27	619.22	191.52
<i>Pseudomys australis</i>	21.03	16.45	156.03	28.01	8.87

Table E.1—continued.

	BIO1	BIO9	BIO12	BIO17	AI
<i>Pseudomys hermannsburgensis</i>	22.45	18.68	263.17	25.89	9.47
<i>Rattus exulans</i>	23.34	22.99	2540.68	332.46	98.56
<i>Rattus norvegicus</i>	11.40	12.93	758.89	124.63	50.34
<i>Rattus praetor</i>	25.49	25.33	2997.42	572.47	139.46
<i>Rattus rattus</i>	17.27	15.94	1115.28	147.57	54.58
<i>Rattus sordidus</i>	24.95	22.63	1440.01	63.47	32.27
<i>Rattus tiomanicus</i>	25.51	25.49	2772.53	444.91	114.26
<i>Rattus verecundus</i>	19.53	18.90	3159.60	567.46	171.32
<i>Rattus villosissimus</i>	23.91	18.25	402.51	21.07	10.41
<i>Rhabdomys pumilio</i>	18.98	14.73	555.46	17.48	13.83
<i>Rhynchomys isarogensis</i>	24.88	24.29	2775.75	284.13	89.51
<i>Stenocephalemys albipes</i>	19.03	18.68	1245.82	56.25	33.23
<i>Stochomys longicaudatus</i>	24.65	24.52	1813.58	194.73	60.01
<i>Sundamys muelleri</i>	25.60	25.61	2795.60	459.08	116.61
<i>Tarsomys apoensis</i>	20.27	20.31	2731.34	439.70	132.16
<i>Uromys caudimaculatus</i>	24.19	23.59	2902.84	500.81	131.91
<i>Vandeleuria oleracea</i>	24.39	21.22	1474.73	31.44	27.48
<i>Zelotomys hildegardeae</i>	22.04	20.85	1205.83	45.35	27.64
<i>Zelotomys woosnami</i>	20.96	15.02	380.64	3.07	6.88
<i>Zyzomys argurus</i>	25.45	21.97	786.83	19.98	14.85
Nesomyidae					
Cricetomyinae					
<i>Beamys hindei</i>	23.33	21.37	1111.03	33.32	23.04
<i>Cricetomys gambianus</i>	24.41	22.77	1047.49	18.56	18.62
<i>Saccostomus campestris</i>	21.11	17.10	779.76	11.77	15.14
Delanonymyinae					
<i>Delanymys brooksi</i>	16.48	16.26	1529.54	140.71	61.03
Dendromurinae					
<i>Dendromus insignis</i>	15.13	14.97	1326.43	151.40	62.77
<i>Dendromus mesomelas</i>	19.67	17.03	780.72	35.42	21.02
<i>Dendromus nyasae</i>	17.40	16.24	1293.38	65.65	38.61
<i>Malacothrix typica</i>	18.55	13.68	302.55	13.85	8.81
<i>Steatomys krebsi</i>	19.60	15.40	802.13	12.14	16.42
<i>Steatomys parvus</i>	21.44	18.43	852.40	30.86	20.07
Mystromyinae					
<i>Mystromys albicaudatus</i>	15.62	11.18	601.85	42.13	23.68
Nesomyinae					
<i>Brachytarsomys albicauda</i>	19.84	17.38	1674.48	136.65	58.01
<i>Brachyuromys betsileoensis</i>	18.94	16.27	1655.62	125.73	57.32
<i>Eliurus minor</i>	20.84	18.46	1644.19	118.32	51.60
<i>Eliurus tanala</i>	20.54	18.23	1755.75	150.25	60.68
<i>Gymnuromys roberti</i>	19.82	17.26	1623.24	130.15	55.86
<i>Hypogeomys antimena</i>	25.90	22.62	948.56	3.75	13.90
<i>Macrotarsomys bastardi</i>	24.52	21.33	846.52	18.33	15.77
<i>Monticolomys koopmani</i>	18.23	15.60	1496.69	113.21	53.05
<i>Nesomys rufus</i>	20.55	18.26	1758.11	150.77	60.78
<i>Voalavo gymno caudus</i>	19.79	17.39	1699.69	157.80	63.10
Petromyscinae					
<i>Petromyscus collinus</i>	18.25	14.98	177.63	12.67	6.19
Platacanthomyidae					
Platacanthomyinae					
<i>Typhlomys cinereus</i>	16.83	8.66	1365.98	104.45	59.03
Spalacidae					

Table E.1—continued.

	BIO1	BIO9	BIO12	BIO17	AI
Myospalacinae					
<i>Eospalax fontanieri cansas</i>	4.44	-7.25	483.27	12.49	44.00
<i>Myospalax aspalax</i>	2.73	-14.90	392.33	9.20	4.13
Rhizomyinae					
<i>Cannomys badius</i>	23.40	19.94	1709.29	32.20	32.04
<i>Rhizomys pruinosus</i>	20.60	15.68	1668.09	77.10	45.27
Tachyoryctinae					
<i>Tachyoryctes splendens</i>	19.49	19.02	1148.60	72.32	34.43
Spalacinae					
<i>Spalax ehrenbergi</i>	18.14	27.99	357.54	3.47	6.90
<u>Sciromorpha</u>					
Gliridae					
Graphiurinae					
<i>Graphiurus oocularis</i>	16.08	15.01	374.96	51.34	19.51
Leithiinae					
<i>Eliomys melanurus</i>	18.19	23.87	206.11	1.70	3.96
<i>Eliomys quercinus</i>	8.85	6.61	721.39	119.28	62.22
Sciuridae					
Xerinae					
Xerini					
<i>Atlantoxerus getulus</i>	17.13	24.25	231.16	14.23	6.75
<i>Xerus erythropus</i>	26.67	25.19	885.45	26.69	16.62
<i>Xerus inauris</i>	18.86	12.87	353.88	11.98	9.28
<i>Xerus princeps</i>	19.64	15.76	249.63	1.73	4.61
Marmotini					
<i>Ammospermophilus harrisii</i>	18.35	21.09	313.08	21.31	9.64
<i>Ammospermophilus interpres</i>	17.81	12.67	321.92	28.23	13.26
<i>Ammospermophilus leucurus</i>	11.25	14.14	261.71	38.01	15.61
<i>Ammospermophilus nelsoni</i>	16.21	24.48	281.24	3.42	5.96
<i>Spermophilus fulvus</i>	8.65	9.87	217.27	30.04	14.90
<i>Spermophilus mexicanus</i>	19.10	12.82	557.36	56.46	24.42
<i>Spermophilus mohavensis</i>	16.27	22.72	156.03	10.17	4.83
<i>Spermophilus pygmaeus</i>	6.85	0.88	287.72	52.88	37.70
<i>Spermophilus spilosoma</i>	14.29	8.63	410.36	35.02	19.72
<i>Spermophilus tereticaudus</i>	19.86	22.80	215.13	13.35	6.05
<i>Spermophilus variegatus</i>	14.98	12.88	456.22	38.42	19.21

Table E.2. Description and units of the bioclimatic variables from Table E.1.

Variable	Description	Unit
BIO1	Mean annual temperature	°C
BIO9	Average temperature of the driest quarter	°C
BIO12	Mean annual rainfall	Millimeters
BIO17	Rainfall of the driest quarter	Millimeters
AI	Aridity index	None

$$AI = \frac{\frac{BIO12}{BIO1 + 10} + \frac{(12)(BIO17)}{BIO9 + 10}}{2}$$

Table E.3. List of all extant rodent species listed in IUCN grouped into desert, mesic, or unknown habitat categories.

Desert

Acomys dimidiatus, Acomys seurati, Akodon oenos, Allactaga balikunica, Allactaga bullata, Allactaga elater, Allactaga firouzi, Allactaga hotsoni, Allactaga major, Allactaga severzovi, Allactaga tetracysta, Allactaga vinogradovi, Allactaga williamsi, Allactodipus bohriskii, Ammospermophilus harrisii, Ammospermophilus insularis, Ammospermophilus interpres, Ammospermophilus leucurus, Ammospermophilus nelsoni, Baiomys taylori, Bathyergus suillus, Blanfordimys afghanus, Brachionomys przewalskii, Calomyscus tsolovi, Cardiocranus paradoxus, Chaetodipus arenarius, Chaetodipus artus, Chaetodipus baileyi, Chaetodipus californicus, Chaetodipus dalquesti, Chaetodipus eremicus, Chaetodipus fallax, Chaetodipus formosus, Chaetodipus intermedius, Chaetodipus lineatus, Chaetodipus nelsoni, Chaetodipus penicillatus, Chaetodipus rufinoris, Chaetodipus spinatus, Cratogeomys goldmani, Crenomys cuchicus, Cricetulus migratorius, Cricetulus sokolovi, Ctenomys emiliae, Ctenomys riogrenensis, Cynomys gunnisoni, Cynomys ludovicianus, Dendromus leucostomus, Dendromus melanotis, Dendromus nyasae, Desmodillus auricularis, Dipodillus campestris, Dipodillus dasyurus, Dipodillus mackilligini, Dipodillus somalicus, Dipodomys deserti, Dipodomys elator, Dipodomys gravipes, Dipodomys heermanni, Dipodomys merriami, Dipodomys microps, Dipodomys nelsoni, Dipodomys nitratoides, Dipodomys panamintinus, Dipodomys phillipsii, Dipodomys simulans, Dipodomys spectabilis, Dipomys sagitta, Eligmodontia moreni, Eligmodontia typus, Eliomys munbyanus, Ellobius tancrei, Eremodipus lichtensteini, Euchoreutes naso, Geomys arenarius, Gerbilliscus afra, Gerbilliscus brantsii, Gerbilliscus leucogaster, Gerbillurus paeba, Gerbillurus setzeri, Gerbillurus tytonis, Gerbillurus vallinus, Gerbillus andersoni, Gerbillus cheesmani, Gerbillus dunnii, Gerbillus famulus, Gerbillus floweri, Gerbillus gladeowii, Gerbillus henleyi, Gerbillus hoogstraali, Gerbillus latastei, Gerbillus mesopotamicus, Gerbillus nanus, Gerbillus nigerrima, Gerbillus perpallidus, Gerbillus poecilops, Gerbillus pulvinatus, Gerbillus pyramidum, Gerbillus tarabuli, Gerbillus watersi, Jaculus blanfordi, Jaculus jaculus, Jaculus orientalis, Lagostomus maximus, Leggadina forresti, Malacothrix typica, Marmota himalayana, Melomys zunigae, Meriones arimalius, Meriones crassus, Meriones dahli, Meriones heermanni, Meriones libycus, Meriones meridianus, Meriones rex, Meriones sacramentoi, Meriones tamarensis, Meriones tristrami, Meriones unguiculatus, Microtus australis, Microtropods megacephalus, Microtropods pallidus, Microtus californicus, Microtus linnophilus, Millardia gleadowii, Mus indutus, Mus macedonicus, Myospalax psilurus, Neotoma albigena, Neotoma anthonyi, Neotoma bryanti, Neotoma bunkeri, Neotoma cinerea, Neotoma devia, Neotoma goldmani, Neotoma lepida, Neotoma leucodon, Neotoma macroura, Neotoma martinensis, Notomys alexis, Notomys cervinus, Notomys fuscus, Notomys longicaudatus, Oligoryzomys arenalis, Onychomys arenicola, Onychomys leucogaster, Onychomys torridus, Oryzomys xanthocephalus, Pachyuromys duprasi, Paradipus ctenodactylus, Paralomys gerbillus, Parotomys littledalei, Perognathus atticolus, Perognathus amplus, Perognathus flavescens, Perognathus flavus, Perognathus inornatus, Perognathus longimembris, Perognathus merriami, Perognathus parvus, Peromyscus boylii, Peromyscus caniceps, Peromyscus dickeyi, Peromyscus difficilis, Peromyscus eremicus, Peromyscus eva, Peromyscus fraterculus, Peromyscus guardia, Peromyscus interparietalis, Peromyscus leucopus, Peromyscus maniculatus, Peromyscus melanophrys, Peromyscus pectoralis, Peromyscus seujezi, Peromyscus stephani, Peromyscus truei, Phodopus campbelli, Phodopus roborowski, Phodopus sungorus, Phyllotis amplus, Phyllotis limatus, Psammomys obesus, Pseudomys australis, Pseudomys desertor, Pseudomys hermannsburgensis, Pygeretmus platyurus, Pygeretmus shikovi, Rattus villosissimus, Reithrodontomys hirsutus, Reithrodontomys megalotis, Rhombomys opimus, Saccostomus campestris, Saccostomus mearnsi, Salpingotulus michaelis, Salpingotus crassicauda, Salpingotus heptneri, Salpingotus kozlovi, Salpingotus pallidus, Sekeetamys calurus, Selevinia betpakdalensis, Sigmodon arizonae, Sigmodon hispidus, Spalax carmeli, Spalax ehrenbergi, Spalax galili, Spalax galani, Spalax judea, Spermophilopsis leptodactylus, Spermophilus alashanicus, Spermophilus atricapillus, Spermophilus canus, Spermophilus fulvus, Spermophilus mohavensis, Spermophilus mollis, Spermophilus pretiosus, Spermophilus spilosoma, Spermophilus tereticaudus, Spermophilus townsendii, Spermophilus undulatus, Stylocitellus andrewsi, Stylocitellus telum, Tamias minimus, Tamias obscurus, Tamias rufus, Taterillus indica, Taterillus emini, Taterillus harringtoni, Thomomys bottae, Thomomys umbrinus, Xerus inauris

Mesic

Abditomys latidens, Abeomelomys sevia, Abrawayaomys ruschii, Abrocoma bennettii, Abrocoma boliviensis, Abrocoma budini, Abrocoma cinerea, Abrocoma famatina, Abrocoma shistacea, Abrocoma uspallata, Abrocoma vaccaram, Abrothrix andinus, Abrothrix herschkovizi, Abrothrix illiteus, Abrothrix jelskii, Abrothrix lanosus, Abrothrix longipilis, Abrothrix markhami, Abrothrix olivaceus, Abrothrix sanborni, Acomys airense, Acomys cahirinus, Acomys chdeau, Acomys cineraceus, Acomys ignitus, Acomys johni, Acomys kempti, Acomys loutiae, Acomys minous, Acomys mullae, Acomys nesiotes, Acomys percivali, Acomys russatus, Acomys spinosissimus, Acomys subspinosus, Acomys wilsoni, Aconaeomys porteri, Aconaeomys sagei, Aepeomys lugens, Aepeomys reigi, Aeretes melanopterus, Aeromys tephromelas, Aeromys thomasi, Aethomys bocagei, Aethomys chrysophilus, Aethomys hindei, Aethomys ineptus, Aethomys kaiseri, Aethomys nyikae, Aethomys silindensis, Aethomys stannarius, Aethomys thomasi, Akodon australis, Akodon affinis, Akodon albiventer, Akodon aliquantulus, Akodon azarae, Akodon bogotensis, Akodon boliviensis, Akodon budini, Akodon cursor, Akodon dayi, Akodon dolores, Akodon fumeus, Akodon iniscatus, Akodon juninensis, Akodon kofordi, Akodon latebricola, Akodon leucomelanus, Akodon lindberghi, Akodon lutescens, Akodon mimus, Akodon molinae, Akodon mollis, Akodon montensis, Akodon mystax, Akodon neocenius, Akodon orophilus, Akodon paranaensis, Akodon pervalens, Akodon reigi, Akodon sanctipaulensis, Akodon siberiae, Akodon simulator, Akodon spegazzinii, Akodon subfuscus, Akodon surdus, Akodon sylvanus, Akodon toba, Akodon torques, Akodon varius, Allactaga euphratica, Allactaga sibirica, Allocricetulus curtaurus, Allocricetulus eversmanni, Alticola albicaudus, Alticola argentatus, Alticola barakshin, Alticola lemminius, Alticola macrotis, Alticola montosa, Alticola olchonensis, Alticola roylei, Alticola semicanus, Alticola stoliczkanus, Alticola strelzovi, Alticola tuvinicus, Ammodillus imbellis, Amphinectomys savamis, Andalgalomys olrogii, Andalgalomys personai, Andalgalomys roigi, Andinomys edax, Anisomys initiator, Anomalurus beecrofti, Anomalurus derbianus, Anomalurus pelii, Anomalurus pusillus, Anonymomys mindorenensis, Anotomys leander, Apodemus agrarius, Apodemus apicola, Apodemus argenteus, Apodemus chevrieri, Apodemus draco, Apodemus epimelas, Apodemus flavicollis, Apodemus gurkha, Apodemus hyrcanicus, Apodemus latronum, Apodemus mystacinus, Apodemus pallipes, Apodemus peninsulae, Apodemus ponticus, Apodemus rusiges, Apodemus semotus, Apodemus speciosus, Apodemus sylvaticus, Apodemus uralensis, Apodemus wutherbyi, Apomys abrae, Apomys datae, Apomys gracilirostris, Apomys hylocetes, Apomys insignis, Apomys littoralis, Apomys microdon, Apomys musculus, Apomys saboianus, Arborimus albipes, Arborimus longicaudus, Arborimus pomo, Archboldomys luzonensis, Archboldomys musseri, Arvicantis abyssinicrus, Arvicantis ansorgei, Arvicantis blicki, Arvicantis nairobae, Arvicantis neumanni, Arvicantis niloticus, Arvicantis rufinus, Arvicola amphibius, Arvicola sapidus, Arvicola scherman, Atherurus africanus, Atherurus macrourus, Atlantorferus getulus, Auliscomys boliviensis, Auliscomys pictus, Auliscomys sublimis, Baiomys musculus, Bandicota bengalensis, Bandicota indica, Bandicota sawilei,

Table E.3—continued.

Table E.3—continued.

sachalinensis, *Microtus savii*, *Microtus schelkovnikovi*, *Microtus schidlovskii*, *Microtus socialis*, *Microtus subterraneus*, *Microtus taticus*, *Microtus thomasi*, *Microtus townsendii*, *Microtus transcaspicus*, *Microtus umbrösus*, *Microtus xanthognathus*, *Millardia kathleenae*, *Millardia kondana*, *Millardia meltada*, *Monticolomys koopmani*, *Muriculus imberbis*, *Mus baoulei*, *Mus booduga*, *Mus bufo*, *Mus callewaerti*, *Mus caroli*, *Mus cervicolor*, *Mus cookii*, *Mus crocidurooides*, *Mus famulus*, *Mus fernandoni*, *Mus fragilicauda*, *Mus goundae*, *Mus haussa*, *Mus mahomet*, *Mus mattheyi*, *Mus majori*, *Mus minutoides*, *Mus musculoides*, *Mus neavei*, *Mus orangiae*, *Mus oubangui*, *Mus pahari*, *Mus phillipsi*, *Mus platythrrix*, *Mus saxicola*, *Mus setulosus*, *Mus setzeri*, *Mus shorridgei*, *Mus sorella*, *Mus spicilegus*, *Mus sprattus*, *Mus tenellus*, *Mus terricolor*, *Mus triton*, *Mus vulcani*, *Muscardinus avellanarius*, *Mylomys dybowskii*, *Myocastor coypus*, *Myodes andersoni*, *Myodes californicus*, *Myodes centralis*, *Myodes gapperi*, *Myodes glareolus*, *Myodes imazumi*, *Myodes regulis*, *Myodes rex*, *Myodes rufocanus*, *Myodes rutilus*, *Myodes shanseus*, *Myodes smithii*, *Myomimus personatus*, *Myomimus roachi*, *Myomimus setzeri*, *Myomyscus angolensis*, *Myomyscus brockmani*, *Myomyscus verreauxii*, *Myomyscus yemeni*, *Myoprocta acouchy*, *Myoprocta pratti*, *Myopus schisticolor*, *Myosciurus pumilio*, *Myospalax aspalax*, *Myospalax myospalax*, *Myotomys sloggetti*, *Myotomys unisulcatus*, *Mysateles garridoi*, *Mysateles meridionalis*, *Mysateles prehensili*, *Mystromys albicaudatus*, *Nannosciurus melanotis*, *Napaeozapus insignis*, *Neacomys dubostii*, *Neacomys guianae*, *Neacomys minutus*, *Neacomys musseri*, *Neacomys paracou*, *Neacomys spinosus*, *Neacomys tenuipes*, *Necromys amoenus*, *Necromys benefactus*, *Necromys lactens*, *Necromys lasiurus*, *Necromys lenguarum*, *Necromys obscurus*, *Necromys punctatus*, *Necromys temchuki*, *Necromys urichi*, *Nectomys apicalis*, *Nectomys magdalena*, *Nectomys palmipes*, *Nectomys ratus*, *Nectomys squamipes*, *Nelsonia goldmani*, *Nelsonia neotomoides*, *Neodon forresti*, *Neodon irene*, *Neodon juldashas*, *Neodon sikimensis*, *Neofiber alleni*, *Neotoma angustipatalata*, *Neotoma chrysomelas*, *Neotoma floridana*, *Neotoma fuscipes*, *Neotoma magister*, *Neotoma mexicana*, *Neotoma micropus*, *Neotoma nelsoni*, *Neotoma palatina*, *Neotoma phenax*, *Neotoma stephensi*, *Neotomodon alstoni*, *Neotomys ebriosus*, *Nesokia bunni*, *Nesokia indica*, *Nesomys audeberti*, *Nesomys lambertoni*, *Nesomys rufus*, *Nesomys ceramicus*, *Nesoryzomys darwini*, *Nesoryzomys fernandinae*, *Nesoryzomys indefessus*, *Nesoryzomys swarthi*, *Neusticomys monticulus*, *Neusticomys muossoi*, *Neusticomys oyapocki*, *Neusticomys peruviensis*, *Neusticomys venezuelae*, *Nilopegamys plumbeus*, *Niviventer andersoni*, *Niviventer brahma*, *Niviventer cameroni*, *Niviventer confucianus*, *Niviventer coninga*, *Niviventer cremerior*, *Niviventer culturatus*, *Niviventer eha*, *Niviventer excelsior*, *Niviventer fraternus*, *Niviventer fulvescens*, *Niviventer hinpoon*, *Niviventer langbianis*, *Niviventer lepturus*, *Niviventer niviventer*, *Niviventer tener*, *Noronhomys vespucci*, *Notomys aquilus*, *Notomys mitchellii*, *Notomys sumichrasti*, *Ochrotomys nuttalli*, *Octodon bridgei*, *Octodon degus*, *Octodon lunatus*, *Octodon pacificus*, *Octodontomys gliroides*, *Oecomys auxantepui*, *Oecomys bicolor*, *Oecomys catherinae*, *Oecomys cleberi*, *Oecomys concolor*, *Oecomys flavicans*, *Oecomys mamoreae*, *Oecomys paricola*, *Oecomys phaeotis*, *Oecomys rex*, *Oecomys roberti*, *Oecomys rutilus*, *Oecomys speciosus*, *Oecomys superans*, *Oecomys trinitatis*, *Oenomys hypoxanthus*, *Oenomys ornatus*, *Oallamys albicauda*, *Oallamys edax*, *Oligoryzomys andinus*, *Oligoryzomys brendae*, *Oligoryzomys chacoensis*, *Oligoryzomys delticola*, *Oligoryzomys destructor*, *Oligoryzomys eliurus*, *Oligoryzomys flavescens*, *Oligoryzomys fornesi*, *Oligoryzomys fulvescens*, *Oligoryzomys griseolus*, *Oligoryzomys longicaudatus*, *Oligoryzomys magellanicus*, *Oligoryzomys microtis*, *Oligoryzomys nigripes*, *Oligoryzomys stramineus*, *Oligoryzomys vegetus*, *Ondatra zibethicus*, *Orthogeomys cavator*, *Orthogeomys cherriei*, *Orthogeomys cuniculus*, *Orthogeomys darriensis*, *Orthogeomys grandis*, *Orthogeomys heterodus*, *Orthogeomys hispidus*, *Orthogeomys lanius*, *Orthogeomys matagalpae*, *Orthogeomys thaieri*, *Orthogeomys underwoodi*, *Oryzomys albicularis*, *Oryzomys alfaroi*, *Oryzomys angouya*, *Oryzomys aviventer*, *Oryzomys baleator*, *Oryzomys bolivaris*, *Oryzomys caracolus*, *Oryzomys chapmani*, *Oryzomys couesi*, *Oryzomys devius*, *Oryzomys dimidiatus*, *Oryzomys emmonsae*, *Oryzomys galapagoensis*, *Oryzomys gorgasi*, *Oryzomys hammondi*, *Oryzomys keyesi*, *Oryzomys lamia*, *Oryzomys laticeps*, *Oryzomys legatus*, *Oryzomys levipes*, *Oryzomys macconnelli*, *Oryzomys marinhus*, *Oryzomys megalcephalus*, *Oryzomys melanotis*, *Oryzomys meridensis*, *Oryzomys nelsoni*, *Oryzomys nitidus*, *Oryzomys palustris*, *Oryzomys perenensis*, *Oryzomys politus*, *Oryzomys rhabdops*, *Oryzomys rostratus*, *Oryzomys russatus*, *Oryzomys saturatus*, *Oryzomys subflavus*, *Oryzomys talamancae*, *Oryzomys tatei*, *Oryzomys yunganus*, *Osgoodomys banderanus*, *Otomys anchietae*, *Otomys barbouri*, *Otomys burtoni*, *Otomys cuanzensis*, *Otomys denti*, *Otomys dollmani*, *Otomys irroratus*, *Otomys lacustris*, *Otomys laminatus*, *Otomys occidentalis*, *Otomys saundersiae*, *Otomys tropicalis*, *Otomys typus*, *Otonyctomys hattii*, *Ototylomys philothys*, *Oxymycterus akondontis*, *Oxymycterus amazonicus*, *Oxymycterus angularis*, *Oxymycterus caparao*, *Oxymycterus dasyrhynchus*, *Oxymycterus delator*, *Oxymycterus hiska*, *Oxymycterus hispidus*, *Oxymycterus huachuca*, *Oxymycterus inca*, *Oxymycterus josei*, *Oxymycterus nasutus*, *Oxymycterus paramensis*, *Oxymycterus quaestor*, *Oxymycterus roberti*, *Oxymycterus rufus*, *Palawanomys furvus*, *Papagomys alcorni*, *Papagomys bulleri*, *Parahydromys asper*, *Paraleptomys rufulatus*, *Paraleptomys wilhelmina*, *Paramelomys gressitti*, *Paramelomys levetipes*, *Paramelomys lorentzii*, *Paramelomys mollis*, *Paramelomys moncktoni*, *Paramelomys naso*, *Paramelomys platyops*, *Paramelomys rubex*, *Paramelomys steini*, *Paraxerus alexandri*, *Paraxerus boehmi*, *Paraxerus cepapi*, *Paraxerus cooperi*, *Paraxerus flavovittatus*, *Paraxerus lucifer*, *Paraxerus ochraceus*, *Paraxerus palliatus*, *Paraxerus poensis*, *Paraxerus varillarius*, *Paraxerus vincenti*, *Parotomys brantsii*, *Paruromys dominator*, *Paulamys naso*, *Pearsonomys annectens*, *Pectinator spekei*, *Pedetes capensis*, *Pedetes surdaster*, *Pelomys campanae*, *Pelomys fallax*, *Pelomys hopkinsi*, *Pelomys minor*, *Pelognathus fasciatus*, *Pelomys attwateri*, *Pelomys aztecus*, *Pelomys beatae*, *Pelomys bullatus*, *Pelomys californicus*, *Pelomys crinitus*, *Pelomys curvus*, *Pelomys gossypinus*, *Pelomys grandis*, *Pelomys gratius*, *Pelomys guatemalensis*, *Pelomys gymnotis*, *Pelomys hooperi*, *Pelomys hylocetes*, *Pelomys keeni*, *Pelomys levipes*, *Pelomys madrensis*, *Pelomys mayensis*, *Pelomys megalops*, *Pelomys mekitisturus*, *Pelomys melanocarpus*, *Pelomys melanotis*, *Pelomys melanurus*, *Pelomys merriami*, *Pelomys mexicanus*, *Pelomys nasutus*, *Pelomys ochraventer*, *Pelomys pembertonii*, *Pelomys perfidus*, *Pelomys polionotus*, *Pelomys polius*, *Pelomys pseudocordatus*, *Pelomys sagax*, *Pelomys simulus*, *Pelomys spicilegus*, *Pelomys stirtoni*, *Pelomys winkelmanni*, *Pelomys yucatanicus*, *Pelomys zarhynchus*, *Petaurillus emiliae*, *Petaurillus hosei*, *Petaurillus kinlochii*, *Petaurista alborus*, *Petaurista elegans*, *Petaurista leucogenys*, *Petaurista magnificus*, *Petaurista nobilis*, *Petaurista petaurista*, *Petaurista philippensis*, *Petaurista xanthoitis*, *Petinomys crinitus*, *Petinomys fasciculatus*, *Petinomys genibarbis*, *Petinomys hageni*, *Petinomys lugens*, *Petinomys mindanensis*, *Petinomys sagitta*, *Petinomys setosus*, *Petinomys vordermanni*, *Petromys tipicus*, *Petromys barbouri*, *Petromys collinus*, *Petromys monticulus*, *Petromys shortridgei*, *Phaenomys ferrugineus*, *Phaiomys leucurus*, *Phenacomys intermedius*, *Phenacomys ungava*, *Phloeomys cumingi*, *Phloeomys pallidus*, *Phyllomys blainvillii*, *Phyllomys dasytrix*, *Phyllomys kerri*, *Phyllomys lamarum*, *Phyllomys lundi*, *Phyllomys maniquairensis*, *Phyllomys medius*, *Phyllomys nigrispinus*, *Phyllomys pattoni*, *Phyllomys thomasi*, *Phyllomys unicolor*, *Phyllotis andium*, *Phyllotis caprinus*, *Phyllotis darwini*, *Phyllotis definitus*, *Phyllotis haggardi*, *Phyllotis magister*, *Phyllotis osgoodi*, *Phyllotis osilae*, *Phyllotis wolffsohni*, *Phyllotis xanthopygus*, *Pipanacotomys aureus*, *Pithecheir melanurus*, *Pithecheir parvus*, *Pithecheirostis otion*, *Plagiodontia aedium*, *Platacanthomys lasiurus*, *Podomys floridanus*, *Podozymys roraiae*, *Pogonomelomys brujni*, *Pogonomelomys Mayeri*, *Pogonomys championi*, *Pogonomys fergusonensis*, *Pogonomys loriae*, *Pogonomys macrourus*, *Pogonomys sylvestris*, *Praomys daltoni*, *Praomys degraafii*, *Praomys delectorum*, *Praomys derooi*, *Praomys hartwigi*, *Praomys jacksoni*, *Praomys lukolelae*, *Praomys minor*, *Praomys misonnei*, *Praomys morio*, *Praomys mutoni*, *Praomys obscurus*, *Praomys petteri*, *Praomys rostratus*, *Praomys tullbergi*, *Praomys verschurenii*, *Prionomys batesi*, *Proechimys brevicauda*, *Proechimys canicollis*, *Proechimys chrysaelous*, *Proechimys cuvieri*, *Proechimys decumanus*, *Proechimys echinotrichus*, *Proechimys gardneri*, *Proechimys goeldii*, *Proechimys guyanensis*, *Proechimys kuliniae*, *Proechimys longicaudatus*, *Proechimys mincae*, *Proechimys oconnelli*, *Proechimys pattoni*, *Proechimys politopus*, *Proechimys quadruplicatus*, *Proechimys roberti*, *Proechimys semispinosus*, *Proechimys simonsi*, *Proechimys steerii*, *Proechimys trinitatis*, *Proechimys urichi*, *Proedromys bedfordi*, *Prometheomys schaposchnikovi*, *Prostirurillus abstrusus*, *Prostirurillus leucomus*, *Prostirurillus rosebergii*, *Prostirurillus weberi*, *Protocadomys fellowsi*, *Protoceromys aubinnii*, *Protoceromys stangeri*, *Psammomys vexillaris*, *Pseudohydromys ellermani*, *Pseudohydromys fuscus*, *Pseudohydromys occidentalis*, *Pseudomys albocinerus*, *Pseudomys apodemoides*, *Pseudomys bolami*, *Pseudomys chapmani*, *Pseudomys delicatus*, *Pseudomys fieldi*, *Pseudomys fumeus*, *Pseudomys gouldii*, *Pseudomys gracilicaudatus*, *Pseudomys higginsi*, *Pseudomys johnsoni*, *Pseudomys laborifex*, *Pseudomys nanus*, *Pseudomys novaehollandiae*, *Pseudomys occidentalis*, *Pseudomys oralis*, *Pseudomys patrius*, *Pseudomys pillaensis*, *Pseudomys shortridgei*, *Pseudoryzomys simplex*, *Pteromys momonga*, *Pteromys volans*, *Pteromys pulverulentus*, *Punomys kafordi*, *Punomys lemminius*, *Pygereomys pumilio*, *Rattus adustus*, *Rattus andamanicus*, *Rattus annandalei*, *Rattus argenteiventer*, *Rattus arragans*, *Rattus baluensis*, *Rattus blangorum*, *Rattus bontanus*, *Rattus burrus*, *Rattus colletti*, *Rattus elaphinus*, *Rattus enganus*, *Rattus everetti*, *Rattus exulans*, *Rattus fuscipes*, *Rattus galienensis*, *Rattus hainaldi*, *Rattus hoffmanni*, *Rattus hoogerwerfi*, *Rattus jobiensis*, *Rattus korinchii*, *Rattus leucopus*, *Rattus losaea*, *Rattus lugens*, *Rattus lutreolus*, *Rattus macleari*, *Rattus marmosurus*, *Rattus mindorensis*, *Rattus mollicomulus*, *Rattus montanus*, *Rattus mordax*, *Rattus morotaiensis*, *Rattus nativitatis*, *Rattus niobe*, *Rattus nitidus*, *Rattus noveaguineae*, *Rattus omichliodes*, *Rattus osgoodi*, *Rattus palmarum*, *Rattus pococki*, *Rattus praeator*, *Rattus pyctoris*, *Rattus rattus*, *Rattus richardsoni*, *Rattus salocco*, *Rattus satarae*, *Rattus simalurensis*, *Rattus sordidus*, *Rattus steini*, *Rattus stoliczki*, *Rattus tanzeumi*, *Rattus taitiwaiensis*, *Rattus timorensis*, *Rattus tiomanicus*, *Rattus tunneyi*, *Rattus vanedeuseni*, *Rattus verecundus*, *Rattus xanthurus*, *Ratufa affinis*, *Ratufa bicolor*, *Ratufa indica*, *Ratufa macroura*, *Reithrodontomys auritus*, *Reithrodontomys brevirostris*, *Reithrodontomys burri*, *Reithrodontomys chrysopsis*, *Reithrodontomys creper*, *Reithrodontomys darrienensis*, *Reithrodontomys fulvescens*, *Reithrodontomys gracilis*, *Reithrodontomys humulis*, *Reithrodontomys mexicanus*, *Reithrodontomys micronotus*, *Reithrodontomys montanus*, *Reithrodontomys paradoxus*, *Reithrodontomys raviventris*, *Reithrodontomys rodriguezi*, *Reithrodontomys spectabilis*, *Reithrodontomys sumichrasti*, *Reithrodontomys tenuirostris*, *Reithrodontomys zacatecae*, *Rhabdomys dilectus*, *Rhabdomys pumilio*, *Rhagomys longilingua*, *Rhagomys rufescens*, *Rheithrodontomys macrotis*, *Rheomys mexicanus*, *Rheomys raptor*, *Rheomys thomasi*, *Rheomys underwoodi*, *Rhinoclemmys laticephala*, *Rhipidomys austriacus*, *Rhipidomys caucensis*, *Rhipidomys coesi*, *Rhipidomys emiliae*, *Rhipidomys fulviventer*, *Rhipidomys gardneri*, *Rhipidomys latimanus*, *Rhipidomys leucodactylus*, *Rhipidomys macconnelli*, *Rhipidomys mastacalis*, *Rhipidomys modicus*, *Rhipidomys nitela*, *Rhipidomys ochrogaster*, *Rhipidomys venezuelae*, *Rhipidomys venustus*, *Rhizomys wetzeli*, *Rhizomys pruinosis*, *Rhizomys sinensis*, *Rhynchosomys soricoides*, *Rubriculus rubrivenus*, *Salinomys loschalcaderosorum*, *Salinomys delicatus*, *Scapteromys aquaticus*, *Scapteromys tunidus*, *Sciurotamias davidiensis*, *Sciurotamias forresti*, *Sciurus granatensis*, *Sciurus griseus*, *Sciurus ignitus*, *Sciurus igniventris*, *Sciurus lis*, *Sciurus nayaritensis*, *Sciurus niger*, *Sciurus oculatus*, *Sciurus richmondi*, *Sciurus sanborni*, *Sciurus spadiceus*, *Sciurus stramineus*, *Sciurus variegatoides*, *Sciurus vulgaris*, *Sciurus yucatanicus*, *Scolomys melanops*, *Scolomys ugraydensis*, *Scotinomys teguina*, *Scotinomys xerampelinus*, *Sicista armenica*, *Sicista betulina*, *Sicista caucasica*, *Sicista caudata*, *Sicista concolor*, *Sicista kazbegica*, *Sicista kluchorica*, *Sicista napaea*, *Sicista pseudonapaea*, *Sicista strandi*, *Sicista subtilis*, *Sicista tianshanica*, *Sigmodon allenii*, *Sigmodon alstoni*, *Sigmodon fulviventer*, *Sigmodon hirsutus*, *Sigmodon inopinatus*, *Sigmodon leucotis*, *Sigmodon mascotensis*, *Sigmodon ochrogaster*, *Sigmodon peruanus*, *Sigmodon planifrons*, *Sigmodon toltecus*, *Sigmodon xanthonensis*, *Sigmodontomys alfaroi*, *Sigmodontomys aphrastus*, *Solomys ponceleti*, *Solomys salebrosus*, *Solomys sapiens*, *Sommeromys macrorhinus*, *Spalacopus cyanocephalus*, *Spalax arenarius*, *Spalax giganteus*, *Spalax leucodon*, *Spalax microphthalmus*, *Spalax nehringi*, *Spalax uralensis*, *Spalax zemni*, *Spermophilus adocetus*, *Spermophilus annulatus*, *Spermophilus armatus*, *Spermophilus beechevi*, *Spermophilus beldingi*, *Spermophilus brevicauda*, *Spermophilus brunneus*, *Spermophilus citellus*, *Spermophilus columbianus*, *Spermophilus dauricus*, *Spermophilus elegans*, *Spermophilus erythrogenys*, *Spermophilus franklinii*, *Spermophilus lateralis*, *Spermophilus maderensis*, *Spermophilus major*, *Spermophilus mexicanus*, *Spermophilus musicus*, *Spermophilus pallidicauda*, *Spermophilus parryi*, *Spermophilus pygmaeus*, *Spermophilus ralloi*, *Spermophilus relicta*, *Spermophilus saturatus*, *Spermophilus suslicus*, *Spermophilus tridecemlineatus*, *Spermophilus variegatus*, *Spermophilus washingtoni*, *Spermophilus xanthoprymnus*, *Sphiggurus ichillus*, *Sphiggurus insidiosus*, *Sphiggurus melanurus*, *Sphiggurus mexicanus*, *Sphiggurus pruinosus*, *Sphiggurus roosmalenorum*, *Sphiggurus spinosus*, *Sphiggurus vestitus*, *Sphiggurus villosus*, *Srilankamys ohiensis*, *Steatomys cairinus*, *Steatomys krebsii*, *Steatomys opimus*, *Steatomys parvus*, *Steatomys pratensis*, *Stenocephalemys albipes*, *Stenocephalemys albocaudata*, *Stenocephalemys griseicauda*, *Stenocephalemys ruppi*, *Stochomys longicaudatus*, *Stylocitellus sungorus*, *Sundamys infraluteus*, *Sundamys maxi*, *Sundamys müelleri*, *Sundasciurus brookei*, *Sundasciurus davensis*, *Sundasciurus fraterculus*, *Sundasciurus hippurus*, *Sundasciurus hoogstraali*, *Sundasciurus jentinki*, *Sundasciurus juvencus*, *Sundasciurus lowii*, *Sundasciurus mindanensis*, *Sundasciurus moellendorffi*, *Sundasciurus philippinensis*.

Table E.3—continued.

Sundasciurus rabori, *Sundasciurus samarensis*, *Sundasciurus steerii*, *Sundasciurus tenuis*, *Synaptomys borealis*, *Synaptomys cooperi*, *Syntheosciurus brochus*, *Tachyoryctes ankoliæ*, *Tachyoryctes annectens*, *Tachyoryctes audax*, *Tachyoryctes daemon*, *Tachyoryctes ibeanus*, *Tachyoryctes macrocephalus*, *Tachyoryctes naivashae*, *Tachyoryctes rex*, *Tachyoryctes ruandae*, *Tachyoryctes ruddi*, *Tachyoryctes spalacinus*, *Tachyoryctes splendens*, *Tachyoryctes storeyi*, *Taeromys arcuatus*, *Taeromys callitrichus*, *Taeromys celebensis*, *Taeromys hamatus*, *Taeromys microbullatus*, *Taeromys punicens*, *Tamias alpinus*, *Tamias amoenus*, *Tamias bulleri*, *Tamias canipes*, *Tamias cinereicollis*, *Tamias dorsalis*, *Tamias durangae*, *Tamias merriami*, *Tamias ochrogenys*, *Tamias palmeri*, *Tamias panamintinus*, *Tamias quadrivittatus*, *Tamias ruficaudus*, *Tamias senex*, *Tamias sibiricus*, *Tamias siskiyou*, *Tamias sonoma*, *Tamias speciosus*, *Tamias striatus*, *Tamias townsendii*, *Tamias umbrinus*, *Tamiasciurus douglasii*, *Tamiasciurus hudsonicus*, *Tamiops maritimus*, *Tamiops mclellandii*, *Tamiops rodolphi*, *Tamiops swinhonis*, *Tapeomys primus*, *Tarsomys apoenisis*, *Tarsomys echinatus*, *Tateomys macrocerus*, *Tateomys rhinogradeoides*, *Taterillus arenarius*, *Taterillus conicus*, *Taterillus gracilis*, *Taterillus lacustris*, *Taterillus petteri*, *Taterillus pygargus*, *Taterillus traniieri*, *Thallomys loringi*, *Thallomys nigricauda*, *Thallomys paedulus*, *Thalpomys cerradensis*, *Thalpomys lasiotis*, *Thamomys kempfi*, *Thamomys major*, *Thamomys venustus*, *Thapomys nigrita*, *Thomasomys apeco*, *Thomasomys aureus*, *Thomasomys baeops*, *Thomasomys bombycinus*, *Thomasomys caudivarius*, *Thomasomys cinereiventer*, *Thomasomys cinereus*, *Thomasomys cinnameus*, *Thomasomys daphne*, *Thomasomys eleusis*, *Thomasomys erro*, *Thomasomys gracilis*, *Thomasomys hudsoni*, *Thomasomys hylophilus*, *Thomasomys incanus*, *Thomasomys ischyrus*, *Thomasomys kalinowskii*, *Thomasomys laevis*, *Thomasomys laniger*, *Thomasomys macrotis*, *Thomasomys monocromos*, *Thomasomys niveipes*, *Thomasomys notatus*, *Thomasomys onkiro*, *Thomasomys oreas*, *Thomasomys paramorum*, *Thomasomys papayanus*, *Thomasomys praeator*, *Thomasomys pyrrhotonotus*, *Thomasomys rhodsi*, *Thomasomys rosalinda*, *Thomasomys silvestris*, *Thomasomys taczanowskii*, *Thomasomys uchua*, *Thomasomys vestitus*, *Thomasomys vulcani*, *Thomomys bulbivorus*, *Thomomys clusius*, *Thomomys idahoensis*, *Thomomys mazama*, *Thomomys monticola*, *Thomomys talpoides*, *Thomomys townsendii*, *Thrichomys aperaeoides*, *Thrichomys inermis*, *Thrichomys pachyurus*, *Thryonomys gregorianus*, *Thryonomys swinderianus*, *Tokudai muenninki*, *Tokudaia osimensis*, *Trichys fasciculata*, *Trinomys albispinus*, *Trinomys dimidiatus*, *Trinomys eliasi*, *Trinomys gratiosus*, *Trinomys iheringi*, *Trinomys mirapitanga*, *Trinomys mojeni*, *Trinomys myosuros*, *Trinomys paratus*, *Trinomys setosus*, *Trinomys yonenagae*, *Trogonterus xanthipes*, *Tryphomys adustus*, *Tscherskia triton*, *Tylomys bullaris*, *Tylomys mirae*, *Tylomys nudicaudus*, *Tylomys tumbalensis*, *Tylomys watsoni*, *Typhlomys cinereus*, *Uromys ruddi*, *Uromys anak*, *Uromys boeadi*, *Uromys caudimaculatus*, *Uromys emmae*, *Uromys hadrourus*, *Uromys imperator*, *Uromys neobritannicus*, *Uromys porculus*, *Uromys rex*, *Uromys sieberi*, *Vandeleuria nilagirica*, *Vandeleuria olereacea*, *Vernaya fulva*, *Voadavo gymnoccadius*, *Volemys millicens*, *Volemys musseri*, *Wiedomys pyrrhorhinus*, *Wilfredomys oenax*, *Xenomys nelsoni*, *Xenuromys barbatus*, *Xeromys myoides*, *Xerus erythropus*, *Xerus princeps*, *Xerus rutilus*, *Zapus hudsonius*, *Zapus princeps*, *Zapus trinotatus*, *Zelotomys hildegardae*, *Zelotomys woosnami*, *Zenkerella insignis*, *Zygodontomys brevicauda*, *Zygodontomys brunneus*, *Zygogeomys trichopus*, *Zyzomys argurus*, *Zyzomys maini*, *Zyzomys palatilis*, *Zyzomys pedunculatus*, *Zyzomys woodwardi*

Unknown

Acomys cilicicus, *Amblyrhiza inundata*, *Boromys offella*, *Boromys torrei*, *Brotomys contractus*, *Brotomys voratus*, *Cavia intermedia*, *Cavia porcellus*, *Clidomys osborni*, *Conilurus albipes*, *Coryphomys buehleri*, *Cratogeomys gymnurus*, *Cratogeomys tylorhinus*, *Cryptomys amatus*, *Ctenomys brasiliensis*, *Ctenomys budini*, *Ctenomys coludo*, *Ctenomys coyhaiquensis*, *Ctenomys famosus*, *Ctenomys fochi*, *Ctenomys goodfellowi*, *Ctenomys johannis*, *Ctenomys juris*, *Ctenomys occultus*, *Ctenomys perrensi*, *Ctenomys pontifex*, *Ctenomys roigi*, *Ctenomys saltarius*, *Ctenomys scagliati*, *Ctenomys sericeus*, *Ctenomys sylvanus*, *Ctenomys tuluco*, *Ctenomys validus*, *Ctenomys viperinus*, *Ctenomys yolanda*, *Cuscomyss oblativa*, *Dasyprocta azarae*, *Dasyprocta fuliginosa*, *Dasyprocta kalinowskii*, *Dendropionomys rousseloti*, *Diplomys rufodorsalis*, *Dipodillus bottai*, *Dipodillus jamesi*, *Dipodillus zakariai*, *Elasmodontomys obliquus*, *Elllobius alaticus*, *Geocapromys thoracatus*, *Gerbillus acticola*, *Gerbillus agay*, *Gerbillus Brockmani*, *Gerbillus burtoni*, *Gerbillus dongolanus*, *Gerbillus garamantis*, *Gerbillus grobbeni*, *Gerbillus mauritaniae*, *Gerbillus muriculus*, *Gerbillus syrticus*, *Graomys centralis*, *Hadromys yunnanensis*, *Heteropsmys amillensis*, *Heteropsmys insulans*, *Hexolobodon phenax*, *Isolobodon portoricensis*, *Juscelinomys candango*, *Lagostomus crassus*, *Lophuromys angolensis*, *Lophuromys ansorgei*, *Lophuromys brunneus*, *Lophuromys dudui*, *Lophuromys verhageni*, *Lophuromys zena*, *Makalata obscura*, *Malpaisomys insularis*, *Megalomys desmarestii*, *Megalomys luciae*, *Melomys spechti*, *Meriones zarudnyi*, *Mesocricetus auratus*, *Microscirtus flavigaster*, *Microscirtus santanderensis*, *Microtus irani*, *Myomys rex*, *Notomys amplius*, *Notomys macrotis*, *Notomys mordax*, *Otomys mimax*, *Oryzomys curasaoe*, *Otomys dartmouthi*, *Otomys jacksoni*, *Otomys maximus*, *Otomys orestes*, *Otomys uzungwensis*, *Papagomys theodoroverhoeveni*, *Pelomys isseli*, *Phyllomys brasiliensis*, *Plagiodontia aereaum*, *Plagiodontia ipnaeum*, *Proechimys guaireae*, *Proechimys holopionoides*, *Pseudomys glaucus*, *Quemisia gravis*, *Rattus arfakiensis*, *Rattus koopmani*, *Rattus norvegicus*, *Rattus pelurus*, *Rattus ranjiniae*, *Rattus sanila*, *Rhagomys orthodon*, *Rhizoplaidontia lemkei*, *Salpingotus thomasi*, *Sciurillus pusillus*, *Sciurus gilvivularis*, *Sciurus pucheranii*, *Sciurus pyrrhinus*, *Sicista severzovi*, *Solomys salomonis*, *Solomys spriggsarum*, *Spelaeomys florensis*, *Steatomys jacksoni*, *Taeromys taerae*, *Tamiasciurus mearnsi*, *Thallomys shortridgei*, *Tylomys fulviventer*, *Tylomys panamensis*, *Typanoctomys barrerae*

Table E.4. Species means of raw distances extracted from the ventral views of crania in millimeters. Taxa sorted taxonomically and a visual representation of distances can be found in the figures below. # = number of specimens used; SL = skull length; SW = skull width; IW = incisor width; DL = diastema length; ML = molar tooth row length; MW = first molar width; PR = pterygoid region length; MB = mesopterygoid breadth; BO = basioccipital length; BL = total length of the tympanic bulla; BW = bulla width; CB = condyle breadth.

	#	SL	SW	IW	DL	ML	MW	PR	MB	BO	BL	BW	CB
Anomaluromorpha													
Pedetidae													
<i>Pedetes capensis</i>	4	84.97	56.12	13.39	26.64	16.29	3.23	14.28	6.40	10.80	15.00	11.35	18.92
Castorimorpha													
Geomyidae													
<i>Cratogeomys castanops</i>	4	41.15	25.24	6.68	15.38	6.78	2.12	6.36	2.57	6.85	11.76	9.29	9.05
<i>Thomomys umbrinus</i>	4	37.01	23.19	5.56	13.81	6.25	2.04	5.97	2.25	4.86	9.13	7.49	7.01
Heteromyidae													
Dipodomysinae													
<i>Dipodomys agilis</i>	4	34.12	17.29	3.45	9.83	4.02	1.30	5.79	1.72	5.22	11.51	9.45	6.07
<i>Dipodomys californicus</i>	4	33.93	18.48	3.45	10.06	4.19	1.33	6.21	1.73	5.06	11.39	8.98	6.44
<i>Dipodomys compactus</i>	4	31.46	16.46	3.21	8.98	3.94	1.15	5.61	1.52	4.78	11.72	8.65	6.06
<i>Dipodomys deserti</i>	5	38.80	19.76	3.53	10.65	4.48	1.56	7.69	2.14	5.19	16.52	12.19	6.87
<i>Dipodomys elator</i>	3	34.13	18.57	3.40	10.30	4.11	1.37	6.36	2.06	4.75	12.46	9.44	6.22
<i>Dipodomys gravipes</i>	3	35.19	18.77	3.07	10.31	4.24	1.44	6.30	2.18	5.32	14.13	10.29	6.27
<i>Dipodomys heermanni</i>	3	33.11	16.82	3.39	9.97	4.18	1.39	6.48	1.77	4.65	13.15	9.86	6.01
<i>Dipodomys ingens</i>	4	39.00	21.92	3.93	12.11	4.38	1.58	7.53	2.41	5.38	15.36	11.13	6.89
<i>Dipodomys merriami</i>	4	30.15	14.27	2.69	8.65	3.49	1.27	5.75	1.77	3.99	11.83	9.32	5.39
<i>Dipodomys micropus</i>	4	32.03	16.53	3.60	9.69	3.87	1.54	6.33	1.75	5.19	12.93	9.79	5.62
<i>Dipodomys nelsoni</i>	4	37.79	21.00	4.14	12.00	4.56	1.70	6.99	2.29	5.73	15.08	11.31	6.98
<i>Dipodomys nitratoides</i>	5	30.45	14.96	2.79	8.44	3.59	1.25	5.81	1.70	4.23	12.29	9.56	5.49
<i>Dipodomys ordii</i>	4	32.59	16.67	3.29	9.55	3.90	1.32	6.28	1.88	4.39	12.30	9.44	5.87
<i>Dipodomys panamintinus</i>	4	32.93	18.38	3.48	9.74	3.78	1.42	6.34	2.07	4.62	12.10	8.87	5.94
<i>Dipodomys phillipsii</i>	4	31.25	15.68	2.88	9.21	3.99	1.31	6.01	1.88	4.21	11.92	8.66	5.84
<i>Dipodomys simulans</i>	4	33.85	17.19	3.18	9.77	3.85	1.36	6.62	2.04	4.70	13.86	9.92	5.98
<i>Dipodomys spectabilis</i>	4	39.43	22.27	4.39	12.35	4.66	1.60	7.59	1.87	5.99	15.82	11.61	7.28
<i>Dipodomys stephensi</i>	4	33.79	17.75	3.32	10.32	3.97	1.33	6.68	1.72	4.50	13.28	9.73	6.15
<i>Dipodomys v. venustus</i>	5	35.80	18.21	3.63	11.01	4.27	1.49	7.17	1.71	4.94	13.44	9.76	6.48
<i>Dipodomys v. elephantinus</i>	4	35.55	17.98	3.64	10.55	4.00	1.45	6.88	2.02	4.97	13.66	9.84	6.40
<i>Microdipodops megacephalus</i>	4	21.82	10.45	1.98	5.67	2.90	0.76	3.97	1.35	3.24	8.76	7.36	4.22
<i>Microdipodops pallidus</i>	4	22.54	11.12	2.04	6.25	2.65	0.94	4.57	1.47	2.84	9.53	8.08	4.38
Heteromyinae													
<i>Heteromys anomalus</i>	4	32.08	15.46	3.01	9.29	4.56	1.13	5.73	1.85	4.91	5.39	5.32	6.36
<i>Heteromys australis</i>	4	31.11	14.33	2.85	8.66	4.37	0.97	5.31	2.02	5.14	5.21	4.91	5.95
<i>Heteromys catoptrius</i>	4	33.87	15.76	3.11	9.95	4.66	1.07	5.93	2.26	5.32	5.53	4.96	6.74
<i>Heteromys d. desmarestianus</i>	4	31.76	14.77	2.88	8.87	4.44	0.95	5.41	1.73	4.82	5.32	5.09	6.18
<i>Heteromys d. goldmani</i>	4	33.20	15.84	3.19	9.70	4.37	1.10	5.99	2.19	5.00	5.45	5.53	6.52
<i>Heteromys gaumeri</i>	4	30.36	14.35	2.81	8.69	4.04	1.00	5.27	1.67	4.58	5.86	5.76	6.24
<i>Heteromys nelsoni</i>	4	36.96	16.03	3.61	9.99	5.00	1.20	6.64	2.06	5.85	6.30	6.03	7.13
<i>Heteromys oasicus</i>	2	27.96	13.35	2.88	8.66	3.87	0.95	4.43	1.69	4.56	5.23	5.46	5.99
<i>Heteromys teleus</i>	1	35.37	17.44	3.36	10.52	4.79	1.31	6.29	2.61	5.37	5.21	5.38	6.86
<i>Liomys adspersus</i>	4	31.21	14.73	2.84	9.60	4.24	1.14	5.60	1.90	4.91	5.29	5.03	6.48
<i>Liomys irroratus</i>	4	28.82	13.87	2.74	8.43	4.24	1.12	5.57	1.53	4.32	5.43	5.98	5.93
<i>Liomys pictus</i>	4	30.57	14.41	2.77	8.60	4.11	1.12	5.56	1.57	4.81	5.04	6.13	5.92
<i>Liomys salvini</i>	4	28.36	13.45	2.67	8.50	3.55	0.98	4.99	1.47	4.54	5.14	5.85	5.60
Perognathinae													
<i>Chaetodipus arenarius</i>	4	21.09	11.12	2.05	5.56	2.79	0.80	3.76	1.00	2.97	5.62	4.55	4.39
<i>Chaetodipus artus</i>	4	22.80	11.60	2.30	6.30	3.06	0.87	4.62	1.28	3.37	5.67	4.92	4.96
<i>Chaetodipus baileyi</i>	4	28.52	15.36	2.86	8.05	3.96	1.04	5.54	1.34	4.70	7.93	6.92	5.39
<i>Chaetodipus californicus</i>	4	24.90	13.20	2.63	6.46	3.17	0.95	4.89	1.24	3.68	6.59	5.27	5.38
<i>Chaetodipus eremicus</i>	4	23.02	12.19	2.34	6.43	3.20	0.82	4.17	1.18	3.32	6.20	5.20	4.39
<i>Chaetodipus fallax</i>	4	23.91	12.51	2.39	6.58	3.31	0.91	4.36	1.24	4.05	6.36	5.37	5.25
<i>Chaetodipus formosus</i>	8	23.66	12.30	2.34	6.46	3.23	0.94	4.57	1.19	3.33	6.89	5.74	4.57
<i>Chaetodipus goldmani</i>	4	24.89	12.70	2.62	6.86	3.30	1.02	4.93	1.17	3.78	6.74	5.64	5.76
<i>Chaetodipus hispidus</i>	4	27.20	14.08	2.98	7.58	3.82	1.02	5.26	1.32	4.34	7.01	6.30	5.49
<i>Chaetodipus intermedius</i>	4	21.94	11.27	2.32	5.79	3.02	0.81	3.90	0.99	3.34	6.00	4.88	4.92
<i>Chaetodipus lineatus</i>	4	23.15	11.88	2.20	6.14	3.10	0.82	4.10	1.11	3.48	6.36	5.01	4.91
<i>Chaetodipus nelsoni</i>	3	23.75	12.26	2.30	6.10	3.31	0.86	4.41	1.14	3.49	6.53	5.36	5.05
<i>Chaetodipus penicillatus</i>	4	22.44	11.54	2.31	6.10	2.87	0.81	4.22	1.21	3.19	5.99	5.00	4.45
<i>Chaetodipus pernix</i>	4	21.87	11.43	2.13	6.19	2.94	0.79	3.82	1.08	3.88	5.91	4.69	4.75
<i>Chaetodipus rudinoris</i>	4	27.29	14.86	2.66	7.78	3.79	1.08	5.01	1.43	4.16	7.81	6.57	5.61
<i>Chaetodipus spinatus</i>	4	21.04	11.32	2.22	6.16	3.09	0.82	4.07	1.15	3.31	6.11	4.92	5.00
<i>Perognathus alticolus</i>	4	22.47	11.11	2.44	6.16	2.89	0.94	4.29	1.23	3.41	6.76	5.02	4.85
<i>Perognathus amplus</i>	4	22.19	12.05	2.17	6.44	2.80	0.85	4.07	0.84	3.84	7.65	6.14	4.35
<i>Perognathus fasciatus</i>	4	19.99	10.54	2.00	5.25	2.58	0.83	3.90	1.06	3.57	6.82	5.03	4.56
<i>Perognathus flavescens</i>	4	20.19	10.81	2.05	5.29	2.52	0.70	3.91	1.09	3.41	6.77	5.18	4.35

Table E.4—continued.

	#	SL	SW	IW	DL	ML	MW	PR	MB	BO	BL	BW	CB
<i>Perognathus flavus</i>	4	18.59	10.02	1.95	5.10	2.60	0.82	3.65	0.97	3.14	6.31	5.31	3.55
<i>Perognathus inornatus</i>	4	20.27	10.61	1.94	5.62	2.50	0.79	3.70	0.97	3.42	6.81	5.49	3.86
<i>Perognathus longimembris</i>	4	19.80	10.30	1.94	5.27	2.47	0.73	3.57	0.90	3.28	7.26	5.50	4.06
<i>Perognathus merriami</i>	4	18.38	9.97	1.84	5.57	2.26	0.70	3.47	0.97	2.74	5.88	4.66	3.81
<i>Perognathus parvus</i>	4	23.05	12.03	2.43	6.31	3.01	0.96	4.26	1.02	3.97	7.28	5.62	4.87
Hystricomorpha													
Ctenodactylomorphi													
Ctenodactylidae													
<i>Ctenodactylus gundi</i>	4	49.77	32.66	4.88	13.14	9.49	1.54	10.27	2.82	7.57	16.10	11.89	8.86
<i>Ctenodactylus vali</i>	1	na	na	2.87	10.55	7.95	1.91	7.75	2.00	8.53	na	na	na
<i>Felovia vae</i>	4	44.52	30.01	4.65	12.71	7.37	1.62	10.17	2.49	6.26	13.48	9.22	8.72
<i>Massoutiera mzabi</i>	4	43.54	26.72	4.23	11.87	7.83	1.55	10.32	1.81	6.06	16.30	11.46	7.53
<i>Pectinator spekei</i>	2	42.94	25.61	3.44	10.99	8.33	1.52	10.07	2.28	6.45	12.76	10.04	8.05
Hystricognathi													
Abrocomidae													
<i>Abrocoma bennettii</i>	4	46.03	21.12	2.92	14.09	9.34	1.90	10.05	1.16	7.67	14.12	10.28	7.62
Bathyergidae													
<i>Bathyergus janetta</i>	4	41.97	26.17	6.21	12.90	7.66	1.96	8.75	2.81	6.14	11.43	7.80	7.78
<i>Cryptomys hottentotus</i>	4	34.15	22.44	5.00	10.08	4.94	1.51	6.79	2.16	3.62	7.52	4.99	6.78
Caviidae													
Caviinae													
<i>Microcavia australis</i>	4	46.93	28.09	3.64	11.66	10.67	2.08	8.48	2.73	7.49	12.45	9.00	8.99
Dolichotinae													
<i>Dolichotis patagonum</i>	4	132.13	66.52	10.01	43.58	26.32	7.38	23.13	8.46	16.39	23.78	19.30	20.39
<i>Dolichotis salinicola</i>	4	101.04	51.16	7.65	33.48	20.05	4.39	17.96	7.14	14.90	19.00	15.29	14.91
Chinchillidae													
<i>Lagidium viscacia</i>	4	87.26	43.91	7.58	24.98	19.18	4.38	16.78	5.99	11.75	18.19	12.51	14.39
<i>Lagostomus maximus</i>	4	105.29	62.94	11.72	34.15	23.28	6.68	20.23	9.20	12.87	20.56	12.92	18.67
Ctenomyidae													
<i>Ctenomys emilianus</i>	1	36.06	25.26	6.67	12.61	8.37	2.01	7.97	3.93	4.38	9.48	6.60	7.97
<i>Ctenomys latro</i>	4	34.41	21.70	4.93	9.63	6.87	1.64	6.33	2.18	6.22	12.31	7.98	6.50
<i>Ctenomys mendocinus</i>	4	35.81	21.12	5.48	9.89	6.97	1.51	7.06	2.02	6.76	13.83	9.03	6.54
<i>Ctenomys occultus</i>	2	37.13	21.36	5.79	9.44	6.84	1.63	7.76	1.99	6.94	13.75	9.45	6.89
Hystricidae													
<i>Hystrix africaeaustralis</i>	4	156.50	84.67	16.77	50.71	36.78	6.21	31.85	14.19	19.63	23.64	19.20	32.31
<i>Hystrix cristata</i>	4	154.00	83.49	16.31	46.38	36.08	6.29	30.26	13.11	24.04	23.45	20.77	30.49
<i>Hystrix indica</i>	4	158.97	82.42	17.42	47.18	34.91	7.29	34.63	14.31	22.82	23.50	20.81	29.20
Octodontidae													
<i>Octodon degus</i>	4	40.07	21.40	3.82	9.98	8.12	1.69	8.53	2.17	6.59	12.16	7.50	7.62
<i>Octodon lunatus</i>	4	44.37	22.95	4.07	10.22	9.46	2.03	9.33	2.37	7.37	13.36	8.40	8.42
Petromuridae													
<i>Petromus typicus</i>	4	39.81	23.15	3.58	10.41	7.70	1.85	8.75	2.05	6.26	11.37	8.41	7.91
Myodonta													
Dipodoidea													
Dipodidae													
Allactaginae													
<i>Allactaga balikunica</i>	1	27.94	19.83	2.48	9.11	5.48	1.13	5.30	0.87	4.47	8.22	5.93	6.34
<i>Allactaga bullata</i>	4	32.27	22.43	2.88	10.31	6.42	1.69	6.33	1.34	5.59	9.17	6.23	7.23
<i>Allactaga e. elater</i>	4	27.07	20.00	2.25	8.31	4.95	0.96	4.87	1.31	4.40	7.17	4.78	6.76
<i>Allactaga e. elater indica</i>	3	28.82	20.99	2.41	8.70	4.95	1.18	5.46	1.41	4.60	7.57	4.89	6.96
<i>Allactaga e. elater turkmeni</i>	1	26.21	19.95	2.40	7.83	5.19	1.55	4.38	1.31	4.35	7.14	4.27	6.85
<i>Allactaga euphratica</i>	8	32.07	22.57	2.96	10.10	6.49	1.39	6.26	2.58	4.47	7.65	5.52	7.44
<i>Allactaga firozzi</i>	3	28.05	20.80	2.44	9.20	5.16	1.38	6.30	1.61	4.70	8.02	5.18	6.60
<i>Allactaga hotsoni</i>	4	31.54	21.57	2.50	9.76	5.36	1.25	6.74	1.72	4.63	8.96	6.16	6.90
<i>Allactaga major</i>	4	47.64	34.19	4.45	15.34	8.66	2.37	9.05	2.99	6.27	10.32	7.16	11.09
<i>Allactaga severzovi</i>	2	38.78	27.51	3.70	12.49	8.87	2.57	5.65	2.20	6.25	9.63	6.61	8.40
<i>Allactaga sibirica</i>	2	38.99	24.95	3.19	12.70	7.66	2.15	7.21	2.00	5.64	9.40	6.18	8.48
<i>Allactaga tetradactyla</i>	6	31.20	21.29	2.40	9.46	5.86	1.48	6.09	2.39	4.13	7.78	5.22	7.59
Pygeretmus platyurus	1	23.32	18.50	1.56	7.89	3.92	1.21	4.86	2.15	2.36	5.78	4.43	5.87
Pygeretmus pumilio	4	26.36	20.46	1.97	8.17	4.26	1.18	5.93	2.64	na	na	na	na
Pygeretmus zhitkovi	3	27.18	21.73	2.23	9.11	4.61	1.35	4.93	2.23	3.98	6.17	5.12	6.42
Cardiocraninae													
<i>Cardiocranus paradoxus</i>	2	19.65	9.52	1.78	4.82	3.38	0.85	4.17	1.23	1.61	8.09	8.02	3.96
<i>Salpingotulus michaelis</i>	2	17.62	10.65	1.44	4.44	2.98	0.61	4.04	1.09	1.15	7.18	5.81	3.88
<i>Salpingotulus crassicauda</i>	2	14.35	8.23	1.21	3.19	2.44	0.57	3.23	0.58	1.09	6.29	4.97	3.03
Dipodinae													
<i>Dipus s. sagitta</i>	4	31.94	21.03	3.02	9.07	6.34	1.26	6.58	1.36	5.31	10.23	8.45	6.77
<i>Dipus s. sowerli</i>	4	29.64	19.76	3.18	8.67	5.41	1.39	7.05	1.50	4.44	9.30	7.81	6.36
<i>Eremodipus lichensteinii</i>	1	27.05	18.19	2.63	7.96	4.29	1.34	4.50	1.85	5.72	10.73	8.44	5.45
<i>Jaculus blanfordi</i>	5	34.41	24.41	3.24	10.25	4.99	1.51	9.21	1.76	4.38	12.69	9.74	6.80
<i>Jaculus jaculus</i>	4	32.18	22.42	3.10	9.48	4.89	1.59	8.04	1.36	3.92	11.57	8.72	6.49
<i>Jaculus orientalis</i>	4	37.52	27.59	3.46	12.27	6.32	1.81	9.22	2.02	4.88	12.69	9.92	7.53
<i>Paradipus ctenodactylus</i>	1	28.32	15.49	2.45	8.09	5.79	1.23	5.09	1.58	4.34	9.66	7.89	6.22
<i>Stylopodus telum</i>	4	24.80	18.10	2.38	8.02	4.18	1.15	5.17	1.93	3.60	8.06	6.56	6.06

Table E.4—continued.

	#	SL	SW	IW	DL	ML	MW	PR	MB	BO	BL	BW	CB
Sicistinae													
<i>Sicista betulina</i>	4	17.96	8.91	1.65	4.76	2.67	0.65	4.11	1.33	2.77	4.16	3.49	4.50
<i>Sicista concolor</i>	5	22.26	10.93	2.16	6.37	3.29	0.86	4.89	1.66	3.52	4.60	3.61	5.27
<i>Sicista napaea</i>	1	19.50	9.82	1.73	4.90	3.09	0.69	4.38	1.14	3.11	4.93	3.94	4.50
<i>Sicista subtilis</i>	4	22.62	13.37	1.96	6.28	3.91	1.01	5.17	1.77	3.20	5.26	4.30	5.40
Zapodinae													
<i>Eozapus setchuanus</i>	4	20.08	10.44	1.95	5.07	3.26	0.67	4.05	1.48	2.95	4.54	3.52	5.14
<i>Napaeozapus insignis</i>	4	22.57	11.78	2.42	6.21	3.47	0.70	4.60	1.95	3.36	4.69	3.37	5.17
<i>Zapus hudsonius</i>	4	21.83	10.97	2.26	5.63	3.38	0.71	4.40	1.77	3.37	4.42	3.58	5.08
<i>Zapus p. oregonus</i>	4	24.74	13.15	2.44	6.44	4.24	0.93	5.03	2.40	3.69	4.78	4.03	6.01
<i>Zapus p. pacificus</i>	1	23.44	13.13	2.44	6.37	3.89	0.99	4.92	2.33	3.72	4.91	3.85	5.65
<i>Zapus p. princeps</i>	3	23.43	12.37	2.24	6.13	3.57	0.89	4.87	2.10	3.66	4.71	3.80	5.53
<i>Zapus trinotatus</i>	4	23.73	12.76	2.50	6.16	3.78	0.75	4.79	2.13	3.68	4.88	4.13	5.66
Muroidea													
Calomyscidae													
Calomyscinae													
<i>Calomyscus baluchi</i>	4	23.65	11.75	2.19	6.64	3.02	0.86	5.37	1.54	3.65	5.04	3.77	5.60
<i>Calomyscus bailwardi</i>	3	22.92	11.72	2.24	6.62	3.07	0.78	4.69	1.57	3.53	4.88	3.73	5.51
Cricetidae													
Arvicolinae													
<i>Alticola strelzowi</i>	6	24.72	14.28	2.83	8.14	5.37	0.97	5.17	1.58	4.07	7.04	5.16	5.80
<i>Arvicola amphibius</i>	3	39.57	22.83	4.85	13.08	9.74	1.86	7.24	2.53	6.29	8.10	7.01	7.91
<i>Chionomys nivalis</i>	4	27.35	15.50	3.29	8.72	6.38	1.11	5.37	1.31	4.46	7.18	6.28	5.69
<i>Dicrostonyx groenlandicus</i>	4	25.62	15.89	2.73	8.30	6.55	1.16	4.05	1.51	4.15	7.38	4.63	5.63
<i>Ellobius talpinus</i>	4	30.78	21.30	3.90	10.37	6.93	1.40	4.10	2.05	4.97	7.20	5.10	6.33
<i>Eolagurus luteus</i>	5	27.42	16.80	3.62	9.37	6.75	1.26	4.74	1.67	5.39	8.55	6.32	5.89
<i>Eolagurus przewalskii</i>	1	29.86	18.55	3.63	10.91	6.04	1.02	5.11	1.63	5.53	8.87	7.22	5.51
<i>Eothenomys custos rubellus</i>	4	21.57	12.55	2.74	6.98	4.94	0.91	4.19	1.26	3.68	5.31	3.90	4.91
<i>Lagurus l. abacaneules</i>	1	20.67	13.29	2.50	6.78	5.20	0.95	3.47	1.25	3.83	7.04	4.50	3.96
<i>Lagurus l. agressus</i>	2	22.67	13.81	2.60	7.35	5.71	1.00	3.77	1.58	3.75	6.62	4.62	4.35
<i>Lagurus l. lagurus</i>	1	23.04	14.14	2.72	7.53	5.49	1.03	4.30	1.71	4.04	7.26	4.54	4.71
<i>Lasiopodomys mandarinus</i>	4	23.88	14.30	3.12	7.66	5.53	1.15	4.30	1.49	3.94	6.98	4.54	4.96
<i>Lemmus sibiricus</i>	4	32.64	21.47	4.13	10.77	8.63	1.69	5.09	1.96	6.05	10.01	6.88	5.92
<i>Microtus arvalis</i>	4	23.70	13.41	2.94	7.30	5.59	1.10	4.31	1.18	4.30	6.94	4.73	4.95
<i>Microtus californicus</i>	4	26.03	14.55	2.97	8.03	6.16	1.26	4.62	1.48	4.47	7.70	5.38	6.02
<i>Microtus chrotorrhinus</i>	4	25.65	13.77	2.93	7.72	5.93	1.08	5.07	1.09	4.51	7.87	5.68	5.48
<i>Microtus kikuchii</i>	4	26.20	14.03	3.20	7.81	6.30	1.23	4.84	1.34	4.48	7.39	5.59	5.26
<i>Microtus montanus</i>	3	26.95	15.18	3.29	8.49	6.16	1.17	4.77	1.54	4.69	7.29	5.23	5.39
<i>Microtus p. acadicus</i>	1	23.60	13.79	2.82	7.73	5.66	1.06	4.84	1.21	4.08	6.70	4.95	4.71
<i>Microtus p. pennsylvanicus</i>	3	24.52	13.38	2.93	7.64	5.84	1.13	4.41	1.23	4.36	6.87	4.80	5.21
<i>Microtus richardsoni</i>	1	29.67	17.72	3.92	10.45	6.16	1.20	4.60	2.07	4.54	7.69	4.96	6.48
<i>Myodes gapperi</i>	4	23.41	12.56	2.64	7.13	4.83	0.88	5.03	1.34	4.15	7.26	5.24	5.54
<i>Neodon irene</i>	4	21.58	12.75	2.50	6.63	4.83	0.94	4.24	1.42	3.67	5.93	4.25	4.84
<i>Neofiber alleni</i>	4	42.05	26.02	5.27	14.37	10.69	2.11	7.42	3.28	6.81	10.45	7.70	9.21
<i>Ondatra z. rivalicetus</i>	1	61.70	37.96	8.12	21.35	14.31	3.53	10.03	4.76	10.08	13.12	8.67	12.19
<i>Ondatra z. zibethicus</i>	2	58.52	34.94	7.50	20.30	13.76	3.28	9.23	4.79	8.68	11.50	9.02	11.16
<i>Phenacomys i. levii</i>	2	21.24	12.69	2.47	6.37	5.41	1.10	4.24	1.55	3.57	5.76	4.37	4.79
<i>Phenacomys i. oramoutis</i>	2	20.28	11.33	2.33	5.88	5.01	1.02	3.94	1.30	3.33	5.68	4.34	4.69
<i>Prometheomys schaposchnikowi</i>	4	30.89	17.37	4.28	9.43	6.91	1.90	5.87	2.51	5.19	8.03	5.30	7.17
<i>Synaptomys c. cooperi</i>	1	24.18	14.13	3.26	6.96	6.07	1.01	4.28	1.26	4.18	7.17	5.08	5.00
<i>Synaptomys c. grossii</i>	2	25.08	15.21	3.80	7.66	6.35	1.22	4.43	1.50	4.47	7.73	5.24	5.20
Cricetinae													
<i>Allocricetus e. curtatus</i>	5	27.60	15.51	3.36	9.20	4.15	1.04	6.79	2.22	4.55	5.97	4.08	6.43
<i>Allocricetus e. microdon</i>	2	24.80	14.45	2.91	9.18	3.96	0.86	5.84	1.89	4.16	5.86	3.84	5.40
<i>Cricetus b. barabensis</i>	4	25.27	13.55	2.35	7.55	3.47	0.71	6.32	1.60	4.62	5.54	4.02	5.80
<i>Cricetus b. griseus</i>	4	25.02	13.29	2.52	7.46	3.39	0.83	6.07	1.85	4.17	5.05	3.69	5.23
<i>Cricetus longicaudatus</i>	4	22.24	11.60	2.08	6.33	3.44	0.62	5.08	1.44	3.61	4.79	3.69	5.20
<i>Cricetus migratorius</i>	7	25.73	13.34	2.59	7.74	3.76	0.71	5.99	1.79	4.45	5.40	3.78	5.58
<i>Cricetus c. canescens</i>	2	37.85	23.00	4.80	12.36	7.13	1.30	8.40	2.21	6.80	9.09	6.40	8.99
<i>Cricetus c. cricetus</i>	2	44.61	26.20	6.00	14.36	7.44	1.60	11.23	3.10	9.22	8.92	9.61	9.46
<i>Mesocricetus auratus</i>	3	32.11	19.23	4.61	10.53	5.42	1.05	7.87	2.59	6.18	6.82	4.75	6.90
<i>Phodopus campbelli</i>	4	23.49	13.42	2.68	7.11	3.29	0.86	5.69	1.82	4.04	4.84	3.54	5.16
<i>Phodopus roborovskii</i>	4	19.78	11.04	1.85	5.65	2.78	0.60	4.36	1.63	3.15	4.11	2.94	4.92
<i>Phodopus sungorus</i>	4	22.46	12.13	2.15	6.68	3.08	0.55	4.93	1.82	3.80	4.75	3.23	5.09
Neotominae													
<i>Baiomys musculus</i>	3	17.64	9.94	1.75	4.94	2.84	0.59	3.98	1.20	2.63	4.34	2.96	4.29
<i>Habromys lepturus</i>	4	26.63	14.24	2.44	7.30	4.10	0.89	6.13	1.77	3.93	5.89	4.13	5.76
<i>Hodomys allenii</i>	4	46.68	23.51	4.64	13.46	9.71	1.83	8.95	3.37	6.97	8.57	6.03	9.74
<i>Isthomys pirrensis</i>	4	38.58	18.56	3.78	11.99	5.46	1.19	9.07	2.90	5.50	6.71	4.90	7.74
<i>Megadontomys thomasi</i>	4	35.28	17.69	3.21	10.26	5.78	1.40	8.30	2.33	5.05	6.98	5.04	7.86
<i>Neotoma albigena</i>	4	41.59	22.20	4.97	12.13	7.86	1.85	9.00	3.08	6.86	8.31	6.44	9.34
<i>Neotoma bryanti</i>	4	40.14	21.97	3.94	12.29	7.33	1.71	9.13	2.77	6.41	8.61	6.51	9.55
<i>Neotoma cinerea</i>	2	44.07	23.01	4.83	13.48	8.22	1.89	9.58	3.16	6.69	8.75	7.22	9.65
<i>Neotoma devia</i>	4	34.88	18.47	3.81	10.30	6.92	1.63	7.28	2.14	5.37	7.42	6.12	7.69
<i>Neotoma floridana</i>	3	47.91	25.02	5.32	15.16	7.82	2.26	11.39	3.75	6.95	8.56	6.63	9.98
<i>Neotoma goldmani</i>	4	35.32	18.40	3.36	10.75	6.85	1.77	7.88	2.47	5.45	7.27	5.75	7.84

Table E.4—continued.

	#	SL	SW	IW	DL	ML	MW	PR	MB	BO	BL	BW	CB
<i>Neotoma lepida</i>	4	40.41	20.81	4.24	12.07	7.26	1.76	8.89	2.62	6.26	8.44	6.57	8.65
<i>Neotoma mexicana</i>	4	39.25	21.30	4.43	11.94	7.94	1.99	8.06	2.76	5.87	7.80	5.72	8.80
<i>Neotomodon alstoni</i>	4	30.23	16.34	2.82	9.45	4.86	1.27	7.21	1.94	4.35	6.33	4.79	6.85
<i>Ochrotomys nuttalli</i>	3	23.07	12.41	2.25	6.75	3.34	0.71	5.15	1.68	3.34	4.91	3.76	5.30
<i>Onychomys l. arcticeps</i>	2	26.25	14.79	3.04	7.22	3.92	0.78	6.57	2.03	4.03	5.38	4.15	5.97
<i>Onychomys l. breviauritus</i>	1	25.87	13.59	2.59	6.75	3.92	0.80	6.56	2.02	4.30	4.60	4.16	5.66
<i>Onychomys ruidosae</i>	3	26.29	14.68	2.82	7.22	3.94	0.97	6.37	2.14	4.29	5.04	4.26	6.13
<i>Onychomys torridus</i>	4	24.23	12.64	2.55	6.18	3.45	0.73	6.27	1.69	3.80	5.33	4.09	5.87
<i>Osgoodomys banderanus</i>	4	28.19	13.31	2.54	7.78	3.62	0.84	6.65	2.17	3.91	5.02	3.99	5.99
<i>Peromyscus a. hylocetes</i>	3	27.97	15.20	2.98	8.93	4.34	0.94	6.72	1.87	4.15	5.99	4.65	6.41
<i>Peromyscus a. oaxacensis</i>	1	26.25	13.01	2.62	7.86	4.02	1.09	5.80	1.64	3.78	5.35	3.94	5.77
<i>Peromyscus b. levipes</i>	3	26.60	13.75	2.54	7.58	4.05	0.93	6.10	1.89	3.73	5.76	4.19	6.23
<i>Peromyscus b. rowleyi</i>	1	26.17	12.98	2.43	7.63	3.66	0.93	5.90	1.71	3.58	5.39	3.83	5.80
<i>Peromyscus californicus</i>	1	26.98	13.64	2.28	7.54	3.50	0.80	6.63	1.52	4.10	6.03	4.75	5.66
<i>Peromyscus c. auripectus</i>	1	22.88	11.36	2.23	6.46	2.83	0.69	5.09	1.52	3.17	5.12	3.84	5.27
<i>Peromyscus c. pergracilis</i>	3	24.58	12.58	2.26	6.95	3.31	0.85	5.55	1.93	3.68	5.39	4.31	5.77
<i>Peromyscus eremicus</i>	4	23.60	12.45	2.30	6.29	3.31	0.84	5.65	1.74	3.51	5.45	4.09	5.72
<i>Peromyscus fraterculus</i>	4	22.93	11.66	2.14	6.34	3.26	0.87	5.46	1.68	3.33	5.32	3.80	5.46
<i>Peromyscus leucopus</i>	4	23.61	12.35	2.18	6.90	3.12	0.78	5.56	1.88	3.30	4.93	3.72	5.56
<i>Peromyscus m. abietorum</i>	1	23.03	11.53	2.11	6.92	2.75	0.56	5.45	1.47	3.22	5.02	3.54	5.30
<i>Peromyscus m. gambelii</i>	2	25.05	11.43	2.00	7.36	3.31	0.62	5.20	1.63	4.23	5.47	3.75	5.83
<i>Peromyscus m. gracilis</i>	1	23.56	12.03	2.27	7.24	3.01	0.64	5.44	1.83	3.31	5.11	3.61	5.43
<i>Peromyscus merriami</i>	4	24.78	13.28	2.44	6.91	3.44	0.88	6.02	1.91	3.84	5.72	4.41	5.90
<i>Peromyscus m. nudipes</i>	1	30.16	14.69	2.75	8.86	4.08	0.88	7.26	2.41	4.45	5.77	4.22	6.81
<i>Peromyscus m. saxatilis</i>	3	29.61	14.08	2.75	8.71	3.83	0.93	6.88	2.00	4.23	5.62	4.19	6.22
<i>Peromyscus pectoralis</i>	4	25.06	13.12	2.28	6.80	3.21	0.79	6.04	1.95	3.64	5.75	4.08	5.95
<i>Peromyscus p. allophys</i>	1	20.36	10.77	1.89	5.71	2.75	0.62	4.68	1.11	3.00	4.63	3.33	4.79
<i>Peromyscus p. subgriseus</i>	3	20.56	10.81	1.89	5.81	2.70	0.68	4.87	1.28	3.00	4.56	3.34	4.66
<i>Reithrodontomys creper</i>	4	27.20	14.51	2.52	7.89	3.86	0.98	6.10	2.11	3.74	5.56	4.05	6.27
<i>Reithrodontomys f. chiapensis</i>	1	20.47	10.26	2.25	5.89	2.72	0.89	4.44	1.59	3.14	4.08	3.30	4.57
<i>Reithrodontomys f. difficilis</i>	1	20.48	10.25	1.94	5.36	2.68	0.68	4.38	1.56	2.90	4.36	3.44	5.00
<i>Reithrodontomys f. helvolus</i>	1	21.35	10.78	1.98	5.84	2.89	0.66	4.57	1.43	3.59	4.62	3.70	5.02
<i>Reithrodontomys f. intermedius</i>	1	20.04	10.27	1.99	5.95	2.82	0.71	4.08	1.20	3.13	4.34	3.55	4.85
<i>Reithrodontomys gracilis</i>	3	20.37	10.09	2.09	5.55	2.71	0.59	4.66	1.58	2.79	4.48	3.36	5.04
<i>Reithrodontomys megalotis</i>	7	20.14	10.60	1.93	5.60	2.72	0.65	4.55	1.66	3.00	4.29	3.56	4.74
<i>Scotinomys teguina</i>	3	21.46	11.39	2.12	5.82	3.64	0.76	4.55	1.67	3.03	4.98	3.43	5.27
<i>Xenomys nelsoni</i>	2	37.73	20.21	3.62	10.91	7.74	1.92	7.71	2.35	6.14	9.39	7.12	8.38
Sigmodontinae													
<i>Abrothrix andinus</i>	4	23.43	12.65	2.39	6.47	3.45	0.85	5.68	1.30	3.49	6.12	4.49	6.06
<i>Abrothrix longipilis</i>	4	27.93	13.58	2.92	7.75	4.08	1.00	6.53	1.90	4.12	5.80	4.43	6.83
<i>Aegialomys xantheolus</i>	4	30.18	15.39	3.29	9.30	4.79	1.10	6.84	2.13	4.56	6.52	4.06	6.82
<i>Akodon aerosus</i>	4	25.86	13.70	2.52	7.58	4.16	0.97	6.12	2.00	4.15	6.13	4.01	6.50
<i>Akodon boliviensis</i>	3	22.85	12.24	2.27	6.57	3.61	0.76	5.63	1.58	3.66	5.73	3.96	5.73
<i>Akodon iniscatus</i>	4	25.33	13.49	2.42	7.43	3.85	2.11	5.12	2.32	4.67	5.54	4.62	5.79
<i>Akodon kofordi</i>	4	24.27	12.25	2.38	6.90	3.53	0.72	5.67	1.67	3.40	5.99	3.94	5.72
<i>Akodon lutescens</i>	1	20.14	10.34	1.95	6.05	3.11	0.65	4.78	1.36	2.97	5.13	3.45	5.15
<i>Akodon minimus</i>	3	24.68	12.28	2.49	7.20	3.97	0.84	5.54	1.70	3.38	5.79	3.72	5.93
<i>Akodon molinae</i>	1	26.88	14.14	2.75	8.32	4.13	1.09	6.85	2.01	4.31	6.50	4.22	6.23
<i>Akodon spegazzinii</i>	4	24.61	12.56	2.46	7.02	4.03	2.00	4.38	2.39	4.36	5.33	4.50	6.04
<i>Akodon torques</i>	4	24.38	12.43	2.37	6.82	3.87	0.68	5.32	1.44	3.64	5.47	3.96	6.04
<i>Andalgalomys pearsoni</i>	4	27.79	13.88	2.40	8.79	4.01	1.10	6.17	1.75	4.27	5.70	4.69	5.95
<i>Andinomys edax</i>	5	32.65	17.96	4.21	10.44	6.45	1.73	7.19	2.74	4.97	6.66	4.90	7.38
<i>Auliscomys sublimis</i>	4	23.27	13.06	2.24	6.75	4.17	0.90	5.24	1.78	3.66	5.36	3.68	5.17
<i>Brucepattersonius igniventris</i>	2	26.57	12.66	2.95	6.98	3.98	0.98	6.26	1.76	3.86	5.09	4.33	6.19
<i>Brucepattersonius soricinus</i>	2	26.71	12.80	2.91	6.91	4.16	0.84	6.45	1.97	3.90	5.60	4.44	6.29
<i>Calomys callosus</i>	7	24.68	13.12	2.59	6.73	3.68	0.90	5.81	1.89	3.96	5.41	3.72	5.58
<i>Calomys lepidus</i>	4	21.61	11.70	2.04	5.73	3.44	0.89	4.96	1.73	3.45	4.80	3.75	5.24
<i>Calomys musculinus</i>	4	20.78	11.22	1.87	5.70	3.27	0.78	4.56	1.55	3.14	4.96	3.50	5.10
<i>Calomys venustus</i>	1	25.23	13.63	2.56	6.80	4.19	0.98	5.71	2.09	3.60	5.86	3.93	5.87
<i>Cerradomys subflavus</i>	4	34.47	17.27	3.43	10.24	4.79	1.07	8.48	2.45	5.35	6.54	4.73	6.62
<i>Chelemys macronyx</i>	4	31.24	17.47	3.81	8.47	5.31	1.27	7.60	2.35	5.01	7.27	5.10	7.82
<i>Chinchilla sahamae</i>	4	36.82	19.88	4.04	11.83	6.39	1.67	8.39	2.39	5.73	8.05	5.64	7.56
<i>Delomys d. collinus</i>	2	31.71	15.78	3.57	9.63	4.44	1.01	7.04	2.24	4.67	6.27	4.22	6.63
<i>Delomys d. dorsalis</i>	2	31.01	15.71	3.24	9.41	4.54	1.02	7.02	2.27	4.83	6.42	4.56	6.66
<i>Deltamys kempi</i>	4	22.24	10.85	2.06	6.29	3.36	0.65	5.34	1.62	3.66	5.17	3.54	5.32
<i>Eligmodontia moreni</i>	3	21.03	10.96	1.83	5.80	3.24	0.96	4.50	1.52	3.09	5.36	3.61	4.79
<i>Eligmodontia morgani</i>	4	23.86	12.84	2.22	6.74	3.39	0.86	5.33	1.67	3.52	5.93	3.97	5.63
<i>Eligmodontia typus</i>	8	22.35	11.79	2.03	6.23	3.29	0.69	4.81	1.65	3.35	5.56	3.76	5.12
<i>Euneomys c. chinchilloides</i>	3	30.02	17.81	3.51	8.99	5.08	1.30	6.63	2.19	5.29	7.28	5.01	6.51
<i>Euneomys c. sublimis</i>	1	27.87	15.77	3.32	7.85	4.76	1.16	6.12	1.71	4.66	7.04	4.45	6.53
<i>Geoxus valdivianus</i>	4	24.60	11.90	2.61	6.60	3.09	0.76	6.54	1.59	3.92	5.65	4.11	6.03
<i>Graomys editiae</i>	1	27.00	13.20	2.25	8.00	4.17	0.98	5.21	1.43	3.95	6.68	4.53	6.41
<i>Graomys griseoflavus</i>	7	31.42	15.83	3.00	9.30	4.83	1.21	7.01	1.92	4.89	7.66	5.28	6.75
<i>Holochilus brasiliensis</i>	4	37.04	20.11	4.64	12.19	6.61	1.55	7.10	2.67	5.99	7.48	4.83	7.40
<i>Holochilus sciureus</i>	3	36.25	19.81	4.58	12.14	6.34	1.61	7.71	2.49	5.61	7.24	4.74	7.04
<i>Ichthyomys stolzmanni</i>	1	30.90	15.18	3.16	8.45	3.55	1.00	9.20	3.25	5.07	6.41	4.16	5.88

Table E.4—continued.

	#	SL	SW	IW	DL	ML	MW	PR	MB	BO	BL	BW	CB
<i>Irenomys tarsalis tarsalis</i>	4	28.08	14.61	2.61	7.55	4.88	1.05	5.64	1.73	4.20	6.04	4.29	6.27
<i>Juliomys pictipes</i>	4	24.23	13.18	2.51	7.02	3.56	0.76	5.18	2.20	3.69	5.05	3.45	5.46
<i>Kunsia tomentosus</i>	4	50.74	27.95	6.50	15.24	8.44	2.54	13.15	4.03	7.87	9.95	7.60	10.16
<i>Lenoxus apicalis apicalis</i>	4	33.80	15.79	3.47	9.40	5.23	1.08	8.12	2.52	5.00	6.30	5.08	7.42
<i>Loxodontomys micropus</i>	4	30.39	16.95	3.59	8.63	5.17	1.27	6.77	2.25	4.61	6.83	4.71	6.26
<i>Melanomys c. chrysomelas</i>	3	29.01	16.22	3.18	8.16	4.33	1.20	6.96	2.61	4.80	5.52	4.08	6.59
<i>Melanomys c. ssp</i>	1	29.55	15.73	3.39	8.35	4.52	1.17	6.67	2.37	4.99	6.40	4.28	6.92
<i>Microryzomys m. azoricus</i>	1	16.04	8.18	1.29	4.44	2.24	0.69	3.50	0.78	2.72	4.17	3.03	4.23
<i>Microryzomys m. soricinus</i>	2	15.77	8.70	1.49	4.13	2.46	0.63	3.66	1.01	2.63	3.97	3.15	4.34
<i>Microryzomys m. ssp</i>	1	19.08	9.37	1.83	4.91	2.93	0.75	4.07	1.00	2.99	4.22	3.30	4.44
<i>Neacomys spinosus</i>	4	22.16	12.05	2.18	6.39	2.69	0.76	5.12	1.82	3.46	4.44	3.20	5.47
<i>Necromys amoeneus</i>	4	26.47	14.71	2.74	7.49	3.71	1.06	6.38	1.78	4.16	6.11	4.03	5.96
<i>Nectomys apicalis</i>	4	46.60	25.37	5.75	13.77	7.55	1.94	11.21	3.79	7.34	8.11	6.08	9.81
<i>Nectomys s. palmipes</i>	1	37.25	19.25	4.29	11.43	5.87	1.43	9.07	3.00	5.31	6.26	4.73	8.05
<i>Nectomys s. pollens</i>	1	39.70	21.99	4.84	11.60	6.38	1.50	9.07	3.34	6.21	6.82	5.52	8.37
<i>Nectomys s. ssp</i>	1	45.38	24.84	5.05	15.39	6.99	2.27	10.43	3.31	7.82	8.00	5.23	9.03
<i>Neotomys ebriosus</i>	5	28.17	15.53	4.09	7.72	4.55	1.23	6.00	2.10	4.52	6.60	4.50	6.52
<i>Nephelomys keaysi</i>	4	32.87	17.88	3.63	9.18	5.16	1.06	7.62	2.53	5.15	6.26	4.50	7.16
<i>Nephelomys levipes</i>	4	33.83	18.79	3.61	9.42	5.44	1.28	7.89	2.41	5.45	6.76	4.68	7.19
<i>Notiomys edwardsii</i>	1	22.53	12.69	2.75	5.64	2.98	0.81	5.51	1.84	3.31	5.32	4.02	5.56
<i>Oecomys bicolor</i>	3	25.29	12.08	2.33	6.42	3.50	0.79	5.17	1.85	3.64	4.98	3.69	5.40
<i>Oecomys concolor</i>	2	29.23	14.98	2.92	8.46	4.66	0.95	6.46	2.46	5.44	6.16	4.13	6.15
<i>Oecomys superans</i>	4	35.63	19.17	4.09	10.06	5.53	1.20	8.55	2.69	5.88	6.40	4.65	7.44
<i>Oligoryzomys fulvescens</i>	3	19.46	10.27	1.65	5.14	2.61	0.55	4.28	1.54	3.09	4.00	3.13	4.83
<i>Oligoryzomys longicaudatus</i>	4	23.71	12.51	2.22	6.43	3.18	0.78	5.39	1.86	3.66	4.80	3.48	5.25
<i>Oligoryzomys microtis</i>	4	21.30	11.72	1.98	5.63	2.83	0.64	4.75	1.73	3.32	4.41	3.27	5.06
<i>Oryzomys couesi</i>	3	26.58	13.80	2.91	7.54	3.92	0.92	5.85	1.94	4.13	5.28	3.80	6.13
<i>Oryzomys palustris</i>	4	28.76	15.50	2.92	8.28	4.26	0.90	6.55	2.18	4.42	5.85	4.21	6.54
<i>Oxymycterus hiska</i>	4	27.72	13.65	2.81	6.42	4.11	0.91	6.43	2.12	4.40	6.19	4.61	6.95
<i>Oxymycterus nasutus</i>	4	33.17	14.64	3.22	8.29	4.38	1.06	8.91	2.39	5.68	6.93	4.89	7.12
<i>Phyllotis amicus</i>	6	24.13	12.53	2.20	6.72	3.34	0.94	5.48	1.70	3.74	5.78	4.28	5.80
<i>Phyllotis andium</i>	4	26.02	13.65	2.50	7.34	3.77	0.91	5.72	1.85	4.11	5.98	4.51	6.48
<i>Phyllotis caprinus</i>	2	29.33	15.21	3.13	8.71	4.22	1.35	6.66	2.23	4.81	6.23	4.49	6.59
<i>Phyllotis darwini</i>	4	30.15	15.37	2.87	8.96	4.05	1.07	6.67	2.24	5.29	6.83	5.26	6.63
<i>Phyllotis gerbillus</i>	4	22.50	12.10	1.99	6.29	3.14	0.89	4.89	1.75	3.45	5.05	3.81	5.28
<i>Phyllotis magister</i>	2	30.10	16.19	3.56	9.34	4.53	1.46	6.86	2.19	4.55	6.33	4.78	7.04
<i>Phyllotis oslae</i>	4	26.46	13.97	2.71	7.56	4.03	1.14	6.18	2.07	3.92	5.74	4.52	6.27
<i>Phyllotis xanthopygus</i>	4	30.91	15.53	3.24	9.07	4.32	1.27	6.75	2.33	4.92	6.18	4.81	6.34
<i>Pseudoryzomys simplex</i>	4	28.58	15.44	3.10	8.62	4.11	1.07	6.46	2.24	4.66	6.01	4.19	5.80
<i>Punomys kofordi</i>	3	34.01	18.75	4.32	8.73	6.51	1.38	8.31	2.30	5.53	8.05	5.86	7.83
<i>Reithrodon a. auritus</i>	4	35.92	20.30	3.42	10.49	5.71	1.57	8.23	2.54	5.42	8.14	5.42	8.00
<i>Reithrodon a. physodes</i>	4	33.12	17.73	3.38	8.76	5.01	1.21	7.61	2.73	4.94	8.06	4.47	6.72
<i>Rhagomys longilingua</i>	1	27.08	15.43	2.90	7.59	4.14	0.87	5.87	2.51	4.19	6.45	3.54	6.26
<i>Rheomys t. stutoni</i>	2	28.62	14.94	2.68	6.79	3.87	1.26	7.17	2.67	5.45	6.29	3.91	7.94
<i>Rheomys t. thomasi</i>	2	26.40	14.40	2.46	6.42	4.02	0.95	6.63	2.35	4.46	5.81	3.90	7.59
<i>Rhipidomys macconnelli</i>	4	30.27	16.06	2.98	8.24	4.75	1.00	7.01	2.81	4.86	6.03	3.93	6.83
<i>Rhipidomys nitela</i>	4	30.38	16.44	3.03	8.24	4.42	0.92	7.14	2.85	4.99	6.23	3.81	6.80
<i>Scapteromys tumidus</i>	4	40.06	20.32	3.91	10.42	6.17	1.55	10.52	3.10	6.63	8.31	6.19	9.12
<i>Scolomys melanops</i>	1	19.56	11.51	1.67	5.26	2.34	0.59	4.77	1.83	3.20	4.55	3.51	5.29
<i>Scolomys ucalensis</i>	4	20.62	11.35	2.05	5.94	2.38	0.56	4.94	2.18	3.01	4.50	3.18	5.44
<i>Sigmodon alstoni</i>	4	29.30	17.13	3.80	8.90	4.92	1.24	6.08	2.11	5.01	6.79	4.64	6.39
<i>Sigmodon arizonae</i>	4	34.68	20.75	4.14	10.35	6.31	1.70	7.63	2.62	5.67	7.28	5.20	7.49
<i>Sigmodon fulviventer</i>	4	31.50	18.86	3.53	9.46	5.47	1.60	7.06	2.35	5.14	7.36	4.71	7.11
<i>Sigmodon hispidus</i>	3	36.07	19.96	4.49	10.48	5.71	1.57	8.15	2.53	6.17	8.07	5.28	7.27
<i>Sigmodon ochrognathus</i>	4	30.97	18.35	3.63	8.71	5.32	1.38	6.83	2.28	5.09	6.99	5.17	6.91
<i>Sigmodontomys alfari</i>	4	33.97	18.64	4.34	10.54	5.09	1.45	7.68	2.82	5.07	5.65	4.17	7.04
<i>Sooretamys angouya</i>	3	35.69	17.64	3.69	10.14	5.54	1.21	8.21	2.49	5.64	6.83	4.57	7.22
<i>Thaptomys nigrita</i>	4	23.30	12.95	2.43	7.05	3.24	0.77	5.64	1.73	4.00	5.50	3.87	5.60
<i>Thomasomys aureus</i>	4	36.89	20.20	3.87	10.21	6.60	1.78	8.18	3.17	5.99	7.19	4.92	7.96
<i>Thomasomys daphne</i>	4	24.92	13.17	2.33	7.15	3.78	0.89	5.36	2.08	3.96	5.15	3.86	6.10
<i>Thomasomys notatus</i>	4	28.43	15.04	2.78	7.92	4.09	0.99	6.50	2.75	4.63	6.15	4.18	6.83
<i>Transandinomys talamancae</i>	4	27.87	14.37	2.70	8.28	3.83	0.89	6.46	2.62	4.31	5.28	3.68	5.98
<i>Wiedomys pyrrhorhinus</i>	3	28.64	14.87	2.70	7.93	4.18	1.01	7.00	1.65	4.59	6.90	5.25	6.37
<i>Zygodontomys brevicauda</i>	3	27.97	14.53	2.65	8.21	3.76	0.92	6.62	2.56	4.58	5.91	3.92	6.05
Tylomyinae													
<i>Nyctomyssumichrasti</i>	5	29.61	16.92	2.94	8.21	4.40	1.02	6.78	2.41	4.57	5.72	4.09	6.92
<i>Ototylomysphyllotis</i>	3	39.20	19.54	3.45	11.28	6.87	1.41	8.75	2.43	5.65	7.42	5.90	7.70
<i>Tylomysnudicaudus</i>	5	42.84	22.83	4.07	12.24	7.99	1.55	9.13	3.41	6.54	7.97	5.77	9.30
Muridae													
Deomyinae													
<i>Acomys cahirinus</i>	7	25.64	12.94	2.08	7.94	3.79	1.23	5.83	1.88	2.97	5.74	3.67	6.12
<i>Acomys cineraceus</i>	4	25.43	12.22	2.24	7.73	3.59	1.16	5.94	1.82	3.66	5.31	3.42	5.97
<i>Acomys dimidiatus</i>	1	27.92	14.19	2.40	8.45	4.10	1.04	7.04	1.71	4.40	5.64	4.24	6.31
<i>Acomys ignitus</i>	4	26.86	13.07	2.05	8.56	3.64	1.11	6.22	1.48	3.73	5.93	3.75	5.77
<i>Acomys percivali</i>	4	27.89	13.72	2.40	8.79	4.02	1.23	6.46	1.74	3.95	5.92	3.87	6.36
<i>Acomys russatus</i>	4	27.84	13.98	2.61	8.61	4.49	1.39	6.33	1.49	3.85	6.21	4.40	6.33

Table E.4—continued.

	#	SL	SW	IW	DL	ML	MW	PR	MB	BO	BL	BW	CB
<i>Acomys spinosissimus</i>	4	25.19	12.48	2.16	7.77	3.98	1.25	5.57	1.84	3.60	5.31	3.54	6.08
<i>Acomys wilsoni</i>	4	27.92	14.00	2.20	8.65	4.10	1.28	6.29	1.84	4.08	6.13	4.25	6.51
<i>Deomys ferrugineus</i>	4	33.42	14.66	2.80	9.99	5.29	1.57	7.96	2.57	4.60	6.03	4.25	7.33
<i>Lophuromys f. flavopunctatus</i>	3	26.94	12.75	2.34	7.35	4.19	1.17	6.50	1.70	4.25	5.71	4.34	6.35
<i>Lophuromys f. zaphiri</i>	1	30.40	15.80	2.83	8.52	4.84	1.37	7.84	2.00	5.09	6.11	5.19	6.79
<i>Lophuromys f. zena</i>	4	28.17	14.09	2.57	7.84	4.11	1.25	6.89	1.73	4.50	6.40	4.55	6.39
<i>Lophuromys sikapusi</i>	4	30.16	15.24	2.94	8.09	4.49	1.60	7.54	2.11	5.21	6.37	4.83	6.56
<i>Uranomys ruddi</i>	4	27.06	13.85	2.52	8.18	4.00	1.25	6.39	2.24	4.20	6.19	3.98	6.10
Gerbillinae													
<i>Ammodillus imbellis</i>	1	29.57	14.29	2.43	8.70	4.49	0.95	6.77	1.43	3.91	9.32	5.37	5.70
<i>Brachiones przewalskii</i>	1	22.62	12.93	2.42	6.68	3.29	1.01	5.76	1.12	3.79	7.59	5.59	5.27
<i>Desmodillus braueri</i>	6	18.89	11.39	1.50	5.78	2.68	0.88	4.47	0.61	2.97	7.46	6.09	3.38
<i>Desmodillus auricularis</i>	8	32.95	18.34	2.71	10.09	3.92	1.19	7.77	1.20	5.46	13.58	9.57	5.50
<i>Dipodillus campestris</i>	4	25.24	13.17	2.10	7.17	3.42	1.03	5.52	1.17	3.38	7.11	4.81	5.43
<i>Dipodillus dasyurus</i>	4	24.92	13.64	2.05	6.98	3.30	1.05	5.37	0.79	3.85	7.44	5.24	5.30
<i>Dipodillus harwoodi</i>	4	23.08	12.29	1.98	6.84	3.34	0.96	4.88	0.65	3.40	7.08	4.96	5.12
<i>Dipodillus lowei</i>	2	28.45	14.20	2.40	8.39	3.91	1.26	6.22	1.29	3.87	7.27	5.39	5.99
<i>Dipodillus mackilligini</i>	1	24.66	12.70	2.40	6.97	3.45	1.02	5.92	0.83	3.51	7.91	5.18	5.02
<i>Dipodillus magharebi</i>	6	27.65	15.26	2.60	8.94	3.76	1.22	6.35	1.33	4.18	7.86	5.82	5.82
<i>Dipodillus simoni</i>	4	22.96	12.93	2.04	7.07	3.11	0.94	5.30	1.04	3.24	6.48	4.75	5.02
<i>Dipodillus stigmonyx</i>	4	22.30	11.82	1.76	6.13	2.94	0.83	5.15	0.88	3.09	7.13	5.30	4.60
<i>Gerbiliscus afra</i>	4	38.01	21.15	4.09	11.73	5.58	1.69	9.00	1.40	5.53	10.44	7.46	8.01
<i>Gerbiliscus boehmi</i>	4	39.83	21.78	4.28	12.10	5.95	1.77	9.54	1.63	5.52	10.31	6.90	7.68
<i>Gerbiliscus b. brantsii</i>	4	36.16	19.35	3.60	11.08	5.20	1.60	8.93	0.88	5.43	10.74	7.18	6.56
<i>Gerbiliscus b. humpatensis</i>	2	38.53	19.55	4.09	11.46	5.72	1.69	8.55	1.33	4.40	10.62	7.75	8.07
<i>Gerbiliscus b. perpallidus</i>	4	34.01	17.91	3.23	9.88	5.06	1.55	7.88	1.13	4.95	9.51	6.86	6.79
<i>Gerbiliscus guineae</i>	4	37.34	18.70	3.54	11.39	5.23	1.51	8.89	1.64	4.94	9.88	6.29	7.11
<i>Gerbiliscus inclusus</i>	4	36.80	19.76	4.29	10.90	5.37	1.58	8.89	1.51	5.01	10.36	6.83	7.10
<i>Gerbiliscus kempti</i>	4	37.95	19.61	3.72	11.89	5.38	1.61	8.89	1.67	5.52	9.19	6.42	7.73
<i>Gerbiliscus leucogaster</i>	4	33.79	18.24	3.42	10.23	4.67	1.51	7.59	1.23	4.67	9.62	6.66	6.59
<i>Gerbiliscus nigricaudus</i>	4	37.49	18.78	3.40	11.25	5.14	1.52	8.45	1.42	5.39	9.79	6.65	7.56
<i>Gerbiliscus phillipsi</i>	4	38.66	20.61	3.37	11.75	5.65	1.70	8.62	1.46	5.61	11.25	6.58	7.69
<i>Gerbiliscus robustus</i>	4	41.29	20.91	3.54	12.52	5.65	1.70	9.57	1.50	5.58	10.86	7.13	8.60
<i>Gerbiliscus validus</i>	4	38.90	21.89	3.92	11.57	5.68	1.67	9.53	1.57	5.54	10.95	6.72	8.00
<i>Gerbillurus paeba</i>	4	27.67	14.81	2.43	7.85	3.54	1.05	6.42	1.41	3.79	8.52	5.36	6.12
<i>Gerbillurus setzeri</i>	4	26.52	14.90	2.34	7.54	3.81	1.08	6.15	0.84	4.37	10.43	7.33	5.30
<i>Gerbillurus tytonis</i>	4	26.87	14.27	2.64	7.85	3.55	1.12	5.90	1.03	3.82	9.35	6.66	5.67
<i>Gerbillurus vallinus</i>	4	27.19	14.89	2.30	7.75	3.56	0.99	6.78	1.03	4.37	10.44	6.97	5.49
<i>Gerbillus agag</i>	4	28.83	15.54	2.34	8.32	3.69	1.11	6.36	0.88	4.20	9.71	6.22	5.91
<i>Gerbillus amoenus</i>	4	22.90	12.63	1.91	6.55	2.99	0.83	5.20	0.90	3.08	7.48	5.65	4.51
<i>Gerbillus andersoni</i>	4	27.58	15.32	2.36	8.12	3.68	1.10	6.16	0.98	3.90	8.40	6.04	5.60
<i>Gerbillus aquilus</i>	4	27.86	15.38	2.28	8.22	3.52	1.11	6.54	0.80	4.14	9.01	6.90	5.37
<i>Gerbillus cheesmani</i>	4	27.20	15.37	2.21	8.05	3.43	1.05	6.25	0.78	4.08	9.17	6.64	5.69
<i>Gerbillus famulus</i>	4	24.75	13.16	1.96	7.04	2.84	0.78	5.92	0.79	3.52	8.07	6.50	4.40
<i>Gerbillus floweri</i>	4	31.99	17.57	2.82	9.79	3.85	1.19	7.22	1.12	4.35	9.01	7.04	6.07
<i>Gerbillus garamantis</i>	1	23.70	12.86	1.87	7.01	2.85	0.83	5.29	0.92	3.54	7.13	5.34	4.78
<i>Gerbillus gerbillus</i>	6	25.78	14.66	2.20	7.75	3.12	1.00	6.02	0.91	3.50	8.17	5.82	5.33
<i>Gerbillus gleadowi</i>	4	27.61	14.74	2.28	8.33	3.53	1.22	6.02	0.95	3.55	8.53	6.14	5.29
<i>Gerbillus henleyi</i>	4	20.89	11.76	1.73	5.96	2.67	0.83	4.74	0.66	3.08	7.27	5.18	4.47
<i>Gerbillus hesperinus</i>	4	28.06	15.69	2.51	8.45	3.63	1.20	6.37	1.16	3.94	8.22	5.94	5.47
<i>Gerbillus hoogstraali</i>	4	26.09	14.26	2.23	7.64	3.30	1.17	5.81	0.83	3.54	8.15	6.03	5.13
<i>Gerbillus latastei</i>	4	27.94	15.28	2.13	8.24	3.40	1.10	6.49	1.04	4.03	9.42	6.35	5.89
<i>Gerbillus mauritaniae</i>	4	20.13	11.20	1.72	5.85	2.71	0.88	4.49	0.76	2.96	6.69	4.84	4.42
<i>Gerbillus mesopotamiae</i>	4	26.04	14.47	2.19	7.94	3.38	1.09	6.10	1.18	3.87	8.22	5.83	5.37
<i>Gerbillus muriculus</i>	4	20.18	10.83	1.62	5.74	2.89	0.80	4.50	0.86	2.84	6.72	4.69	4.37
<i>Gerbillus nanus</i>	6	24.76	13.17	1.96	7.33	3.17	0.96	5.72	0.87	3.71	8.56	6.15	5.07
<i>Gerbillus nigeriae</i>	2	25.40	13.15	2.05	7.56	3.43	0.99	5.79	1.10	3.66	7.00	4.96	4.11
<i>Gerbillus occiduus</i>	1	29.96	16.66	2.96	9.38	3.59	1.21	7.08	1.37	4.17	9.46	6.65	5.60
<i>Gerbillus perpallidus</i>	4	28.75	15.71	2.60	8.83	3.66	1.27	6.40	1.08	3.97	8.97	6.03	5.62
<i>Gerbillus poecilops</i>	4	27.88	15.06	2.54	9.29	3.20	0.94	6.18	1.10	4.09	8.83	6.22	5.12
<i>Gerbillus pulvinatus</i>	4	24.34	14.68	2.22	7.19	2.97	0.88	6.31	1.10	3.64	8.62	5.89	5.21
<i>Gerbillus pusillus</i>	4	22.03	11.17	1.81	6.59	2.84	0.84	4.72	0.64	3.03	6.86	4.83	4.26
<i>Gerbillus pyramidum</i>	4	31.97	18.01	2.72	10.35	4.00	1.35	7.39	1.33	5.09	10.32	6.88	6.09
<i>Gerbillus tarabuli</i>	4	29.38	15.95	2.43	9.19	3.53	1.10	6.63	0.93	4.26	9.77	6.62	5.72
<i>Meriones crassus</i>	4	33.96	18.97	2.75	10.17	4.25	1.30	8.57	1.02	5.90	14.29	10.52	5.70
<i>Meriones grandis</i>	4	41.47	22.97	4.37	13.08	5.23	1.64	9.65	1.74	6.48	13.75	9.55	7.81
<i>Meriones hurrianae</i>	4	34.34	20.25	3.56	10.25	4.64	1.53	8.12	1.62	5.33	11.28	7.92	7.25
<i>Meriones l. erythrourus</i>	1	38.67	22.18	3.21	11.70	4.70	1.34	10.09	2.39	6.39	15.15	11.58	6.41
<i>Meriones l. libycus</i>	4	40.69	22.29	3.50	11.78	5.12	1.71	10.26	1.46	6.66	15.67	11.50	7.68
<i>Meriones meridianus</i>	4	33.00	18.70	2.73	9.64	4.37	1.38	7.64	1.32	5.48	12.89	9.46	5.92
<i>Meriones persicus</i>	4	46.53	25.80	4.15	15.72	5.72	1.58	10.77	2.49	6.72	13.11	10.14	8.64
<i>Meriones rex</i>	4	36.89	20.84	4.00	11.71	5.02	1.52	8.44	1.83	5.49	12.00	8.80	7.13
<i>Meriones shawi</i>	4	38.08	21.84	3.54	11.97	5.04	1.59	9.21	1.48	6.21	13.84	9.94	7.01
<i>Meriones tamariscinus</i>	4	38.53	21.88	3.75	12.41	4.83	1.54	8.56	2.00	5.63	11.24	8.65	7.67
<i>Meriones tristrami</i>	4	36.84	20.32	3.45	11.67	4.43	1.23	8.31	1.46	5.31	11.08	8.24	7.23
<i>Meriones unguiculatus</i>	8	33.54	20.04	3.30	10.33	4.18	1.40	8.16	1.75	5.46	11.49	8.41	6.56

Table E.4—continued.

	#	SL	SW	IW	DL	ML	MW	PR	MB	BO	BL	BW	CB
<i>Merioness vinogradovi</i>	4	36.25	19.86	3.49	11.32	4.71	1.25	8.45	1.74	5.57	12.01	8.39	7.74
<i>Pachyuromys duprasi</i>	9	31.80	18.66	2.74	9.46	4.21	1.37	8.04	1.15	5.29	15.71	10.73	5.04
<i>Psammomys obesus</i>	9	38.97	23.48	4.09	12.78	5.71	1.73	8.67	1.74	6.24	13.30	10.62	7.52
<i>Rhombomys o. sodalis</i>	4	39.34	23.58	4.72	12.26	6.17	1.85	8.43	2.04	5.97	13.37	9.68	7.60
<i>Rhombomys o. ssp</i>	5	37.94	22.08	4.69	11.37	5.48	1.65	8.34	1.92	5.87	12.55	9.65	7.25
<i>Sekeetamys calurus</i>	8	32.28	16.73	2.78	9.77	4.11	1.37	7.35	1.07	4.68	11.62	8.27	5.80
<i>Tatera indica</i>	8	41.26	22.40	3.52	12.19	5.41	1.83	9.43	2.05	5.68	11.92	7.66	8.48
<i>Taterillus arenarius</i>	4	32.23	16.55	2.56	9.65	3.36	1.34	7.22	1.46	4.24	9.25	5.80	6.67
<i>Taterillus congicus</i>	4	32.76	16.52	2.70	9.65	4.29	1.40	6.98	1.66	4.49	9.21	5.59	6.95
<i>Taterillus emini</i>	4	31.51	16.13	2.49	9.19	4.31	1.44	6.93	1.63	4.21	8.98	5.42	6.72
<i>Taterillus gracilis</i>	4	32.35	16.42	2.71	9.52	3.92	1.43	7.28	1.65	4.21	9.19	5.93	6.79
<i>Taterillus harringtoni</i>	4	33.10	17.15	2.56	10.00	4.23	1.40	7.69	1.53	4.80	9.88	6.19	6.23
<i>Taterillus lacustris</i>	4	32.22	16.43	2.57	9.59	4.57	1.59	7.10	1.47	4.43	9.07	5.92	6.71
<i>Taterillus pygargus</i>	4	33.68	17.44	2.74	10.13	4.35	1.66	7.42	1.63	4.72	9.39	6.09	6.44
Lophiomyinae													
<i>Lophiomys i. imhausi</i>	2	59.01	38.14	8.11	16.14	12.80	2.44	13.30	3.31	9.33	10.15	6.90	11.31
<i>Lophiomys i. thomasi</i>	2	55.87	34.79	7.81	14.68	12.70	2.62	11.56	3.03	8.41	10.74	7.01	11.44
Murinae													
<i>Abeomelomys sevia</i>	4	31.46	15.86	3.04	9.22	5.47	1.33	6.71	2.55	5.56	5.52	4.06	7.41
<i>Aethomys chrysophilus</i>	4	35.89	18.17	3.71	11.15	5.74	1.65	8.49	2.28	5.71	7.29	4.60	8.21
<i>Anisomys imitator</i>	4	64.00	32.70	7.77	20.56	10.53	2.73	14.58	6.27	9.24	9.60	6.92	13.96
<i>Apodemus agrarius</i>	4	26.10	12.70	2.45	7.66	3.72	1.09	6.47	1.96	3.95	5.05	4.13	5.69
<i>Apodemus mystacinus</i>	4	29.28	14.49	2.76	8.85	4.44	1.15	7.02	2.04	3.91	5.83	4.33	6.33
<i>Apodemus semotus</i>	4	25.24	12.43	2.32	7.61	3.81	0.97	5.51	1.92	3.28	4.79	3.64	5.65
<i>Apodemus speciosus</i>	2	25.27	13.10	2.32	7.76	3.65	0.91	5.82	1.81	3.45	4.90	3.62	5.53
<i>Apodemus sylvaticus</i>	4	23.88	12.18	2.21	6.69	3.49	0.85	5.42	1.64	3.45	4.93	3.85	5.40
<i>Apomys dattae</i>	4	36.42	17.44	3.65	9.49	6.62	1.33	7.85	3.06	4.75	5.96	4.48	7.67
<i>Apomys hylocoetes</i>	4	28.06	13.10	2.66	6.86	5.10	1.27	5.53	2.33	3.67	4.93	4.08	6.34
<i>Archboldomys luzonensis</i>	4	24.89	12.67	2.40	6.79	4.47	1.20	5.69	2.01	3.65	5.12	4.02	6.35
<i>Arvicathis neumanni</i>	2	28.70	15.25	3.31	8.09	5.50	1.54	6.58	1.93	5.13	6.28	4.42	6.32
<i>Arvicathis niloticus</i>	4	30.09	15.56	3.41	8.26	5.94	1.58	6.70	1.83	5.05	6.60	4.52	6.37
<i>Bandicota bengalensis</i>	3	41.76	25.15	5.18	13.65	7.82	2.20	9.28	2.89	6.64	8.26	6.72	8.32
<i>Batomys salomonensi</i>	4	38.65	19.86	3.98	11.97	7.05	1.52	7.58	3.48	5.62	5.75	4.72	8.09
<i>Berylmys bowersi</i>	4	54.21	27.95	5.88	17.34	8.79	2.23	13.67	4.16	8.34	9.14	6.96	11.94
<i>Bullimus bagobus</i>	6	60.58	29.85	6.48	18.47	9.07	2.44	13.90	3.84	9.24	12.21	8.55	11.48
<i>Bunomys chrysocomus</i>	4	37.51	18.40	3.59	10.99	5.66	1.58	9.15	2.82	5.47	6.75	5.27	8.50
<i>Carpomys phaeurus</i>	1	36.36	19.77	3.53	10.57	5.96	1.79	8.04	2.77	6.49	6.18	5.43	8.35
<i>Chromomys chiropus</i>	4	36.51	17.92	3.81	10.72	6.48	1.64	8.39	3.37	5.09	6.17	4.44	7.26
<i>Chiropodomys gliroides</i>	4	23.61	13.59	2.57	7.21	3.33	0.85	5.52	2.31	3.63	4.97	3.64	5.43
<i>Chrotomys gonzalesi</i>	2	37.12	19.41	3.54	12.39	5.38	1.22	8.52	3.38	4.96	7.25	4.43	8.95
<i>Colomys goslingi</i>	4	30.51	14.71	2.75	9.18	4.81	1.36	7.35	2.89	4.37	5.80	4.16	6.74
<i>Conilurus penicillatus</i>	4	38.24	20.44	4.20	11.95	7.42	1.97	8.84	3.05	5.50	7.08	4.87	8.14
<i>Cremnomys cutchicus</i>	4	30.27	14.14	3.00	9.08	4.66	1.26	6.60	1.86	4.27	5.46	4.08	6.49
<i>Crunomys melanius</i>	2	26.93	12.35	2.74	7.25	3.56	1.13	7.14	2.46	4.09	5.60	4.17	7.13
<i>Dacnomys millardi</i>	4	54.79	26.40	5.92	16.30	10.88	2.64	12.71	5.21	7.14	8.60	5.41	11.04
<i>Dasyomys i. mediuss</i>	3	32.31	17.64	3.70	10.33	6.18	1.70	7.07	2.67	4.90	7.06	4.47	7.29
<i>Dasyomys i. nudipes</i>	1	36.57	18.18	3.94	11.21	7.08	1.96	7.91	3.16	3.81	6.78	5.51	7.63
<i>Golunda ellioti</i>	3	30.00	14.63	3.33	8.80	5.55	1.56	6.12	1.91	4.89	7.04	4.38	6.39
<i>Grammomys d. dolichurus</i>	3	29.50	14.64	2.44	8.11	4.09	0.92	7.37	1.58	4.41	6.24	4.91	6.58
<i>Grammomys d. sardasler</i>	1	28.63	14.66	2.96	8.07	4.20	1.13	6.72	1.91	4.72	6.10	4.39	6.02
<i>Grammomys ibeanus</i>	4	29.05	14.32	2.65	8.18	4.15	1.03	6.86	1.99	4.34	5.67	4.43	5.93
<i>Grammomys macmillani</i>	4	25.93	12.97	2.34	7.16	3.55	0.91	6.16	1.76	3.89	5.71	4.03	5.47
<i>Hapalomys delacouri</i>	1	29.53	16.40	3.46	8.29	4.76	1.27	6.26	2.02	5.44	6.40	5.34	5.52
<i>Heimyscus fumosus</i>	4	23.42	10.57	2.31	7.27	3.30	0.81	5.46	1.74	3.56	4.67	3.55	4.98
<i>Hybomys univittatus</i>	4	30.53	14.69	3.41	8.70	4.79	1.33	6.45	2.16	4.32	5.81	4.20	6.27
<i>Hydromys c. chrysogaster</i>	1	55.52	29.24	5.89	15.04	7.30	2.34	15.45	6.32	9.13	8.41	7.68	12.89
<i>Hydromys c. fowlavatus</i>	2	58.98	29.11	5.68	16.92	8.35	1.98	15.09	5.76	8.59	9.22	7.57	13.66
<i>Hydromys c. ssp</i>	1	55.75	27.30	5.69	15.71	8.23	2.06	14.72	5.75	8.51	8.73	7.61	12.72
<i>Hylomyscus parvus</i>	4	22.34	11.00	1.89	6.48	3.13	0.76	5.62	1.86	3.37	4.47	3.26	5.02
<i>Hylomyscus stella</i>	4	23.97	11.52	2.19	7.32	3.30	0.82	5.78	1.85	3.60	4.45	3.59	5.30
<i>Hyomys goliath</i>	4	73.90	40.31	11.69	23.91	16.02	4.54	14.57	7.23	10.50	10.29	8.06	15.15
<i>Leggadina forresti</i>	3	18.16	9.25	1.66	5.72	3.31	0.92	3.67	1.36	2.71	4.44	3.26	4.56
<i>Lemniscomys barbarus</i>	4	29.23	14.11	3.02	8.15	4.74	1.30	6.74	1.92	4.74	6.80	4.26	5.78
<i>Lemniscomys striatus</i>	3	29.23	14.07	2.98	7.91	4.73	1.35	6.99	2.04	4.82	6.06	4.33	5.83
<i>Leopoldamys sabanus</i>	4	52.47	23.81	5.33	15.90	9.19	2.13	12.17	4.85	7.25	8.08	5.55	9.73
<i>Leptomys elegans</i>	4	34.72	15.66	3.85	9.16	5.86	1.10	8.64	3.22	5.25	6.15	4.85	8.21
<i>Limnomyss sibuanus</i>	4	30.32	15.39	2.59	8.16	4.25	1.21	7.48	2.53	4.54	5.95	4.94	6.65
<i>Lorentzimys nouhuysi</i>	3	19.56	11.03	1.65	5.76	2.28	0.58	5.23	1.90	2.99	4.14	3.02	5.20
<i>Macruromys major</i>	4	49.19	23.89	5.55	14.49	6.03	1.42	14.28	5.50	7.64	7.17	5.52	11.93
<i>Malacomys longipes</i>	4	37.07	16.66	3.41	12.12	4.70	1.17	8.49	2.93	5.37	5.59	4.93	7.21
<i>Margaretomys elegans</i>	4	40.72	19.50	3.67	12.80	6.09	1.51	10.08	3.48	6.30	7.01	5.52	8.56
<i>Mastacomys fuscus</i>	1	41.21	22.73	4.99	12.50	8.61	2.53	9.00	3.42	5.82	8.55	5.25	8.87
<i>Mastomys erythroleucus</i>	4	29.54	14.86	2.73	9.10	4.02	1.26	7.38	2.46	4.84	5.83	4.30	6.36
<i>Maxomys bartelsii</i>	4	35.77	15.83	3.64	10.99	4.76	1.20	8.86	2.86	5.35	6.57	4.50	7.32
<i>Maxomys surifer</i>	4	39.86	18.48	4.01	12.10	5.65	1.53	9.22	3.63	5.88	7.08	4.60	7.93
<i>Melasmotherix naso</i>	4	30.92	13.33	2.40	7.35	4.22	1.42	8.09	1.97	4.61	6.56	4.92	7.52

Table E.4—continued.

	#	SL	SW	IW	DL	ML	MW	PR	MB	BO	BL	BW	CB
<i>Melomys cervinipes</i>	4	32.70	17.57	3.39	9.56	5.92	1.46	7.13	2.64	4.59	5.90	4.74	7.30
<i>Melomys rufescens</i>	2	30.13	15.35	3.36	8.92	5.63	1.39	6.45	2.69	4.58	5.06	4.26	6.85
<i>Mesembriomys gouldii</i>	3	60.06	29.63	7.07	20.43	10.58	2.57	13.79	4.81	8.53	10.18	7.69	12.03
<i>Micaelamys namaquensis</i>	3	27.90	14.39	2.90	8.10	4.88	1.46	6.36	2.30	3.84	5.70	3.84	6.58
<i>Micromys minutus</i>	4	20.31	10.74	1.81	5.76	2.45	0.58	4.30	1.57	3.17	4.78	3.20	5.30
<i>Millardia gladowi</i>	4	25.19	12.21	2.15	7.56	4.05	1.06	5.71	1.50	3.93	6.04	4.28	5.58
<i>Millardia kathleenae</i>	2	32.93	14.33	3.15	10.20	5.44	1.50	8.04	2.04	4.91	7.72	5.65	7.13
<i>Mus booduga</i>	5	18.74	9.74	1.81	5.38	2.80	0.71	4.37	1.41	3.10	4.35	2.89	4.44
<i>Mus cervicolor</i>	4	20.68	11.10	2.02	6.31	2.87	0.84	5.40	1.39	3.45	4.70	3.17	5.06
<i>Mus cookii</i>	4	23.75	11.68	2.25	6.84	3.48	1.06	5.67	1.90	3.79	4.77	3.39	5.32
<i>Mus minutoides</i>	9	17.98	9.18	1.51	4.92	2.55	0.74	3.96	1.38	2.88	4.08	2.81	4.42
<i>Mus m. bactrianus</i>	1	19.13	9.70	1.79	5.51	2.64	0.77	4.41	1.13	3.19	4.20	3.04	na
<i>Mus m. ssp</i>	2	19.61	10.32	1.68	5.20	2.64	0.67	4.70	1.38	3.25	4.54	3.31	5.05
<i>Mus m. yamashinai</i>	1	19.41	10.27	1.79	5.28	3.11	0.72	4.51	1.36	3.27	4.45	3.42	4.80
<i>Mus pahari</i>	4	24.87	12.28	2.21	7.18	3.43	0.92	5.98	2.14	3.60	5.05	3.54	5.87
<i>Mus saxicola</i>	4	26.14	12.85	2.22	8.26	3.77	0.94	6.53	1.56	4.10	5.34	3.49	5.58
<i>Mus spretus</i>	4	20.03	10.57	1.92	5.73	2.99	0.78	4.71	1.32	3.08	4.53	3.36	4.68
<i>Mus terricolor</i>	4	17.70	8.90	1.64	5.30	2.52	0.63	4.22	1.23	2.83	3.85	2.87	4.32
<i>Myomys dybowskii</i>	4	33.10	15.67	4.18	9.22	6.89	2.14	6.63	2.16	5.51	6.80	4.75	6.42
<i>Myomyscus brockmani</i>	4	27.28	12.71	2.55	8.18	4.09	1.06	6.32	1.97	4.10	5.17	3.96	5.93
<i>Niviventer c. confucianus</i>	3	35.86	16.54	3.28	9.72	5.68	1.46	7.95	2.62	5.08	6.49	4.95	7.61
<i>Niviventer c. lotipes</i>	1	34.91	15.35	3.22	9.92	5.36	1.43	8.42	2.67	5.14	5.32	4.55	6.73
<i>Niviventer cremoriventer</i>	4	33.76	15.87	3.46	9.91	5.30	1.21	7.59	3.01	4.75	5.56	4.51	6.92
<i>Niviventer excelsior</i>	2	36.12	16.88	3.49	10.03	5.61	1.32	7.71	3.06	5.07	6.29	5.12	7.91
<i>Notomys alexis</i>	4	27.27	13.79	2.32	7.59	4.27	1.27	6.03	1.84	3.79	6.84	4.53	5.97
<i>Notomys cervinus</i>	4	27.48	14.34	2.18	7.96	4.18	1.28	6.07	2.03	3.84	6.49	4.45	5.99
<i>Notomys fuscus</i>	4	28.26	14.69	2.28	8.19	4.22	1.33	6.83	1.77	4.14	7.19	5.13	6.18
<i>Oenomys h. editus</i>	2	32.93	16.26	4.16	9.40	6.01	1.48	7.19	1.85	5.20	6.45	5.38	6.59
<i>Oenomys h. hypoxanthus</i>	2	32.95	15.03	3.83	9.62	6.10	1.62	6.69	2.06	4.88	6.14	5.19	6.48
<i>Otomys angoniensis</i>	4	37.00	18.66	5.60	9.68	8.05	1.99	7.01	2.34	6.11	8.26	5.85	7.29
<i>Otomys denti</i>	4	36.17	17.87	5.23	10.22	7.39	1.87	7.33	2.19	6.12	8.27	6.07	7.60
<i>Parotomys brantsii</i>	4	35.31	18.68	4.73	9.70	7.17	1.95	7.46	1.11	6.16	11.71	9.87	6.86
<i>Parotomys littledalei</i>	5	34.43	18.18	4.10	9.84	6.75	1.78	7.74	1.47	5.90	11.47	8.82	7.26
<i>Paruromys dominator</i>	4	55.62	26.93	6.01	16.77	8.23	2.12	12.95	4.25	8.24	9.49	6.93	11.13
<i>Pogonomys loriae</i>	2	33.49	18.54	3.88	10.71	5.63	1.55	7.64	3.28	5.08	5.87	4.69	7.59
<i>Pogonomys macrourus</i>	4	30.03	16.70	3.20	8.74	4.90	1.40	6.82	2.80	4.64	5.75	4.35	7.02
<i>Praomys jacksoni montis</i>	1	27.81	13.82	2.63	8.42	3.94	1.20	6.43	2.20	3.99	5.25	4.13	6.00
<i>Praomys jacksoni ssp</i>	3	30.79	13.95	2.70	9.31	4.09	1.12	7.40	2.34	4.46	5.57	4.07	6.32
<i>Praomys misonnei</i>	4	31.22	14.17	2.94	10.07	4.41	1.18	7.02	2.34	4.35	5.48	4.33	6.28
<i>Praomys tullbergi</i>	3	30.71	14.39	2.72	10.13	4.13	1.11	7.05	2.71	4.20	5.47	4.17	6.32
<i>Pseudohydromys ellermani</i>	3	22.10	9.75	2.43	6.66	1.80	0.51	7.08	1.84	3.65	4.59	3.88	5.36
<i>Pseudomys australis</i>	5	31.19	16.08	3.13	9.18	5.26	1.46	7.14	2.62	4.48	6.85	4.76	7.19
<i>Pseudomys hermannsburgensis</i>	4	22.11	11.08	1.78	6.15	3.10	0.97	5.19	1.57	3.07	5.56	4.25	5.20
<i>Rattus exulans</i>	4	28.86	14.19	2.90	8.43	4.30	1.18	6.65	2.30	4.21	5.89	4.93	6.40
<i>Rattus norvegicus</i>	3	44.12	21.96	4.91	13.99	5.93	1.63	11.58	3.57	7.10	8.88	6.21	9.14
<i>Rattus praeator</i>	4	44.19	22.24	5.16	13.27	6.81	2.02	11.21	3.57	6.90	8.08	6.10	9.03
<i>Rattus rattus</i>	4	38.99	18.85	3.93	12.14	5.31	1.64	9.53	3.17	6.14	7.91	6.16	8.00
<i>Rattus sordidus</i>	4	33.29	17.54	3.64	9.23	6.10	1.56	7.53	2.47	5.18	7.52	5.83	7.97
<i>Rattus tiomanicus</i>	4	40.09	19.72	4.35	12.10	5.97	1.50	9.90	3.04	6.05	8.00	5.80	8.28
<i>Rattus verecundus</i>	4	35.20	16.33	3.25	10.40	5.48	1.44	8.56	3.15	4.88	6.24	4.91	7.58
<i>Rattus villosissimus</i>	4	38.30	19.48	3.81	11.68	6.31	2.01	9.38	3.05	6.05	8.29	6.13	7.82
<i>Rhabdomys pumilio</i>	4	26.18	13.27	2.68	7.04	4.07	1.16	6.15	1.60	3.88	6.36	4.26	5.80
<i>Rhynchosomys isarogensis</i>	4	40.82	16.24	2.10	12.91	2.11	0.71	13.87	3.57	5.63	7.32	4.65	9.37
<i>Stenocephalemys albipes</i>	4	29.89	14.71	2.69	9.26	4.87	1.29	7.26	2.65	4.47	5.77	4.44	6.16
<i>Stochomys longicaudatus</i>	4	36.82	18.37	4.26	10.83	6.04	1.75	7.95	3.49	5.50	6.82	4.68	7.32
<i>Sundamys muelleri muelleri</i>	4	50.55	25.54	5.92	15.60	8.69	2.41	11.80	4.90	7.81	8.44	6.60	10.28
<i>Tarsomys apoensis</i>	3	35.97	17.86	3.10	11.24	5.42	1.56	8.55	3.18	5.06	6.79	5.26	7.78
<i>Uromys caudimaculatus</i>	4	71.27	36.88	7.75	23.78	11.90	2.92	16.48	6.95	9.57	10.60	7.19	14.19
<i>Vandeleuria oleracea</i>	4	19.02	10.12	2.01	5.43	2.65	0.73	4.46	1.50	2.89	4.12	3.33	4.31
<i>Zelotomys h. ssp</i>	1	28.01	15.00	3.09	8.48	4.58	1.56	7.05	2.42	4.40	5.30	4.43	6.54
<i>Zelotomys h. vinaceus</i>	3	28.66	15.37	3.15	8.71	4.63	1.60	6.90	2.56	4.39	5.80	4.48	6.58
<i>Zelotomys woosnami</i>	4	28.39	14.86	3.35	8.41	4.42	1.27	7.04	2.60	4.77	6.24	4.34	6.83
<i>Zyzomys argurus</i>	4	29.65	13.71	2.55	8.92	4.64	1.06	6.71	2.17	4.18	5.64	4.47	6.68
<i>Nesomyidae</i>													
<i>Cricetomyinae</i>													
<i>Beamys hindei</i>	4	32.38	15.37	3.39	11.06	4.69	1.17	7.33	2.33	4.88	6.05	4.08	6.86
<i>Cricetomys gambianus</i>	3	58.90	27.92	5.88	20.33	9.40	2.18	12.67	5.53	8.18	8.66	6.60	13.48
<i>Saccostomus campestris</i>	4	30.04	14.90	2.94	9.95	4.07	1.24	7.04	2.35	4.55	6.42	4.55	6.72
<i>Delanymyinae</i>													
<i>Delanymys brooksi</i>	4	16.45	9.07	1.34	4.38	2.28	0.46	3.67	1.31	2.64	4.48	3.11	4.27
<i>Dendromurinae</i>													
<i>Dendromys insignis</i>	4	22.84	11.10	1.96	6.33	3.54	0.86	4.77	1.49	3.28	5.79	3.71	5.23
<i>Dendromys mesomelas</i>	1	21.23	10.77	1.95	5.59	3.28	0.66	4.89	1.48	3.15	5.47	3.82	5.17
<i>Dendromys nyasae</i>	4	20.97	10.39	1.78	5.68	3.09	0.64	4.52	1.50	2.91	5.23	3.48	4.81
<i>Malacothrix typica</i>	4	23.09	12.68	1.97	7.05	3.53	0.83	5.37	1.84	3.47	4.95	4.35	5.02
<i>Steatomys krebsi</i>	1	20.77	10.65	2.10	5.85	3.09	0.72	4.86	1.38	3.31	5.35	4.36	5.22

Table E.4—continued.

	#	SL	SW	IW	DL	ML	MW	PR	MB	BO	BL	BW	CB
<i>Steatomys p. athi</i>	1	22.71	11.64	2.49	6.77	3.14	1.04	5.92	1.26	3.38	6.24	4.82	4.95
<i>Steatomys p. kalaharicus</i>	1	22.09	11.86	2.15	6.25	2.90	0.91	5.54	1.17	3.46	6.51	4.87	5.04
<i>Steatomys p. ssp</i>	1	20.93	10.94	2.12	5.67	3.06	0.97	5.23	1.09	3.04	5.86	4.39	4.83
<i>Steatomys p. tongensis</i>	1	18.12	10.16	1.86	5.40	2.88	0.75	4.39	1.28	2.97	5.51	4.13	4.90
Mystromyinae													
<i>Mystromys albicaudatus</i>	4	32.59	16.99	3.23	10.58	5.58	1.27	8.08	2.07	4.71	7.17	5.48	7.09
Nesomyinae													
<i>Brachytarsomys albicauda</i>	4	43.60	24.90	4.88	13.22	8.08	1.72	10.99	3.87	7.35	8.77	5.26	9.55
<i>Brachyuromys betsileoensis</i>	4	32.53	19.66	4.10	8.77	6.08	1.66	7.62	2.59	5.61	7.43	5.69	7.50
<i>Eliurus minor</i>	4	28.01	14.40	2.88	8.59	3.78	0.86	6.34	2.39	4.13	5.42	4.12	6.05
<i>Eliurus tanala</i>	4	38.60	18.38	3.89	12.32	5.35	1.23	9.12	3.24	5.64	7.05	4.98	7.85
<i>Gymnuromys roberti</i>	4	37.93	19.77	3.64	12.24	5.42	1.27	8.31	3.64	6.11	6.87	4.97	8.10
<i>Hypogeomys antimena</i>	1	66.80	37.61	6.87	20.86	12.84	3.06	13.68	7.06	15.27	9.99	10.72	na
<i>Macrotarsomys bastardi</i>	4	26.16	13.32	2.18	7.97	3.43	0.89	5.91	1.54	3.86	5.74	4.69	5.35
<i>Monticolomys koopmani</i>	2	27.86	14.53	2.36	8.63	3.53	0.83	6.51	1.87	3.83	7.01	4.70	6.56
<i>Nesomys rufus</i>	4	43.45	23.09	4.73	12.89	6.45	1.55	10.06	3.96	6.52	8.31	6.53	9.42
<i>Voalavo gymnochaeus</i>	4	24.46	13.00	2.46	7.40	3.48	0.99	5.30	2.22	3.66	4.75	3.62	5.85
Petromyinae													
<i>Petromyscus collinus</i>	8	23.16	11.09	1.97	6.89	2.94	0.81	5.57	1.57	3.32	5.35	3.63	5.82
Platacanthomyinae													
<i>Typhlomys c. chapensis</i>	1	25.65	13.39	2.25	7.29	3.94	0.87	5.90	2.96	3.49	4.49	3.77	6.32
<i>Typhlomys c. cinereus</i>	3	21.57	11.89	1.90	6.29	3.45	0.73	4.82	2.50	3.15	4.08	3.46	5.33
Spalacidae													
Myospalacinae													
<i>Eospalax f. cansas</i>	2	39.44	27.78	6.74	13.04	8.78	1.90	4.79	3.43	7.07	9.66	6.69	10.05
<i>Myospalax aspalax</i>	2	37.54	23.89	5.17	12.61	9.03	1.86	4.66	3.51	6.21	8.48	6.01	10.68
Rhizomyinae													
<i>Cannomys badius</i>	4	44.63	32.54	7.09	16.33	10.03	3.52	6.52	3.65	5.98	10.67	8.33	9.88
<i>Rhizomys pruinosus</i>	4	68.17	49.27	11.01	22.52	13.84	3.85	13.85	6.83	11.56	14.51	11.04	14.40
Tachyoryctinae													
<i>Tachyoryctes splendens</i>	4	45.42	31.60	7.11	16.97	8.57	2.85	8.08	3.56	6.68	10.96	7.80	9.60
Spalacinae													
<i>Spalax ehrenbergi</i>	4	38.37	27.45	5.71	13.47	6.15	1.64	6.72	3.83	5.92	8.28	6.63	8.87
Sciuromorpha													
Gliridae													
Graphiurinae													
<i>Graphiurus ocularis</i>	3	30.92	16.62	3.79	8.50	3.11	0.78	8.53	2.54	5.65	8.30	6.85	7.15
Leithiinae													
<i>Eliomys melanurus</i>	4	30.92	17.62	3.53	7.57	4.44	1.24	7.26	1.56	6.00	8.88	7.94	6.19
<i>Eliomys quercinus</i>	4	32.15	19.05	3.82	7.56	5.18	1.34	7.54	2.37	6.24	8.55	7.51	6.61
Sciuridae													
Kerinae													
Xerini													
<i>Atlantoxerus getulus</i>	4	43.27	26.68	4.78	10.68	8.56	2.15	10.34	3.64	7.40	9.97	9.01	10.20
<i>Xerus erythropus</i>	4	57.18	31.29	6.77	13.87	11.83	3.02	13.55	4.61	10.05	13.85	9.77	13.00
<i>Xerus inauris</i>	4	55.61	34.52	6.50	14.99	10.93	3.17	13.16	5.60	9.84	13.72	11.41	13.10
<i>Xerus princeps</i>	3	60.39	36.21	7.03	16.45	11.40	3.25	13.67	5.68	10.12	15.59	11.69	13.50
Marmotini													
<i>Ammospermophilus harrisi</i>	4	38.82	22.62	4.38	11.27	6.77	1.55	9.02	3.54	6.52	9.20	8.00	8.79
<i>Ammospermophilus interpres</i>	4	36.96	21.74	4.15	10.63	5.05	1.41	8.61	3.46	6.15	8.59	7.78	8.36
<i>Ammospermophilus leucurus</i>	4	37.39	21.50	4.12	10.18	6.62	1.64	8.69	3.38	6.14	8.85	8.42	8.35
<i>Ammospermophilus nelsoni</i>	4	39.49	23.58	3.73	10.74	7.37	1.59	8.73	3.37	7.00	9.83	9.04	8.72
<i>Spermophilus fulvus</i>	4	54.82	36.62	6.48	13.63	11.92	2.47	12.35	5.54	8.69	11.28	10.49	12.11
<i>Spermophilus mexicanus</i>	4	48.87	29.04	5.53	12.76	9.14	2.06	11.11	4.57	8.19	10.23	8.28	10.40
<i>Spermophilus mohavensis</i>	4	37.15	23.61	3.86	9.35	7.39	1.80	8.62	3.06	6.53	8.96	7.74	8.02
<i>Spermophilus pygmaeus</i>	4	38.79	25.23	4.62	10.47	8.75	1.86	8.63	4.75	6.27	8.59	6.88	8.89
<i>Spermophilus spilosoma</i>	4	37.43	22.48	4.18	9.33	6.78	1.68	8.66	3.13	6.04	9.37	7.97	8.30
<i>Spermophilus tereticaudus</i>	4	36.30	23.07	4.09	8.97	7.36	1.81	8.15	3.24	5.99	8.82	7.38	7.84
<i>Spermophilus variegatus</i>	4	63.14	39.39	7.06	17.33	12.19	2.77	15.42	6.96	9.99	13.13	10.35	14.30

Table E.5. Species means of raw distances extracted from the lateral and dorsal views of crania in millimeters. See Table E.4 legend for more information. ID= incisor depth; IH= incisor height; RD= rostral depth; LML= lateral molar row length; MH= first molar height (hypodonty measurement); LBL= maximum lateral bulla length; BH= bulla height across auditory meatus and perpendicular to LBL; NB= nasal breadth; NSL= nasal length; IOB= interorbital breadth; DSW= dorsal skull width; DSL= dorsal skull length.

	#	ID	IH	RD	LML	MH	LBL	BH	NB	NSL	IOB	DSW	DSL
Anomaluromorphia													
Pedetidae													
<i>Pedetes capensis</i>	4	6.48	17.68	36.38	16.15	3.54	19.91	23.85	21.34	32.72	39.69	52.23	89.58
Castorimorpha													
Geomyidae													
<i>Cratogeomys castanops</i>	4	2.96	10.79	15.12	7.20	2.61	12.14	9.74	5.82	12.43	7.12	26.96	43.03
<i>Thomomys umbrinus</i>	4	2.24	9.54	12.00	6.81	2.12	8.14	6.88	4.14	11.31	7.15	23.22	36.35
Heteromyidae													
Dipodomysinae													
<i>Dipodomys agilis</i>	4	1.89	5.96	8.20	4.50	1.57	12.04	7.29	3.68	12.53	14.25	18.32	37.80
<i>Dipodomys californicus</i>	4	1.84	5.78	8.26	3.84	1.53	10.88	6.73	3.65	11.72	12.81	17.31	35.45
<i>Dipodomys compactus</i>	4	1.78	5.82	8.25	4.19	1.58	10.07	5.61	3.63	11.73	13.87	16.04	34.32
<i>Dipodomys deserti</i>	5	2.29	6.16	9.63	5.04	1.67	16.26	9.34	3.79	14.46	17.01	18.49	41.59
<i>Dipodomys elator</i>	3	2.33	6.72	9.72	4.89	1.68	11.76	6.99	3.94	13.89	14.59	17.58	37.59
<i>Dipodomys gravipes</i>	3	1.81	6.15	9.06	4.76	1.46	12.60	7.36	3.81	13.28	14.66	18.25	38.97
<i>Dipodomys heermanni</i>	3	1.74	5.85	8.72	4.13	1.50	11.52	6.39	3.69	11.32	13.57	16.20	35.78
<i>Dipodomys ingens</i>	4	2.30	7.95	10.97	5.14	1.78	15.22	8.17	4.52	14.77	15.66	21.17	43.11
<i>Dipodomys merriami</i>	4	1.73	5.51	7.49	3.87	1.40	10.77	5.66	3.07	11.25	14.92	13.93	32.94
<i>Dipodomys microps</i>	4	1.71	5.99	8.19	4.21	1.52	12.08	6.83	3.48	11.39	13.29	15.71	34.09
<i>Dipodomys nelsoni</i>	4	2.26	7.61	9.82	4.94	1.73	13.12	9.05	4.20	14.25	16.62	19.88	40.62
<i>Dipodomys nitratoides</i>	5	1.62	5.36	7.78	4.02	1.29	10.62	5.79	3.14	11.01	13.31	14.18	32.34
<i>Dipodomys ordii</i>	4	1.86	6.18	8.32	4.05	1.26	10.43	5.85	3.34	11.22	13.95	15.61	33.52
<i>Dipodomys panamintinus</i>	4	1.49	6.00	8.70	4.25	1.21	10.78	5.61	3.39	12.59	13.71	17.44	35.28
<i>Dipodomys phillipsii</i>	4	1.81	5.61	8.04	4.26	1.51	10.56	6.05	3.18	11.04	14.28	15.41	32.86
<i>Dipodomys simulans</i>	4	1.91	6.32	8.74	4.38	1.47	11.52	7.46	3.58	12.18	13.61	16.19	36.41
<i>Dipodomys spectabilis</i>	4	2.36	7.14	10.63	4.84	2.04	13.70	8.00	4.40	14.03	16.62	21.14	41.31
<i>Dipodomys stephensi</i>	4	1.93	6.40	8.95	4.46	1.67	11.96	7.72	3.94	13.00	14.27	17.98	37.96
<i>Dipodomys v. venustus</i>	5	2.15	6.56	9.40	4.74	1.66	12.40	7.02	4.24	13.74	14.26	18.06	39.36
<i>Dipodomys v. elephantinus</i>	4	2.16	6.85	9.38	4.51	1.81	12.08	7.49	3.59	13.34	13.43	17.22	38.30
<i>Microdipodops megacephalus</i>	4	1.00	3.20	5.17	2.82	1.16	8.79	4.64	2.26	8.06	6.92	10.52	23.23
<i>Microdipodops pallidus</i>	4	1.15	3.86	5.44	3.02	1.00	10.01	4.75	2.07	8.11	7.56	11.04	24.02
Heteromyiinae													
<i>Heteromys anomalus</i>	4	1.60	4.12	8.18	4.83	1.51	7.57	5.06	4.26	12.20	8.34	15.00	32.78
<i>Heteromys australis</i>	4	1.49	3.81	7.82	4.61	1.36	7.18	5.15	4.00	11.92	9.25	14.43	32.80
<i>Heteromys catopterius</i>	4	1.67	3.99	8.52	4.90	1.52	6.59	4.55	4.73	12.71	9.25	15.32	34.45
<i>Heteromys d. desmarestianus</i>	4	1.52	3.62	7.34	4.40	1.54	6.22	4.51	3.81	12.30	9.82	14.50	32.47
<i>Heteromys d. goldmani</i>	4	1.66	4.76	8.09	4.64	1.46	7.81	4.73	3.93	12.82	10.47	15.85	35.00
<i>Heteromys gaumeri</i>	4	1.49	4.45	7.61	4.47	1.26	7.72	5.36	3.36	11.12	8.82	13.81	30.49
<i>Heteromys nelsoni</i>	4	1.81	5.21	7.51	5.40	1.68	7.73	4.99	4.81	13.62	9.58	15.80	37.44
<i>Heteromys oasicus</i>	2	1.53	3.89	6.65	4.16	1.25	6.64	4.57	3.81	10.42	7.45	12.58	27.95
<i>Heteromys teleus</i>	1	1.75	4.04	8.74	5.18	1.22	7.22	5.31	5.12	13.34	9.25	16.33	35.39
<i>Liomys adspersus</i>	4	1.72	5.01	7.22	4.53	1.32	5.91	4.51	3.34	11.73	8.09	14.40	31.85
<i>Liomys irroratus</i>	4	1.49	4.35	6.75	4.38	1.44	5.23	4.28	3.16	10.68	7.52	13.34	28.88
<i>Liomys pictus</i>	4	1.75	4.71	7.27	4.82	1.37	5.69	4.63	3.57	12.46	8.02	14.41	31.81
<i>Liomys salvini</i>	4	1.56	4.38	6.97	4.24	1.26	5.31	4.37	3.19	9.99	7.31	13.34	28.99
Perognathinae													
<i>Chaetodipus arenarius</i>	4	1.06	3.54	5.11	2.85	0.81	5.78	3.36	2.19	7.30	6.73	10.68	21.81
<i>Chaetodipus artus</i>	4	1.24	4.19	5.66	3.22	0.86	6.15	3.56	2.62	8.13	7.50	11.82	24.77
<i>Chaetodipus baileyi</i>	4	1.48	4.25	6.89	3.92	1.06	7.47	4.92	2.99	9.87	8.76	14.71	28.61
<i>Chaetodipus californicus</i>	4	1.34	4.11	6.31	3.47	0.96	6.71	4.23	2.77	8.22	7.86	12.89	25.33
<i>Chaetodipus eremicus</i>	4	1.42	4.61	5.90	3.19	0.92	6.01	3.31	2.47	7.60	7.60	11.86	23.21
<i>Chaetodipus fallax</i>	4	1.11	3.80	5.79	3.41	1.02	6.40	3.72	2.69	8.39	8.70	12.97	25.78
<i>Chaetodipus formosus</i>	8	1.26	4.25	5.67	3.36	1.00	6.68	4.09	2.58	8.75	8.23	12.24	25.28
<i>Chaetodipus goldmani</i>	4	1.27	4.03	5.91	3.42	1.00	6.80	4.22	3.13	8.86	7.52	12.53	26.00
<i>Chaetodipus hispidus</i>	4	1.45	4.59	7.05	3.75	1.06	7.44	4.55	3.14	9.19	8.81	13.45	27.54
<i>Chaetodipus intermedius</i>	4	1.23	3.41	4.90	3.15	0.78	5.60	3.15	2.32	7.38	7.88	10.04	21.96
<i>Chaetodipus lineatus</i>	4	1.46	3.85	5.38	3.20	0.85	6.31	3.61	2.59	8.19	8.35	12.01	24.32
<i>Chaetodipus nelsoni</i>	3	1.23	3.89	5.34	3.37	0.85	6.34	3.55	2.60	8.38	8.03	12.48	24.92
<i>Chaetodipus penicillatus</i>	4	1.34	3.95	5.50	3.01	0.82	5.90	3.29	2.45	8.05	7.30	11.65	23.50
<i>Chaetodipus pernix</i>	4	1.12	3.70	5.34	3.05	0.90	5.82	3.48	2.61	7.28	6.39	11.06	22.38
<i>Chaetodipus ruddinoris</i>	4	1.61	4.87	6.59	3.86	1.07	7.41	5.02	2.73	9.62	8.39	14.27	27.51
<i>Chaetodipus spinatus</i>	4	1.24	3.82	5.35	3.14	0.87	6.36	3.58	2.51	6.80	7.13	11.64	22.35
<i>Perognathus alticola</i>	4	1.13	3.63	5.44	3.08	0.93	6.48	4.35	2.34	7.67	6.49	11.33	22.63
<i>Perognathus amplus</i>	4	1.10	3.78	5.26	3.13	0.93	6.78	4.50	2.19	7.91	5.97	11.54	22.47
<i>Perognathus fasciatus</i>	4	0.99	3.10	4.85	2.65	0.75	5.98	4.09	2.10	5.98	6.33	10.45	19.76
<i>Perognathus flavescens</i>	4	1.07	3.13	4.92	2.76	0.70	5.81	3.91	2.18	6.39	6.21	10.45	20.67

Table E.5—continued.

	#	ID	IH	RD	LML	MH	LBL	BH	NB	NSL	IOB	DSW	DSL
<i>Perognathus flavus</i>	4	1.02	3.21	4.77	2.89	0.72	5.96	4.10	1.95	5.71	6.53	10.42	19.42
<i>Perognathus inornatus</i>	4	0.96	3.68	4.87	2.85	0.88	5.90	3.91	2.01	6.88	6.00	10.55	20.89
<i>Perognathus longimembris</i>	4	1.11	3.23	4.65	2.75	0.81	6.27	4.00	2.00	7.38	6.24	9.88	20.28
<i>Perognathus merriami</i>	4	1.05	3.29	4.46	2.55	0.72	4.88	3.62	1.89	5.73	5.70	9.91	18.78
<i>Perognathus parvus</i>	4	1.21	3.93	5.46	3.26	0.87	6.58	4.59	2.33	7.30	6.44	11.31	22.55
Hystricomorpha													
Ctenodactylophorii													
Ctenodactylidae													
<i>Ctenodactylus gundi</i>	4	3.55	7.11	11.28	na	1.95	15.59	15.77	6.26	14.75	15.51	34.07	49.60
<i>Ctenodactylus vali</i>	1	na	na	na	na	na	na	na	na	na	na	na	na
<i>Felovia vae</i>	4	2.97	6.38	9.23	na	1.83	10.89	7.95	5.57	15.45	15.26	29.70	45.09
<i>Massoutiera mzabi</i>	4	2.53	5.80	8.51	na	1.35	16.26	15.51	5.11	14.82	13.60	26.66	43.59
<i>Pectinator spekei</i>	2	2.16	5.15	7.56	8.00	1.49	12.00	12.37	4.96	14.45	13.51	25.65	44.56
Hystricognathi													
Abrocomidae													
<i>Abrocoma bennettii</i>	4	1.96	4.32	8.06	9.13	1.43	15.24	12.03	5.33	16.76	8.77	22.00	44.92
Bathyergidae													
<i>Bathyergus janetta</i>	4	3.02	7.57	10.88	8.44	2.08	11.23	9.55	3.34	14.96	9.09	26.97	43.58
<i>Cryptomys hottentotus</i>	4	2.36	7.78	9.26	5.51	1.69	8.03	7.04	2.29	11.27	6.64	21.89	29.80
Caviidae													
Caviinae													
<i>Microcavia australis</i>	4	2.27	6.52	11.19	8.45	2.13	14.07	11.32	6.85	13.47	11.22	27.42	46.40
Dolichotinae													
<i>Dolichotis patagonum</i>	4	5.33	16.97	34.65	na	na	27.33	22.02	18.89	43.46	43.47	61.52	124.48
<i>Dolichotis salinicola</i>	4	5.28	12.22	25.26	na	4.80	23.79	18.85	15.74	32.67	34.17	48.17	97.45
Chinchillidae													
<i>Lagidium viscacia</i>	4	3.49	13.04	17.63	18.69	1.87	20.87	21.58	11.36	25.07	18.87	42.67	80.40
<i>Lagostomus maximus</i>	4	5.37	21.19	26.04	23.31	3.03	21.77	19.54	18.92	42.53	33.32	61.61	105.65
Ctenomyidae													
<i>Ctenomys emilianus</i>	1	3.11	8.45	11.86	8.73	2.39	na	na	6.51	17.48	11.32	na	na
<i>Ctenomys latro</i>	4	2.18	7.71	9.24	7.22	1.67	12.33	9.08	5.04	10.76	9.41	21.94	32.75
<i>Ctenomys mendocinus</i>	4	2.68	8.34	9.96	7.51	1.53	13.07	9.25	5.83	12.39	9.73	22.62	36.54
<i>Ctenomys occultus</i>	2	2.92	7.91	10.39	7.19	1.60	12.74	9.92	5.43	12.07	9.78	22.15	36.06
Hystricidae													
<i>Hystrix africaeaustralis</i>	4	8.62	26.34	60.14	35.01	5.00	23.72	17.88	52.55	68.02	70.74	81.17	140.58
<i>Hystrix cristata</i>	4	7.70	26.59	62.17	33.68	6.47	23.11	18.73	51.09	80.83	67.33	78.50	140.45
<i>Hystrix indica</i>	4	8.68	25.22	54.47	32.39	5.77	21.45	16.43	40.67	61.92	59.12	73.00	135.13
Octodontidae													
<i>Octodon degus</i>	4	2.11	6.05	9.95	8.47	1.63	11.55	9.32	5.17	13.04	10.52	21.25	39.66
<i>Octodon lunatus</i>	4	2.40	6.31	10.33	9.70	1.89	12.99	10.12	5.35	13.74	10.62	22.96	42.80
Petromuridae													
<i>Petromus typicus</i>	4	2.13	5.04	7.98	8.25	1.98	11.98	10.48	5.51	12.95	12.65	23.01	40.80
Myodonta													
Dipodoidea													
Dipodidae													
Allactaginae													
<i>Allactaga balikunica</i>	1	1.36	5.79	7.81	5.30	1.29	8.58	7.47	4.21	9.43	10.15	18.92	28.17
<i>Allactaga bullata</i>	4	1.86	6.06	na	na	9.02	9.21	7.82	4.43	11.01	11.89	21.40	31.87
<i>Allactaga e. elater</i>	4	1.57	4.96	7.85	4.16	1.10	6.47	5.46	3.70	8.07	10.72	18.21	25.89
<i>Allactaga e. elater indica</i>	3	1.92	5.05	8.52	4.14	0.98	6.37	5.94	4.22	8.69	11.83	20.02	28.35
<i>Allactaga e. elater turkmeni</i>	1	1.38	na	8.67	4.73	1.09	6.01	5.10	3.81	6.64	10.77	17.44	24.19
<i>Allactaga euphratica</i>	8	1.91	5.88	8.91	5.74	3.76	7.00	6.33	4.95	11.01	11.20	20.68	31.42
<i>Allactaga firozzi</i>	3	1.61	5.59	8.23	4.60	1.20	7.88	7.05	4.12	9.09	11.36	19.87	28.35
<i>Allactaga hotsoni</i>	4	1.68	5.20	8.61	5.15	1.00	8.46	7.41	3.88	8.48	11.78	18.78	28.32
<i>Allactaga major</i>	4	2.70	8.16	15.47	7.89	1.87	8.95	7.75	7.46	16.26	14.74	30.06	42.76
<i>Allactaga severtzovi</i>	2	2.34	6.76	13.12	na	1.56	8.30	7.85	5.52	12.69	13.69	26.68	39.15
<i>Allactaga sibirica</i>	2	1.71	5.62	11.70	5.43	1.46	8.20	7.48	5.38	13.18	13.71	24.08	39.54
<i>Allactaga tetradactyla</i>	6	1.58	4.74	9.41	5.17	1.12	6.83	5.89	3.98	9.73	11.75	19.65	29.48
<i>Pygeretmus platyurus</i>	1	1.14	4.13	5.26	na	0.86	4.67	4.79	2.82	8.43	6.32	17.03	21.81
<i>Pygeretmus pumilio</i>	4	na	na	na	na	na	na	na	na	na	na	na	na
<i>Pygeretmus zhitkovi</i>	3	1.51	5.10	7.55	4.66	0.88	5.34	5.54	3.84	8.47	9.29	20.04	25.94
Cardiocraninae													
<i>Cardiocranus paradoxus</i>	2	0.85	3.71	4.87	3.49	0.79	7.83	7.17	1.99	4.15	4.64	10.09	21.36
<i>Salpingotulus michaelis</i>	2	1.13	2.87	na	3.71	0.89	4.92	5.34	1.77	6.76	5.65	10.67	18.48
<i>Salpingotulus crassicauda</i>	2	0.99	2.35	3.06	2.03	0.50	4.29	5.11	1.77	5.75	5.20	8.10	16.20
Dipodinae													
<i>Dipus s. sagitta</i>	4	1.87	5.67	9.81	5.66	1.37	10.02	9.58	4.45	10.27	13.50	19.46	32.29
<i>Dipus s. sowerli</i>	4	2.07	6.51	8.74	6.69	0.99	9.43	9.53	4.82	11.71	12.63	19.11	31.50
<i>Eremodipus lichensteinii</i>	1	1.43	5.11	5.97	na	na	na	na	3.77	9.81	10.22	17.78	29.47
<i>Jaculus blanfordi</i>	5	2.54	6.93	8.63	na	1.20	11.51	12.71	4.65	11.53	15.32	21.89	34.43
<i>Jaculus jaculus</i>	4	2.16	5.97	8.22	na	1.33	10.23	10.30	4.39	9.75	15.40	20.99	31.39
<i>Jaculus orientalis</i>	4	2.24	6.64	9.34	6.27	1.57	11.10	12.24	5.54	12.79	16.92	24.80	36.48
<i>Paradipus ctenodactylus</i>	1	1.40	3.57	6.70	na	na	9.99	11.71	4.00	10.01	11.71	16.48	31.01
<i>Stylocitellus telum</i>	4	1.62	5.04	7.01	4.46	1.17	6.58	6.94	3.78	9.01	10.89	17.26	26.32

Table E.5—continued.

	#	ID	IH	RD	LML	MH	LBL	BH	NB	NSL	IOB	DSW	DSL
Sicistinae													
<i>Sicista betulina</i>	4	0.88	2.54	4.00	2.66	0.69	3.51	2.84	2.14	6.40	4.04	8.40	18.44
<i>Sicista concolor</i>	5	1.11	3.19	4.70	3.27	0.79	3.56	2.95	2.51	7.49	4.43	10.14	22.30
<i>Sicista napaea</i>	1	1.01	2.64	4.02	3.28	0.75	3.87	2.76	1.99	6.46	4.20	8.67	19.12
<i>Sicista subtilis</i>	4	1.09	2.91	4.43	3.05	0.69	3.64	2.88	2.22	5.88	4.33	8.28	18.13
Zapodinae													
<i>Eozapus setchuanus</i>	4	1.15	3.34	5.32	3.44	0.75	3.76	3.14	7.95	6.28	5.46	9.72	22.21
<i>Napaeozapus insignis</i>	4	1.19	3.67	6.03	3.63	0.75	3.94	3.01	2.69	8.51	5.31	11.52	23.18
<i>Zapus hudsonius</i>	4	1.38	3.85	5.96	3.58	0.66	3.64	2.93	2.72	7.58	4.80	10.40	22.01
<i>Zapus p. oregonus</i>	4	1.31	4.13	6.36	4.25	0.78	3.82	3.09	3.15	9.09	5.22	12.07	24.38
<i>Zapus p. pacificus</i>	1	1.32	3.82	5.97	3.69	0.69	3.58	2.61	2.64	6.73	4.12	10.71	20.35
<i>Zapus p. princeps</i>	3	1.40	3.92	6.09	3.75	0.63	3.81	3.12	3.05	9.05	4.96	11.85	23.94
<i>Zapus trimotatus</i>	4	1.31	4.21	6.22	3.85	0.64	4.00	3.21	2.65	8.63	4.68	12.22	23.81
Muroidea													
Calomyscidae													
Calomyscinae													
<i>Calomyscus baluchi</i>	4	1.29	3.25	4.85	3.14	0.72	4.83	3.05	2.68	7.98	5.27	11.22	24.15
<i>Calomyscus bailwardi</i>	3	1.36	3.26	4.98	3.37	0.82	4.56	3.04	2.75	7.44	5.76	12.04	24.02
Cricetidae													
Arvicolinea													
<i>Alticola strelzowi</i>	6	1.44	3.88	4.79	5.45	0.95	6.22	4.09	3.16	7.39	4.80	14.67	25.84
<i>Arvicola amphibius</i>	3	2.49	7.28	11.36	9.01	1.78	8.42	5.77	5.12	10.76	4.67	22.39	38.30
<i>Chionomys nivalis</i>	4	1.50	5.13	6.91	6.42	1.21	8.45	5.86	3.34	6.19	4.22	15.05	27.07
<i>Dicrostonyx groenlandicus</i>	4	1.30	5.26	7.34	6.52	1.62	7.79	5.57	3.34	6.68	4.11	16.72	26.13
<i>Ellobius talpinus</i>	4	1.93	7.22	10.34	6.91	1.75	7.22	4.23	3.29	7.27	6.39	21.20	26.81
<i>Eolagurus luteus</i>	5	1.74	5.40	8.57	6.30	1.74	9.40	7.88	3.49	6.87	4.49	17.08	28.38
<i>Eolagurus przewalskii</i>	1	1.79	5.61	8.98	6.25	1.69	10.19	8.41	3.32	7.97	4.78	18.89	30.61
<i>Eothenomys custos rubellus</i>	4	1.36	3.80	6.21	5.12	1.08	5.56	3.69	2.78	6.27	4.15	12.48	22.02
<i>Lagurus l. abacaneus</i>	1	1.35	4.31	6.00	5.77	1.06	7.63	5.19	2.70	6.01	3.05	14.46	22.46
<i>Lagurus l. agressus</i>	2	0.98	3.62	5.53	5.58	1.12	6.28	4.59	2.70	7.00	2.97	13.73	22.53
<i>Lagurus l. lagurus</i>	1	1.11	4.36	6.48	5.57	0.80	7.30	4.81	3.05	6.83	2.78	14.95	23.77
<i>Lasiopodomys mandarinus</i>	4	1.48	5.08	6.83	5.85	1.33	6.64	5.23	2.97	5.83	3.89	14.37	23.18
<i>Lemmus sibiricus</i>	4	2.13	7.07	9.56	8.46	1.51	8.97	7.01	4.04	7.92	3.87	21.67	31.42
<i>Microtus arvalis</i>	4	1.52	4.61	6.64	6.07	1.15	7.14	4.75	3.14	6.24	3.54	13.80	24.02
<i>Microtus californicus</i>	4	1.57	4.31	7.83	6.40	1.39	7.15	5.38	3.50	7.17	3.80	14.77	26.89
<i>Microtus chrotorrhinus</i>	4	1.48	4.65	6.82	6.24	1.11	7.67	5.24	3.07	6.40	3.94	14.44	26.43
<i>Microtus kikuchii</i>	4	1.68	4.45	7.21	6.82	1.33	7.94	5.62	3.22	7.20	3.98	14.91	28.02
<i>Microtus montanus</i>	3	1.67	5.18	7.87	6.20	1.18	7.00	4.89	3.28	7.60	3.72	15.37	26.74
<i>Microtus p. acadicus</i>	1	1.45	4.45	7.26	5.91	1.09	6.34	4.84	3.07	6.67	3.37	15.08	25.58
<i>Microtus p. pennsylvanicus</i>	3	1.53	4.24	7.42	6.08	1.05	6.37	4.24	2.92	6.20	3.69	12.68	24.39
<i>Microtus richardsoni</i>	1	1.67	6.52	9.56	6.91	1.48	6.82	4.48	3.86	7.97	4.96	18.42	29.39
<i>Myodes gapperi</i>	4	1.11	3.42	5.61	4.90	1.35	6.88	4.11	2.86	6.17	4.24	12.82	24.60
<i>Neodon irene</i>	4	1.23	4.04	5.96	4.90	1.05	5.60	3.92	2.65	5.93	3.45	12.73	21.43
<i>Neofiber alleni</i>	4	2.86	8.21	13.60	10.48	2.15	9.29	7.51	5.00	10.16	5.18	25.72	41.69
<i>Ondatra z. rivaliculus</i>	1	4.08	12.11	18.15	13.84	3.80	12.42	10.25	8.63	16.60	6.58	36.83	60.16
<i>Ondatra z. zibethicus</i>	2	3.84	11.63	16.70	14.30	4.03	11.60	9.71	8.56	16.83	6.95	35.53	59.19
<i>Phenacomys i. levis</i>	2	1.06	3.60	5.43	5.63	1.53	5.40	4.35	2.58	5.80	4.01	12.83	22.41
<i>Phenacomys i. oramoutis</i>	2	0.99	3.00	5.05	5.20	1.47	5.31	4.36	2.74	4.82	3.64	11.41	20.79
<i>Prometheomys schaposchnikowi</i>	4	1.97	5.31	8.70	7.17	1.89	7.97	5.94	4.14	8.99	4.10	17.36	30.80
<i>Synaptomys c. cooperi</i>	1	1.15	3.71	6.58	5.92	1.12	6.18	4.46	3.32	5.66	3.23	14.23	24.91
<i>Synaptomys c. gossii</i>	2	1.67	4.70	7.46	6.54	1.34	7.08	5.53	3.45	6.01	3.63	14.86	25.54
Cricetinae													
<i>Allocricetus e. curtatus</i>	5	1.89	4.74	7.08	4.26	0.96	5.37	3.43	3.34	9.89	5.27	15.16	28.14
<i>Allocricetus e. microdon</i>	2	1.60	4.18	6.68	4.13	1.02	4.85	3.07	3.19	8.84	4.97	14.08	25.29
<i>Cricetus b. barabensis</i>	4	1.47	3.87	6.57	3.76	0.87	5.73	3.44	2.87	8.17	5.40	13.37	26.63
<i>Cricetus b. griseus</i>	4	1.50	3.60	6.30	3.76	0.90	5.34	3.37	2.74	7.58	4.53	12.75	24.75
<i>Cricetus longicaudatus</i>	4	1.11	3.30	5.68	3.72	0.85	5.44	3.25	2.68	7.93	4.12	11.52	23.53
<i>Cricetus migratorius</i>	7	1.39	3.77	6.44	4.11	0.96	5.21	3.32	2.85	8.03	4.60	12.80	26.08
<i>Cricetus c. canescens</i>	2	2.29	6.42	10.39	7.76	1.57	8.64	5.65	5.60	15.06	6.59	23.85	40.56
<i>Cricetus c. cricetus</i>	2	2.42	6.56	11.27	7.78	1.92	8.79	8.52	6.12	14.29	6.25	24.75	42.42
<i>Mesocricetus auratus</i>	3	2.03	5.61	8.27	5.37	1.20	6.45	5.18	3.99	12.90	4.72	18.37	32.06
<i>Phodopus campbelli</i>	4	1.32	3.37	6.12	3.60	0.81	4.13	3.27	2.80	8.05	4.03	13.24	23.80
<i>Phodopus roborovskii</i>	4	1.10	2.91	5.03	3.11	0.75	3.11	2.45	2.35	6.53	3.63	10.79	19.94
<i>Phodopus sungorus</i>	4	1.25	3.15	5.64	3.27	0.68	4.30	2.93	2.54	7.10	4.06	11.71	21.86
Neotominae													
<i>Baiomys musculus</i>	3	1.15	2.85	4.15	2.96	0.64	3.53	2.18	2.12	6.47	4.49	9.75	18.34
<i>Habromys lepturus</i>	4	1.44	3.51	5.65	4.65	1.05	4.94	3.90	3.13	9.32	4.62	13.55	27.05
<i>Hodomys allenii</i>	4	2.53	6.55	10.14	11.14	2.73	8.53	5.63	5.00	14.56	6.23	22.60	46.47
<i>Isthomys pirrensis</i>	4	2.20	5.79	8.41	5.88	1.46	5.87	4.08	4.55	14.78	6.17	18.07	39.59
<i>Megadontomys thomasi</i>	4	1.91	4.50	7.09	5.91	1.42	5.65	4.90	4.00	12.55	6.02	17.34	35.69
<i>Neotoma albicula</i>	4	2.71	6.37	9.61	7.93	2.27	7.84	5.33	4.91	14.58	6.16	21.89	42.98
<i>Neotoma bryanti</i>	4	2.32	5.60	9.32	7.99	2.28	7.25	5.22	4.46	13.38	7.50	21.57	41.09
<i>Neotoma cinerea</i>	2	2.67	6.73	9.49	8.83	3.39	7.73	5.96	5.06	16.51	5.79	22.06	44.46
<i>Neotoma devia</i>	4	2.01	5.29	8.30	7.43	2.27	7.14	5.76	3.96	12.04	5.04	17.87	35.33
<i>Neotoma floridana</i>	3	2.84	6.28	11.05	8.34	2.39	7.50	6.14	5.37	16.43	7.05	23.37	47.06
<i>Neotoma goldmani</i>	4	2.06	5.16	8.13	7.46	2.04	7.10	5.20	4.03	10.96	6.28	17.87	35.69

Table E.5—continued.

	#	ID	IH	RD	LML	MH	LBL	BH	NB	NSL	IOB	DSW	DSL
<i>Neotoma lepida</i>	4	2.44	5.68	9.39	7.97	2.42	7.89	5.84	4.34	14.41	5.47	19.38	39.65
<i>Neotoma mexicana</i>	4	2.36	5.66	9.14	8.52	2.22	6.82	5.18	4.58	14.78	6.12	21.19	40.56
<i>Neotomodon alstoni</i>	4	1.48	4.20	6.44	5.23	1.23	5.67	4.15	3.39	11.12	4.55	15.57	29.99
<i>Ochrotomys nuttalli</i>	3	1.48	3.18	5.68	3.63	0.63	4.48	3.15	2.63	7.58	4.55	12.21	23.51
<i>Onychomys l. arcticeps</i>	2	1.61	4.59	6.58	4.50	1.16	5.27	3.42	3.26	9.84	4.64	13.92	26.30
<i>Onychomys l. breviauritus</i>	1	1.57	3.64	6.45	4.37	1.10	4.30	3.10	2.90	9.33	4.55	13.15	26.30
<i>Onychomys l. ruidosae</i>	3	1.54	4.38	6.37	4.34	1.00	4.67	3.28	3.01	9.36	4.87	13.62	26.37
<i>Onychomys torridus</i>	4	1.41	3.57	5.40	3.55	0.88	4.44	2.93	2.48	7.74	4.56	10.88	22.68
<i>Osgoodomys banderanus</i>	4	1.54	3.66	6.09	4.12	0.85	4.32	3.43	3.10	10.26	6.31	13.20	29.01
<i>Peromyscus a. hylocetes</i>	3	1.42	4.25	6.24	4.71	1.29	4.96	3.85	3.21	11.07	4.26	14.70	28.46
<i>Peromyscus a. oaxacensis</i>	1	1.60	3.26	5.84	4.46	0.86	4.64	3.61	3.27	10.07	4.89	12.82	27.30
<i>Peromyscus b. levipes</i>	3	1.66	3.30	5.96	4.39	0.91	4.78	3.58	2.99	9.30	4.76	12.89	26.18
<i>Peromyscus b. rowleyi</i>	1	1.52	3.34	5.81	4.23	0.95	4.37	3.27	2.77	9.63	4.69	12.78	26.64
<i>Peromyscus californicus</i>	1	1.34	2.94	5.89	3.70	0.81	5.15	3.44	2.99	9.51	4.52	13.39	27.44
<i>Peromyscus c. auripectus</i>	1	1.35	2.96	5.13	3.22	0.78	3.97	2.89	2.60	8.41	4.68	10.99	23.02
<i>Peromyscus c. pergracilis</i>	3	1.54	3.13	5.54	3.75	0.72	4.42	3.10	2.67	8.64	5.15	12.21	24.72
<i>Peromyscus eremicus</i>	4	1.43	3.41	5.21	3.66	0.75	4.48	3.37	2.53	8.45	4.27	12.17	23.99
<i>Peromyscus fraterculus</i>	4	1.31	3.07	4.86	3.50	0.71	4.29	3.10	2.37	7.84	3.96	11.21	22.93
<i>Peromyscus leucopus</i>	4	1.33	3.08	5.63	3.43	0.64	4.15	3.00	2.63	8.47	3.97	11.84	23.72
<i>Peromyscus m. abietorum</i>	1	1.20	3.36	4.91	3.13	0.70	4.46	3.09	2.58	9.23	3.80	11.82	24.45
<i>Peromyscus m. gambelii</i>	2	1.23	3.37	5.17	3.65	0.85	4.43	3.19	2.77	9.36	3.90	11.23	25.63
<i>Peromyscus m. gracilis</i>	1	1.37	3.26	5.26	3.27	0.65	4.10	3.06	2.64	8.99	4.22	11.81	24.04
<i>Peromyscus merriami</i>	4	1.61	3.42	5.55	3.72	0.76	4.82	3.49	2.70	8.47	4.07	12.57	24.49
<i>Peromyscus m. nudipes</i>	1	1.57	4.21	6.20	4.58	0.96	4.72	4.07	3.57	12.23	4.91	14.65	31.95
<i>Peromyscus m. saxatilis</i>	3	1.74	3.86	6.27	4.33	0.90	4.52	3.35	3.53	10.61	5.77	13.49	29.62
<i>Peromyscus pectoralis</i>	4	1.43	3.44	5.56	3.75	0.75	4.72	3.60	2.75	8.30	4.92	12.72	25.79
<i>Peromyscus p. allophys</i>	1	1.12	3.08	4.81	3.14	0.62	4.56	3.25	2.39	7.31	3.95	10.80	20.80
<i>Peromyscus p. subgriseus</i>	3	1.24	2.76	5.07	3.06	0.65	3.94	2.79	2.26	7.05	3.85	10.44	20.76
<i>Reithrodontomys creper</i>	4	1.43	3.90	5.96	4.21	0.78	4.32	3.35	2.73	8.85	5.22	13.27	26.57
<i>Reithrodontomys f. chiapensis</i>	1	1.21	2.94	5.19	3.13	0.61	3.46	2.53	2.40	8.01	3.58	10.01	20.71
<i>Reithrodontomys f. difficilis</i>	1	1.27	3.05	4.72	2.81	0.67	3.58	3.03	2.03	6.78	4.33	9.92	20.83
<i>Reithrodontomys f. helvolus</i>	1	1.27	3.41	4.85	3.34	0.60	3.81	2.64	2.17	7.95	3.96	10.43	21.81
<i>Reithrodontomys f. intermedius</i>	1	1.21	2.83	4.93	3.38	0.60	3.40	2.88	2.08	6.56	3.32	9.48	19.23
<i>Reithrodontomys gracilis</i>	3	1.25	3.18	4.73	2.99	0.57	3.36	2.74	2.11	6.59	4.03	9.42	19.89
<i>Reithrodontomys megalotis</i>	7	1.13	2.88	4.53	2.98	0.69	3.25	2.83	2.00	6.58	3.55	9.46	18.84
<i>Scotinomys teguina</i>	3	1.20	3.11	4.86	4.02	0.81	3.52	2.80	2.38	7.37	4.87	10.80	21.41
<i>Xenomys nelsoni</i>	2	2.09	5.11	8.36	7.88	1.65	9.51	7.64	3.82	11.19	7.17	18.88	37.84
Sigmodontinae													
<i>Abrothrix andinus</i>	4	1.34	3.64	4.26	3.60	0.90	5.24	3.60	2.86	7.65	5.03	11.79	23.52
<i>Abrothrix longipilis</i>	4	1.38	3.66	5.22	4.17	0.99	4.66	2.56	3.69	11.53	5.33	13.01	28.63
<i>Aegialomys xanthaeolus</i>	4	2.07	5.15	6.95	4.93	1.12	4.82	3.31	3.57	10.32	7.25	14.34	29.41
<i>Akodon aerosus</i>	4	1.46	3.96	5.85	4.46	1.01	4.19	3.02	3.00	8.66	6.76	13.31	26.65
<i>Akodon boliviensis</i>	3	1.14	3.41	5.05	3.72	1.02	3.95	2.44	2.88	6.51	5.27	11.43	22.20
<i>Akodon iniscatus</i>	4	1.32	3.58	5.41	3.93	0.83	4.16	3.08	2.84	7.95	4.90	12.34	24.67
<i>Akodon kofordi</i>	4	1.28	3.37	5.28	3.86	0.91	4.24	2.97	2.70	7.82	5.75	11.61	24.16
<i>Akodon lutescens</i>	1	1.23	2.39	4.64	3.54	0.92	3.73	2.39	2.64	6.09	4.93	9.85	19.73
<i>Akodon mimus</i>	3	1.24	3.31	5.09	4.24	0.92	3.88	2.47	2.84	8.78	6.39	11.71	24.58
<i>Akodon molinae</i>	1	1.81	5.15	6.92	4.38	0.98	4.88	3.44	3.61	8.63	6.27	14.71	27.31
<i>Akodon spegazzinii</i>	4	1.34	3.47	5.48	4.13	1.04	3.80	2.42	2.89	8.14	5.35	11.81	24.48
<i>Akodon torques</i>	4	1.22	3.38	5.32	4.21	0.95	4.06	2.85	2.82	8.41	5.89	11.79	24.33
<i>Andalgalomys pearsoni</i>	4	1.77	4.36	6.79	4.12	0.98	5.83	3.77	2.81	9.66	6.81	13.60	28.47
<i>Andinomys edax</i>	5	2.07	5.50	8.19	6.39	1.41	5.04	4.16	5.11	11.62	4.57	18.23	34.09
<i>Auliscomys sublimis</i>	4	1.16	3.58	5.68	4.26	1.03	4.25	2.87	3.05	8.19	4.20	12.82	24.04
<i>Brucepattersonius igniventris</i>	2	1.27	3.15	5.46	4.18	0.96	5.31	2.86	3.48	10.68	6.20	12.29	27.55
<i>Brucepattersonius soricinus</i>	2	1.26	3.66	5.67	4.39	1.07	5.33	3.14	3.15	9.67	5.95	11.92	26.38
<i>Calomys callosus</i>	7	1.66	4.13	6.07	3.86	0.91	4.81	3.09	2.98	8.52	5.65	12.65	24.92
<i>Calomys lepidus</i>	4	1.07	3.14	5.06	3.40	0.76	3.88	2.63	2.70	7.11	4.07	11.21	21.43
<i>Calomys musculinus</i>	4	1.22	3.28	4.87	3.49	0.76	3.91	2.94	2.71	7.16	4.91	10.96	21.30
<i>Calomys venustus</i>	1	1.56	4.09	5.80	3.98	0.83	4.09	2.88	3.33	8.20	5.72	12.61	24.07
<i>Cerradomys subflavus</i>	4	2.24	5.36	8.69	5.12	1.00	5.74	3.44	3.67	11.37	8.53	16.73	35.22
<i>Chelemys macronyx</i>	4	1.89	5.59	7.30	5.55	1.39	6.14	4.19	4.18	9.67	5.37	16.40	30.64
<i>Chinchillula sahamae</i>	4	2.31	6.48	9.37	6.87	2.09	6.82	4.96	5.19	13.38	4.86	19.42	36.74
<i>Delomys d. collinus</i>	2	1.60	4.71	7.27	4.60	0.95	5.96	3.43	4.19	10.79	5.29	15.06	31.51
<i>Delomys d. dorsalis</i>	2	1.51	4.18	7.02	4.47	0.95	5.66	3.48	3.89	10.43	5.47	15.15	31.22
<i>Deltamys kempi</i>	4	1.29	3.54	5.50	3.74	0.88	4.22	2.59	2.68	7.92	4.65	10.72	23.27
<i>Eligmodontia moreni</i>	3	1.26	3.35	4.90	3.58	0.78	4.22	3.44	2.17	7.63	3.74	10.69	21.43
<i>Eligmodontia morgani</i>	4	1.39	3.66	5.57	3.58	0.88	4.34	3.50	2.61	8.54	4.86	12.26	24.00
<i>Eligmodontia typus</i>	8	1.40	3.57	5.47	3.63	0.91	4.63	3.49	2.53	8.10	4.36	11.73	22.99
<i>Euneomys c. chinchilloides</i>	3	1.96	5.17	7.55	5.30	1.32	5.80	4.51	4.39	11.20	3.89	17.33	29.76
<i>Euneomys c. sublimis</i>	1	1.70	4.43	6.87	5.18	1.33	5.81	4.22	3.94	9.63	4.00	15.12	26.96
<i>Geoxus valdivianus</i>	4	1.13	3.29	5.36	3.10	0.76	4.43	3.09	2.78	8.59	5.16	11.75	25.60
<i>Graomys edithae</i>	1	1.56	4.43	6.34	4.76	1.41	5.51	4.01	3.11	8.87	5.33	12.25	25.99
<i>Graomys griseoflavus</i>	7	2.01	5.05	7.68	5.34	1.39	6.84	5.13	3.69	11.21	7.20	15.30	31.95
<i>Holochilus brasiliensis</i>	4	2.39	5.98	10.38	6.67	1.34	6.98	4.93	4.40	12.98	4.67	19.13	36.67
<i>Holochilus sciureus</i>	3	2.44	6.28	10.46	6.39	1.46	7.11	4.65	4.45	13.11	4.73	19.49	37.20
<i>Ichthyomys stolzmanni</i>	1	1.72	3.86	5.46	3.73	1.00	4.00	2.53	3.80	10.04	4.57	14.85	29.76

Table E.5—continued.

	#	ID	IH	RD	LML	MH	LBL	BH	NB	NSL	IOB	DSW	DSL
<i>Irenomys tarsalis tarsalis</i>	4	1.54	4.11	6.32	4.85	1.23	5.09	3.61	3.01	9.28	3.65	13.95	27.74
<i>Juliomys pictipes</i>	4	1.55	3.81	5.99	3.63	0.73	3.97	2.78	2.58	6.77	4.22	12.37	23.60
<i>Kunsia tomentosus</i>	4	3.51	8.71	14.10	9.62	2.33	9.51	6.81	6.57	18.22	8.58	27.07	50.57
<i>Lenoxus apicalis apicalis</i>	4	1.59	4.24	7.58	5.49	1.27	5.87	3.32	4.30	14.17	7.89	15.32	34.48
<i>Loxodontomys micropus</i>	4	1.80	5.04	8.05	5.58	1.30	5.68	3.89	4.29	11.91	4.15	17.34	31.25
<i>Melanomys c. chrysomelas</i>	3	1.79	5.36	7.84	4.79	0.96	5.04	3.10	3.41	9.97	7.76	15.30	29.42
<i>Melanomys c. ssp</i>	1	1.77	4.76	7.13	4.61	0.89	4.07	2.76	3.52	10.24	6.98	15.25	29.85
<i>Microryzomys m. azoricus</i>	1	1.02	2.40	3.95	2.56	0.53	3.74	2.87	2.02	4.76	3.75	7.86	16.44
<i>Microryzomys m. soricinus</i>	2	0.94	2.39	3.92	2.67	0.63	3.61	2.28	1.60	4.13	4.63	8.28	15.97
<i>Microryzomys m. ssp</i>	1	1.12	2.78	3.98	3.43	0.70	4.32	2.64	1.89	4.72	4.48	8.93	18.57
<i>Neacomys spinosus</i>	4	1.29	3.70	5.82	2.97	0.73	3.26	2.35	2.55	7.91	5.40	11.44	22.78
<i>Necromys amoenus</i>	4	1.45	3.64	6.93	4.36	0.88	5.11	3.20	3.20	7.22	5.46	14.14	25.56
<i>Nectomys apicalis</i>	4	3.52	7.79	12.05	7.84	1.54	6.88	4.42	5.17	15.54	9.51	24.72	47.84
<i>Nectomys s. palmipes</i>	1	2.66	6.67	10.18	6.10	1.05	5.68	3.37	4.88	12.93	7.38	18.80	37.75
<i>Nectomys s. pollens</i>	1	2.73	7.34	10.76	7.08	1.27	6.82	3.96	4.49	13.89	7.36	21.35	40.04
<i>Nectomys s. ssp</i>	1	3.34	7.50	12.19	7.30	1.23	6.57	4.13	5.48	18.33	7.62	24.28	47.39
<i>Neotomys ebriosus</i>	5	1.94	4.66	7.69	5.40	1.46	5.76	4.16	5.22	11.29	3.97	16.19	29.36
<i>Nephelomys keyssi</i>	4	2.06	4.67	7.89	5.42	1.04	4.45	3.13	3.96	10.85	6.12	17.11	33.15
<i>Nephelomys levipes</i>	4	2.10	5.42	8.48	5.95	1.06	5.48	3.74	4.41	11.12	6.24	18.29	34.46
<i>Notiomys edwardsii</i>	1	na	na	6.58	3.31	0.88	5.58	3.09	3.06	8.16	5.40	13.26	24.57
<i>Oecomys bicolor</i>	3	1.50	3.52	6.62	3.87	0.75	3.57	2.78	2.91	7.92	6.45	13.29	27.18
<i>Oecomys concolor</i>	2	1.92	4.55	7.52	4.95	0.95	4.45	3.39	3.33	8.83	6.69	14.38	28.77
<i>Oecomys superans</i>	4	2.47	5.88	9.03	5.90	1.16	5.43	3.61	3.78	10.23	8.41	17.73	35.02
<i>Oligoryzomys fulvescens</i>	3	1.08	3.26	5.09	2.86	0.60	2.96	2.41	2.30	6.97	3.90	10.25	19.98
<i>Oligoryzomys longicaudatus</i>	4	1.45	3.85	6.03	3.43	0.68	4.32	2.99	2.91	8.49	3.50	12.50	24.63
<i>Oligoryzomys microtis</i>	4	1.33	3.55	5.58	3.25	0.71	3.61	2.57	2.43	7.77	4.30	11.71	22.19
<i>Oryzomys couesi</i>	3	1.81	4.95	7.23	4.43	0.82	4.43	2.92	3.20	9.70	5.70	13.37	27.36
<i>Oryzomys palustris</i>	4	1.87	5.09	7.54	4.40	0.89	4.70	3.13	3.28	10.29	6.57	14.70	29.11
<i>Oxymycterus hiska</i>	4	1.33	3.64	5.80	4.31	1.10	4.66	2.97	3.68	10.52	7.15	13.54	29.39
<i>Oxymycterus nasutus</i>	4	1.54	3.90	6.64	4.62	1.12	5.71	3.37	2.80	10.54	6.33	13.47	31.29
<i>Phyllotis amicus</i>	6	1.55	3.73	5.93	3.88	0.87	4.90	3.82	3.11	8.87	4.84	12.44	24.80
<i>Phyllotis andium</i>	4	1.45	3.57	6.15	4.51	1.19	5.11	3.91	3.45	8.57	4.51	13.31	26.21
<i>Phyllotis caprinus</i>	2	1.82	4.60	6.88	4.81	1.35	5.00	3.87	3.99	11.64	4.67	14.90	29.90
<i>Phyllotis darwini</i>	4	1.87	4.98	7.67	4.66	1.27	6.03	4.71	3.60	11.49	4.43	14.73	29.86
<i>Phyllotis gerbillus</i>	4	1.40	3.56	5.33	3.52	0.82	4.24	3.27	2.55	8.24	4.55	11.50	22.58
<i>Phyllotis magister</i>	2	2.03	5.04	7.27	5.18	1.27	5.55	4.09	4.23	11.80	4.73	15.65	30.86
<i>Phyllotis osilae</i>	4	1.51	4.31	6.36	4.50	1.21	4.71	3.53	3.53	10.63	4.21	14.30	28.10
<i>Phyllotis xanthopygus</i>	4	2.04	5.22	7.39	5.03	1.39	5.46	3.99	4.11	12.26	4.20	15.27	30.75
<i>Pseudoryzomys simplex</i>	4	1.85	4.91	7.54	4.64	0.92	4.95	3.55	3.47	11.13	4.28	15.08	29.28
<i>Punomys kofordi</i>	3	1.99	5.10	7.92	6.77	1.78	6.12	4.89	4.78	10.66	4.78	17.57	33.03
<i>Reithrodon a. auritus</i>	4	1.95	5.14	9.38	6.44	1.76	6.01	5.61	4.28	11.22	4.54	19.19	34.75
<i>Reithrodon a. physodes</i>	4	1.68	4.03	8.22	5.68	1.44	6.48	4.74	4.12	10.89	3.89	16.63	31.28
<i>Rhagomys longilingua</i>	1	1.86	4.49	7.09	4.28	0.81	3.93	3.01	2.83	6.71	6.34	13.67	25.43
<i>Rheomys t. stutoni</i>	2	1.80	4.88	6.31	4.12	0.88	3.53	2.48	3.33	10.92	5.58	14.87	29.72
<i>Rheomys t. thomasi</i>	2	1.36	3.83	5.84	4.25	1.06	2.82	2.22	3.12	9.20	5.31	13.83	26.73
<i>Rhipidomys macconnelli</i>	4	1.77	4.10	7.35	4.80	0.99	4.29	3.03	3.33	10.02	5.81	14.97	29.26
<i>Rhipidomys nitela</i>	4	1.82	4.56	7.71	4.71	0.88	4.27	3.27	3.19	9.19	6.35	15.21	30.03
<i>Scapteromys tumidus</i>	4	2.11	5.54	8.98	6.79	1.30	6.05	3.95	4.45	13.20	5.89	18.67	39.07
<i>Scolomys melanops</i>	1	1.14	3.26	5.68	2.39	0.51	2.90	2.38	2.28	5.63	4.93	10.86	19.34
<i>Scolomys ucayalensis</i>	4	1.19	3.27	5.82	2.56	0.55	3.07	2.60	2.58	7.03	6.25	10.97	21.27
<i>Sigmodon alstoni</i>	4	2.06	5.29	8.48	5.58	1.15	6.36	4.17	3.33	9.16	5.41	16.33	28.85
<i>Sigmodon arizonae</i>	4	2.32	6.18	9.77	6.84	1.36	6.35	4.54	3.93	11.19	6.72	19.99	34.29
<i>Sigmodon fulviventer</i>	4	1.92	5.20	9.26	5.77	1.21	6.19	4.55	3.61	9.74	5.56	18.48	32.08
<i>Sigmodon hispidus</i>	3	2.33	6.02	9.66	5.79	1.33	6.33	4.47	4.05	11.42	5.95	18.20	34.03
<i>Sigmodon ochrognathus</i>	4	1.95	4.75	8.55	5.47	1.22	5.66	3.62	3.35	9.07	6.67	17.14	29.90
<i>Sigmodontomys alfari</i>	4	2.52	6.29	9.14	5.51	1.09	4.32	3.17	3.97	12.47	8.32	17.78	34.09
<i>Sooretamys angouya</i>	3	2.23	5.33	8.85	5.69	1.08	5.13	3.21	4.34	12.09	5.25	16.61	34.49
<i>Thaptomys nigrita</i>	4	1.30	3.64	5.90	3.48	0.86	3.89	2.42	2.75	7.50	5.63	12.24	22.77
<i>Thomasomys aureus</i>	4	2.10	6.08	8.64	7.20	1.37	5.64	4.28	4.30	12.55	5.10	19.40	37.31
<i>Thomasomys daphne</i>	4	1.36	4.01	5.84	4.12	0.88	4.08	3.16	2.69	7.85	5.11	12.73	25.23
<i>Thomasomys notatus</i>	4	1.72	4.69	6.93	4.31	0.82	4.88	3.37	3.10	9.24	4.35	14.45	28.40
<i>Transandinomys talamancae</i>	4	1.69	4.46	7.25	4.27	0.76	4.22	2.97	3.10	8.94	5.55	13.91	28.09
<i>Wiedomys pyrrhorhinos</i>	3	1.78	4.30	6.52	4.30	0.82	5.98	4.17	3.11	8.96	5.56	13.80	28.05
<i>Zygodontomys brevicauda</i>	3	1.66	4.32	7.11	4.23	1.01	4.19	2.96	3.03	9.59	5.89	13.79	27.97
Tylomyinae													
<i>Nyctomys sumichrasti</i>	5	1.68	4.42	7.64	4.69	0.86	4.78	3.41	3.22	8.83	8.48	16.27	29.70
<i>Ototylomys phyllotis</i>	3	2.25	4.86	8.09	6.92	1.17	7.08	5.23	3.49	12.82	7.84	19.10	39.90
<i>Tylomys nudicaudus</i>	5	2.19	5.68	9.87	7.78	1.58	6.36	4.54	4.29	13.10	10.64	21.64	42.59
Muridae													
Deomyinae													
<i>Acomys cahirinus</i>	7	1.60	3.69	4.92	4.12	0.86	4.14	3.05	2.77	9.39	6.26	12.62	26.49
<i>Acomys cineraceus</i>	4	1.61	3.53	4.86	3.94	0.82	4.06	3.09	2.82	9.69	6.42	11.90	26.40
<i>Acomys dimidiatus</i>	1	1.72	4.62	5.80	3.91	1.11	4.78	3.95	2.69	9.85	7.39	13.74	28.27
<i>Acomys ignitus</i>	4	1.64	3.87	5.37	4.02	0.92	5.10	3.50	2.59	9.85	6.95	12.72	27.40
<i>Acomys percivali</i>	4	1.81	4.23	5.42	4.31	0.84	4.54	3.35	2.54	9.74	6.77	12.50	26.47
<i>Acomys russatus</i>	4	1.71	4.05	5.39	4.62	0.88	5.17	3.59	2.97	9.92	6.98	13.34	27.73

Table E.5—continued.

	#	ID	IH	RD	LML	MH	LBL	BH	NB	NSL	IOB	DSW	DSL
<i>Acomys spinosissimus</i>	4	1.56	3.62	4.75	4.12	0.94	3.76	2.69	2.76	8.70	6.73	12.15	25.14
<i>Acomys wilsoni</i>	4	1.66	4.07	5.41	4.26	1.07	5.03	3.48	2.51	9.08	7.55	12.56	26.35
<i>Deomys ferrugineus</i>	4	1.66	4.41	6.31	5.64	1.37	5.89	4.16	3.76	13.78	7.25	14.40	34.64
<i>Lophuromys f. flavopunctatus</i>	3	1.43	3.79	5.74	4.75	0.96	5.51	3.38	2.61	10.14	6.62	12.89	27.74
<i>Lophuromys f. zaphiri</i>	1	1.42	3.79	6.21	5.08	0.97	6.10	3.52	2.76	10.56	6.75	14.84	29.46
<i>Lophuromys f. zena</i>	4	1.49	3.82	5.86	4.72	1.07	5.40	3.50	2.53	10.67	6.52	13.19	27.52
<i>Lophuromys sikapusi</i>	4	1.54	4.30	6.02	5.15	1.26	5.66	3.87	2.95	10.56	7.52	14.70	30.12
<i>Uranomys ruddi</i>	4	1.53	4.43	6.50	4.53	0.88	3.94	2.82	2.92	8.58	6.08	13.41	24.69
Gerbillinae													
<i>Ammodillus imbellis</i>	1	1.57	2.89	5.85	4.14	1.07	8.22	5.77	2.20	10.54	8.61	13.66	28.41
<i>Brachiones przewalskii</i>	1	1.46	3.59	5.97	3.53	1.42	8.35	6.52	2.76	6.63	7.05	13.71	23.25
<i>Desmodillus braueri</i>	6	1.09	3.62	5.06	3.07	0.93	6.82	5.46	1.95	5.89	4.85	11.57	20.02
<i>Desmodillus auricularis</i>	8	2.22	5.43	8.02	4.17	1.27	13.49	9.59	3.13	11.33	9.16	18.67	34.37
<i>Dipodillus campestris</i>	4	1.76	4.23	5.93	3.61	1.09	7.83	5.10	2.46	8.66	6.62	12.89	25.71
<i>Dipodillus dasyurus</i>	4	1.62	3.99	6.09	3.64	1.14	8.75	5.76	2.52	8.31	6.53	13.16	25.55
<i>Dipodillus harwoodi</i>	4	1.52	3.97	5.60	3.53	1.08	7.15	5.06	2.39	8.12	6.23	12.14	23.82
<i>Dipodillus lowei</i>	2	1.76	4.35	6.37	4.20	1.32	8.81	6.40	2.87	10.15	6.64	12.68	29.45
<i>Dipodillus mackillagini</i>	1	1.52	4.08	6.18	3.80	1.29	10.01	7.38	2.57	7.59	7.17	13.29	25.95
<i>Dipodillus magharebi</i>	6	1.99	5.32	7.46	4.25	1.21	8.54	6.19	3.23	10.44	7.73	15.71	30.38
<i>Dipodillus simoni</i>	4	1.36	3.71	5.67	3.33	0.94	7.46	4.94	2.21	7.17	5.66	12.34	22.76
<i>Dipodillus stigmonyx</i>	4	1.43	3.62	5.37	3.26	1.00	8.25	5.77	2.08	6.88	6.70	11.62	23.15
<i>Gerbiliscus afra</i>	4	2.51	7.05	9.31	6.55	2.25	10.87	8.99	3.98	12.31	8.95	19.64	37.48
<i>Gerbiliscus boehmi</i>	4	2.56	7.06	10.07	7.16	2.10	11.02	8.63	4.38	14.76	9.13	21.38	41.39
<i>Gerbiliscus b. brantsii</i>	4	2.58	6.41	9.50	6.29	1.83	11.82	9.65	3.62	12.27	7.81	19.17	36.85
<i>Gerbiliscus b. humpatensis</i>	2	2.47	6.69	9.59	6.92	2.50	10.92	8.99	4.12	12.24	8.38	19.96	39.87
<i>Gerbiliscus b. perpallidus</i>	4	2.16	5.09	7.97	5.83	1.88	10.43	7.91	3.46	11.30	7.90	17.72	34.88
<i>Gerbiliscus guineae</i>	4	2.20	6.10	8.84	5.66	1.89	9.91	7.75	4.01	13.29	7.76	17.42	37.05
<i>Gerbiliscus inclusus</i>	4	2.27	6.21	9.55	6.52	2.53	10.98	8.76	3.87	13.04	7.12	18.90	37.29
<i>Gerbiliscus kempfi</i>	4	2.50	6.83	9.39	6.39	2.07	10.45	8.06	3.96	13.67	8.61	18.95	38.72
<i>Gerbiliscus leucogaster</i>	4	2.39	5.93	8.88	5.82	1.80	10.43	8.23	3.46	12.36	7.91	18.44	35.15
<i>Gerbiliscus nigricaudus</i>	4	2.02	6.06	8.92	5.81	1.77	10.37	8.02	3.75	14.30	9.61	18.47	38.90
<i>Gerbiliscus phillipsi</i>	4	2.21	6.23	9.39	5.86	1.67	10.86	8.22	3.70	14.40	8.65	18.77	38.05
<i>Gerbiliscus robustus</i>	4	2.48	6.22	9.71	6.46	2.01	11.10	8.13	3.92	14.22	9.91	20.03	40.70
<i>Gerbiliscus validus</i>	4	2.53	6.98	10.27	6.62	2.18	10.79	8.68	4.03	12.60	9.05	20.28	38.66
<i>Gerbilurus paeba</i>	4	1.82	4.21	6.30	4.10	1.13	8.07	5.78	2.55	9.57	7.55	13.37	27.76
<i>Gerbilurus setzeri</i>	4	1.68	4.43	6.32	4.14	1.24	10.50	7.87	2.61	8.41	8.16	15.18	28.13
<i>Gerbilurus tytonis</i>	4	1.61	4.45	6.17	4.09	1.20	9.39	7.40	2.67	8.86	7.42	14.37	27.39
<i>Gerbilurus vallinus</i>	4	1.68	4.04	6.29	3.89	1.07	9.94	8.05	2.60	8.95	8.21	14.53	27.85
<i>Gerbilus agag</i>	4	1.62	4.49	6.39	4.05	1.31	8.01	6.98	2.52	9.06	7.40	13.93	27.78
<i>Gerbilus amoenus</i>	4	1.48	3.85	5.35	3.27	0.91	6.76	5.83	2.12	7.59	6.02	12.28	23.64
<i>Gerbilus andersoni</i>	4	1.65	4.42	6.67	4.03	1.23	8.63	6.54	2.57	9.18	8.05	15.05	28.40
<i>Gerbilus aquilus</i>	4	1.64	4.25	6.30	3.66	1.27	8.82	7.39	2.54	8.58	8.52	14.93	28.47
<i>Gerbilus cheesmani</i>	4	1.64	4.38	6.44	3.71	1.41	9.06	7.11	2.52	8.35	8.46	15.13	28.06
<i>Gerbilus famulus</i>	4	1.51	3.98	5.90	3.21	1.16	8.37	6.89	2.34	8.12	6.84	12.86	25.61
<i>Gerbilus floweri</i>	4	1.84	4.94	7.15	4.19	1.47	9.04	7.25	2.88	11.59	9.05	16.81	32.12
<i>Gerbilus garamantis</i>	1	1.73	4.07	5.36	3.36	0.89	6.65	5.83	2.24	7.68	6.23	12.11	23.11
<i>Gerbilus gerbillus</i>	6	1.51	4.08	5.94	3.55	1.01	8.18	5.98	2.48	8.59	8.11	14.60	27.00
<i>Gerbilus gleadowi</i>	4	1.65	4.52	6.60	3.91	1.18	8.71	7.06	2.52	9.58	7.35	14.43	28.39
<i>Gerbilus henleyi</i>	4	1.25	3.65	5.34	2.98	0.93	6.78	5.54	2.00	6.40	6.79	11.55	21.90
<i>Gerbilus hesperinus</i>	4	1.86	4.48	6.67	4.17	1.23	8.03	6.32	2.95	9.69	7.28	15.15	28.85
<i>Gerbilus hoogstraali</i>	4	1.56	4.15	6.16	3.61	1.22	7.90	6.33	2.50	8.48	7.47	14.29	27.31
<i>Gerbilus latastei</i>	4	1.76	4.65	6.75	4.06	1.28	8.49	6.92	2.54	9.50	7.77	14.57	28.11
<i>Gerbilus mauritaniae</i>	4	1.39	3.38	4.92	3.00	0.92	6.13	4.91	1.94	6.34	5.70	11.04	20.70
<i>Gerbilus mesopotamiae</i>	4	1.64	4.83	6.72	3.59	1.18	7.75	6.05	2.63	8.88	7.15	14.12	26.85
<i>Gerbilus muriculus</i>	4	1.21	3.16	4.79	3.06	0.99	6.04	4.71	1.98	6.04	5.49	10.08	20.96
<i>Gerbilus nanus</i>	6	1.55	4.06	5.91	3.45	1.14	7.61	6.48	2.26	8.07	7.35	13.08	25.79
<i>Gerbilus nigeriae</i>	2	1.43	3.86	5.86	3.55	1.29	na	na	2.38	8.97	6.62	12.34	24.95
<i>Gerbilus occiduus</i>	1	2.04	4.64	6.81	3.82	1.28	8.79	6.74	2.78	10.53	8.17	16.55	30.55
<i>Gerbilus perpallidus</i>	4	1.87	4.78	7.17	4.19	1.32	8.58	6.68	2.68	10.49	8.22	15.63	29.65
<i>Gerbilus poecilops</i>	4	1.77	4.61	6.92	3.61	1.26	8.35	6.39	2.74	9.31	6.98	14.61	27.91
<i>Gerbilus pulvinatus</i>	4	1.70	4.36	6.61	3.78	1.26	8.29	6.56	2.67	9.84	7.82	14.20	28.26
<i>Gerbilus pusillus</i>	4	1.32	3.23	5.14	2.98	0.98	6.22	4.69	1.95	7.29	6.32	10.83	22.23
<i>Gerbilus pyramidum</i>	4	2.13	5.84	7.73	4.44	1.50	9.62	7.12	3.04	11.18	8.84	17.60	33.51
<i>Gerbilus tarabuli</i>	4	1.81	4.92	7.17	4.00	1.41	8.78	6.85	2.65	9.84	8.98	15.63	30.34
<i>Meriones crassus</i>	4	2.15	5.03	8.10	5.12	1.77	12.25	9.37	3.32	10.73	9.41	18.39	34.20
<i>Meriones grandis</i>	4	2.61	6.99	10.47	6.11	2.08	11.90	8.73	3.96	14.54	9.93	22.30	41.93
<i>Meriones hurrianae</i>	4	2.09	6.05	9.13	5.62	2.10	9.96	8.09	3.28	10.45	8.76	19.19	33.77
<i>Meriones l. erythrourus</i>	1	2.54	6.46	9.18	5.47	1.86	13.25	9.46	3.21	13.64	9.77	20.97	38.88
<i>Meriones l. libycus</i>	4	2.27	6.55	9.21	5.87	1.96	13.55	10.30	3.54	13.45	10.88	20.94	40.38
<i>Meriones meridianus</i>	4	2.12	5.31	7.64	4.84	1.51	11.71	8.48	3.15	11.55	9.23	17.60	32.52
<i>Meriones persicus</i>	4	2.84	7.84	10.87	6.28	2.40	11.69	8.71	4.59	16.00	11.77	24.61	46.00
<i>Meriones rex</i>	4	2.50	6.28	9.73	5.96	2.00	11.58	8.32	4.21	12.73	10.11	20.87	38.33
<i>Meriones shawi</i>	4	1.95	5.37	9.20	5.29	1.69	12.61	8.76	3.64	13.01	9.71	20.64	37.50
<i>Meriones tamariscinus</i>	4	2.34	6.61	9.56	5.93	2.29	10.48	8.32	4.05	14.62	10.59	21.40	40.08
<i>Meriones tristrami</i>	4	2.18	6.00	8.95	5.42	1.98	10.17	7.82	3.86	13.45	9.59	20.11	38.46
<i>Meriones unguiculatus</i>	8	2.17	5.59	8.39	4.71	1.65	10.29	7.39	3.55	11.17	9.22	19.29	34.18

Table E.5—continued.

	#	ID	IH	RD	LML	MH	LBL	BH	NB	NSL	IOB	DSW	DSL
<i>Meriones vinogradovi</i>	4	2.32	5.85	8.88	5.47	2.00	11.21	8.00	3.65	12.97	10.69	20.86	38.84
<i>Pachyuromys duprasi</i>	9	1.86	4.76	7.29	4.78	1.34	15.46	10.23	2.96	10.61	9.59	17.68	32.23
<i>Psammomys obesus</i>	9	2.29	6.88	10.68	6.50	2.08	12.70	8.76	3.59	12.95	9.33	23.13	39.05
<i>Rhombomys o. sodalis</i>	4	2.70	6.32	11.96	6.57	1.39	11.70	8.22	3.81	12.36	10.31	23.50	40.00
<i>Rhombomys o. ssp</i>	5	2.16	6.26	11.02	6.26	1.61	12.39	8.99	3.76	12.22	9.91	21.86	38.66
<i>Sekeetamys calurus</i>	8	2.09	4.93	7.40	4.64	1.24	10.76	7.94	2.88	11.35	8.10	16.59	33.47
<i>Tatera indica</i>	8	2.60	6.59	10.22	6.02	2.00	11.13	9.29	3.98	14.65	10.44	20.95	40.68
<i>Taterillus arenarius</i>	4	1.92	5.13	7.49	4.98	1.34	8.96	7.01	2.70	10.79	8.02	15.63	32.05
<i>Taterillus congicus</i>	4	1.87	5.08	7.88	5.14	1.74	8.82	6.23	3.01	11.09	8.65	15.73	32.59
<i>Taterillus emini</i>	4	1.86	5.16	7.68	4.94	1.56	8.34	6.48	2.88	11.67	7.66	15.66	32.43
<i>Taterillus gracilis</i>	4	2.58	5.66	6.87	3.87	1.21	8.34	6.58	3.08	10.71	8.75	15.37	32.04
<i>Taterillus harringtoni</i>	4	2.07	4.69	8.06	4.82	1.30	9.71	7.19	3.05	11.28	8.36	16.45	33.36
<i>Taterillus lacustris</i>	4	1.94	5.00	7.33	5.03	1.51	8.33	6.46	2.88	11.47	8.23	15.59	31.96
<i>Taterillus pygargus</i>	4	2.00	5.13	7.58	4.89	1.28	8.87	6.74	3.09	12.02	8.36	16.80	34.00
Lophiomyinae													
<i>Lophiomys i. imhausi</i>	2	3.68	10.55	16.58	13.83	3.38	9.69	6.30	7.93	20.66	16.49	34.34	60.21
<i>Lophiomys i. thomasi</i>	2	3.26	8.82	15.22	13.79	2.97	9.85	6.51	7.89	16.34	17.52	31.98	56.03
Murinae													
<i>Abeomelomys sevia</i>	4	1.93	4.60	6.49	6.11	1.11	4.19	3.43	3.47	9.68	6.74	15.94	33.42
<i>Aethomys chrysophilus</i>	4	2.40	5.52	7.33	5.82	1.27	6.21	4.90	4.14	11.25	7.64	17.19	34.87
<i>Anisomys imitator</i>	4	4.64	10.34	18.21	9.89	1.84	6.79	5.69	8.54	24.04	12.85	31.85	68.57
<i>Apodemus agrarius</i>	4	1.55	3.31	5.94	3.92	0.91	4.79	3.53	2.83	7.29	6.29	11.43	25.57
<i>Apodemus mystacinus</i>	4	1.68	4.12	6.29	4.52	0.89	4.74	3.71	3.40	9.65	5.05	13.29	29.19
<i>Apodemus semotus</i>	4	1.46	3.16	5.54	3.98	0.92	4.18	3.06	2.72	9.06	5.77	11.68	25.76
<i>Apodemus speciosus</i>	2	1.32	3.30	5.74	3.93	1.03	4.30	3.14	2.79	8.78	5.75	12.18	25.31
<i>Apodemus sylvaticus</i>	4	1.38	3.34	5.39	3.74	0.91	4.46	3.21	2.58	7.76	4.55	11.51	23.65
<i>Apomys datae</i>	4	2.00	5.37	7.89	6.70	1.59	5.32	4.21	3.87	13.31	6.36	16.78	36.93
<i>Apomys hylocoetes</i>	4	1.47	4.08	5.75	5.34	1.10	3.99	3.33	3.12	9.89	5.18	12.45	28.61
<i>Archboldomys luzonensis</i>	4	1.37	3.45	5.35	4.47	1.11	4.13	3.00	2.86	8.65	6.14	12.35	26.51
<i>Arvicantis neumanni</i>	2	1.96	4.77	7.73	5.73	1.32	6.08	4.89	3.58	9.43	7.07	15.93	31.04
<i>Arvicantis niloticus</i>	4	2.09	4.96	7.99	6.44	1.41	6.69	4.73	3.28	9.48	7.40	15.50	31.06
<i>Bandicota bengalensis</i>	3	2.88	8.32	12.86	8.06	2.18	9.29	7.15	4.54	13.44	7.27	24.52	40.69
<i>Batomys salomonensi</i>	4	1.96	6.03	9.72	7.44	1.55	5.02	3.99	4.97	15.58	6.27	19.91	40.34
<i>Berylmys bowersi</i>	4	3.43	8.25	12.56	9.44	2.13	8.91	7.28	6.23	19.64	9.20	26.35	53.54
<i>Bullimus bagobus</i>	6	3.84	9.37	15.02	9.80	2.54	13.28	9.79	6.08	21.80	8.49	27.86	60.22
<i>Bunomys chrysocomus</i>	4	2.11	5.62	8.36	6.10	1.51	7.33	5.02	4.13	13.55	6.86	17.87	38.82
<i>Carpomys phaeurus</i>	1	2.39	6.21	9.38	6.18	1.43	6.49	4.33	4.06	12.21	5.89	19.71	36.35
<i>Chiromys chiropus</i>	4	2.27	5.50	8.41	6.98	1.47	6.48	4.41	3.98	12.44	7.76	16.89	37.65
<i>Chiropodomys gliroides</i>	4	1.77	4.29	6.22	3.54	0.81	4.31	3.32	2.50	7.41	5.87	13.53	24.12
<i>Chrotomys gonzalesi</i>	2	1.67	3.64	8.64	6.33	1.49	5.89	4.95	3.47	11.08	6.96	19.26	34.95
<i>Colomys goslingi</i>	4	1.94	5.19	6.92	5.20	1.20	5.42	3.67	3.49	11.87	4.57	14.71	32.36
<i>Conilurus penicillatus</i>	4	2.58	6.21	9.90	7.65	1.61	7.30	5.94	4.75	13.48	6.68	20.81	40.82
<i>Cremonomys cutchicus</i>	4	2.21	4.80	6.71	5.31	1.11	5.84	4.19	3.27	10.65	5.66	13.13	30.53
<i>Crunomys melanius</i>	2	1.70	4.45	5.91	4.03	1.22	5.41	3.14	3.05	9.59	7.05	12.51	28.70
<i>Dacnomyss millardi</i>	4	3.26	8.59	12.26	11.63	2.64	7.43	5.43	6.34	20.39	8.85	25.08	56.20
<i>Dasymys i. mediuss</i>	3	2.14	5.76	9.35	6.80	1.72	6.17	4.53	4.09	11.28	4.65	17.32	32.59
<i>Dasymys i. nudipes</i>	1	2.30	7.10	10.41	7.67	1.60	6.31	4.27	4.80	14.31	4.92	18.96	39.46
<i>Golunda ellioti</i>	3	1.81	4.77	7.25	5.84	1.29	5.70	4.43	3.07	8.92	5.68	13.75	28.92
<i>Grammomys d. dolichurus</i>	3	1.93	4.44	7.04	4.53	1.03	6.14	4.82	3.15	9.14	6.09	13.50	28.71
<i>Grammomys d. sardaster</i>	1	1.92	3.98	6.74	4.47	0.75	4.77	3.47	2.83	8.39	6.23	13.44	27.81
<i>Grammomys ibeanus</i>	4	1.86	4.67	6.53	4.50	1.11	5.14	4.31	3.06	10.07	6.05	13.79	29.39
<i>Grammomys macmillani</i>	4	1.72	3.94	6.21	4.07	0.96	4.90	3.67	2.99	8.38	5.09	12.66	26.65
<i>Hapalomys delacouri</i>	1	2.15	4.69	6.99	5.35	1.12	6.40	5.43	2.78	7.95	7.76	15.36	28.57
<i>Heimyscus fumosus</i>	4	1.38	3.35	5.25	3.59	0.79	4.65	2.95	2.63	8.21	4.87	10.36	23.89
<i>Hybomys univittatus</i>	4	1.75	4.29	7.51	5.26	1.13	5.32	4.28	3.93	10.44	6.68	14.50	31.04
<i>Hydromys c. chrysogaster</i>	1	4.21	8.97	12.74	8.59	1.94	8.19	4.73	6.55	16.55	7.08	26.92	51.18
<i>Hydromys c. fowlavatus</i>	2	3.65	10.53	13.10	9.61	2.65	8.70	6.21	6.13	19.41	7.93	28.20	55.80
<i>Hydromys c. ssp</i>	1	3.32	na	na	9.25	2.23	9.20	5.80	5.71	18.17	7.50	26.87	54.39
<i>Hylomys parvus</i>	4	1.44	3.23	5.35	3.42	0.77	3.95	2.87	2.49	6.83	4.87	11.06	22.97
<i>Hylomys stella</i>	4	1.29	3.31	5.54	3.46	0.81	4.23	2.93	2.61	7.75	4.86	11.32	24.12
<i>Hyomys goliath</i>	4	5.33	11.10	21.78	16.22	4.39	10.33	6.76	12.19	29.25	10.70	38.08	73.92
<i>Leggadina forresti</i>	3	1.05	3.30	4.69	3.60	0.85	4.25	3.28	2.00	5.99	3.41	10.18	19.29
<i>Lemniscomys barbarus</i>	4	1.87	4.65	7.26	5.06	1.06	6.35	5.17	3.28	9.89	5.45	13.50	29.63
<i>Lemniscomys striatus</i>	3	1.64	3.82	7.26	4.98	0.98	5.92	4.45	3.47	10.09	5.85	13.41	29.49
<i>Leopoldamys sabanus</i>	4	3.44	7.99	12.96	9.69	2.04	8.90	5.79	5.92	18.99	10.00	23.66	54.06
<i>Leptomys elegans</i>	4	2.00	5.35	7.51	6.17	1.36	5.99	4.40	4.08	12.28	6.03	15.01	35.88
<i>Limnomys sibuanus</i>	4	1.83	4.80	7.33	4.71	1.20	6.72	5.18	3.48	10.03	5.69	14.28	31.05
<i>Lorentzimys nouhuysi</i>	3	1.36	3.54	5.66	2.58	0.74	3.22	2.61	2.33	5.47	5.24	11.10	20.46
<i>Macruromys major</i>	4	2.86	6.33	13.26	6.63	1.41	5.98	4.35	6.57	18.69	8.20	24.29	53.02
<i>Malacomys longipes</i>	4	1.91	4.67	8.26	5.16	1.18	5.42	3.76	3.76	12.60	6.70	15.42	36.04
<i>Margaretomys elegans</i>	4	2.38	6.66	9.34	6.47	1.62	6.24	4.96	4.07	14.02	5.60	18.80	41.96
<i>Mastacomys fuscus</i>	1	2.20	5.58	10.25	8.39	1.70	7.64	5.10	6.35	14.02	4.94	23.77	42.38
<i>Mastomys erythroleucus</i>	4	1.98	4.70	7.05	4.80	1.22	5.26	3.69	3.16	9.88	4.54	13.86	29.23
<i>Maxomys bartelsii</i>	4	1.93	4.79	8.00	5.28	1.17	5.40	4.54	3.79	12.88	7.01	15.59	37.49
<i>Maxomys surifer</i>	4	2.23	5.23	9.14	5.74	1.37	5.78	4.12	4.34	13.48	7.22	17.45	40.02
<i>Melasmotherix naso</i>	4	1.39	3.65	5.25	4.59	1.05	5.78	3.28	2.87	11.10	6.53	12.45	30.79

Table E.5—continued.

	#	ID	IH	RD	LML	MH	LBL	BH	NB	NSL	IOB	DSW	DSL
<i>Melomys cervinipes</i>	4	2.03	5.09	8.18	6.76	1.44	5.47	4.39	3.78	10.84	5.39	16.95	33.40
<i>Melomys rufescens</i>	2	1.90	4.78	8.32	6.20	1.22	5.12	3.44	3.50	9.65	6.21	15.05	31.61
<i>Mesembriomys gouldii</i>	3	4.22	10.30	17.38	11.51	2.26	8.89	9.32	7.71	22.52	11.14	28.39	61.17
<i>Micralamys namaquensis</i>	3	1.76	4.25	6.68	5.02	1.03	4.85	3.94	3.33	9.74	5.84	13.72	28.21
<i>Micromys minutus</i>	4	1.21	3.35	5.17	2.70	0.61	3.42	2.33	2.24	6.33	3.45	10.33	20.23
<i>Millardia gleadowi</i>	4	1.43	3.67	5.75	4.31	0.92	5.47	4.34	2.57	8.64	5.06	11.50	25.06
<i>Millardia kathleenae</i>	2	1.77	4.09	7.54	5.36	1.17	6.32	4.75	2.97	10.01	6.54	13.94	31.39
<i>Mus booduga</i>	5	1.13	2.89	4.42	3.25	0.66	3.62	2.46	2.03	6.28	3.67	9.21	18.55
<i>Mus cervicolor</i>	4	1.21	3.06	4.73	3.35	0.85	3.89	2.60	2.17	6.74	4.03	10.41	20.98
<i>Mus cookii</i>	4	1.28	3.36	4.95	3.97	0.95	3.87	2.87	2.33	7.82	4.45	11.19	23.51
<i>Mus minutoides</i>	9	1.04	2.68	3.90	3.18	0.70	3.19	2.31	2.06	6.38	3.95	9.00	18.01
<i>Mus m. bactrianus</i>	1	1.08	2.68	4.69	3.06	0.70	3.43	2.13	2.28	5.93	4.02	9.42	20.04
<i>Mus m. ssp</i>	2	1.08	3.09	4.60	3.09	0.74	3.57	2.40	2.14	6.53	4.25	9.97	20.37
<i>Mus m. yamashinai</i>	1	1.00	2.88	4.16	3.18	0.71	3.60	2.58	2.02	6.35	3.90	9.66	18.99
<i>Mus pahari</i>	4	1.40	3.75	5.52	4.02	0.93	4.28	2.89	2.70	9.72	5.10	11.99	25.68
<i>Mus saxicola</i>	4	1.40	3.44	5.78	4.34	0.91	4.94	2.97	2.53	8.84	4.85	11.97	25.00
<i>Mus spretus</i>	4	1.22	3.05	4.83	3.40	0.71	3.63	2.42	2.31	6.90	3.98	10.38	20.74
<i>Mus terricolor</i>	4	0.92	2.64	4.24	3.12	0.72	4.12	2.56	1.84	6.42	3.49	9.03	18.36
<i>Myomys dybowskii</i>	4	1.95	5.13	7.70	7.66	1.47	6.69	5.29	4.31	11.44	6.45	15.77	34.17
<i>Myomyscus brockmani</i>	4	1.65	4.09	5.88	4.53	0.99	4.89	3.54	3.16	9.22	4.43	12.60	27.52
<i>Niviventer c. confucianus</i>	3	2.02	5.26	7.12	6.89	1.40	6.00	4.54	3.51	10.30	6.83	15.59	35.09
<i>Niviventer c. lotipes</i>	1	2.44	4.95	8.34	6.11	1.68	6.71	4.61	4.21	11.93	7.70	15.93	37.77
<i>Niviventer cremoniventer</i>	4	1.98	5.10	7.41	5.36	1.19	4.71	3.86	4.09	12.30	7.13	15.40	34.76
<i>Niviventer excelsior</i>	2	2.15	4.88	7.06	6.17	1.42	5.30	4.14	3.68	12.40	5.27	15.97	35.95
<i>Notomys alexis</i>	4	1.62	3.92	6.04	4.48	1.24	6.47	5.13	2.71	8.00	5.37	12.36	26.03
<i>Notomys cervinus</i>	4	1.57	3.54	6.80	4.76	1.21	6.27	5.02	2.64	8.11	5.77	13.10	26.41
<i>Notomys fuscus</i>	4	1.75	4.30	6.70	4.56	1.00	6.48	5.37	2.80	9.15	6.08	14.92	30.08
<i>Oenomys h. editus</i>	2	1.77	4.87	7.13	6.31	1.44	6.07	4.63	4.47	11.57	6.75	15.53	33.67
<i>Oenomys h. hypoxanthus</i>	2	1.92	5.28	7.68	6.59	1.61	6.02	4.88	4.16	12.03	6.48	15.10	34.13
<i>Otomys angoniensis</i>	4	2.49	6.40	10.19	8.51	1.95	8.09	6.85	7.46	14.04	4.17	18.48	36.98
<i>Otomys denti</i>	4	2.36	6.45	9.75	7.84	1.67	7.57	6.65	6.25	13.81	4.60	17.49	36.25
<i>Parotomys brantsii</i>	4	2.50	6.29	10.28	7.47	1.68	11.67	9.71	4.41	8.70	6.41	18.82	35.03
<i>Parotomys littledalei</i>	5	2.11	6.21	9.61	7.33	1.83	11.55	9.38	4.32	10.75	6.08	18.20	35.55
<i>Paruromys dominator</i>	4	4.21	8.51	14.68	9.38	2.05	8.60	7.00	6.07	20.56	9.01	25.72	55.58
<i>Pogonomys loriae</i>	2	1.96	4.27	8.08	6.01	1.31	4.36	3.46	3.86	12.10	5.10	18.09	34.33
<i>Pogonomys macrourus</i>	4	1.80	5.00	7.48	5.36	1.16	4.79	3.83	3.09	9.23	5.27	16.12	30.46
<i>Praomys jacksoni montis</i>	1	1.75	4.58	6.48	4.68	0.88	4.38	3.39	3.26	10.37	5.39	13.72	28.41
<i>Praomys jacksoni ssp</i>	3	1.91	4.62	6.51	4.69	1.01	5.23	3.89	3.23	10.43	5.86	13.78	31.02
<i>Praomys missonnei</i>	4	1.85	4.33	6.72	4.74	0.85	4.61	3.72	3.24	11.88	5.43	14.09	31.60
<i>Praomys tullbergi</i>	3	1.81	4.55	7.19	4.74	0.91	4.82	3.41	3.27	10.82	5.38	13.87	30.49
<i>Pseudohydromys ellermani</i>	3	1.23	2.73	4.36	0.79	0.57	2.41	2.07	2.59	6.52	4.09	9.72	21.23
<i>Pseudomys australis</i>	5	1.69	4.87	7.59	5.76	1.10	5.14	4.46	3.43	9.39	4.36	14.76	29.81
<i>Pseudomys hermannsburgensis</i>	4	1.18	3.16	4.97	3.70	0.83	4.73	3.98	2.06	6.55	3.88	10.01	21.03
<i>Rattus exulans</i>	4	1.73	4.78	7.05	5.03	1.17	5.93	4.41	3.18	9.47	6.46	13.79	29.43
<i>Rattus norvegicus</i>	3	2.83	7.32	11.57	7.03	1.68	7.54	5.26	5.22	16.11	6.30	21.68	45.87
<i>Rattus praetor</i>	4	2.68	7.33	11.01	7.19	1.48	6.93	5.45	5.60	17.38	7.02	21.58	46.29
<i>Rattus rattus</i>	4	2.30	6.37	9.25	6.06	1.38	7.79	6.03	4.33	14.60	6.95	18.36	40.63
<i>Rattus sordidus</i>	4	2.02	5.69	8.78	7.31	1.68	7.91	6.43	3.83	10.11	5.91	16.78	33.11
<i>Rattus tiomanicus</i>	4	2.60	6.78	10.25	7.08	1.46	7.79	6.17	4.69	13.46	7.20	18.50	40.57
<i>Rattus verecundus</i>	4	2.03	5.06	7.14	5.81	1.10	5.10	4.26	3.70	11.99	5.66	15.01	34.34
<i>Rattus villosissimus</i>	4	2.34	6.91	10.47	7.07	1.45	8.71	6.73	4.05	11.76	4.90	18.19	37.03
<i>Rhabdomys pumilio</i>	4	1.50	4.18	6.97	4.68	0.96	5.75	4.33	3.10	7.64	6.58	12.80	26.44
<i>Rhynchosomys isarogensis</i>	4	1.05	3.08	6.41	2.18	0.67	5.44	3.83	3.18	15.26	6.67	15.67	41.70
<i>Stenocephalemys albipes</i>	4	1.90	4.83	6.75	5.50	0.99	4.88	3.94	3.44	10.61	4.82	14.33	30.59
<i>Stochomys longicaudatus</i>	4	2.47	6.30	9.20	6.59	1.46	4.99	4.17	4.67	13.33	8.60	17.72	37.07
<i>Sundamys muelleri muelleri</i>	4	3.59	8.92	13.23	9.25	1.87	7.65	6.86	5.73	19.20	9.62	24.09	50.75
<i>Tarsomys apoenensis</i>	3	2.06	5.43	8.03	5.88	1.27	5.95	4.88	3.60	13.40	6.19	16.85	35.88
<i>Uromys caudimaculatus</i>	4	4.60	11.49	18.87	12.19	2.24	7.77	6.59	8.14	25.31	13.52	34.23	72.23
<i>Vandeleuria olereacea</i>	4	1.16	3.13	4.71	3.02	0.58	3.49	2.58	1.93	6.68	3.70	10.18	19.91
<i>Zelotomys h. ssp</i>	1	2.03	4.56	8.04	5.43	1.08	4.41	3.79	3.37	10.54	4.42	14.68	27.30
<i>Zelotomys h. vinaceus</i>	3	1.65	5.73	7.04	4.94	1.16	4.84	3.28	3.60	10.49	4.83	14.81	27.37
<i>Zelotomys woosnami</i>	4	1.91	5.13	7.05	5.07	1.22	5.08	3.60	3.25	10.58	5.12	14.13	29.75
<i>Zyzomys argurus</i>	4	1.51	3.95	6.21	4.69	1.03	4.19	3.88	2.73	10.10	4.62	12.93	29.45
<i>Nesomyidae</i>													
<i>Cricetomyinae</i>													
<i>Beamys hindei</i>	4	1.63	4.52	7.44	4.84	1.23	5.59	3.70	3.42	10.62	5.47	15.05	33.61
<i>Cricetomys gambianus</i>	3	3.40	7.61	14.67	10.64	2.09	9.68	6.68	7.83	21.78	11.03	26.76	59.58
<i>Saccostomus campestris</i>	4	1.41	4.09	7.13	4.53	0.93	6.14	4.41	3.40	9.69	4.73	14.32	29.50
<i>Delanomyinae</i>													
<i>Delanomyss brooksi</i>	4	0.99	2.89	4.34	2.38	0.48	3.68	2.19	1.60	4.89	3.06	8.75	16.24
<i>Dendromurinae</i>													
<i>Dendromys insignis</i>	4	1.32	3.55	4.92	3.63	0.73	4.52	3.21	2.54	8.32	3.25	10.63	22.56
<i>Dendromys mesomelas</i>	1	1.12	3.13	4.80	3.19	0.65	4.40	2.88	2.14	6.66	3.02	10.12	21.31
<i>Dendromys nyasae</i>	4	1.23	3.40	4.81	3.33	0.75	4.29	2.91	2.18	7.33	3.25	10.14	21.49
<i>Malacothrix typica</i>	4	1.36	3.74	5.51	3.81	0.95	4.47	3.75	2.27	8.22	3.07	12.45	23.17
<i>Steatomys krebsi</i>	1	0.98	3.17	4.36	3.56	0.75	4.98	3.21	2.32	7.38	3.59	10.08	20.27

Table E.5—continued.

	#	ID	IH	RD	LML	MH	LBL	BH	NB	NSL	IOB	DSW	DSL
<i>Steatomys p. athi</i>	1	1.21	3.57	5.09	3.20	0.77	5.21	3.72	2.64	8.62	3.96	10.83	22.17
<i>Steatomys p. kalaharicus</i>	1	1.15	3.66	5.17	3.46	0.76	5.95	3.76	2.56	8.66	4.28	11.56	22.93
<i>Steatomys p. ssp</i>	1	1.09	3.01	4.20	3.14	0.69	4.54	3.25	2.30	7.81	3.67	10.05	20.47
<i>Steatomys p. tongensis</i>	1	1.06	2.73	4.48	3.24	0.86	5.08	2.97	2.32	5.99	3.72	9.64	18.36
Mystromyinae													
<i>Mystromys albicaudatus</i>	4	2.05	5.54	7.63	6.10	1.41	6.55	4.69	3.87	12.52	4.31	16.56	32.87
Nesomyinae													
<i>Brachytarsomys albicauda</i>	4	2.76	6.10	11.95	8.27	1.70	8.32	4.79	4.83	15.07	5.69	24.66	45.02
<i>Brachytarsomys betsileoensis</i>	4	2.15	6.00	9.09	6.63	1.39	7.91	5.23	4.32	10.77	4.91	19.82	33.59
<i>Eliurus minor</i>	4	1.68	4.03	6.97	4.12	1.03	4.95	3.78	3.13	10.00	5.22	14.64	29.33
<i>Eliurus tanala</i>	4	2.48	5.30	8.81	5.97	1.43	5.90	4.69	4.20	15.68	5.69	18.38	39.66
<i>Gymnuromys roberti</i>	4	2.09	4.52	9.37	5.59	1.42	5.86	4.21	4.50	13.07	5.78	18.58	37.42
<i>Hypogeomys antimena</i>	1	na	na	na	na	na	na	na	na	na	na	na	na
<i>Macrotarsomys bastardii</i>	4	1.54	3.47	6.12	3.86	0.92	6.03	4.47	2.73	9.83	5.09	12.99	26.68
<i>Monticolomys koopmani</i>	2	1.45	3.96	6.36	3.66	0.85	5.47	3.61	2.40	8.37	3.71	12.52	24.74
<i>Nesomys rufus</i>	4	2.39	5.28	10.36	6.77	1.54	7.61	5.71	5.65	14.86	9.25	22.38	43.98
<i>Voalavo gymnochadus</i>	4	1.43	3.65	5.90	3.71	0.82	3.87	2.90	2.43	8.20	4.96	12.60	24.55
Petromyscinae													
<i>Petromyscus collinus</i>	8	1.54	3.22	5.06	3.31	0.71	4.17	2.89	2.26	8.11	3.98	10.64	22.90
Platacanthomysinae													
<i>Typhlomys c. chapensis</i>	1	1.49	4.32	5.95	4.17	0.79	3.60	3.29	2.68	7.24	6.19	12.44	25.13
<i>Typhlomys c. cinereus</i>	3	1.26	3.22	5.11	3.55	0.47	3.12	2.68	2.40	6.36	4.88	11.44	21.83
Spalacidae													
Myospalacinae													
<i>Eospalax f. kansus</i>	2	2.80	8.06	11.80	9.33	2.52	11.23	8.76	6.37	11.45	8.59	28.93	40.44
<i>Myospalax aspalax</i>	2	2.09	4.79	10.06	9.19	2.46	9.36	8.33	6.54	10.50	8.39	22.75	36.51
Rhizomysinae													
<i>Cannomys badius</i>	4	3.24	10.88	16.46	11.16	3.73	11.70	11.04	6.76	14.79	13.43	34.17	43.25
<i>Rhizomys pruinosus</i>	4	5.52	14.50	24.74	14.51	2.89	14.17	16.14	9.60	23.52	12.21	48.94	66.74
Tachyoryctinae													
<i>Tachyoryctes splendens</i>	4	3.18	11.33	16.05	8.53	2.28	11.08	9.83	6.49	16.95	8.78	31.05	43.95
Spalacinae													
<i>Spalax ehrenbergi</i>	4	2.26	7.12	11.48	6.91	1.83	8.23	6.97	5.10	13.22	13.22	27.51	37.48
Sciuroidea													
Gliridae													
Graphiurinae													
<i>Graphiurus oocularis</i>	3	2.07	4.82	6.89	3.39	1.08	9.54	6.48	3.90	11.78	5.07	16.98	32.76
Leithiinae													
<i>Eliomys melanurus</i>	4	1.70	4.32	6.66	4.73	1.11	10.17	7.50	2.94	10.01	4.68	17.42	31.76
<i>Eliomys quercinus</i>	4	1.90	5.05	6.82	5.45	1.31	10.22	7.38	3.43	9.94	4.41	18.88	32.76
Sciuridae													
Xerinae													
Xerini													
<i>Atlantoxerus getulus</i>	4	3.08	7.19	11.35	8.55	1.42	12.06	8.48	5.26	10.28	13.49	25.30	42.78
<i>Xerus erythropus</i>	4	3.66	8.11	15.26	11.66	1.86	13.94	9.46	7.43	13.40	20.71	29.57	56.42
<i>Xerus inauris</i>	4	3.86	9.14	15.61	10.95	2.12	13.27	10.66	8.51	13.83	22.14	33.13	55.47
<i>Xerus princeps</i>	3	4.46	9.85	17.43	10.27	2.06	13.86	10.74	7.69	14.84	24.90	33.25	57.53
Marmotini													
<i>Ammospermophilus harrisi</i>	4	2.49	5.10	10.07	6.67	1.22	10.05	7.75	4.24	8.63	12.87	21.30	37.95
<i>Ammospermophilus interpres</i>	4	2.66	5.32	10.00	6.47	1.14	10.24	7.86	4.29	7.34	11.61	20.03	35.83
<i>Ammospermophilus leucurus</i>	4	2.37	5.31	9.80	6.12	1.03	9.95	7.45	4.27	7.92	11.12	20.85	37.22
<i>Ammospermophilus nelsoni</i>	4	2.28	4.95	10.08	7.09	1.24	10.89	8.45	4.35	7.81	12.93	22.27	38.51
<i>Spermophilus fulvus</i>	4	3.04	9.30	13.88	13.73	2.71	11.09	9.80	8.38	16.14	17.72	36.90	54.47
<i>Spermophilus mexicanus</i>	4	2.84	7.55	12.08	9.78	1.69	11.39	8.07	6.81	13.41	15.19	29.17	49.51
<i>Spermophilus mohavensis</i>	4	2.15	5.91	9.90	7.40	1.19	9.71	7.56	4.22	9.65	13.21	22.64	35.66
<i>Spermophilus pygmaeus</i>	4	2.02	5.84	10.63	8.41	1.55	8.73	6.53	6.30	10.45	12.18	24.94	38.38
<i>Spermophilus spilosoma</i>	4	2.25	5.20	10.25	7.19	1.36	10.12	6.86	4.69	8.10	12.24	21.10	35.67
<i>Spermophilus tereticaudus</i>	4	2.11	5.59	9.73	7.53	1.46	9.39	7.62	4.04	8.06	12.49	22.40	35.54
<i>Spermophilus variegatus</i>	4	3.75	9.13	16.60	12.44	2.42	14.20	10.74	9.50	16.62	19.55	37.88	61.62

Table E.6. Species means of raw distances extracted from the occlusal and lateral views of mandibles in millimeters. See Table E.4 legend for more information. LIW= width across both lower incisors; IL= incisor length; JDL= jaw diastema length; JML= jaw molar tooth row length; JMW= jaw first molar width; TJL= total jaw length; JID= jaw insisor depth; IL2= incisor length; JLS= jaw length measurement I; MAM= moment arm masseter; JLB= jaw length measurement II; JMH= jaw molar 1 height.

	#	LIW	IL	JDL	JML	JMW	TJL	JID	IL2	JLS	MAM	JLB	JMH
Anomaluromorpha													
Pedetidae													
<i>Pedetes capensis</i>	4	9.25	5.51	8.43	14.6	3.33	55.3	4.29	12.5	49.0	26.0	49.1	2.55
Castorimorpha													
Geomysidae													
<i>Cratogeomys castanops</i>	4	4.70	5.06	8.27	5.5	2.17	na	2.48	14.4	33.5	9.6	28.4	1.94
<i>Thomomys umbrinus</i>	4	4.34	5.45	6.44	6.3	1.97	28.7	2.35	13.8	29.7	9.6	26.7	1.92
Heteromyidae													
Dipodomysinae													
<i>Dipodomys agilis</i>	4	2.04	2.92	4.32	3.7	1.43	18.0	1.32	5.7	18.1	5.5	17.1	1.27
<i>Dipodomys californicus</i>	4	2.05	3.23	4.28	3.6	1.47	19.5	1.45	6.5	19.1	5.6	17.8	1.31
<i>Dipodomys compactus</i>	4	1.88	3.00	4.13	3.5	1.34	18.8	1.32	5.9	18.6	5.6	17.8	1.46
<i>Dipodomys deserti</i>	5	2.34	3.21	5.06	4.2	1.80	20.0	1.58	5.6	20.1	7.7	19.0	1.58
<i>Dipodomys elator</i>	3	2.17	3.09	4.36	3.7	1.58	19.7	1.40	6.1	20.9	6.5	18.6	1.58
<i>Dipodomys gravipes</i>	3	1.72	2.90	4.59	3.9	1.52	18.9	1.31	5.5	19.6	7.2	18.7	1.43
<i>Dipodomys heermanni</i>	3	2.03	3.15	4.44	3.5	1.44	18.8	1.31	6.1	20.4	5.9	18.0	1.45
<i>Dipodomys ingens</i>	4	2.43	3.22	5.98	3.9	1.66	22.3	1.63	7.0	24.2	7.8	21.6	1.66
<i>Dipodomys merriami</i>	4	1.68	2.56	3.71	3.3	1.38	16.3	1.25	5.4	16.7	5.3	15.5	1.29
<i>Dipodomys microps</i>	4	2.41	2.79	4.71	3.4	1.49	18.4	1.32	5.6	18.2	6.1	16.7	1.54
<i>Dipodomys nelsoni</i>	4	2.98	3.87	5.71	4.2	1.92	21.5	1.64	7.8	23.8	8.2	20.9	1.72
<i>Dipodomys nitratoides</i>	5	1.72	2.53	3.80	3.6	1.35	16.7	1.17	5.2	17.0	5.3	15.6	1.31
<i>Dipodomys ordii</i>	4	1.92	2.63	4.04	3.0	1.28	17.2	1.37	5.7	18.2	5.6	16.7	1.25
<i>Dipodomys panamintinus</i>	4	2.14	2.83	4.72	3.9	1.52	19.0	1.41	5.9	18.3	6.0	17.7	1.40
<i>Dipodomys phillipsii</i>	4	1.73	2.66	4.12	3.3	1.39	17.3	1.21	5.3	18.7	5.4	16.7	1.50
<i>Dipodomys simulans</i>	4	2.13	2.82	4.20	3.7	1.44	18.5	1.45	6.2	20.1	6.4	18.0	1.47
<i>Dipodomys spectabilis</i>	4	2.73	3.95	5.67	4.1	1.85	na	1.76	6.9	24.6	8.6	21.3	1.92
<i>Dipodomys stephensi</i>	4	1.89	2.76	4.55	3.9	1.43	18.8	1.42	6.3	20.8	6.5	18.4	1.44
<i>Dipodomys v. venustus</i>	5	2.07	2.52	4.67	3.6	1.51	19.2	1.40	6.5	21.1	6.3	19.2	1.49
<i>Dipodomys v. elephantinus</i>	4	2.03	2.64	4.48	3.5	1.48	18.7	1.46	5.8	19.7	6.2	18.0	1.44
<i>Microdipodops megacephalus</i>	4	1.18	1.90	2.58	2.5	0.80	11.0	0.81	3.6	10.8	4.1	10.6	0.92
<i>Microdipodops pallidus</i>	4	1.43	1.95	2.84	2.7	0.97	13.0	0.95	4.7	12.1	4.6	12.2	0.91
Heteromyinae													
<i>Heteromys anomalus</i>	4	2.03	2.99	3.85	4.2	1.08	18.3	1.67	6.6	18.5	6.7	17.4	1.25
<i>Heteromys australis</i>	4	2.20	2.67	3.89	4.0	1.16	18.3	1.49	5.8	17.1	6.5	16.1	1.22
<i>Heteromys catopterius</i>	4	2.23	3.01	4.28	4.2	1.21	19.1	1.59	6.1	19.1	6.9	18.4	1.53
<i>Heteromys d. desmarestianus</i>	4	1.98	2.74	3.74	3.7	1.04	18.0	1.46	6.1	17.5	6.6	16.8	1.02
<i>Heteromys d. goldmani</i>	4	1.78	3.23	3.93	4.2	1.07	18.4	1.40	6.7	17.9	6.0	16.6	1.33
<i>Heteromys gauameri</i>	4	1.95	3.05	3.35	4.0	1.08	17.0	1.27	5.9	16.2	5.7	15.0	1.09
<i>Heteromys nelsoni</i>	4	1.99	3.49	4.12	4.7	1.36	19.7	1.41	6.7	19.6	7.4	18.5	1.54
<i>Heteromys oasicus</i>	2	1.49	2.61	2.70	3.5	0.75	13.6	1.27	5.5	14.1	5.0	13.4	0.96
<i>Heteromys teleus</i>	1	2.28	3.47	3.71	4.5	1.30	18.7	1.70	6.8	18.8	7.2	17.9	1.31
<i>Liomys adspersus</i>	4	2.02	3.04	4.05	3.8	1.19	18.8	1.42	6.3	17.9	6.3	17.0	1.08
<i>Liomys irroratus</i>	4	1.92	3.03	3.61	4.2	1.11	18.0	1.32	6.3	16.8	6.3	16.0	1.15
<i>Liomys pictus</i>	4	1.46	2.93	3.56	3.9	1.25	17.4	1.49	6.6	16.9	6.4	15.9	1.21
<i>Liomys salvini</i>	4	1.75	2.80	3.65	3.6	1.11	16.9	1.42	6.2	16.2	6.0	15.4	1.02
Perognathinae													
<i>Chaetodipus arenarius</i>	4	1.21	1.85	2.45	2.6	0.82	11.8	0.93	4.1	11.7	3.9	10.7	0.77
<i>Chaetodipus artus</i>	4	1.33	2.05	2.83	2.9	0.95	13.1	1.08	4.9	13.5	4.7	12.7	0.89
<i>Chaetodipus baileyi</i>	4	1.66	2.51	3.58	3.4	1.10	16.6	1.33	5.9	16.9	5.4	15.5	1.01
<i>Chaetodipus californicus</i>	4	1.46	2.00	2.59	2.9	0.94	13.6	1.08	4.8	14.1	4.6	12.9	0.80
<i>Chaetodipus eremicus</i>	4	1.54	1.84	2.54	2.6	0.83	12.4	1.00	4.7	12.6	4.5	11.6	0.81
<i>Chaetodipus fallax</i>	4	1.62	1.90	2.72	3.2	1.01	13.3	1.09	4.7	14.2	4.3	12.8	0.89
<i>Chaetodipus formosus</i>	8	1.48	1.89	2.71	2.9	0.97	13.2	0.99	4.5	13.0	4.6	12.5	0.88
<i>Chaetodipus goldmani</i>	4	1.38	1.91	2.68	2.8	0.88	13.5	1.19	5.1	14.2	5.3	13.0	0.82
<i>Chaetodipus hispidus</i>	4	1.78	2.69	3.39	3.6	0.91	15.9	1.25	5.4	15.4	5.3	14.4	0.89
<i>Chaetodipus intermedius</i>	4	1.31	1.65	2.55	2.7	0.88	11.8	1.05	4.2	12.7	4.2	11.2	0.81
<i>Chaetodipus lineatus</i>	4	1.34	1.73	2.34	2.8	0.81	11.9	1.06	4.8	13.4	4.7	12.3	0.85
<i>Chaetodipus nelsoni</i>	3	1.34	1.64	2.43	2.8	0.75	12.4	1.13	4.6	12.5	4.6	12.1	0.96
<i>Chaetodipus penicillatus</i>	4	1.50	2.17	2.75	2.9	0.88	13.3	1.11	4.4	12.2	4.1	11.8	0.82
<i>Chaetodipus pernix</i>	4	1.36	1.52	2.52	2.4	0.69	11.1	0.97	4.7	12.5	4.0	11.4	0.81
<i>Chaetodipus rulinoris</i>	4	1.35	2.16	2.87	2.9	0.88	13.5	1.19	5.7	15.9	5.5	14.2	0.92
<i>Chaetodipus spinatus</i>	4	1.22	2.15	2.82	2.9	0.80	12.8	1.08	4.6	12.8	4.4	11.5	0.81
<i>Perognathus alcticolus</i>	4	1.56	1.99	2.75	3.0	0.97	12.9	0.86	4.2	12.4	4.3	12.0	0.79
<i>Perognathus amplus</i>	4	1.38	2.25	2.55	2.8	0.96	11.6	0.91	4.1	11.9	4.3	11.3	0.93
<i>Perognathus fasciatus</i>	4	1.22	1.72	2.12	2.6	0.77	10.5	0.80	3.7	10.4	3.7	10.2	0.61
<i>Perognathus flavescens</i>	4	1.30	1.70	2.15	2.5	0.86	10.7	0.83	3.7	10.7	3.6	9.9	0.68

Table E.6—continued.

	#	LIW	IL	JDL	JML	JMW	TJL	JID	IL2	JLS	MAM	JLB	JMH
<i>Perognathus flavus</i>	4	1.32	1.53	2.10	2.8	0.87	10.5	0.87	3.8	10.6	3.8	10.1	0.72
<i>Perognathus inornatus</i>	4	1.36	1.57	2.40	2.5	0.85	10.7	0.87	3.9	11.2	3.5	10.8	0.82
<i>Perognathus longimembris</i>	4	1.20	1.70	2.19	2.4	0.73	10.2	0.84	3.6	10.0	3.3	9.7	0.68
<i>Perognathus merriami</i>	4	1.38	1.92	2.20	2.5	0.77	10.7	0.95	4.1	10.8	3.8	10.3	0.81
<i>Perognathus parvus</i>	4	1.55	1.95	2.75	2.9	0.97	12.7	1.13	4.6	13.4	4.4	12.5	0.84
Hystricomorpha													
Ctenodactylomorphi													
Ctenodactylidae													
<i>Ctenodactylus gundi</i>	4	4.27	4.58	8.24	10.9	2.07	36.6	1.81	7.2	40.8	13.2	33.2	1.48
<i>Ctenodactylus vali</i>	1	na	na	na	na	na	na	na	na	na	na	na	na
<i>Felovia vae</i>	4	3.77	3.52	7.10	8.2	1.82	26.7	1.57	5.7	33.7	10.3	28.3	1.28
<i>Massoutiera mzabi</i>	4	3.22	3.50	6.77	8.0	1.78	28.1	1.47	5.4	29.4	9.7	26.1	1.23
<i>Pectinator spekei</i>	2	2.88	3.97	6.12	8.8	1.83	na	1.48	5.9	28.3	7.8	28.3	1.54
Hystricognathi													
Abrocomidae													
<i>Abrocoma bennettii</i>	4	2.46	3.59	8.72	9.2	1.87	32.8	2.88	4.9	30.3	13.5	30.9	1.88
Bathyergidae													
<i>Bathyergus janetta</i>	4	5.78	8.40	5.47	8.5	2.08	33.2	3.38	15.4	39.7	13.7	29.6	2.44
<i>Cryptomys hottentotus</i>	4	4.33	8.53	4.92	5.0	1.54	26.8	2.30	13.1	31.3	10.9	25.6	1.48
Caviidae													
Caviinae													
<i>Microcavia australis</i>	4	2.98	4.69	7.36	10.8	1.94	33.2	1.77	7.5	37.0	12.0	30.3	2.07
Dolichotinae													
<i>Dolichotis patagonum</i>	4	6.99	14.11	28.72	24.9	4.85	92.8	5.58	19.8	101.9	39.7	86.3	5.85
<i>Dolichotis salinicola</i>	4	4.74	10.48	20.44	20.1	3.06	59.3	3.78	14.9	77.6	26.7	64.9	4.32
Chinchillidae													
<i>Lagidium viscacia</i>	4	5.38	7.09	14.92	16.9	4.12	62.5	2.29	11.9	51.3	19.9	46.9	2.06
<i>Lagostomus maximus</i>	4	9.30	16.05	20.50	23.0	7.44	109.9	4.84	23.1	92.3	30.7	84.1	3.48
Ctenomyidae													
<i>Ctenomys emilianus</i>	1	5.83	5.60	6.49	9.7	2.01	na	2.84	10.4	39.9	14.0	31.1	1.88
<i>Ctenomys latro</i>	4	3.84	4.39	5.15	7.0	1.61	26.5	1.88	9.0	27.5	10.6	23.5	1.56
<i>Ctenomys mendocinus</i>	4	4.50	5.33	5.05	7.1	1.84	na	2.27	9.5	32.2	12.0	25.8	1.74
<i>Ctenomys occultus</i>	2	4.50	4.65	5.14	7.0	2.02	na	2.24	9.8	31.3	11.9	25.2	1.86
Hystricidae													
<i>Hystrix africaeaustralis</i>	4	11.25	23.68	23.19	32.8	6.10	114.1	6.46	34.1	112.9	38.2	102.5	6.11
<i>Hystrix cristata</i>	4	12.95	15.85	23.67	32.4	6.27	113.2	6.33	28.5	105.1	39.2	94.7	7.86
<i>Hystrix indica</i>	4	8.75	20.11	22.80	33.6	6.49	111.6	5.93	27.3	107.0	38.9	94.8	6.67
Octodontidae													
<i>Octodon degus</i>	4	3.21	4.34	5.23	7.9	1.63	27.5	1.79	8.3	29.5	10.7	26.5	1.74
<i>Octodon lunatus</i>	4	3.13	3.69	5.42	8.7	1.88	25.9	1.81	8.3	31.0	11.2	27.7	1.57
Petromuridae													
<i>Petromus typicus</i>	4	3.35	3.82	5.07	8.7	1.82	30.2	1.57	6.5	29.5	11.8	25.8	2.18
Myodonta													
Dipodoidea													
Dipodidae													
Allactaginae													
<i>Allactaga balikunica</i>	1	1.80	4.76	4.42	5.2	1.53	20.2	1.24	8.1	22.7	5.3	21.1	1.55
<i>Allactaga bullata</i>	4	2.25	5.37	4.97	6.1	1.69	na	1.35	9.2	23.9	5.6	22.2	1.46
<i>Allactaga e. elater</i>	4	1.84	4.20	4.30	4.7	1.06	19.4	1.21	7.0	19.8	4.6	17.7	1.07
<i>Allactaga e. elater indica</i>	3	2.10	4.25	4.28	4.9	1.27	20.2	1.34	6.9	20.5	5.2	18.1	1.19
<i>Allactaga e. elater turkmeni</i>	1	na	na	na	na	na	na	1.27	5.6	19.2	4.9	17.4	0.81
<i>Allactaga euphratica</i>	8	2.10	4.72	4.95	6.0	1.33	21.6	1.45	8.1	22.7	5.5	20.7	1.44
<i>Allactaga firozzi</i>	3	1.88	4.68	4.60	5.2	1.50	20.5	1.20	7.9	21.8	5.2	19.4	1.22
<i>Allactaga hotsoni</i>	4	1.56	4.16	4.29	4.9	1.32	19.3	1.15	7.2	20.3	5.0	18.6	1.18
<i>Allactaga major</i>	4	3.76	9.04	7.78	8.3	2.09	36.5	1.97	13.3	36.3	8.8	33.5	2.23
<i>Allactaga severzovi</i>	2	5.79	7.35	na	7.6	2.51	na	1.96	11.1	31.3	7.7	28.3	1.77
<i>Allactaga sibirica</i>	2	2.51	7.14	6.22	6.6	1.78	na	1.42	10.5	30.5	6.4	27.6	1.79
<i>Allactaga tetradactyla</i>	6	2.01	5.04	4.94	5.9	1.47	22.1	1.22	7.7	22.0	4.9	20.2	1.37
<i>Pygeretmus platyurus</i>	1	1.30	3.43	4.01	4.1	1.14	16.5	0.95	5.8	17.8	4.4	15.9	0.88
<i>Pygeretmus pumilio</i>	4	na	na	na	na	na	na	na	na	na	na	na	na
<i>Pygeretmus zhittkovi</i>	3	1.80	4.73	4.70	5.6	1.53	19.6	1.22	7.2	21.2	6.0	19.1	1.26
Cardiocrainiinae													
<i>Cardiocranus paradoxus</i>	2	1.50	1.69	2.59	2.7	0.64	11.4	0.74	4.0	10.3	3.6	10.1	0.67
<i>Salpingotulus michaelis</i>	2	1.20	1.23	2.18	2.3	0.65	9.3	0.75	3.3	8.8	4.2	9.8	0.71
<i>Salpingotulus crassicauda</i>	2	1.54	0.98	1.58	2.3	0.62	8.7	0.69	2.6	7.6	3.2	8.2	0.61
Dipodinae													
<i>Dipus s. sagitta</i>	4	2.08	3.74	4.16	5.7	1.23	19.4	1.30	6.7	18.7	6.3	17.8	1.15
<i>Dipus s. sowerli</i>	4	na	na	na	na	na	na	1.52	7.6	19.4	6.7	19.2	1.23
<i>Eremodipus lichtensteinii</i>	1	na	na	na	na	na	na	na	na	na	na	na	na
<i>Jaculus blanfordi</i>	5	2.23	4.36	4.53	4.8	1.46	21.4	1.57	7.3	20.3	7.5	19.8	1.24
<i>Jaculus jaculus</i>	4	1.89	3.87	3.62	5.1	1.39	18.8	1.42	6.4	17.7	6.3	17.2	1.18
<i>Jaculus orientalis</i>	4	2.03	4.65	5.14	5.3	1.71	23.2	1.73	8.1	23.1	8.2	22.4	1.41
<i>Paradipus ctenodactylus</i>	1	2.16	2.39	4.75	6.0	1.13	na	1.03	5.7	18.0	8.1	19.0	1.37
<i>Styloctenus telum</i>	4	1.77	3.80	3.98	4.5	1.30	18.2	1.25	7.0	17.5	5.7	16.6	1.07

Table E.6—continued.

	#	LIW	IL	JDL	JML	JMW	TJL	JID	IL2	JLS	MAM	JLB	JMH
Sicistinae													
<i>Sicista betulina</i>	4	1.17	1.94	2.41	2.6	0.70	11.2	0.75	3.9	10.0	4.0	10.6	0.80
<i>Sicista concolor</i>	5	1.48	2.80	3.23	3.3	0.87	14.7	0.91	5.0	13.0	4.7	13.6	0.77
<i>Sicista napaea</i>	1	1.24	1.97	2.22	2.8	0.73	11.2	0.79	4.2	11.1	4.4	11.5	0.77
<i>Sicista subtilis</i>	4	1.16	1.81	2.12	2.4	0.71	10.4	0.87	4.3	10.0	4.2	10.8	0.69
Zapodinae													
<i>Eozapus setchuanus</i>	4	1.42	1.86	2.71	3.0	0.64	11.9	0.89	4.4	12.0	3.9	11.9	0.90
<i>Napaeozapus insignis</i>	4	1.46	2.35	2.80	3.6	0.70	13.2	0.88	4.5	12.7	4.6	12.9	1.05
<i>Zapus hudsonius</i>	4	1.29	2.04	2.66	3.0	0.70	12.1	0.94	4.3	12.0	4.6	11.9	0.86
<i>Zapus p. oregonus</i>	4	1.56	2.58	3.12	3.8	0.84	14.1	0.91	4.7	13.5	4.8	13.2	1.15
<i>Zapus p. pacificus</i>	1	na	na	na	na	na	na	0.95	5.2	14.0	5.2	13.1	1.00
<i>Zapus p. princeps</i>	3	1.61	2.50	3.01	3.4	0.91	14.2	0.98	5.2	13.6	5.1	13.3	0.97
<i>Zapus trinotatus</i>	4	1.54	1.92	3.06	3.4	0.84	13.0	0.92	4.3	12.7	4.9	12.4	0.96
Muroidea													
Calomyscidae													
Calomyscinae													
<i>Calomyscus baluchi</i>	4	1.71	2.31	3.40	3.0	0.80	15.2	1.13	5.4	14.2	5.7	14.6	0.75
<i>Calomyscus bailwardi</i>	3	1.64	2.61	3.44	3.2	0.81	15.4	1.13	5.4	13.4	5.2	14.3	0.81
Cricetidae													
Arvicolinae													
<i>Alticola strelzowi</i>	6	1.50	3.40	3.64	4.9	0.83	17.7	1.11	6.8	17.4	5.4	16.9	1.28
<i>Arvicola amphibius</i>	3	9.07	1.72	3.61	5.9	5.80	na	2.11	12.5	28.9	11.3	27.3	1.76
<i>Chionomys nivalis</i>	4	2.32	3.65	3.89	5.7	1.01	19.9	1.28	7.5	19.0	7.8	18.0	1.07
<i>Dicrostonyx groenlandicus</i>	4	1.77	3.72	4.97	6.3	1.16	21.4	1.37	7.0	21.2	9.0	19.9	2.06
<i>Ellotis talpinus</i>	4	3.04	5.36	4.51	6.3	1.24	24.2	1.53	11.5	23.6	7.5	22.1	1.59
<i>Eolagurus luteus</i>	5	2.62	4.43	4.32	6.8	1.14	na	1.32	7.9	21.4	9.1	20.2	1.55
<i>Eolagurus przewalskii</i>	1	2.38	4.28	4.62	5.6	0.94	22.4	1.60	7.7	21.1	10.1	20.3	1.63
<i>Eothenomys custos rubellus</i>	4	2.08	2.87	2.85	4.6	0.78	16.3	1.13	6.9	16.3	6.8	15.5	0.98
<i>Lagurus l. abacaneules</i>	1	2.08	1.50	3.35	4.4	0.81	15.8	1.25	5.3	16.0	7.0	15.8	1.19
<i>Lagurus l. agressus</i>	2	1.90	1.90	3.42	4.5	0.78	15.5	1.13	5.8	16.5	6.0	15.3	1.07
<i>Lagurus l. lagurus</i>	1	1.88	2.62	3.54	5.4	0.78	17.6	1.03	5.5	17.8	7.0	16.4	0.99
<i>Lasiopodomys mandarinus</i>	4	1.81	4.05	3.45	5.3	1.07	18.8	1.29	7.7	18.5	6.5	17.1	1.22
<i>Lemmus sibiricus</i>	4	2.94	5.26	5.28	7.9	1.69	23.8	1.79	9.0	26.0	11.2	23.1	1.57
<i>Microtus arvalis</i>	4	2.55	2.43	3.75	5.2	0.98	18.7	1.31	7.0	18.9	7.6	17.7	1.06
<i>Microtus californicus</i>	4	1.89	3.04	3.91	5.6	1.07	19.0	1.46	7.5	19.2	8.0	17.8	1.21
<i>Microtus chrotorrhinus</i>	4	1.98	3.92	3.60	5.6	1.08	19.5	1.15	6.8	17.4	7.5	17.2	1.22
<i>Microtus kikuchii</i>	4	2.50	3.63	3.79	5.8	1.18	19.8	1.42	8.0	19.8	8.3	18.3	1.18
<i>Microtus montanus</i>	3	2.34	4.39	4.16	6.2	1.14	21.5	1.22	8.4	20.6	7.6	18.7	1.15
<i>Microtus p. acadicus</i>	1	2.04	3.08	3.28	5.2	0.96	17.2	1.29	7.7	18.7	7.8	17.2	1.05
<i>Microtus p. pennsylvanicus</i>	3	2.11	3.89	3.72	6.0	1.07	19.0	1.23	7.1	18.4	7.5	17.2	0.89
<i>Microtus richardsoni</i>	1	2.47	na	4.33	5.7	1.04	na	1.21	na	na	2.0	8.5	1.21
<i>Myodes gapperi</i>	4	1.54	3.13	3.19	4.3	0.78	15.8	0.89	5.3	14.5	5.7	14.5	0.83
<i>Neodon irene</i>	4	1.73	3.31	3.29	4.7	0.87	16.8	1.02	6.8	16.5	5.9	15.8	1.17
<i>Neofiber allenii</i>	4	4.31	5.82	6.76	9.4	2.02	33.5	2.53	12.5	31.9	12.5	29.8	1.88
<i>Ondatra z. rivalicetus</i>	1	2.82	10.53	8.75	13.0	2.82	48.6	3.87	19.1	44.9	18.5	40.1	3.09
<i>Ondatra z. zibethicus</i>	2	5.57	8.72	8.73	12.4	2.63	44.3	3.28	16.9	45.0	17.5	41.5	3.31
<i>Phenacomys i. levis</i>	2	1.85	2.52	3.44	5.0	0.99	16.4	0.92	5.6	15.9	6.6	15.4	1.49
<i>Phenacomys i. oramoutis</i>	2	1.59	2.29	2.92	5.1	1.01	14.6	0.78	4.3	12.8	5.9	13.0	1.07
<i>Prometheomys schaposchnikowi</i>	4	3.10	4.56	4.13	6.6	1.60	23.9	1.81	9.3	23.5	8.8	22.4	2.03
<i>Synaptomyces c. cooperi</i>	1	2.57	2.32	3.73	4.9	1.03	17.1	1.47	5.7	18.7	8.1	16.7	0.82
<i>Synaptomyces c. gossii</i>	2	1.36	3.01	4.12	5.9	1.20	19.1	1.56	6.2	18.7	8.0	17.2	0.82
Cricetinae													
<i>Allocricetus e. curtatus</i>	5	2.44	3.68	4.62	4.0	0.85	18.9	1.51	7.4	18.9	5.4	18.0	1.40
<i>Allocricetus e. microdon</i>	2	2.13	4.22	4.64	4.2	0.74	19.9	1.43	7.8	18.2	5.6	18.2	1.18
<i>Cricetus b. barabensis</i>	4	1.53	2.89	3.76	3.2	0.61	15.3	1.05	5.6	14.4	4.8	14.1	0.89
<i>Cricetus b. griseus</i>	4	1.78	2.84	3.97	3.4	0.76	16.0	1.09	6.1	16.1	5.3	15.5	1.05
<i>Cricetus longicaudatus</i>	4	1.66	2.10	3.74	3.1	0.65	14.4	0.94	5.2	13.9	4.8	13.9	0.96
<i>Cricetus migratorius</i>	7	1.75	3.17	4.22	3.7	0.74	17.6	1.22	6.2	16.9	5.8	16.3	1.13
<i>Cricetus c. canescens</i>	2	3.82	5.42	7.13	7.0	1.18	na	2.20	11.0	28.6	10.2	27.2	2.07
<i>Cricetus c. cricetus</i>	2	3.30	7.66	7.19	7.0	1.32	32.7	2.31	12.3	31.0	10.7	29.5	2.47
<i>Mesocricetus auratus</i>	3	3.59	4.12	6.35	5.4	1.05	23.8	1.97	9.1	24.6	8.6	22.8	1.47
<i>Phodopus campbelli</i>	4	1.77	2.25	3.67	3.1	0.76	14.8	1.15	4.8	14.6	4.7	14.3	1.06
<i>Phodopus roborovskii</i>	4	1.44	1.68	3.08	2.9	0.69	12.0	0.90	4.1	12.0	3.6	12.0	0.98
<i>Phodopus sungorus</i>	4	1.64	2.31	3.33	2.9	0.63	13.6	0.98	4.2	13.3	4.2	13.0	1.05
Neotominae													
<i>Baiomys musculus</i>	3	1.35	2.16	2.12	2.7	0.57	11.5	0.94	3.6	10.1	4.0	10.5	0.63
<i>Habromys lepturus</i>	4	1.86	3.46	3.37	4.6	0.94	18.1	1.22	6.1	17.0	5.9	17.2	1.34
<i>Hodomys allenii</i>	4	3.66	4.99	6.56	9.2	1.89	32.3	1.96	9.3	30.0	13.2	28.2	2.82
<i>Isthmomys pirrensis</i>	4	2.90	6.37	4.96	5.9	1.30	26.6	2.86	6.0	19.9	5.6	13.2	8.29
<i>Megadontomys thomasi</i>	4	2.63	5.01	3.88	5.8	1.33	na	1.45	7.0	20.9	7.6	21.1	1.43
<i>Neotoma albigenula</i>	4	3.96	5.21	5.60	7.3	1.62	29.6	2.07	9.3	25.3	11.6	27.0	2.50
<i>Neotoma bryanti</i>	4	2.91	4.44	4.56	7.3	1.48	25.1	1.69	8.0	25.6	9.9	26.0	2.16
<i>Neotoma cinerea</i>	2	3.40	5.44	6.51	7.6	1.64	na	2.01	10.6	29.6	10.7	29.4	2.84
<i>Neotoma devia</i>	4	2.85	4.11	4.33	6.5	1.36	23.8	2.22	7.6	18.3	9.2	17.7	9.92
<i>Neotoma floridana</i>	3	4.08	5.03	6.94	7.9	1.71	na	2.19	10.0	30.1	11.2	30.1	2.68
<i>Neotoma goldmani</i>	4	2.67	4.29	5.02	6.7	1.49	24.7	1.62	7.7	23.7	9.4	23.7	1.91

Table E.6—continued.

	#	LIW	IL	JDL	JML	JMW	TJL	JID	IL2	JLS	MAM	JLB	JMH
<i>Neotoma lepida</i>	4	3.32	4.82	5.27	7.1	1.54	27.7	1.81	8.9	26.4	10.6	26.3	2.15
<i>Neotoma mexicana</i>	4	2.86	4.90	5.74	7.5	1.49	29.4	1.75	9.3	26.3	10.1	25.9	2.68
<i>Neotomodon alstoni</i>	4	2.20	4.08	3.88	5.3	1.30	20.5	1.17	6.3	18.2	6.5	18.4	1.32
<i>Ochrotomys nuttalli</i>	3	1.38	2.30	3.19	3.3	0.81	14.8	1.20	5.3	14.4	5.1	14.6	0.81
<i>Onychomys l. arcticeps</i>	2	2.19	3.17	3.63	4.5	1.15	17.1	1.28	6.4	17.1	5.9	17.2	1.37
<i>Onychomys l. breviauritus</i>	1	1.81	2.27	3.43	3.9	1.18	15.7	1.15	5.4	15.9	5.4	15.4	1.14
<i>Onychomys l. ruidosae</i>	3	2.01	3.05	4.03	4.6	1.16	18.6	1.24	5.1	15.6	5.6	15.9	1.12
<i>Onychomys torridus</i>	4	1.40	2.45	2.78	3.1	0.85	13.3	0.97	4.8	13.1	4.4	13.2	0.90
<i>Osgoodomys banderanus</i>	4	1.67	3.33	3.35	4.1	1.10	17.4	1.14	5.7	15.9	5.4	15.8	0.88
<i>Peromyscus a. hylocetes</i>	3	2.17	4.31	4.22	4.9	1.12	20.7	1.25	6.9	19.1	6.7	18.6	1.26
<i>Peromyscus a. oaxacensis</i>	1	1.74	3.08	3.60	4.2	1.07	17.3	1.35	6.2	17.7	6.1	18.4	1.29
<i>Peromyscus b. levipes</i>	3	1.92	3.24	3.59	4.3	1.05	17.5	1.30	5.9	16.1	6.2	16.1	1.08
<i>Peromyscus b. rowleyi</i>	1	1.66	3.02	4.11	4.4	1.48	19.4	1.20	5.2	15.7	5.9	16.7	1.22
<i>Peromyscus californicus</i>	1	1.56	2.50	3.45	3.8	0.86	16.5	1.32	5.5	15.7	5.8	16.4	0.94
<i>Peromyscus c. auripectus</i>	1	1.22	2.26	2.60	3.1	0.81	13.3	1.08	5.4	13.3	5.3	13.9	0.98
<i>Peromyscus c. pergracilis</i>	3	1.37	2.59	3.41	3.6	0.93	15.4	1.15	5.1	13.7	5.1	14.3	0.92
<i>Peromyscus eremicus</i>	4	1.73	2.17	2.90	3.5	0.87	14.7	1.12	4.9	13.8	5.6	14.1	0.91
<i>Peromyscus fraterculus</i>	4	1.42	2.44	3.08	3.6	0.96	15.1	0.95	4.7	13.1	4.9	13.5	0.77
<i>Peromyscus leucopus</i>	4	1.53	2.75	2.97	3.2	0.72	15.1	1.15	5.6	14.5	5.3	15.0	0.94
<i>Peromyscus m. abietorum</i>	1	1.23	2.24	3.02	2.7	0.71	13.0	0.93	5.5	14.9	5.3	15.4	0.87
<i>Peromyscus m. gambelii</i>	2	1.64	2.72	3.89	3.5	0.91	16.4	0.94	5.3	14.8	4.7	15.2	0.95
<i>Peromyscus m. gracilis</i>	1	1.70	2.29	3.78	3.1	0.83	15.3	0.95	4.8	13.8	4.5	14.2	0.90
<i>Peromyscus merriami</i>	4	1.62	2.47	2.92	3.5	0.89	14.7	1.09	4.5	13.6	5.0	13.8	0.73
<i>Peromyscus m. nudipes</i>	1	1.87	3.61	3.91	4.1	0.99	18.5	1.27	6.9	19.5	6.8	19.6	1.27
<i>Peromyscus m. saxatilis</i>	3	1.98	3.59	3.94	4.5	1.09	19.5	1.36	6.6	18.7	6.9	18.5	1.06
<i>Peromyscus pectoralis</i>	4	1.45	2.57	2.75	3.3	0.74	14.2	0.94	4.5	13.1	4.8	13.5	0.78
<i>Peromyscus p. allophrys</i>	1	1.11	1.53	2.47	2.4	0.61	10.7	0.87	4.3	12.1	4.1	12.5	0.83
<i>Peromyscus p. subgriseus</i>	3	1.36	1.95	2.88	2.8	0.82	13.2	0.98	4.6	12.7	4.7	13.1	0.95
<i>Reithrodontomys creper</i>	4	1.99	3.53	3.39	4.3	1.05	17.8	0.99	5.0	14.2	4.9	14.3	0.90
<i>Reithrodontomys f. chiapensis</i>	1	1.46	2.31	2.42	3.1	0.69	13.2	0.89	4.8	11.7	4.5	12.7	0.82
<i>Reithrodontomys f. difficilis</i>	1	1.34	2.44	2.35	3.2	0.73	12.5	0.93	4.0	11.3	4.4	11.4	0.56
<i>Reithrodontomys f. helvolus</i>	1	1.37	1.72	2.58	2.5	0.70	11.3	1.09	4.4	12.7	4.7	13.0	0.82
<i>Reithrodontomys f. intermedius</i>	1	1.60	2.08	2.96	3.2	0.74	13.7	0.93	4.0	11.7	4.7	12.2	0.71
<i>Reithrodontomys gracilis</i>	3	1.37	2.03	2.25	2.7	0.68	11.6	0.94	4.6	11.3	4.4	11.6	0.62
<i>Reithrodontomys megalotis</i>	7	1.42	1.68	2.54	2.8	0.69	11.7	0.85	3.8	10.9	4.3	11.2	0.77
<i>Scotinomys teguina</i>	3	1.52	2.16	2.61	3.5	0.88	13.0	0.95	4.9	13.6	4.5	13.6	0.97
<i>Xenomys nelsoni</i>	2	2.81	4.27	5.50	7.7	1.59	25.0	1.65	8.1	25.3	11.9	24.4	2.14
Sigmodontinae													
<i>Abrothrix andinus</i>	4	1.31	2.52	2.50	3.3	0.70	13.3	0.91	4.0	11.2	4.6	11.9	0.64
<i>Abrothrix longipilis</i>	4	1.73	2.66	2.96	4.1	0.79	16.1	1.16	4.4	13.8	5.3	15.5	0.93
<i>Aegialomys xanthaeolus</i>	4	2.25	3.20	3.41	4.4	1.00	18.7	1.45	6.1	17.2	6.7	17.1	0.99
<i>Akodon aerosus</i>	4	1.81	3.52	3.18	4.3	0.84	17.6	1.11	6.1	17.2	5.8	17.3	0.98
<i>Akodon boliviensis</i>	3	1.55	2.78	2.91	3.7	0.81	15.2	0.92	5.2	14.3	4.9	14.3	0.96
<i>Akodon iniscatus</i>	4	1.71	3.24	2.57	3.8	0.87	15.2	0.98	4.7	13.5	4.9	13.6	0.91
<i>Akodon kofordi</i>	4	1.48	2.86	3.12	3.7	0.71	15.0	0.91	4.1	13.4	4.5	13.8	0.97
<i>Akodon lutescens</i>	1	1.11	2.47	2.35	3.0	0.58	11.5	0.81	4.5	12.2	3.8	11.8	0.94
<i>Akodon mimus</i>	3	1.48	3.22	3.37	4.5	0.95	17.1	0.99	5.4	16.3	4.7	16.2	1.26
<i>Akodon molinae</i>	1	1.80	3.15	3.09	3.8	0.86	16.7	1.20	6.1	15.7	5.3	16.5	1.06
<i>Akodon spegazzinii</i>	4	1.52	2.85	2.96	3.9	0.77	15.5	1.04	5.1	15.0	4.8	15.1	1.10
<i>Akodon torques</i>	4	1.54	3.07	3.02	3.9	0.83	15.9	0.88	5.3	14.9	4.4	15.0	0.96
<i>Andalgalomys pearsoni</i>	4	1.79	3.03	3.54	3.9	1.04	17.7	1.29	5.6	16.3	6.3	16.4	0.92
<i>Andinomys edax</i>	5	3.08	3.97	4.10	6.1	1.41	21.4	1.55	7.2	22.0	8.6	21.7	1.88
<i>Auliscomys sublimis</i>	4	1.74	2.48	3.20	4.3	0.95	15.3	0.90	3.9	14.8	5.5	14.2	1.12
<i>Brucepattersonius igniventris</i>	2	1.57	2.75	3.01	3.7	0.79	14.3	0.86	5.0	14.1	4.6	14.4	1.05
<i>Brucepattersonius soricinus</i>	2	1.53	3.47	3.09	4.3	0.79	16.3	0.84	5.0	13.6	5.0	13.4	1.02
<i>Calomys callosus</i>	7	1.95	2.69	2.99	3.5	0.85	15.5	1.16	5.2	15.1	5.7	14.5	1.03
<i>Calomys lepidus</i>	4	1.40	2.40	2.49	3.4	0.72	13.3	0.97	4.1	12.0	4.8	12.3	0.87
<i>Calomys musculinus</i>	4	1.34	1.76	2.59	2.9	0.69	11.8	0.89	3.4	11.2	4.6	10.9	0.68
<i>Calomys venustus</i>	1	2.18	3.55	4.12	4.7	1.11	19.8	1.28	5.4	16.3	6.2	15.4	1.04
<i>Cerradomys subflavus</i>	4	2.20	4.13	4.26	4.5	1.02	21.1	1.59	7.0	20.5	8.0	19.8	1.11
<i>Chelemys macronyx</i>	4	2.31	4.04	3.50	5.2	1.16	20.2	1.23	6.5	18.8	7.1	18.4	1.25
<i>Chinchillula sahamae</i>	4	2.23	5.26	4.75	6.3	1.60	26.0	1.67	9.1	24.6	10.7	24.4	1.69
<i>Delomys d. collinus</i>	2	1.79	3.50	3.65	4.6	0.96	18.7	1.29	5.7	18.5	6.7	17.7	1.41
<i>Delomys d. dorsalis</i>	2	2.07	3.72	3.81	4.2	0.94	18.0	1.23	6.4	18.1	6.9	17.5	0.96
<i>Deltamys kempi</i>	4	1.49	3.42	3.03	3.6	0.74	15.1	0.95	5.9	15.3	4.7	14.6	0.98
<i>Eligmodontia moreni</i>	3	1.42	1.99	2.42	3.3	0.89	12.5	0.88	4.3	12.7	5.2	12.4	0.86
<i>Eligmodontia morganii</i>	4	1.60	2.67	2.54	3.4	0.81	13.8	0.95	4.7	13.2	5.1	13.1	0.88
<i>Eligmodontia typus</i>	8	1.57	2.18	2.88	3.3	0.70	14.0	0.95	4.5	13.2	5.2	13.1	0.98
<i>Euneomys c. chinchilloides</i>	3	2.89	1.84	3.81	5.3	1.32	20.5	1.36	6.0	19.6	8.9	19.0	1.42
<i>Euneomys c. sublimis</i>	1	2.16	2.41	2.96	5.0	1.05	16.7	1.15	4.3	17.0	7.7	16.3	1.19
<i>Geoxus valdivianus</i>	4	1.62	2.99	3.24	3.1	0.65	15.6	0.81	4.5	14.2	5.2	14.5	0.84
<i>Graomys edithae</i>	1	1.53	2.31	3.50	4.1	1.08	16.4	1.21	5.6	15.9	5.9	15.9	1.26
<i>Graomys griseoflavus</i>	7	2.26	3.43	3.84	4.7	1.30	20.2	1.45	6.5	18.9	8.0	18.8	1.18
<i>Holochilus brasiliensis</i>	4	3.59	5.03	4.86	6.3	1.69	na	1.93	9.3	25.8	10.5	23.3	1.12
<i>Holochilus sciureus</i>	3	3.58	5.11	5.16	6.5	1.64	na	2.15	10.0	27.2	10.4	24.4	1.28
<i>Ichthyomys stolzmanni</i>	1	1.93	3.21	4.59	3.1	1.07	18.5	1.39	6.4	19.1	5.5	17.0	1.02

Table E.6—continued.

	#	LIW	IL	JDL	JML	JMW	TJL	JID	IL2	JLS	MAM	JLB	JMH
<i>Irenomys tarsalis tarsalis</i>	4	1.85	3.27	2.88	4.5	0.96	16.6	1.04	5.2	15.0	5.9	14.8	1.08
<i>Juliomys pictipes</i>	4	1.39	2.65	2.53	3.4	0.73	14.2	1.15	4.7	13.8	5.5	13.6	0.82
<i>Kunsia tomentosus</i>	4	4.87	6.80	7.06	9.6	2.54	37.8	2.94	12.1	37.3	15.6	34.3	2.28
<i>Lenoxus apicalis apicalis</i>	4	1.95	4.47	4.13	5.3	1.13	21.1	1.14	6.3	19.4	5.4	19.3	1.32
<i>Loxodontomys micropus</i>	4	2.24	3.22	3.59	5.3	1.11	18.5	1.29	5.7	17.7	7.0	16.7	1.25
<i>Melanomys c. chrysomelas</i>	3	1.75	4.52	2.96	4.5	1.11	18.4	1.36	7.2	17.9	6.8	16.9	1.10
<i>Melanomys c. ssp</i>	1	1.91	4.24	3.36	4.5	1.00	18.6	1.31	7.0	18.2	6.3	17.9	1.24
<i>Microryzomys m. azoricus</i>	1	1.19	1.81	2.18	2.6	0.57	10.8	0.75	3.2	8.9	4.2	9.9	0.64
<i>Microryzomys m. soricinus</i>	2	1.38	1.61	1.89	2.4	0.50	9.1	0.64	2.9	8.6	3.2	8.6	0.55
<i>Microryzomys m. ssp</i>	1	1.04	2.09	1.70	2.6	0.59	10.3	0.78	3.6	9.8	4.1	10.0	0.53
<i>Neacomys spinosus</i>	4	1.38	2.38	2.41	2.9	0.66	12.8	0.98	4.3	12.2	4.7	12.3	0.62
<i>Necromys amoenus</i>	4	1.91	4.40	2.74	3.9	0.85	17.5	1.11	5.5	15.5	5.5	15.7	0.94
<i>Nectomys apicalis</i>	4	3.31	5.46	5.74	7.6	1.76	29.4	2.26	9.7	27.8	10.2	27.2	1.83
<i>Nectomys s. palmipes</i>	1	3.38	4.42	5.42	6.0	1.46	na	1.81	8.3	25.0	9.6	23.0	1.35
<i>Nectomys s. pollens</i>	1	3.27	4.92	5.46	6.2	1.70	na	2.31	10.1	26.9	9.6	25.6	1.99
<i>Nectomys s. ssp</i>	1	3.38	6.29	6.55	6.3	1.65	na	2.24	11.5	29.4	10.3	28.0	1.75
<i>Neotomys eriosos</i>	5	3.19	2.19	3.11	5.0	1.32	17.5	1.29	4.7	16.1	8.6	16.4	1.11
<i>Nephelomys keaysi</i>	4	2.11	4.11	3.57	5.1	0.99	19.9	1.56	6.9	19.7	7.3	18.4	1.22
<i>Nephelomys levipes</i>	4	2.69	4.23	4.54	5.6	1.44	na	1.81	8.4	22.5	8.5	21.4	1.51
<i>Notiomys edwardsii</i>	1	1.40	2.73	2.67	2.8	0.74	13.1	1.02	4.1	12.3	4.1	12.4	0.47
<i>Oecomys bicolor</i>	3	1.71	3.01	3.39	4.1	0.87	17.2	1.16	5.1	14.8	6.2	15.4	0.74
<i>Oecomys concolor</i>	2	1.85	3.16	3.53	4.6	1.06	17.8	1.49	6.2	17.9	6.8	18.3	1.21
<i>Oecomys superans</i>	4	1.98	4.65	3.94	5.4	1.13	22.4	1.73	7.8	21.2	7.7	20.6	1.46
<i>Oligoryzomys fulvescens</i>	3	1.31	1.93	2.47	2.7	0.72	11.9	0.90	4.2	11.0	4.2	11.4	0.66
<i>Oligoryzomys longicaudatus</i>	4	1.44	2.40	2.89	3.2	0.86	13.9	1.21	4.9	14.3	5.3	14.1	0.83
<i>Oligoryzomys microtis</i>	4	1.37	2.06	2.53	2.8	0.70	12.4	1.01	4.4	12.6	4.6	12.7	0.71
<i>Oryzomys couesi</i>	3	1.98	3.21	3.39	4.4	1.05	18.0	1.33	5.8	17.0	5.6	16.3	1.01
<i>Oryzomys palustris</i>	4	2.04	3.48	3.71	4.2	1.08	18.7	1.37	6.9	17.7	6.3	17.9	1.04
<i>Oxymycterus hiska</i>	4	1.50	2.95	3.38	4.5	1.17	16.7	0.98	4.7	15.4	4.9	15.4	1.16
<i>Oxymycterus nasutus</i>	4	2.07	3.61	4.33	4.8	1.08	20.5	1.12	5.9	19.9	5.4	19.8	1.34
<i>Phyllotis amicus</i>	6	1.56	2.29	2.82	3.5	1.05	14.4	1.10	4.5	13.5	5.6	14.1	0.92
<i>Phyllotis andium</i>	4	1.49	2.91	3.09	3.9	0.97	15.3	1.03	4.6	14.8	5.6	14.7	0.91
<i>Phyllotis caprinus</i>	2	2.26	3.37	3.80	5.1	1.33	19.7	1.47	6.8	19.5	7.9	19.2	1.20
<i>Phyllotis darwini</i>	4	1.07	3.36	4.21	4.5	1.36	19.8	1.45	6.7	19.0	7.7	19.2	1.49
<i>Phyllotis gerbillus</i>	4	1.37	2.71	2.69	3.2	1.02	13.8	1.04	4.9	13.1	4.9	13.3	0.81
<i>Phyllotis magister</i>	2	2.34	3.55	4.40	4.9	1.58	20.2	1.41	6.4	19.7	8.3	19.5	1.46
<i>Phyllotis osilae</i>	4	2.04	2.64	3.58	4.2	1.25	17.4	1.17	5.9	17.7	6.5	17.4	1.28
<i>Phyllotis xanthopygus</i>	4	2.44	4.13	3.94	4.8	1.27	21.2	1.47	7.5	19.6	8.0	20.0	1.45
<i>Pseudoryzomys simplex</i>	4	2.10	3.22	4.03	4.6	1.18	19.2	1.45	5.8	18.4	7.0	17.2	1.12
<i>Punomys kofordi</i>	3	2.61	4.08	3.52	6.1	1.53	21.7	1.49	6.8	20.1	8.3	20.0	1.77
<i>Reithrodon a. auritus</i>	4	1.79	3.42	3.88	5.8	1.21	20.9	1.23	5.9	21.3	7.8	20.2	1.41
<i>Reithrodon a. physodes</i>	4	2.50	3.76	4.08	2.6	1.15	18.2	1.19	4.6	17.9	7.6	17.2	1.21
<i>Rhagomys longilingua</i>	1	2.33	3.67	3.00	3.9	1.10	18.1	1.31	6.9	16.7	6.6	17.5	0.83
<i>Rheomys t. stutoni</i>	2	1.52	4.29	2.71	3.9	1.15	17.7	1.21	6.6	16.6	5.4	16.2	1.15
<i>Rheomys t. thomasi</i>	2	1.43	3.34	2.70	4.0	1.01	15.9	1.01	5.6	15.1	5.2	14.9	1.04
<i>Rhipidomys macconnelli</i>	4	2.00	3.07	3.22	4.7	1.13	17.8	1.36	5.4	16.6	6.6	16.7	1.21
<i>Rhipidomys nitela</i>	4	2.25	3.57	3.95	4.8	1.19	18.1	1.52	6.3	19.4	7.5	19.6	1.20
<i>Scapteromys tumidus</i>	4	2.52	4.74	4.66	6.6	1.57	25.7	1.51	8.0	24.4	8.1	23.3	1.55
<i>Scolomys melanops</i>	1	1.20	2.82	2.33	2.3	0.50	12.4	0.87	5.2	13.2	4.2	12.3	0.53
<i>Scolomys ucalensis</i>	4	1.40	2.28	3.37	2.6	0.64	13.4	0.93	4.2	12.6	4.5	13.0	0.62
<i>Sigmodon alstoni</i>	4	2.75	3.59	3.45	5.3	1.17	19.8	1.59	6.8	19.8	8.5	18.5	1.34
<i>Sigmodon arizonae</i>	4	3.07	5.04	3.85	6.4	1.50	23.6	1.76	8.2	23.8	9.3	21.6	1.41
<i>Sigmodon fulviventer</i>	4	2.90	3.86	3.58	5.6	1.46	21.1	1.56	7.6	21.7	8.7	20.5	1.43
<i>Sigmodon hispidus</i>	3	2.98	3.98	3.82	5.6	1.35	na	1.92	7.9	23.3	8.9	21.6	1.74
<i>Sigmodon ochrognathus</i>	4	2.62	3.77	3.64	5.5	1.31	19.9	1.50	7.4	20.8	8.2	19.3	1.46
<i>Sigmodontomys alfaroi</i>	4	2.85	4.54	4.47	5.2	1.33	22.1	1.91	8.7	22.9	8.8	22.2	1.63
<i>Sooretamys angouya</i>	3	2.34	3.07	4.21	5.0	1.13	19.3	1.65	6.8	20.1	7.7	19.7	1.20
<i>Thaptomys nigrita</i>	4	1.58	3.51	3.11	3.3	0.78	16.0	1.08	5.9	15.2	5.4	15.1	0.90
<i>Thomasomys aureus</i>	4	2.42	5.12	3.28	6.6	1.50	22.4	1.59	8.1	23.3	9.1	21.5	1.71
<i>Thomasomys daphne</i>	4	1.76	2.96	3.62	3.8	0.97	16.8	1.07	6.1	16.1	5.6	16.0	1.06
<i>Thomasomys notatus</i>	4	1.50	2.93	3.35	3.8	0.89	16.5	1.38	6.3	16.9	6.3	17.0	0.94
<i>Transandinomys talamancae</i>	4	1.54	3.40	3.29	4.3	0.94	17.7	1.30	6.2	17.7	6.6	16.8	1.12
<i>Wiedomys pyrrhorhinus</i>	3	1.79	3.12	3.11	4.1	0.95	17.1	1.35	7.3	16.4	6.9	16.1	0.99
<i>Zygodontomys brevicauda</i>	3	1.68	3.27	3.86	4.0	0.98	18.3	1.37	6.3	17.4	6.1	17.0	1.15
Tylomyinae													
<i>Nyctomys sumichrasti</i>	5	2.42	3.36	3.75	4.4	1.07	19.3	1.49	6.8	17.9	7.2	18.3	1.14
<i>Ototylomys phyllostis</i>	3	2.93	3.82	5.42	6.5	1.61	na	1.64	7.1	24.7	10.2	23.5	1.86
<i>Tylomys nudicaudus</i>	5	2.75	4.78	5.43	7.7	1.71	26.7	3.43	12.4	20.3	10.3	24.1	2.02
Muridae													
Deomyinae													
<i>Acomys cahirinus</i>	7	1.53	2.89	3.25	3.4	0.87	16.2	1.13	5.4	14.8	5.8	15.4	0.96
<i>Acomys cinereus</i>	4	1.78	3.00	3.45	3.5	0.91	16.4	1.05	5.1	14.4	5.4	14.8	0.90
<i>Acomys dimidiatus</i>	1	1.55	3.57	3.18	3.5	1.01	18.1	1.28	6.0	15.7	6.9	16.0	0.81
<i>Acomys ignitus</i>	4	1.59	3.02	3.35	3.5	0.87	16.5	1.17	5.1	11.6	5.1	11.4	5.20
<i>Acomys percivali</i>	4	1.67	3.01	3.36	3.8	1.03	17.0	1.03	4.9	14.6	5.5	15.0	0.99
<i>Acomys russatus</i>	4	2.14	2.93	3.65	4.4	1.23	18.4	1.31	5.3	15.3	6.0	15.7	0.96

Table E.6—continued.

	#	LIW	IL	JDL	JML	JMW	TJL	JID	IL2	JLS	MAM	JLB	JMH
<i>Acomys spinosissimus</i>	4	1.87	2.46	3.22	3.5	1.01	15.6	0.99	5.5	13.9	5.6	14.9	0.99
<i>Acomys wilsoni</i>	4	1.53	2.73	2.96	3.7	0.92	15.9	0.95	4.4	14.1	5.3	14.5	0.93
<i>Deomys ferrugineus</i>	4	2.28	3.78	5.53	5.4	1.19	22.4	1.21	6.1	22.1	6.4	21.1	1.76
<i>Lophuromys f. flavopunctatus</i>	3	1.30	3.61	4.30	4.0	0.88	19.0	1.02	6.5	18.7	5.9	18.0	1.12
<i>Lophuromys f. zaphiri</i>	1	2.31	4.68	4.34	5.0	1.27	22.6	1.25	7.7	22.5	7.4	21.7	1.53
<i>Lophuromys f. zena</i>	4	1.94	3.63	4.05	3.9	0.93	18.6	1.13	6.2	18.3	5.9	17.7	1.15
<i>Lophuromys sikapusi</i>	4	1.59	3.92	3.95	4.5	1.06	19.9	1.24	6.2	18.8	5.6	18.3	1.39
<i>Uranomys ruddi</i>	4	1.80	3.70	4.15	3.7	1.06	19.0	1.25	6.7	18.5	6.5	18.1	0.97
Gerbilinae													
<i>Ammodillus imbellis</i>	1	1.04	2.42	3.37	3.4	0.87	16.7	1.09	4.9	13.4	7.5	16.4	0.94
<i>Brachionomys przewalskii</i>	1	1.98	2.73	3.32	3.1	0.93	16.0	0.99	4.8	13.1	5.7	13.4	0.60
<i>Desmodillus braueri</i>	6	1.16	1.83	2.77	2.3	0.62	12.2	0.82	3.9	11.5	5.2	11.4	0.92
<i>Desmodillus auricularis</i>	8	1.85	3.90	5.02	3.6	1.14	21.2	1.53	6.3	19.1	8.7	19.4	1.14
<i>Dipodillus campestris</i>	4	1.51	2.52	3.21	3.2	0.99	15.3	1.12	5.3	15.1	6.3	14.9	0.76
<i>Dipodillus dasyurus</i>	4	1.43	2.47	3.78	3.7	1.14	17.4	1.17	4.4	13.8	6.2	14.3	0.85
<i>Dipodillus harwoodi</i>	4	1.32	2.16	3.01	3.1	0.95	14.2	0.98	4.5	12.5	5.5	13.2	0.83
<i>Dipodillus lowei</i>	2	1.45	2.72	3.13	3.2	0.92	15.3	1.13	5.3	16.4	6.6	15.7	0.93
<i>Dipodillus mackilligini</i>	1	1.63	3.25	4.10	3.8	1.17	18.1	1.23	5.1	15.1	5.8	14.8	1.09
<i>Dipodillus magharebi</i>	6	1.95	2.96	4.44	3.7	1.18	18.6	1.42	6.2	17.6	7.2	16.9	1.05
<i>Dipodillus simoni</i>	4	1.27	2.17	3.10	3.0	0.85	13.8	0.95	4.4	12.3	5.3	12.8	0.82
<i>Dipodillus stigmonyx</i>	4	1.45	2.20	3.07	3.0	0.91	14.5	0.88	4.1	12.2	5.5	12.2	0.78
<i>Gerbilliscus afra</i>	4	2.51	4.39	4.96	5.2	1.72	24.9	1.56	6.7	22.9	8.1	21.4	1.54
<i>Gerbilliscus boehmi</i>	4	1.77	4.33	5.81	5.6	1.92	26.8	1.77	7.8	25.9	8.8	24.5	1.53
<i>Gerbilliscus b. brantsii</i>	4	2.59	3.75	4.74	4.9	1.79	24.7	1.75	6.7	23.6	9.8	22.3	1.40
<i>Gerbilliscus b. humpatensis</i>	2	2.62	4.20	5.64	5.5	1.79	26.8	1.48	7.2	23.7	9.1	22.8	1.65
<i>Gerbilliscus b. perpallidus</i>	4	2.50	3.05	4.66	4.6	1.64	19.9	1.61	6.3	21.2	8.1	20.3	1.22
<i>Gerbilliscus guineae</i>	4	2.05	3.90	5.29	4.7	1.52	23.4	1.35	7.2	22.6	8.5	21.8	1.20
<i>Gerbilliscus inclusus</i>	4	2.66	4.52	5.58	5.5	1.82	25.3	1.69	8.6	25.1	8.8	23.1	1.33
<i>Gerbilliscus kempti</i>	4	2.49	4.65	5.73	5.1	1.72	24.7	1.68	8.1	24.5	9.1	23.7	1.55
<i>Gerbilliscus leucogaster</i>	4	2.15	3.34	4.46	4.8	1.74	22.8	1.56	6.4	22.1	8.3	20.6	1.24
<i>Gerbilliscus nigricaudus</i>	4	1.87	3.73	5.04	4.8	1.58	23.4	1.44	7.1	22.8	8.8	21.7	1.44
<i>Gerbilliscus phillipsi</i>	4	2.15	3.98	5.14	5.3	1.65	24.3	1.62	6.9	24.6	9.9	23.1	1.48
<i>Gerbilliscus robustus</i>	4	2.24	3.09	5.54	5.4	1.73	24.9	1.49	5.7	23.3	9.1	22.5	1.49
<i>Gerbilliscus validus</i>	4	2.49	4.34	5.00	5.5	2.00	25.7	1.87	7.9	26.6	9.7	25.0	1.53
<i>Gerbillurus paeba</i>	4	1.50	2.53	3.34	3.4	1.09	16.3	1.20	5.0	15.5	6.3	14.7	0.84
<i>Gerbillurus setzeri</i>	4	1.20	2.31	3.32	3.7	1.14	17.1	1.05	4.3	15.9	7.8	16.3	1.08
<i>Gerbillurus tytonis</i>	4	1.48	2.64	3.62	3.5	1.24	17.3	1.15	5.5	15.9	7.0	15.8	0.97
<i>Gerbillurus vallinus</i>	4	1.56	2.74	3.38	3.5	1.05	16.4	1.06	4.4	14.6	7.2	15.2	0.87
<i>Gerbillus agag</i>	4	1.68	2.69	3.29	3.4	1.18	16.2	1.05	4.3	13.9	6.2	14.1	1.00
<i>Gerbillus amoenus</i>	4	1.21	2.18	2.92	2.8	0.85	13.6	1.03	4.3	12.6	6.1	12.6	0.71
<i>Gerbillus andersoni</i>	4	1.87	2.68	3.62	2.8	0.80	17.1	1.10	4.8	14.7	6.4	15.0	0.98
<i>Gerbillus aquilus</i>	4	1.38	2.44	3.88	3.3	1.07	16.7	1.10	5.2	15.8	6.7	15.6	1.02
<i>Gerbillus cheesmani</i>	4	1.38	2.30	4.17	3.2	1.04	16.7	1.10	4.5	14.9	6.6	15.2	0.95
<i>Gerbillus famulus</i>	4	1.37	2.10	3.15	2.7	0.85	14.1	0.97	4.7	13.8	6.5	13.6	0.86
<i>Gerbillus floweri</i>	4	1.61	2.75	4.13	3.4	1.15	18.3	1.41	5.7	18.0	7.6	18.1	1.15
<i>Gerbillus garamantis</i>	1	1.23	2.02	3.30	3.0	0.83	14.3	1.14	4.5	13.6	6.1	13.6	0.86
<i>Gerbillus gerbillus</i>	6	1.31	2.57	3.40	3.1	0.87	15.9	1.04	4.9	14.4	6.5	14.8	0.85
<i>Gerbillus gleadowi</i>	4	1.59	2.41	3.61	3.3	1.12	16.1	1.13	4.8	14.5	6.2	14.6	1.19
<i>Gerbillus henleyi</i>	4	1.17	1.84	2.50	2.5	0.82	12.0	0.86	3.7	11.1	5.3	11.4	0.64
<i>Gerbillus hesperinus</i>	4	1.33	2.52	3.17	3.3	1.01	15.9	1.17	5.1	15.5	6.5	15.3	0.92
<i>Gerbillus hoogstraali</i>	4	1.61	2.69	3.45	3.6	1.13	16.7	1.03	4.6	14.2	6.0	14.0	0.99
<i>Gerbillus latastei</i>	4	1.56	2.19	3.24	3.0	0.99	15.2	1.13	5.1	15.6	6.9	15.8	1.10
<i>Gerbillus mauritaniae</i>	4	1.52	2.80	3.70	3.5	1.16	17.4	0.81	3.0	10.2	4.5	10.1	0.73
<i>Gerbillus mesopotamiae</i>	4	1.48	2.68	3.40	3.1	0.94	15.6	1.08	5.1	14.5	6.1	14.2	0.88
<i>Gerbillus muriculus</i>	4	1.13	1.78	2.66	2.6	0.80	11.7	0.85	3.6	11.2	5.0	11.5	0.75
<i>Gerbillus nanus</i>	6	1.31	2.28	3.11	3.0	1.02	14.3	1.06	3.9	12.8	6.3	13.2	0.78
<i>Gerbillus nigeriae</i>	2	1.81	2.72	3.39	3.1	0.98	15.8	1.14	5.1	14.0	6.4	14.6	1.00
<i>Gerbillus occiduus</i>	1	1.68	2.72	3.51	3.2	1.19	16.7	1.33	5.0	15.6	6.9	15.4	1.03
<i>Gerbillus perpallidus</i>	4	1.81	2.85	3.96	3.7	1.30	18.3	1.33	5.7	17.1	7.6	17.4	1.11
<i>Gerbillus poecilops</i>	4	1.58	2.82	3.94	2.7	0.88	17.0	1.29	5.9	16.1	6.8	15.6	0.93
<i>Gerbillus pulvinatus</i>	4	1.49	2.55	3.89	3.5	1.16	16.9	1.13	4.8	15.7	6.5	15.2	0.99
<i>Gerbillus pusillus</i>	4	1.29	2.03	2.70	2.8	0.80	13.1	1.02	4.0	11.7	5.3	12.0	0.73
<i>Gerbillus pyramidum</i>	4	1.38	3.48	4.17	3.8	1.26	19.7	1.40	6.2	18.8	8.1	18.6	1.31
<i>Gerbillus tarabuli</i>	4	1.63	2.89	3.98	3.4	1.08	17.7	1.45	6.3	18.3	7.9	17.9	1.09
<i>Meriones crassus</i>	4	1.85	3.12	4.70	4.1	1.39	21.7	1.47	6.0	19.0	9.7	20.3	1.32
<i>Meriones grandis</i>	4	3.01	4.75	5.91	5.2	1.65	28.1	2.07	9.6	27.5	11.2	27.1	1.68
<i>Meriones hurrianae</i>	4	2.20	3.41	4.14	4.5	1.52	20.5	1.59	6.6	20.2	8.4	20.1	1.52
<i>Meriones l. erythrourus</i>	1	2.38	3.50	5.48	4.5	1.50	na	1.59	7.7	21.6	11.2	24.1	1.56
<i>Meriones l. libycus</i>	4	2.08	3.80	4.87	4.8	1.58	23.5	1.68	7.1	21.2	11.0	23.0	1.70
<i>Meriones meridianus</i>	4	1.66	3.51	3.96	4.0	1.26	19.6	1.37	6.8	17.2	8.5	18.5	1.18
<i>Meriones persicus</i>	4	2.69	5.47	6.72	5.2	1.60	28.9	2.03	9.4	26.6	11.2	27.1	1.85
<i>Meriones rex</i>	4	2.74	4.00	4.93	4.7	1.59	24.9	1.81	7.8	22.8	10.3	22.9	1.45
<i>Meriones shawi</i>	4	2.06	3.43	4.52	4.5	1.43	20.3	1.52	7.6	22.8	9.8	22.3	1.46
<i>Meriones tamariscinus</i>	4	2.71	4.55	5.44	5.0	1.66	24.6	1.82	8.4	23.7	9.2	23.7	1.55
<i>Meriones tristrami</i>	4	2.22	4.28	5.55	4.6	1.34	24.0	1.77	8.3	22.4	8.7	22.7	1.48
<i>Meriones unguiculatus</i>	8	1.96	3.05	4.27	4.2	1.33	20.3	1.46	6.2	17.8	8.6	18.9	1.23

Table E.6—continued.

	#	LIW	IL	JDL	JML	JMW	TJL	JID	IL2	JLS	MAM	JLB	JMH
<i>Meriones vinogradovi</i>	4	2.32	4.41	5.39	5.3	1.43	25.0	1.77	8.2	24.0	10.0	23.4	1.62
<i>Pachyuromys duprasi</i>	9	1.82	3.19	4.25	4.3	1.48	18.7	1.45	6.4	18.0	8.5	18.6	1.26
<i>Psammomys obesus</i>	9	2.88	4.14	5.87	5.4	1.77	25.0	1.86	7.7	24.4	10.8	24.2	1.92
<i>Rhombomys o. sodalis</i>	4	3.34	4.71	5.61	6.0	1.82	na	1.90	8.6	25.9	10.8	24.5	1.37
<i>Rhombomys o. ssp</i>	5	3.17	4.26	5.24	5.8	1.64	26.6	1.86	7.5	24.4	10.4	24.5	1.57
<i>Sekeetamys calurus</i>	8	1.85	2.65	4.49	4.1	1.40	19.5	1.49	5.6	19.0	8.4	18.8	1.20
<i>Tatera indica</i>	8	2.58	4.12	5.39	5.2	1.82	25.5	1.76	7.7	24.3	9.2	22.8	1.64
<i>Taterillus arenarius</i>	4	1.38	2.97	4.02	3.9	1.25	18.5	1.30	5.8	16.8	7.0	17.4	1.33
<i>Taterillus congicus</i>	4	1.42	2.94	4.16	4.4	1.20	18.4	1.34	6.4	19.8	6.9	18.3	1.43
<i>Taterillus emini</i>	4	1.72	3.81	4.23	4.5	1.38	19.5	1.20	5.8	16.8	6.6	17.6	1.23
<i>Taterillus gracilis</i>	4	1.44	2.99	3.74	3.8	1.27	18.1	1.20	5.5	17.0	6.6	17.2	1.23
<i>Taterillus harringtoni</i>	4	1.35	3.08	4.35	4.0	1.30	19.6	1.29	5.6	17.0	7.1	18.0	1.10
<i>Taterillus lacustris</i>	4	1.41	2.53	4.11	4.0	1.36	17.8	1.31	5.3	18.3	7.2	17.9	1.13
<i>Taterillus pygargus</i>	4	1.68	3.40	4.53	4.3	1.38	20.2	1.26	6.2	18.4	7.6	18.4	1.20
Lophiomyinae													
<i>Lophiomys i. imhausi</i>	2	5.57	6.18	8.43	11.7	2.41	41.6	3.05	11.5	42.6	18.2	39.7	4.42
<i>Lophiomys i. thomasi</i>	2	2.24	5.85	8.08	11.1	2.09	38.2	2.97	12.6	39.4	16.3	36.2	3.57
Murinae													
<i>Abeomelomys sevia</i>	4	2.41	3.56	3.76	5.2	1.26	20.7	1.49	7.3	18.9	7.5	19.6	1.23
<i>Aethomys chrysophilus</i>	4	2.28	3.92	3.69	5.0	1.22	21.3	1.54	6.9	20.0	8.4	20.3	1.17
<i>Anisomys imitator</i>	4	3.60	7.37	9.95	9.6	2.52	46.4	4.77	15.2	38.3	18.4	41.6	2.10
<i>Apodemus agrarius</i>	4	1.73	3.51	3.63	3.8	0.87	17.0	1.07	5.4	14.8	5.3	14.7	0.87
<i>Apodemus mystacinus</i>	4	1.88	3.10	3.69	4.2	1.01	17.8	1.35	6.6	17.7	6.7	18.0	1.01
<i>Apodemus semotus</i>	4	1.40	2.63	3.11	3.5	0.79	15.4	1.03	5.2	14.0	5.4	14.6	0.83
<i>Apodemus speciosus</i>	2	1.50	3.43	3.66	3.8	0.77	17.6	1.09	5.4	14.9	5.1	15.5	0.97
<i>Apodemus sylvaticus</i>	4	1.60	2.60	3.20	3.4	0.73	15.3	1.13	4.6	14.0	5.3	14.6	0.82
<i>Apomys datae</i>	4	2.66	4.51	4.54	6.2	1.51	24.4	1.73	8.2	23.4	7.4	22.7	1.01
<i>Apomys hylocoetes</i>	4	1.83	3.15	3.38	4.9	1.15	17.1	1.11	5.7	16.8	5.5	16.3	0.98
<i>Archboldomys luzonensis</i>	4	1.73	3.97	2.97	4.7	1.19	18.2	1.00	5.3	15.4	5.4	15.9	1.09
<i>Arvicantis neumanni</i>	2	1.68	3.61	3.63	5.2	1.21	20.8	1.46	5.9	19.6	8.3	18.8	1.29
<i>Arvicantis niloticus</i>	4	2.86	3.89	4.25	6.0	1.34	25.7	1.62	6.7	20.4	8.9	20.0	1.22
<i>Bandicota bengalensis</i>	3	4.65	7.11	6.92	6.3	1.87	na	2.27	13.1	32.6	12.1	29.2	1.71
<i>Batomys salomonensi</i>	4	2.61	4.85	5.07	7.0	1.76	na	2.08	10.0	25.7	11.1	25.1	1.83
<i>Berylmus bowersi</i>	4	4.65	6.72	7.65	8.0	2.00	36.9	2.32	11.0	34.4	14.0	33.1	2.14
<i>Bullimus bagobus</i>	6	4.23	6.82	7.89	8.9	2.25	40.0	2.98	11.5	37.9	15.8	36.2	1.73
<i>Bunomys chrysocomus</i>	4	2.67	4.96	5.08	5.7	1.44	26.1	1.55	8.1	24.3	9.2	24.1	1.37
<i>Carpomys phaeurus</i>	1	2.60	4.47	4.84	6.1	1.90	na	1.98	9.1	24.2	10.2	23.2	1.38
<i>Chromyssus chiropus</i>	4	2.88	3.85	5.06	6.0	1.33	22.8	1.69	7.3	23.3	8.7	22.2	1.52
<i>Chiropodomys gliroides</i>	4	1.92	2.80	3.39	3.1	0.71	16.5	1.36	5.8	15.3	6.8	15.7	0.84
<i>Chrotomys gonzalesi</i>	2	3.04	6.43	5.73	5.9	1.27	28.2	1.57	9.8	26.2	9.3	26.1	1.11
<i>Colomys goslingi</i>	4	1.76	3.83	4.96	4.6	1.21	19.5	1.26	6.6	19.1	6.5	18.6	0.90
<i>Conilurus penicillatus</i>	4	2.64	4.26	5.33	6.6	1.90	26.9	1.91	8.0	25.9	9.8	25.6	1.31
<i>Cremnomys cutchicus</i>	4	1.92	3.54	4.23	4.8	1.16	20.2	1.34	6.3	18.6	6.8	18.5	1.06
<i>Crunomys melanius</i>	2	1.88	3.19	3.38	3.6	0.98	16.5	1.22	6.6	16.6	5.7	16.0	0.96
<i>Dacnomyss millardi</i>	4	3.92	6.52	7.61	10.7	2.30	40.2	2.38	12.4	36.9	14.4	34.2	2.57
<i>Dasymys i. medius</i>	3	3.25	4.58	5.51	5.9	1.56	na	1.70	9.3	23.4	10.5	23.0	1.28
<i>Dasymys i. nudipes</i>	1	3.54	6.15	4.76	7.1	2.06	28.1	1.90	10.1	27.1	12.1	25.9	1.44
<i>Golunda elliotti</i>	3	2.86	2.63	3.82	4.8	1.32	19.6	1.46	5.6	19.2	8.6	18.2	0.91
<i>Grammomys d. dolichurus</i>	3	1.86	3.58	2.87	3.8	0.90	17.4	1.25	5.7	16.4	6.6	16.1	0.89
<i>Grammomys d. sardasler</i>	1	1.94	3.18	2.83	4.0	0.80	16.3	1.31	5.5	15.8	6.2	15.7	1.08
<i>Grammomys ibeanus</i>	4	1.75	3.58	3.94	4.3	0.99	19.9	1.40	7.0	18.4	7.2	18.1	1.04
<i>Grammomys macmillani</i>	4	1.84	2.57	3.27	3.4	0.74	15.6	1.25	5.7	15.7	6.1	15.4	0.85
<i>Hapalomys delacouri</i>	1	3.07	3.57	3.58	5.0	1.37	20.6	1.47	6.6	19.3	7.8	19.2	1.07
<i>Heimyscus fumosus</i>	4	1.39	2.78	3.73	3.3	0.72	15.5	0.98	5.3	14.6	5.1	14.9	0.78
<i>Hybomys univittatus</i>	4	2.10	3.28	3.77	4.7	1.06	19.0	1.34	6.2	18.6	7.3	18.3	1.12
<i>Hydromys c. chrysogaster</i>	1	4.45	7.62	6.20	8.0	2.38	34.9	2.50	11.9	32.6	12.0	30.7	2.30
<i>Hydromys c. fowlavolatus</i>	2	3.11	8.52	7.22	8.6	2.22	39.4	2.30	12.0	32.3	11.7	32.4	2.17
<i>Hydromys c. ssp</i>	1	4.27	7.07	6.72	8.5	2.46	37.0	2.41	11.8	35.7	12.2	33.7	2.59
<i>Hylomys parvus</i>	4	1.50	2.82	3.49	3.2	0.78	15.8	1.07	5.4	14.4	6.2	14.5	0.72
<i>Hylomyscuss stella</i>	4	1.48	2.81	3.63	3.2	0.83	15.7	1.12	6.0	15.5	6.1	15.6	0.80
<i>Hyomys goliath</i>	4	8.18	8.66	10.91	14.4	4.62	56.2	4.19	16.6	49.5	21.4	46.3	3.09
<i>Leggadina forresti</i>	3	1.17	2.23	3.49	2.7	0.85	13.3	0.89	4.8	12.6	4.8	12.9	0.68
<i>Lemniscomys barbarus</i>	4	2.15	2.88	3.54	4.4	1.11	18.2	1.33	5.3	17.9	7.4	16.9	0.86
<i>Lemniscomys striatus</i>	3	1.83	3.21	3.70	4.6	1.07	18.9	1.39	5.8	18.9	7.3	17.9	0.99
<i>Leopoldamys sabanus</i>	4	3.74	5.51	6.94	8.3	2.15	32.8	2.59	10.1	34.6	13.2	32.7	2.18
<i>Leptomys elegans</i>	4	2.19	4.06	4.73	5.2	1.06	19.9	1.48	7.9	22.7	7.0	21.6	1.34
<i>Limnomyss sibuanus</i>	4	1.69	3.58	3.77	4.2	1.03	18.1	1.43	6.6	18.5	7.1	18.4	0.82
<i>Lorentzimys nouhuysi</i>	3	1.58	2.66	3.16	2.3	0.70	14.5	1.08	5.1	12.7	6.0	13.3	0.49
<i>Macrouromys major</i>	4	4.45	6.15	8.12	5.8	1.35	na	2.44	10.7	31.5	11.7	31.0	1.24
<i>Malacomys longipes</i>	4	1.96	3.68	5.82	4.5	1.12	22.2	1.54	7.3	21.0	8.3	21.3	1.19
<i>Margaretamys elegans</i>	4	2.65	4.28	5.78	5.4	1.35	na	1.86	8.5	25.2	9.4	25.0	1.44
<i>Mastacomys fuscus</i>	1	2.74	4.00	5.30	7.3	2.26	27.3	1.99	8.3	27.1	10.0	25.4	1.18
<i>Mastomys erythroleucus</i>	4	1.69	3.86	4.19	4.1	0.96	19.6	1.41	6.5	19.5	7.3	18.2	1.04
<i>Maxomys bartelsii</i>	4	2.48	4.08	5.82	5.1	1.32	25.0	1.45	7.4	22.2	7.1	22.9	1.12
<i>Maxomys surifer</i>	4	2.28	4.14	5.12	5.0	1.11	23.1	1.59	7.2	22.0	8.7	21.9	1.20
<i>Melasmotherix naso</i>	4	1.72	3.12	3.66	3.8	1.03	18.6	0.88	5.1	17.5	5.1	18.5	0.98

Table E.6—continued.

	#	LIW	IL	JDL	JML	JMW	TJL	JID	IL2	JLS	MAM	JLB	JMH
<i>Melomys cervinipes</i>	4	2.03	3.60	4.12	5.8	1.36	21.3	1.36	6.5	19.9	7.7	19.7	1.17
<i>Melomys rufescens</i>	2	1.91	3.57	4.18	5.4	1.37	20.6	1.45	6.1	19.4	7.3	19.1	1.08
<i>Mesembriomys gouldii</i>	3	3.54	7.28	10.04	10.5	2.60	44.9	3.06	12.2	40.0	14.9	39.5	1.80
<i>Micaelamys namaquensis</i>	3	2.13	3.19	3.25	4.8	1.26	18.1	1.18	4.7	17.0	6.5	16.7	1.04
<i>Micromys minutus</i>	4	1.18	2.10	2.46	2.4	0.56	11.7	0.82	3.3	10.1	4.1	10.7	0.53
<i>Millardia gladowi</i>	4	1.64	2.73	4.10	3.9	0.98	17.4	1.17	5.2	16.0	6.6	16.5	0.98
<i>Millardia kathleenae</i>	2	1.31	3.70	4.49	4.6	1.11	20.6	1.52	7.2	20.3	7.8	20.9	1.27
<i>Mus booduga</i>	5	1.43	2.35	2.95	2.6	0.68	12.9	0.82	4.5	12.0	4.2	11.9	0.71
<i>Mus cervicolor</i>	4	1.50	2.81	3.27	2.9	0.80	14.7	0.92	4.8	13.9	4.9	13.9	0.84
<i>Mus cookii</i>	4	1.69	3.42	3.47	3.4	0.92	16.5	1.03	5.7	15.1	5.4	15.4	0.88
<i>Mus minutoides</i>	9	1.37	1.69	2.62	2.5	0.71	11.2	0.80	3.7	10.6	3.7	10.7	0.71
<i>Mus m. bactrianus</i>	1	1.23	1.83	2.62	2.5	0.71	11.9	0.94	3.5	12.3	4.2	11.9	0.79
<i>Mus m. ssp</i>	2	1.31	2.00	2.94	2.6	0.71	11.4	0.98	3.9	12.0	4.1	11.6	0.79
<i>Mus m. yamashinai</i>	1	1.08	1.90	2.71	2.5	0.70	11.6	0.93	4.1	11.7	4.4	11.8	0.80
<i>Mus pahari</i>	4	1.63	2.74	3.74	3.4	0.91	16.2	1.00	5.1	15.5	5.1	15.4	0.82
<i>Mus saxicola</i>	4	1.72	3.58	4.44	3.6	0.87	18.6	1.00	5.8	18.6	5.5	18.0	0.98
<i>Mus spretus</i>	4	1.34	2.37	2.84	2.9	0.76	12.7	0.94	4.5	12.5	4.3	12.5	0.76
<i>Mus terricolor</i>	4	1.18	1.91	3.03	2.4	0.61	12.0	0.73	4.2	12.3	4.1	12.4	0.67
<i>Myomys dybowskii</i>	4	2.02	3.30	3.84	7.0	1.70	22.2	1.53	6.5	21.4	8.8	20.3	1.11
<i>Myomyscus Brockmani</i>	4	1.78	2.84	3.66	3.8	0.90	17.0	1.13	5.6	16.5	6.0	16.6	0.95
<i>Niviventer c. confucianus</i>	3	1.99	3.53	4.85	5.7	1.38	21.1	1.35	6.1	19.8	6.5	19.3	1.24
<i>Niviventer c. lotipes</i>	1	2.68	4.03	4.42	5.5	1.37	na	1.53	6.4	22.0	7.5	21.8	1.34
<i>Niviventer cremoriventer</i>	4	2.48	3.76	4.75	5.0	1.27	21.2	1.52	6.9	21.0	7.1	20.0	1.13
<i>Niviventer excelsior</i>	2	1.86	3.19	4.65	5.4	1.33	21.3	1.50	6.1	21.0	6.8	20.9	1.19
<i>Notomys alexis</i>	4	1.72	2.41	4.03	4.1	1.14	17.8	1.14	4.5	15.4	6.9	16.4	0.88
<i>Notomys cervinus</i>	4	1.42	2.65	4.35	4.3	1.02	18.4	1.03	5.1	16.9	6.3	17.3	0.78
<i>Notomys fuscus</i>	4	1.40	2.87	3.63	4.1	1.24	17.6	1.02	4.5	14.4	6.4	15.3	0.88
<i>Oenomys h. editus</i>	2	2.19	3.29	4.21	5.9	1.58	20.7	1.38	5.9	21.5	8.0	20.2	1.36
<i>Oenomys h. hypoxanthus</i>	2	2.89	3.41	4.60	6.2	1.48	21.7	1.36	6.6	21.9	8.3	20.5	1.61
<i>Otomys angoniensis</i>	4	3.58	3.45	4.15	7.1	1.86	24.2	1.78	6.2	23.3	11.9	23.6	1.32
<i>Otomys denti</i>	4	3.65	3.59	3.96	6.6	1.94	24.4	1.75	6.8	21.7	9.6	20.8	1.60
<i>Parotomys brantsii</i>	4	3.78	3.59	4.00	6.7	1.92	23.2	1.78	6.5	23.6	12.5	23.8	1.76
<i>Parotomys littledalei</i>	5	3.25	3.31	5.31	6.6	1.97	25.7	1.80	6.8	23.6	10.9	23.2	1.81
<i>Paruromys dominator</i>	4	3.53	5.97	6.71	7.6	2.04	35.3	2.88	11.4	36.4	13.6	35.7	1.69
<i>Pogonomys loriae</i>	2	2.91	4.05	4.82	5.9	1.48	23.7	1.59	7.3	21.8	8.9	23.2	1.37
<i>Pogonomyms macrourus</i>	4	2.50	4.27	4.04	5.0	1.31	21.8	1.39	7.4	19.3	7.4	19.7	1.22
<i>Praomys jacksoni montis</i>	1	1.80	3.23	4.49	3.9	1.02	19.9	1.39	7.0	19.2	7.1	19.0	0.96
<i>Praomys jacksoni ssp</i>	3	1.65	3.54	4.18	4.2	1.02	19.2	1.43	6.7	17.8	6.7	17.6	0.92
<i>Praomys misonnei</i>	4	1.66	3.36	4.90	4.3	1.14	20.6	1.54	7.4	19.5	7.7	19.6	1.01
<i>Praomys tullbergi</i>	3	1.86	3.79	5.06	4.4	1.16	21.4	1.46	7.5	20.0	7.4	19.9	1.07
<i>Pseudohydromys ellermani</i>	3	1.62	3.61	3.36	0.6	0.39	13.8	1.04	5.5	13.6	4.7	13.6	0.27
<i>Pseudomys australis</i>	5	2.28	3.56	3.21	5.0	1.31	19.6	1.39	5.8	18.5	7.5	18.7	1.11
<i>Pseudomys hermannsburgensis</i>	4	1.24	1.64	2.98	3.0	0.87	12.7	0.89	4.0	12.5	4.9	12.8	0.78
<i>Rattus exulans</i>	4	1.72	3.24	3.92	4.7	1.07	18.6	1.30	6.3	18.6	6.5	18.3	1.09
<i>Rattus norvegicus</i>	3	3.39	5.12	7.06	6.0	1.37	30.6	2.33	10.5	29.7	9.8	28.2	1.46
<i>Rattus praetor</i>	4	2.25	5.68	6.34	6.9	1.69	30.9	2.19	10.8	29.7	11.2	28.8	1.66
<i>Rattus rattus</i>	4	2.74	4.76	5.59	5.6	1.45	27.2	1.85	8.3	25.1	9.5	24.5	1.26
<i>Rattus sordidus</i>	4	2.75	4.65	4.04	6.2	1.57	22.9	1.58	7.6	22.5	8.4	21.7	1.19
<i>Rattus tiomanicus</i>	4	3.03	5.35	5.92	6.0	1.44	25.9	2.01	10.4	28.2	10.4	26.8	1.40
<i>Rattus verecundus</i>	4	2.20	3.42	4.80	5.6	1.43	22.4	1.42	6.4	20.9	7.0	21.1	1.36
<i>Rattus villosissimus</i>	4	3.10	5.46	5.24	6.4	1.72	na	2.14	9.7	27.9	11.3	25.9	1.40
<i>Rhabdomys pumilio</i>	4	1.79	3.26	3.00	4.4	1.03	16.8	1.23	5.3	16.2	6.5	15.5	0.92
<i>Rhynchosomys isarogensis</i>	4	1.75	4.93	8.96	2.1	0.71	28.1	1.10	7.7	28.5	5.6	27.3	0.62
<i>Stenocephalemys albipes</i>	4	1.89	3.43	4.63	4.7	1.20	19.9	1.40	6.9	20.3	7.1	19.4	1.12
<i>Stochomys longicaudatus</i>	4	2.74	4.25	4.73	5.7	1.73	20.7	1.82	8.7	23.0	9.9	22.5	1.39
<i>Sundamys muelleri muelleri</i>	4	3.74	6.80	7.42	8.3	2.22	36.2	2.67	12.6	35.0	13.3	32.8	1.92
<i>Tarsomys apoensis</i>	3	2.12	4.34	4.71	5.5	1.41	24.5	1.56	7.7	22.0	7.6	21.7	1.15
<i>Uromys caudimaculatus</i>	4	4.43	8.91	10.69	11.4	2.82	49.7	4.31	15.5	47.2	20.2	46.1	2.56
<i>Vandeleuria olereacea</i>	4	1.63	2.09	2.57	2.9	0.68	12.2	1.02	4.1	11.5	4.7	11.6	0.59
<i>Zelotomys h. ssp</i>	1	1.28	5.13	3.86	4.9	1.33	22.9	1.38	7.9	20.3	7.5	20.7	1.14
<i>Zelotomys h. vinaceus</i>	3	1.72	4.66	4.06	4.7	1.29	20.9	1.47	7.9	20.3	7.5	20.4	1.30
<i>Zelotomys woosnami</i>	4	2.39	3.89	4.13	4.4	1.15	19.9	1.54	8.0	20.2	7.3	19.9	1.27
<i>Zyzomys argurus</i>	4	1.67	3.20	3.95	4.2	1.02	18.6	1.27	6.0	17.5	6.4	17.9	0.90
<i>Nesomyidae</i>													
<i>Cricetomyinae</i>													
<i>Beamys hindei</i>	4	1.89	3.82	5.85	4.4	0.91	22.2	1.52	7.7	21.5	8.6	21.1	1.26
<i>Cricetomys gambianus</i>	3	4.23	5.15	10.69	8.6	1.84	na	2.91	12.9	40.6	15.3	39.6	2.37
<i>Saccostomus campestris</i>	4	2.15	3.67	5.30	4.2	1.18	20.8	1.35	6.6	17.9	7.9	18.5	1.16
<i>Delanymyinae</i>													
<i>Delanymys brooksi</i>	4	1.22	1.54	2.09	2.1	0.51	9.7	0.75	3.1	8.8	3.6	9.3	0.49
<i>Dendromurinae</i>													
<i>Dendromus insignis</i>	4	1.50	2.20	2.91	3.0	0.74	13.4	0.87	4.4	12.5	5.2	12.6	0.91
<i>Dendromus mesomelas</i>	1	1.19	1.88	2.48	2.7	0.67	11.5	0.85	3.9	10.8	5.5	11.1	0.89
<i>Dendromus nyasae</i>	4	1.46	2.02	3.00	2.9	0.71	12.9	0.89	4.2	12.2	5.1	12.3	0.87
<i>Malacothrix typica</i>	4	1.45	2.21	3.33	3.3	0.75	14.5	0.92	3.9	13.3	5.4	13.4	1.09
<i>Steatomys krebsi</i>	1	1.50	2.07	3.21	3.3	0.94	14.1	1.03	5.1	14.4	6.1	14.4	1.08

Table E.6—continued.

	#	LIW	IL	JDL	JML	JMW	TJL	JID	IL2	JLS	MAM	JLB	JMH
<i>Steatomys p. athi</i>	1	1.48	2.18	3.54	2.8	0.80	14.3	1.01	4.8	12.5	6.1	14.1	1.18
<i>Steatomys p. kalaharicus</i>	1	1.30	2.37	2.92	2.7	0.74	13.2	1.08	5.4	13.4	5.6	13.8	1.26
<i>Steatomys p. ssp</i>	1	1.41	2.36	2.89	2.9	0.80	13.3	0.94	4.1	12.4	5.3	12.8	0.95
<i>Steatomys p. tongensis</i>	1	0.94	2.32	3.14	3.2	0.93	14.1	0.80	4.2	12.3	5.2	12.1	0.99
Mystromyinae													
<i>Mystromys albicaudatus</i>	4	2.38	4.98	4.92	5.8	1.37	23.5	1.57	8.1	22.1	7.9	22.5	1.69
Nesomyinae													
<i>Brachytarsomys albicauda</i>	4	3.69	5.57	5.63	7.3	1.79	31.8	2.37	9.9	30.1	13.2	29.2	1.77
<i>Brachyuromys betsileoensis</i>	4	3.25	4.28	4.42	6.4	1.67	23.4	1.58	8.2	23.5	10.5	20.8	1.19
<i>Eliurus minor</i>	4	1.86	2.99	4.36	3.5	0.83	18.2	1.17	6.0	16.2	6.9	16.7	0.94
<i>Eliurus tanala</i>	4	2.54	4.57	6.72	5.4	1.29	27.0	1.87	9.1	23.7	9.8	24.2	1.31
<i>Gymnuromys roberti</i>	4	2.49	4.30	6.48	5.9	1.33	26.0	1.76	8.6	23.4	9.9	22.9	1.53
<i>Hypogeomys antimena</i>	1	na	na	na	na	na	na	na	na	na	na	na	na
<i>Macrotarsomys bastardi</i>	4	1.40	2.99	3.73	3.5	0.92	17.0	0.94	5.4	14.9	6.3	15.8	0.83
<i>Monticolomys koopmani</i>	2	1.60	2.70	3.87	3.1	0.78	15.8	1.21	5.3	15.5	5.7	16.2	0.78
<i>Nesomys rufus</i>	4	3.27	4.98	6.07	7.2	1.69	27.3	1.86	8.5	26.7	10.3	26.6	1.59
<i>Voalavo gymnocaudus</i>	4	1.67	2.45	3.95	3.3	0.94	16.0	1.26	6.0	15.4	6.2	15.8	0.86
Petromyscinae													
<i>Petromyscus collinus</i>	8	1.61	2.33	3.07	3.1	0.87	14.5	1.08	4.6	13.2	5.5	14.1	0.76
Platacanthomyinae													
<i>Typhlomys c. chapensis</i>	1	1.52	3.17	3.65	3.8	0.74	16.2	1.22	6.7	15.6	6.0	15.3	0.86
<i>Typhlomys c. cinereus</i>	3	1.70	3.39	2.82	3.6	0.80	15.0	1.19	6.2	13.9	5.7	14.0	0.81
Spalacidae													
Myospalacinae													
<i>Eospalax f. canus</i>	2	4.55	6.32	5.09	9.0	1.75	29.1	2.51	12.0	30.9	14.3	29.5	2.64
<i>Myospalax aspalax</i>	2	3.77	4.54	5.69	8.1	1.96	na	1.81	8.1	25.6	11.6	25.6	1.96
Rhizomyinae													
<i>Cannomys badius</i>	4	6.69	8.22	7.75	11.1	3.34	40.7	3.04	14.7	39.1	17.6	36.7	2.74
<i>Rhizomys pruinosus</i>	4	13.94	10.18	11.22	12.9	3.44	48.1	5.09	19.5	57.8	24.7	51.4	2.77
Tachyoryctinae													
<i>Tachyoryctes splendens</i>	4	4.85	9.64	7.38	8.9	2.53	36.6	2.56	16.5	37.0	15.2	31.5	1.73
Spalacinae													
<i>Spalax ehrenbergi</i>	4	3.43	7.78	5.49	5.8	1.50	na	2.51	14.4	30.2	11.3	29.4	1.83
Sciuromorpha													
Gliridae													
Graphiurinae													
<i>Graphiurus ocularis</i>	3	2.05	4.28	4.43	3.0	0.77	20.1	1.40	7.2	17.6	6.8	18.8	0.59
Leithiinae													
<i>Eliomys melanurus</i>	4	2.36	3.83	3.88	4.4	1.25	19.2	1.51	7.2	19.4	7.3	19.0	1.30
<i>Eliomys quercinus</i>	4	2.04	4.11	4.05	5.2	1.41	20.2	1.53	7.8	21.1	7.2	20.1	1.65
Sciuridae													
Kerinae													
Xerini													
<i>Atlantoxerus getulus</i>	4	3.83	5.27	4.71	8.2	1.95	29.3	2.26	9.2	28.0	12.3	28.2	2.02
<i>Xerus erythropus</i>	4	4.15	6.25	6.20	10.6	2.57	39.6	2.65	12.0	38.3	15.1	36.0	2.28
<i>Xerus inauris</i>	4	4.10	5.37	6.17	10.8	2.74	34.3	2.79	10.6	35.1	16.3	33.9	2.19
<i>Xerus princeps</i>	3	4.98	5.46	7.14	10.6	2.80	37.6	3.08	14.1	39.3	16.6	37.0	2.48
Marmotini													
<i>Ammospermophilus harrisii</i>	4	2.74	4.40	5.01	6.0	1.28	22.9	1.95	8.1	22.5	9.9	23.8	1.29
<i>Ammospermophilus interpres</i>	4	2.49	4.02	5.02	5.7	1.25	23.7	1.88	7.5	22.0	9.4	23.6	1.47
<i>Ammospermophilus leucurus</i>	4	2.46	4.54	4.87	6.0	1.27	25.2	1.56	7.1	21.0	8.2	22.1	1.46
<i>Ammospermophilus nelsoni</i>	4	2.45	3.78	5.18	6.0	1.33	24.7	1.68	6.5	23.0	10.3	24.8	1.54
<i>Spermophilus fulvus</i>	4	4.26	7.05	7.56	12.3	3.29	39.6	2.53	10.7	42.3	15.1	38.9	3.64
<i>Spermophilus mexicanus</i>	4	3.14	6.79	7.07	8.2	2.36	34.1	2.01	10.0	32.1	12.4	30.6	2.47
<i>Spermophilus mohavensis</i>	4	2.86	4.24	5.31	6.7	1.82	24.3	1.92	7.9	25.7	10.1	25.4	1.75
<i>Spermophilus pygmaeus</i>	4	3.27	5.46	5.92	7.9	2.20	31.1	1.78	9.3	30.6	10.8	27.7	2.47
<i>Spermophilus spilosoma</i>	4	2.82	4.17	4.96	6.3	1.74	20.5	1.76	7.4	24.6	9.7	23.6	1.81
<i>Spermophilus tereticaudus</i>	4	2.45	3.97	4.97	6.9	1.77	23.2	1.77	7.6	25.2	11.0	23.5	1.77
<i>Spermophilus variegatus</i>	4	4.47	7.49	9.30	10.5	2.76	42.2	3.14	13.3	43.5	17.4	41.7	2.88

Table E.7. Species means of characters derived from raw distances described above. See Table E.4 legend for more information. AJL=average jaw length; AIL= average incisor length; ASL= average skull length; ASW= average skull width; AML= average molar length; ABL= average bulla length; BI= bullar index; BV= bulla volume; NI= nasal index; NV= nasal volume; LII= lower incisor index.

	#	AJL	AIL	ASL	ASW	AML	ABL	BI	BV	NI	NV	LII
Anomaluromorpha												
Pedetidae												
<i>Pedetes capensis</i>	4	49.70	9.01	87.27	54.2	16.40	17.5	0.20	1240.9	0.7	25509.5	1.0
Castorimorpha												
Geomysidae												
<i>Cratogeomys castanops</i>	4	30.92	9.72	42.09	26.1	6.99	12.0	0.28	284.1	0.5	1118.3	0.5
<i>Thomomys umbrinus</i>	4	28.46	10.90	36.68	23.2	6.53	8.6	0.24	115.7	0.4	564.2	0.4
Heteromyidae												
Dipodomysinae												
<i>Dipodomys agilis</i>	4	17.76	4.33	35.96	17.8	4.26	11.8	0.33	214.1	0.3	378.5	0.5
<i>Dipodomys californicus</i>	4	18.80	4.86	34.69	17.9	4.01	11.1	0.32	175.8	0.3	354.6	0.4
<i>Dipodomys compactus</i>	4	18.38	4.44	32.89	16.2	4.06	10.9	0.33	139.1	0.3	350.2	0.4
<i>Dipodomys deserti</i>	5	19.81	4.43	40.20	19.1	4.76	16.4	0.41	492.3	0.3	528.7	0.5
<i>Dipodomys elator</i>	3	19.72	4.58	35.86	18.1	4.50	12.1	0.34	209.5	0.3	534.6	0.5
<i>Dipodomys gravipes</i>	3	19.04	4.22	37.08	18.5	4.50	13.4	0.36	265.0	0.3	460.2	0.4
<i>Dipodomys heermanni</i>	3	19.04	4.62	34.45	16.5	4.16	12.3	0.36	204.9	0.3	364.2	0.4
<i>Dipodomys ingens</i>	4	22.70	5.10	41.05	21.5	4.76	15.3	0.37	363.7	0.3	733.3	0.5
<i>Dipodomys merriami</i>	4	16.17	3.96	31.54	14.1	3.68	11.3	0.36	156.5	0.3	259.2	0.4
<i>Dipodomys microps</i>	4	17.76	4.17	33.06	16.1	4.04	12.5	0.38	219.4	0.3	324.8	0.6
<i>Dipodomys nelsoni</i>	4	22.53	5.84	39.20	20.4	4.75	14.1	0.36	379.8	0.3	588.5	0.5
<i>Dipodomys nitratoides</i>	5	16.47	3.85	31.40	14.6	3.81	11.5	0.36	167.3	0.3	272.7	0.4
<i>Dipodomys ordii</i>	4	17.42	4.14	33.06	16.1	3.97	11.4	0.34	164.4	0.3	311.3	0.5
<i>Dipodomys panamintinus</i>	4	18.34	4.35	34.11	17.9	4.01	11.4	0.34	150.0	0.3	374.5	0.5
<i>Dipodomys phillipsii</i>	4	17.59	3.98	32.06	15.5	4.12	11.2	0.35	156.4	0.3	283.8	0.4
<i>Dipodomys simulans</i>	4	18.89	4.52	35.13	16.7	4.12	12.7	0.36	245.3	0.3	380.7	0.5
<i>Dipodomys spectabilis</i>	4	22.94	5.43	40.37	21.7	4.75	14.8	0.37	359.0	0.3	664.7	0.5
<i>Dipodomys stephensi</i>	4	19.37	4.54	35.87	17.9	4.21	12.6	0.35	248.2	0.3	459.8	0.4
<i>Dipodomys v. venustus</i>	5	19.68	4.00	37.58	18.1	4.51	12.9	0.34	234.8	0.3	551.3	0.7
<i>Dipodomys v. elephantinus</i>	4	18.80	4.23	36.92	17.6	4.26	12.9	0.35	249.5	0.3	449.7	0.5
<i>Microdipodops megacephalus</i>	4	10.81	2.77	22.53	10.5	2.86	8.8	0.39	78.3	0.3	95.5	0.4
<i>Microdipodops pallidus</i>	4	12.42	3.31	23.28	11.1	2.83	9.8	0.42	99.2	0.3	91.6	0.4
Heteromyinae												
<i>Heteromys anomalus</i>	4	18.06	4.81	32.43	15.2	4.69	6.5	0.20	45.5	0.4	429.3	0.4
<i>Heteromys australis</i>	4	17.16	4.22	31.96	14.4	4.49	6.2	0.19	41.1	0.3	373.6	0.5
<i>Heteromys catopterius</i>	4	18.86	4.58	34.16	15.5	4.78	6.1	0.18	35.9	0.4	515.4	0.5
<i>Heteromys d. desmarestianus</i>	4	17.41	4.41	32.11	14.6	4.42	5.8	0.18	34.7	0.3	344.6	0.5
<i>Heteromys d. goldmani</i>	4	17.65	4.96	34.10	15.8	4.50	6.6	0.20	45.7	0.3	420.3	0.4
<i>Heteromys gaumeri</i>	4	16.07	4.47	30.43	14.1	4.25	6.8	0.22	55.0	0.3	295.9	0.4
<i>Heteromys nelsoni</i>	4	19.31	5.11	37.20	15.9	5.20	7.0	0.19	55.6	0.4	553.4	0.4
<i>Heteromys oasicus</i>	2	13.69	4.08	27.96	13.0	4.01	5.9	0.21	38.9	0.4	265.8	0.4
<i>Heteromys teleus</i>	1	18.44	5.13	35.38	16.9	4.99	6.2	0.18	46.5	0.4	596.9	0.4
<i>Liomys adspersus</i>	4	17.88	4.68	31.53	14.6	4.38	5.6	0.18	33.1	0.3	283.0	0.4
<i>Liomys irroratus</i>	4	16.93	4.65	28.85	13.6	4.31	5.3	0.19	36.2	0.3	237.8	0.4
<i>Liomys pictus</i>	4	16.73	4.77	31.19	14.4	4.46	5.5	0.18	40.5	0.3	322.8	0.3
<i>Liomys salvini</i>	4	16.14	4.50	28.67	13.4	3.89	5.2	0.18	35.2	0.3	221.8	0.4
Perognathinae												
<i>Chaetodipus arenarius</i>	4	11.42	2.96	21.45	10.9	2.82	5.7	0.27	23.1	0.3	82.3	0.4
<i>Chaetodipus artus</i>	4	13.06	3.49	23.78	11.7	3.14	5.9	0.25	27.1	0.3	121.4	0.4
<i>Chaetodipus baileyi</i>	4	16.34	4.66	28.57	15.0	3.94	7.7	0.27	68.7	0.3	203.3	0.4
<i>Chaetodipus californicus</i>	4	13.52	3.41	25.11	13.0	3.32	6.6	0.26	39.2	0.3	144.9	0.4
<i>Chaetodipus eremicus</i>	4	12.22	3.26	23.11	12.0	3.19	6.1	0.26	27.5	0.3	111.7	0.5
<i>Chaetodipus fallax</i>	4	13.44	3.30	24.84	12.7	3.36	6.4	0.26	33.6	0.3	131.2	0.5
<i>Chaetodipus formosus</i>	8	12.90	3.22	24.47	12.3	3.29	6.8	0.28	41.8	0.3	128.5	0.5
<i>Chaetodipus goldmani</i>	4	13.54	3.52	25.44	12.6	3.36	6.8	0.27	42.3	0.4	165.3	0.4
<i>Chaetodipus hispidus</i>	4	15.23	4.06	27.37	13.8	3.78	7.2	0.26	54.4	0.3	209.9	0.4
<i>Chaetodipus intermedius</i>	4	11.92	2.90	21.95	10.7	3.09	5.8	0.26	23.4	0.3	84.4	0.5
<i>Chaetodipus lineatus</i>	4	12.54	3.28	23.74	11.9	3.15	6.3	0.27	30.1	0.3	115.5	0.4
<i>Chaetodipus nelsoni</i>	3	12.36	3.14	24.34	12.4	3.34	6.4	0.26	32.2	0.3	116.6	0.4
<i>Chaetodipus penicillatus</i>	4	12.40	3.27	22.97	11.6	2.94	5.9	0.26	25.7	0.3	109.1	0.5
<i>Chaetodipus pernix</i>	4	11.66	3.12	22.13	11.2	2.99	5.9	0.27	25.2	0.4	101.3	0.4
<i>Chaetodipus rudinoris</i>	4	14.55	3.93	27.40	14.6	3.83	7.6	0.28	65.6	0.3	174.8	0.3
<i>Chaetodipus spinatus</i>	4	12.35	3.38	21.69	11.5	3.11	6.2	0.29	29.0	0.4	91.4	0.4
<i>Perognathus alticulus</i>	4	12.43	3.07	22.55	11.4	2.98	6.6	0.29	38.1	0.3	99.4	0.5
<i>Perognathus amplus</i>	4	11.59	3.15	22.33	11.8	2.96	7.2	0.32	52.6	0.3	91.4	0.4
<i>Perognathus fasciatus</i>	4	10.35	2.71	19.87	10.5	2.62	6.4	0.32	35.6	0.4	61.5	0.5
<i>Perognathus flavescens</i>	4	10.41	2.72	20.43	10.6	2.64	6.3	0.31	34.4	0.3	68.7	0.5
<i>Perognathus flavus</i>	4	10.38	2.67	19.01	10.2	2.74	6.1	0.32	35.6	0.3	53.2	0.5
<i>Perognathus inornatus</i>	4	10.90	2.75	20.58	10.6	2.68	6.4	0.31	36.1	0.3	67.3	0.5

Table E.7—continued.

	#	AJL	AIL	ASL	ASW	AML	ABL	BI	BV	NI	NV	LII
<i>Perognathus longimembris</i>	4	9.96	2.64	20.04	10.1	2.61	6.8	0.34	39.0	0.3	68.8	0.5
<i>Perognathus merriami</i>	4	10.59	3.03	18.58	9.9	2.40	5.4	0.29	23.7	0.3	48.3	0.5
<i>Perognathus parvus</i>	4	12.85	3.29	22.80	11.7	3.13	6.9	0.30	47.8	0.3	93.4	0.5
Hystricomorpha												
Ctenodactylophorii												
Ctenodactylidae												
<i>Ctenodactylus gundi</i>	4	36.97	5.88	49.69	33.4	9.49	15.8	0.32	791.2	0.4	1085.9	0.7
<i>Ctenodactylus vali</i>	1	na	na	na	na	na	na	na	na	na	na	na
<i>Felovia vae</i>	4	30.69	4.62	44.80	29.9	7.37	12.2	0.27	233.4	0.4	801.6	0.8
<i>Massoutiera mzabi</i>	4	27.48	4.45	43.57	26.7	7.83	16.3	0.37	759.4	0.3	644.7	0.7
<i>Pectinator spekei</i>	2	28.32	4.96	43.75	25.6	8.16	12.4	0.28	404.7	0.3	540.1	0.6
Hystricognathi												
Abrocomidae												
<i>Abrocoma bennettii</i>	4	30.91	4.23	45.47	21.6	9.23	14.7	0.32	511.6	0.3	729.7	0.7
Bathyergidae												
<i>Bathyergus janetta</i>	4	34.17	11.92	42.77	26.6	8.05	11.3	0.27	221.6	0.2	549.6	0.5
<i>Cryptomys hottentotus</i>	4	28.51	10.83	31.98	22.2	5.23	7.8	0.24	71.9	0.2	242.5	0.4
Caviidae												
Caviinae												
<i>Microcavia australis</i>	4	33.63	6.09	46.67	27.8	10.55	13.1	0.28	341.4	0.5	984.6	0.5
Dolichotinae												
<i>Dolichotis patagonum</i>	4	91.75	16.96	128.31	64.0	26.32	25.6	0.20	2908.0	0.4	29245.4	0.4
<i>Dolichotis salinicola</i>	4	70.96	12.67	99.24	49.7	20.05	21.4	0.22	1661.7	0.5	14177.0	0.4
Chinchillidae												
<i>Lagidium viscacia</i>	4	49.14	9.36	83.83	43.3	18.93	19.2	0.23	1337.0	0.5	5132.7	0.5
<i>Lagostomus maximus</i>	4	88.17	19.58	105.47	62.3	23.30	21.2	0.20	1443.9	0.4	23273.5	0.5
Ctenomyidae												
<i>Ctenomys emilianus</i>	1	35.50	8.01	36.06	25.3	8.55	9.5	0.26	na	0.4	1349.6	0.7
<i>Ctenomys latro</i>	4	25.54	6.68	33.58	21.8	7.05	12.3	0.37	235.0	0.5	501.0	0.6
<i>Ctenomys mendocinus</i>	4	29.04	7.41	36.17	21.9	7.24	13.5	0.37	295.5	0.5	719.1	0.6
<i>Ctenomys occultus</i>	2	28.23	7.23	36.59	21.8	7.02	13.2	0.36	325.1	0.4	691.8	0.6
Hystricidae												
<i>Hystrix africaeaustralis</i>	4	109.84	28.89	148.54	82.9	35.90	23.7	0.16	2148.6	0.8	218706.1	0.4
<i>Hystrix cristata</i>	4	102.31	22.20	147.22	81.0	34.88	23.3	0.16	2416.2	0.6	287603.0	0.6
<i>Hystrix indica</i>	4	104.44	23.72	147.05	77.7	33.65	22.5	0.15	2064.4	0.7	144352.0	0.4
Octodontidae												
<i>Octodon degus</i>	4	27.85	6.33	39.86	21.3	8.29	11.9	0.30	217.1	0.4	675.6	0.5
<i>Octodon lunatus</i>	4	29.09	6.01	43.59	23.0	9.58	13.2	0.30	294.0	0.4	771.6	0.5
Petromuridae												
<i>Petromus typicus</i>	4	27.62	5.18	40.31	23.1	7.99	11.7	0.29	271.8	0.4	574.1	0.7
Myodonta												
Dipodoidea												
Dipodidae												
Allactaginae												
<i>Allactaga balikunica</i>	1	21.32	6.45	28.06	19.4	5.39	8.4	0.30	97.4	0.4	310.1	0.3
<i>Allactaga bullata</i>	4	23.06	7.27	32.07	21.9	6.42	9.2	0.29	118.8	0.4	na	na
<i>Allactaga e. elater</i>	4	18.96	5.62	26.48	19.1	4.55	6.8	0.26	46.9	0.5	235.2	0.3
<i>Allactaga e. elater indica</i>	3	19.58	5.56	28.59	20.5	4.65	7.0	0.24	53.2	0.5	313.5	0.4
<i>Allactaga e. elater turkmeni</i>	1	18.28	5.57	25.20	18.7	4.96	6.6	0.26	37.5	0.6	219.3	na
<i>Allactaga euphratica</i>	8	21.83	6.43	31.64	21.5	6.24	7.3	0.23	67.2	0.5	456.7	0.3
<i>Allactaga firozzi</i>	3	20.59	6.29	28.00	20.3	4.88	7.9	0.28	75.9	0.5	307.7	0.3
<i>Allactaga hotsoni</i>	4	19.39	5.66	29.93	20.2	5.25	8.7	0.29	104.2	0.5	284.6	0.3
<i>Allactaga major</i>	4	35.03	11.55	45.20	32.1	8.33	9.6	0.21	139.5	0.5	1892.6	0.3
<i>Allactaga severtzovi</i>	2	29.78	9.21	38.96	27.1	8.87	9.0	0.23	122.2	0.4	918.7	0.6
<i>Allactaga sibirica</i>	2	29.06	8.82	39.26	24.5	7.20	8.8	0.22	106.4	0.4	831.2	0.3
<i>Allactaga tetradactyla</i>	6	21.33	6.38	30.34	20.5	5.51	7.3	0.24	60.9	0.4	366.5	0.3
<i>Pygeretmus platyrurus</i>	1	16.73	4.60	22.57	17.8	3.92	5.2	0.23	29.0	0.3	125.0	0.3
<i>Pygeretmus pumilio</i>	4	na	na	na	na	na	na	na	na	na	na	na
<i>Pygeretmus zhikovi</i>	3	20.18	5.94	26.56	20.9	4.75	5.8	0.22	43.3	0.5	244.5	0.3
Cardiocrainiinae												
<i>Cardiocranus paradoxus</i>	2	10.59	2.83	20.51	9.8	3.44	8.0	0.39	119.8	0.5	40.2	0.5
<i>Salpingotulus michaelis</i>	2	9.31	2.25	18.05	10.7	3.34	6.0	0.34	49.0	0.3	na	na
<i>Salpingotulus crassicauda</i>	2	8.15	1.80	15.27	8.2	2.23	5.3	0.35	35.6	0.3	31.2	0.9
Dipodinae												
<i>Dipus s. sagitta</i>	4	18.74	5.22	32.11	20.2	6.00	10.1	0.32	214.8	0.4	459.8	0.4
<i>Dipus s. sowerli</i>	4	19.31	7.60	30.57	19.4	5.57	9.4	0.31	182.6	0.4	494.7	na
<i>Eremodipus lichensteinii</i>	1	na	na	na	na	na	na	na	na	na	na	na
<i>Jaculus blanfordi</i>	5	20.47	5.84	34.42	23.1	4.99	12.1	0.35	392.5	0.4	466.3	0.4
<i>Jaculus jaculus</i>	4	17.87	5.14	31.78	21.7	4.89	10.9	0.34	256.6	0.5	350.6	0.4
<i>Jaculus orientalis</i>	4	22.90	6.39	37.00	26.2	6.36	11.9	0.32	380.9	0.4	666.7	0.3
<i>Paradipus ctenodactylus</i>	1	18.47	4.05	29.67	16.0	5.79	9.8	0.33	237.6	0.4	268.3	0.5
<i>Stylocitellus telum</i>	4	17.42	5.38	25.79	17.7	4.24	6.8	0.26	109.0	0.4	239.1	0.3
Sicistinae												
<i>Sicista betulina</i>	4	10.60	2.92	18.20	8.7	2.66	3.8	0.21	9.9	0.3	55.2	0.4

Table E.7—continued.

	#	AJL	AIL	ASL	ASW	AML	ABL	BI	BV	NI	NV	LII
<i>Sicista concolor</i>	5	13.73	3.91	21.90	10.5	3.28	4.1	0.19	11.7	0.3	93.9	0.4
<i>Sicista napaea</i>	1	11.27	3.08	19.31	9.2	3.19	4.4	0.23	12.5	0.3	51.7	0.4
<i>Sicista subtilis</i>	4	10.39	3.39	19.82	10.1	3.37	4.3	0.21	15.6	0.4	57.5	0.4
Zapodinae												
<i>Eozapus setchuanus</i>	4	11.93	3.13	21.14	10.1	3.35	4.2	0.20	12.0	2.3	176.2	0.5
<i>Napaeozapus insignis</i>	4	12.94	3.40	22.88	11.6	3.55	4.3	0.19	11.5	0.3	139.1	0.4
<i>Zapus hudsonius</i>	4	12.01	3.17	21.92	10.7	3.48	4.0	0.18	11.1	0.4	122.9	0.4
<i>Zapus p. oregonus</i>	4	13.60	3.65	24.56	12.6	4.24	4.3	0.18	14.1	0.3	182.4	0.4
<i>Zapus p. pacificus</i>	1	13.57	5.15	21.90	11.9	3.79	4.2	0.19	11.2	0.4	106.1	na
<i>Zapus p. princeps</i>	3	13.70	3.87	23.69	12.1	3.66	4.3	0.18	13.2	0.3	168.3	0.4
<i>Zapus trinotatus</i>	4	12.72	3.12	23.77	12.5	3.81	4.4	0.19	15.4	0.3	142.3	0.5
Muroidea												
Calomyscidae												
Calomyscinae												
<i>Calomyscus baluchi</i>	4	14.68	3.83	23.90	11.5	3.08	4.9	0.21	14.9	0.3	104.2	0.4
<i>Calomyscus bailwardi</i>	3	14.34	3.99	23.47	11.9	3.22	4.7	0.20	14.1	0.4	102.1	0.4
Cricetidae												
Arvicolinae												
<i>Alticola strelzowi</i>	6	17.37	5.12	25.19	14.4	5.41	6.6	0.26	36.9	0.4	112.4	0.3
<i>Arvicola amphibius</i>	3	28.06	7.09	38.94	22.6	9.38	8.3	0.21	89.6	0.5	631.8	1.3
<i>Chionomys nivalis</i>	4	18.95	5.59	27.21	15.3	6.40	7.8	0.29	76.0	0.5	144.9	0.4
<i>Dicrostonyx groenlandicus</i>	4	20.74	5.37	25.87	16.3	6.53	7.6	0.29	51.7	0.5	163.8	0.3
<i>Ellobius talpinus</i>	4	23.30	8.43	28.80	21.2	6.92	7.2	0.25	41.0	0.5	248.9	0.4
<i>Eolagurus luteus</i>	5	20.83	6.19	27.90	16.9	6.63	9.0	0.32	117.5	0.5	206.2	0.4
<i>Eolagurus przewalskii</i>	1	21.28	5.98	30.24	18.7	6.15	9.5	0.32	151.5	0.4	237.6	0.4
<i>Eothenomys custos rubellus</i>	4	16.02	4.91	21.79	12.5	5.03	5.4	0.25	20.6	0.4	108.5	0.4
<i>Lagurus l. abacaneus</i>	1	15.86	3.39	21.57	13.9	5.49	7.3	0.34	44.8	0.4	97.4	0.6
<i>Lagurus l. agressus</i>	2	15.78	3.85	22.60	13.8	5.64	6.4	0.29	35.8	0.4	104.2	0.5
<i>Lagurus l. lagurus</i>	1	17.24	4.08	23.41	14.5	5.53	7.3	0.31	41.6	0.4	135.0	0.5
<i>Lastiopodomys mandarinus</i>	4	18.13	5.86	23.53	14.3	5.69	6.8	0.29	42.2	0.5	118.8	0.3
<i>Lemmus sibiricus</i>	4	24.28	7.11	32.03	21.6	8.55	9.5	0.30	120.0	0.5	306.0	0.4
<i>Microtus arvalis</i>	4	18.42	4.71	23.86	13.6	5.83	7.0	0.30	42.1	0.5	133.5	0.6
<i>Microtus californicus</i>	4	18.68	5.27	26.46	14.7	6.28	7.4	0.28	56.8	0.5	198.8	0.4
<i>Microtus chrotorrhinus</i>	4	18.03	5.34	26.04	14.1	6.08	7.8	0.30	60.6	0.5	134.1	0.4
<i>Microtus kikuchii</i>	4	19.32	5.80	27.11	14.5	6.56	7.7	0.28	63.7	0.4	166.7	0.4
<i>Microtus montanus</i>	3	20.27	6.42	26.85	15.3	6.18	7.1	0.27	48.3	0.4	196.3	0.4
<i>Microtus p. acadicus</i>	1	17.68	5.41	24.59	14.4	5.79	6.5	0.27	40.9	0.5	148.7	0.4
<i>Microtus p. pennsylvanicus</i>	3	18.18	5.51	24.46	13.0	5.96	6.6	0.27	35.5	0.5	133.9	0.4
<i>Microtus richardsoni</i>	1	8.54	na	29.53	18.1	6.54	7.3	0.25	42.2	0.5	294.1	na
<i>Myodes gapperi</i>	4	14.92	4.21	24.00	12.7	4.86	7.1	0.29	40.2	0.5	99.7	0.4
<i>Neodon irene</i>	4	16.37	5.06	21.51	12.7	4.87	5.8	0.27	25.3	0.4	95.9	0.3
<i>Neofiber alleni</i>	4	31.73	9.17	41.87	25.9	10.59	9.9	0.24	149.5	0.5	693.9	0.5
<i>Ondatra z. rivaliculus</i>	1	44.51	14.84	60.93	37.4	14.08	12.8	0.21	297.1	0.5	2600.1	0.2
<i>Ondatra z. zibethicus</i>	2	43.61	12.83	58.85	35.2	14.03	11.5	0.20	265.4	0.5	2404.7	0.4
<i>Phenacomys i. levius</i>	2	15.90	4.03	21.83	12.8	5.52	5.6	0.26	27.7	0.4	82.7	0.5
<i>Phenacomys i. oramoutis</i>	2	13.45	3.32	20.53	11.4	5.10	5.5	0.27	27.1	0.6	66.5	0.5
<i>Prometheomys schaposchnikowi</i>	4	23.10	6.93	30.84	17.4	7.04	8.0	0.26	66.0	0.5	323.2	0.4
<i>Synaptomys c. cooperi</i>	1	17.48	4.00	24.55	14.2	6.00	6.7	0.27	39.6	0.6	123.6	0.6
<i>Synaptomys c. gossii</i>	2	18.33	4.61	25.31	15.0	6.44	7.4	0.29	56.2	0.6	154.3	0.3
Cricetinae												
<i>Allocricetus e. curtatus</i>	5	18.66	5.53	27.87	15.3	4.21	5.7	0.20	20.8	0.3	234.9	0.4
<i>Allocricetus e. microdon</i>	2	18.76	6.00	25.05	14.3	4.04	5.4	0.21	16.6	0.4	188.1	0.4
<i>Cricetus b. barabensis</i>	4	14.61	4.24	25.95	13.5	3.61	5.6	0.22	20.4	0.4	153.3	0.4
<i>Cricetus b. griseus</i>	4	15.87	4.48	24.88	13.0	3.57	5.2	0.21	16.8	0.4	130.9	0.4
<i>Cricetus longicaudatus</i>	4	14.08	3.64	22.89	11.6	3.58	5.0	0.22	16.3	0.3	121.5	0.5
<i>Cricetus migratorius</i>	7	16.93	4.69	25.91	13.1	3.94	5.3	0.20	17.6	0.4	148.0	0.4
<i>Cricetus c. canescens</i>	2	27.92	8.23	39.20	23.4	7.44	8.9	0.23	83.6	0.4	878.0	0.5
<i>Cricetus c. cricetus</i>	2	31.06	9.96	43.52	25.5	7.61	8.6	0.20	149.1	0.4	1006.7	0.3
<i>Mesocricetus auratus</i>	3	23.77	6.60	32.09	18.8	5.40	6.6	0.21	43.7	0.3	425.2	0.6
<i>Phodopus campbelli</i>	4	14.57	3.54	23.64	13.3	3.44	4.5	0.19	13.5	0.3	138.9	0.5
<i>Phodopus roborovskii</i>	4	11.98	2.87	19.86	10.9	2.94	3.6	0.18	6.8	0.4	77.6	0.5
<i>Phodopus sungorus</i>	4	13.31	3.26	22.16	11.9	3.17	4.5	0.20	11.3	0.4	102.8	0.5
Neotominae												
<i>Baiomys musculus</i>	3	10.66	2.89	17.99	9.8	2.90	3.9	0.22	6.7	0.3	58.3	0.5
<i>Habromys lepturus</i>	4	17.44	4.77	26.84	13.9	4.37	5.4	0.20	22.9	0.3	165.0	0.4
<i>Hodomys allenii</i>	4	30.17	7.14	46.57	23.1	10.43	8.6	0.18	77.4	0.3	750.4	0.5
<i>Isthmomys pirrensis</i>	4	17.10	5.35	39.08	18.3	5.67	6.3	0.16	32.8	0.3	565.8	0.4
<i>Megadontomys thomasi</i>	4	21.01	6.02	35.49	17.5	5.84	6.3	0.18	40.8	0.3	355.8	0.4
<i>Neotoma albigenula</i>	4	26.19	7.25	42.28	22.0	7.90	8.1	0.19	72.8	0.3	691.8	0.5
<i>Neotoma bryanti</i>	4	25.55	6.20	40.62	21.8	7.66	7.9	0.20	71.6	0.3	565.1	0.5
<i>Neotoma cinerea</i>	2	29.53	8.03	44.26	22.5	8.53	8.2	0.19	92.8	0.3	792.9	0.4
<i>Neotoma devia</i>	4	17.62	6.06	35.10	18.2	7.18	7.3	0.21	67.0	0.3	399.5	0.4
<i>Neotoma floridana</i>	3	30.13	7.49	47.49	24.2	8.08	8.0	0.17	86.7	0.3	1007.8	0.5
<i>Neotoma goldmani</i>	4	23.85	5.97	35.50	18.1	7.15	7.2	0.20	57.4	0.4	357.8	0.4
<i>Neotoma lepida</i>	4	26.42	6.88	40.03	20.1	7.62	8.2	0.20	82.9	0.3	589.8	0.5
<i>Neotoma mexicana</i>	4	26.29	7.57	39.90	21.2	8.23	7.5	0.19	54.8	0.3	623.2	0.4

Table E.7—continued.

	#	AJL	AIL	ASL	ASW	AML	ABL	BI	BV	NI	NV	LII
<i>Neotomodon alstoni</i>	4	19.03	5.22	30.11	16.0	5.04	6.0	0.20	31.3	0.3	243.7	0.4
<i>Ochrotomys nuttalli</i>	3	14.60	3.81	23.29	12.3	3.49	4.7	0.20	14.7	0.3	114.5	0.4
<i>Onychomys l. arcticeps</i>	2	17.24	4.81	26.27	14.4	4.21	5.3	0.20	19.8	0.3	212.8	0.5
<i>Onychomys l. breviauritus</i>	1	15.67	3.83	26.09	13.4	4.15	4.5	0.17	15.0	0.3	174.5	0.5
<i>Onychomys l. ruidosae</i>	3	16.71	4.05	26.33	14.2	4.14	4.9	0.18	17.8	0.3	179.3	0.5
<i>Onychomys torridus</i>	4	13.21	3.61	23.46	11.8	3.50	4.9	0.21	15.3	0.3	103.3	0.4
<i>Osgoodomys banderanus</i>	4	16.38	4.53	28.60	13.3	3.87	4.7	0.16	16.8	0.3	193.6	0.4
<i>Peromyscus a. hylocetes</i>	3	19.44	5.62	28.22	14.9	4.53	5.5	0.19	25.6	0.3	221.3	0.4
<i>Peromyscus a. oaxacensis</i>	1	17.78	4.64	26.78	12.9	4.24	5.0	0.19	18.6	0.3	192.3	0.4
<i>Peromyscus b. levipes</i>	3	16.56	4.55	26.39	13.3	4.22	5.3	0.20	20.7	0.3	166.1	0.4
<i>Peromyscus b. rowleyi</i>	1	17.27	4.12	26.41	12.9	3.95	4.9	0.18	16.0	0.3	155.0	0.4
<i>Peromyscus californicus</i>	1	16.20	4.01	27.21	13.5	3.60	5.6	0.21	23.9	0.3	167.5	0.4
<i>Peromyscus c. auripectus</i>	1	13.48	3.83	22.95	11.2	3.03	4.5	0.20	13.2	0.3	112.2	0.3
<i>Peromyscus c. pergracilis</i>	3	14.47	3.85	24.65	12.4	3.53	4.9	0.20	17.2	0.3	128.0	0.4
<i>Peromyscus eremicus</i>	4	14.21	3.53	23.79	12.3	3.49	5.0	0.21	18.0	0.3	112.0	0.5
<i>Peromyscus fraterculus</i>	4	13.90	3.58	22.93	11.4	3.38	4.8	0.21	14.8	0.3	90.4	0.4
<i>Peromyscus leucopus</i>	4	14.88	4.19	23.66	12.1	3.27	4.5	0.19	13.3	0.3	126.5	0.4
<i>Peromyscus m. abietorum</i>	1	14.40	3.88	23.74	11.7	2.94	4.7	0.20	13.6	0.3	116.9	0.3
<i>Peromyscus m. gambelii</i>	2	15.45	3.98	25.34	11.3	3.48	5.0	0.20	15.5	0.3	134.1	0.4
<i>Peromyscus m. gracilis</i>	1	14.44	3.53	23.80	11.9	3.14	4.6	0.19	13.3	0.3	124.8	0.5
<i>Peromyscus m. merriami</i>	4	14.03	3.48	24.64	12.9	3.58	5.3	0.21	21.2	0.3	126.7	0.5
<i>Peromyscus m. nudipes</i>	1	19.20	5.27	31.06	14.7	4.33	5.2	0.17	23.6	0.3	270.7	0.4
<i>Peromyscus m. saxatilis</i>	3	18.90	5.08	29.62	13.8	4.08	5.1	0.17	18.6	0.3	236.4	0.4
<i>Peromyscus pectoralis</i>	4	13.58	3.54	25.42	12.9	3.48	5.2	0.21	20.2	0.3	127.7	0.4
<i>Peromyscus p. allophrys</i>	1	11.74	2.94	20.58	10.8	2.95	4.6	0.22	13.0	0.3	84.0	0.4
<i>Peromyscus p. subgriseus</i>	3	13.03	3.25	20.66	10.6	2.88	4.2	0.21	10.4	0.3	81.5	0.4
<i>Reithrodontomys creper</i>	4	15.41	4.27	26.88	13.9	4.04	4.9	0.18	17.6	0.3	143.9	0.5
<i>Reithrodontomys f. chiapensis</i>	1	12.50	3.54	20.59	10.1	2.93	3.8	0.18	8.2	0.3	99.8	0.4
<i>Reithrodontomys f. difficilis</i>	1	11.76	3.24	20.66	10.1	2.75	4.0	0.19	10.8	0.3	65.0	0.4
<i>Reithrodontomys f. helvolus</i>	1	12.34	3.06	21.58	10.6	3.12	4.2	0.20	10.8	0.3	83.7	0.4
<i>Reithrodontomys f. intermedius</i>	1	12.53	3.04	19.64	9.9	3.10	3.9	0.20	10.4	0.3	67.3	0.5
<i>Reithrodontomys gracilis</i>	3	11.53	3.30	20.13	9.8	2.85	3.9	0.19	9.4	0.3	65.8	0.4
<i>Reithrodontomys megalotis</i>	7	11.28	2.74	19.49	10.0	2.85	3.8	0.19	10.0	0.3	60.2	0.5
<i>Scotinomys teguina</i>	3	13.44	3.55	21.43	11.1	3.83	4.2	0.20	10.7	0.3	85.3	0.4
<i>Xenomys nelsoni</i>	2	24.91	6.19	37.79	19.5	7.81	9.4	0.25	134.7	0.3	359.8	0.5
Sigmodontinae												
<i>Abrothrix andinus</i>	4	12.15	3.27	23.48	12.2	3.53	5.7	0.24	24.1	0.4	93.4	0.4
<i>Abrothrix longipilis</i>	4	15.14	3.52	28.28	13.3	4.12	5.2	0.18	15.6	0.3	221.9	0.5
<i>Aegialomys xanthaeolus</i>	4	17.68	4.64	29.79	14.9	4.86	5.7	0.19	19.9	0.4	261.3	0.5
<i>Akodon aerosus</i>	4	17.37	4.81	26.26	13.5	4.31	5.2	0.20	16.3	0.3	153.2	0.4
<i>Akodon boliviensis</i>	3	14.62	3.99	22.53	11.8	3.67	4.8	0.22	12.2	0.4	95.1	0.4
<i>Akodon iniscatus</i>	4	14.09	3.97	25.00	12.9	3.89	4.9	0.19	17.6	0.4	123.2	0.4
<i>Akodon kofordi</i>	4	14.07	3.50	24.21	11.9	3.70	5.1	0.21	15.7	0.3	111.4	0.4
<i>Akodon lutescens</i>	1	11.83	3.49	19.94	10.1	3.33	4.4	0.22	9.6	0.4	74.6	0.3
<i>Akodon mimus</i>	3	16.54	4.32	24.63	12.0	4.11	4.8	0.20	11.6	0.3	126.9	0.3
<i>Akodon molinae</i>	1	16.31	4.63	27.10	14.4	4.26	5.7	0.21	21.6	0.4	215.6	0.4
<i>Akodon spegazzinii</i>	4	15.21	3.96	24.54	12.2	4.08	4.6	0.19	12.7	0.4	129.8	0.4
<i>Akodon torques</i>	4	15.24	4.18	24.35	12.1	4.04	4.8	0.20	14.1	0.3	127.8	0.4
<i>Andalgalomys pearsoni</i>	4	16.79	4.32	28.13	13.7	4.06	5.8	0.20	27.1	0.3	187.9	0.4
<i>Andinomys edax</i>	5	21.99	5.60	33.37	18.1	6.42	5.8	0.18	31.0	0.4	489.7	0.6
<i>Auliscomys sublimis</i>	4	14.79	3.18	23.66	12.9	4.21	4.8	0.20	13.3	0.4	141.7	0.6
<i>Brucepattersonius igniventris</i>	2	14.25	3.86	27.06	12.5	4.08	5.2	0.19	16.9	0.3	202.8	0.4
<i>Brucepattersonius soricinus</i>	2	14.45	4.25	26.54	12.4	4.27	5.5	0.21	20.4	0.3	174.1	0.4
<i>Calomys callosus</i>	7	15.03	3.94	24.80	12.9	3.77	5.1	0.21	15.4	0.4	154.3	0.5
<i>Calomys lepidus</i>	4	12.53	3.24	21.52	11.5	3.42	4.3	0.20	11.2	0.4	97.5	0.4
<i>Calomys musculinus</i>	4	11.29	2.57	21.04	11.1	3.38	4.4	0.21	12.0	0.4	94.4	0.5
<i>Calomys venustus</i>	1	17.14	4.49	24.65	13.1	4.09	5.0	0.20	14.7	0.4	158.4	0.5
<i>Cerradomys subflavus</i>	4	20.48	5.54	34.84	17.0	4.95	6.1	0.18	26.3	0.3	368.1	0.4
<i>Chelemys macronyx</i>	4	19.14	5.25	30.94	16.9	5.43	6.7	0.22	37.7	0.4	294.5	0.4
<i>Chinchillula sahamae</i>	4	25.01	7.18	36.78	19.7	6.63	7.4	0.20	54.4	0.4	653.8	0.3
<i>Delomys d. collinus</i>	2	18.32	4.58	31.61	15.4	4.52	6.1	0.19	23.1	0.4	328.9	0.4
<i>Delomys d. dorsalis</i>	2	17.88	5.07	31.12	15.4	4.51	6.0	0.19	25.2	0.4	284.5	0.4
<i>Deltamyces kempfi</i>	4	15.01	4.65	22.76	10.8	3.55	4.7	0.21	11.4	0.3	116.8	0.3
<i>Eligmodontia moreni</i>	3	12.52	3.16	21.23	10.8	3.41	4.8	0.23	15.5	0.3	81.8	0.4
<i>Eligmodontia morgani</i>	4	13.38	3.97	23.93	12.5	3.48	5.1	0.21	18.8	0.3	125.2	0.4
<i>Eligmodontia typus</i>	8	13.44	3.33	22.67	11.8	3.46	5.2	0.23	17.1	0.3	113.1	0.5
<i>Euneomys c. chinchilloides</i>	3	19.69	3.90	29.89	17.6	5.19	6.5	0.22	39.0	0.4	380.2	0.7
<i>Euneomys c. sublimis</i>	1	16.66	3.34	27.42	15.4	4.97	6.4	0.23	31.6	0.4	260.7	0.6
<i>Geoxus valdivianus</i>	4	14.78	3.75	25.10	11.8	3.10	5.0	0.20	16.6	0.3	128.4	0.4
<i>Graomys edithae</i>	1	16.06	3.93	26.50	12.7	4.47	6.1	0.23	29.0	0.4	174.9	0.4
<i>Graomys griseoflavus</i>	7	19.25	4.96	31.68	15.6	5.09	7.2	0.23	51.7	0.3	320.1	0.5
<i>Holochilus brasiliensis</i>	4	24.50	7.17	36.86	19.6	6.64	7.2	0.20	46.1	0.3	625.0	0.5
<i>Holochilus sciureus</i>	3	25.82	7.53	36.73	19.6	6.36	7.2	0.20	42.8	0.3	611.0	0.5
<i>Ichthyomys stolzmanni</i>	1	18.20	4.81	30.33	15.0	3.64	5.2	0.17	14.3	0.4	208.3	0.4
<i>Irenomys tarsalis tarsalis</i>	4	15.47	4.25	27.91	14.3	4.87	5.6	0.20	22.5	0.3	182.5	0.4
<i>Juliomys pictipes</i>	4	13.87	3.66	23.92	12.8	3.60	4.5	0.19	11.4	0.4	106.9	0.4

Table E.7—continued.

	#	AJL	AIL	ASL	ASW	AML	ABL	BI	BV	NI	NV	LII
<i>Kunsia tomentosus</i>	4	36.00	9.45	50.66	27.5	9.03	9.7	0.19	132.2	0.4	1698.5	0.5
<i>Lenoxus apicalis apicalis</i>	4	19.94	5.41	34.14	15.6	5.36	6.1	0.18	26.9	0.3	460.5	0.4
<i>Loxodontomys micropus</i>	4	17.64	4.45	30.82	17.1	5.37	6.3	0.20	30.1	0.4	414.1	0.5
<i>Melanomys c. chrysomelas</i>	3	17.73	5.87	29.22	15.8	4.56	5.3	0.18	17.5	0.3	267.8	0.3
<i>Melanomys c. ssp</i>	1	18.23	5.64	29.70	15.5	4.57	5.2	0.18	16.2	0.3	257.0	0.3
<i>Microryzomys m. azoricus</i>	1	9.86	2.49	16.24	8.0	2.40	4.0	0.24	9.0	0.4	38.0	0.5
<i>Microryzomys m. soricinus</i>	2	8.78	2.26	15.87	8.5	2.57	3.8	0.24	7.1	0.4	25.8	0.6
<i>Microryzomys m. ssp</i>	1	10.02	2.83	18.83	9.2	3.18	4.3	0.23	9.7	0.4	35.5	0.4
<i>Neacomys spinosus</i>	4	12.38	3.56	22.47	11.7	2.83	3.8	0.17	7.6	0.3	117.2	0.4
<i>Necromys amoenus</i>	4	16.25	4.95	26.01	14.4	4.03	5.6	0.22	19.0	0.4	160.2	0.4
<i>Nectomys apicalis</i>	4	27.93	7.57	47.22	25.0	7.69	7.5	0.16	52.8	0.3	968.7	0.4
<i>Nectomys s. palmipes</i>	1	23.99	6.37	37.50	19.0	5.99	6.0	0.16	24.9	0.4	642.3	0.5
<i>Nectomys s. pollenis</i>	1	26.24	7.53	39.87	21.7	6.73	6.8	0.17	39.0	0.3	671.1	0.4
<i>Nectomys s. ssp</i>	1	28.72	8.88	46.39	24.6	7.15	7.3	0.16	41.2	0.3	1224.5	0.4
<i>Neotomys ebriosus</i>	5	16.65	3.46	28.77	15.9	4.97	6.2	0.21	30.4	0.5	452.4	0.9
<i>Nephelomys keaysi</i>	4	19.34	5.51	33.01	17.5	5.29	5.4	0.16	19.8	0.4	338.1	0.4
<i>Nephelomys levipes</i>	4	21.92	6.32	34.14	18.5	5.69	6.1	0.18	28.1	0.4	416.9	0.4
<i>Notiomys edwardsii</i>	1	12.57	3.44	23.55	13.0	3.15	5.5	0.23	17.7	0.4	164.3	0.4
<i>Oecomys bicolor</i>	3	15.79	4.06	26.39	12.7	3.68	4.3	0.16	11.5	0.4	152.4	0.4
<i>Oecomys concolor</i>	2	17.96	4.66	29.00	14.7	4.80	5.3	0.18	19.6	0.4	220.3	0.4
<i>Oecomys superans</i>	4	21.43	6.25	35.32	18.4	5.72	5.9	0.17	26.1	0.4	349.5	0.3
<i>Oligoryzomys fulvescens</i>	3	11.41	3.05	19.72	10.3	2.73	3.5	0.18	6.9	0.3	81.9	0.4
<i>Oligoryzomys longicaudatus</i>	4	14.13	3.63	24.17	12.5	3.30	4.6	0.19	12.5	0.3	148.8	0.4
<i>Oligoryzomys microtis</i>	4	12.57	3.25	21.75	11.7	3.04	4.0	0.18	8.8	0.3	105.8	0.4
<i>Oryzomys couesi</i>	3	17.10	4.49	26.97	13.6	4.18	4.9	0.18	14.2	0.3	232.1	0.4
<i>Oryzomys palustris</i>	4	18.08	5.20	28.93	15.1	4.33	5.3	0.18	18.2	0.3	256.1	0.4
<i>Oxymycterus hiska</i>	4	15.81	3.82	28.55	13.6	4.21	5.4	0.19	19.6	0.4	225.8	0.4
<i>Oxymycterus nasutus</i>	4	20.06	4.75	32.23	14.1	4.50	6.3	0.20	27.4	0.3	198.8	0.4
<i>Phyllostis amicus</i>	6	13.98	3.41	24.46	12.5	3.61	5.3	0.22	22.9	0.4	164.3	0.5
<i>Phyllostis andium</i>	4	14.95	3.75	26.11	13.5	4.14	5.5	0.21	25.5	0.4	181.6	0.4
<i>Phyllostis caprinus</i>	2	19.47	5.08	29.61	15.1	4.51	5.6	0.19	25.6	0.3	320.3	0.4
<i>Phyllostis darwini</i>	4	19.26	5.04	30.00	15.0	4.35	6.4	0.21	41.9	0.3	317.2	0.2
<i>Phyllostis gerbillus</i>	4	13.39	3.82	22.54	11.8	3.33	4.6	0.21	15.2	0.3	112.5	0.4
<i>Phyllostis magister</i>	2	19.82	4.98	30.48	15.9	4.85	5.9	0.20	30.4	0.4	367.7	0.5
<i>Phyllostis osilae</i>	4	17.52	4.26	27.28	14.1	4.26	5.2	0.19	22.1	0.3	243.3	0.5
<i>Phyllostis xanthopygus</i>	4	19.90	5.80	30.83	15.4	4.67	5.8	0.19	29.3	0.3	372.5	0.4
<i>Pseudoryzomys simplex</i>	4	18.25	4.50	28.93	15.3	4.37	5.5	0.19	21.3	0.3	291.3	0.5
<i>Punomys kofordi</i>	3	20.60	5.43	33.52	18.2	6.64	7.1	0.21	53.3	0.4	403.8	0.5
<i>Reithrodon a. auritus</i>	4	20.79	4.66	35.33	19.7	6.07	7.1	0.20	56.4	0.4	453.7	0.4
<i>Reithrodon a. physodes</i>	4	17.75	4.30	32.20	17.2	5.34	7.7	0.24	39.9	0.4	373.4	0.6
<i>Rhagomys longilingua</i>	1	17.41	5.27	26.26	14.6	4.21	5.2	0.20	14.5	0.4	134.6	0.4
<i>Rheomys t. stutoni</i>	2	16.85	5.42	29.17	14.9	3.99	4.9	0.17	12.4	0.3	229.3	0.3
<i>Rheomys t. thomasi</i>	2	15.30	4.45	26.56	14.1	4.13	4.3	0.16	9.9	0.3	167.6	0.3
<i>Rhipidomys macconnelli</i>	4	17.04	4.22	29.77	15.5	4.77	5.2	0.17	16.2	0.3	246.3	0.5
<i>Rhipidomys nitela</i>	4	19.46	4.95	30.20	15.8	4.56	5.2	0.17	17.1	0.3	227.9	0.5
<i>Scapteromys tumidus</i>	4	24.15	6.35	39.57	19.5	6.48	7.2	0.18	47.0	0.3	532.7	0.4
<i>Scolomys melanops</i>	1	12.63	4.01	19.45	11.2	2.37	3.7	0.19	8.1	0.4	72.9	0.3
<i>Scolomys uacayalensis</i>	4	13.03	3.26	20.95	11.2	2.47	3.8	0.18	8.3	0.4	108.1	0.4
<i>Sigmodon alstoni</i>	4	19.28	5.17	29.07	16.7	5.25	6.6	0.23	33.3	0.4	259.7	0.5
<i>Sigmodon arizonae</i>	4	23.02	6.59	34.49	20.4	6.57	6.8	0.20	42.2	0.4	430.5	0.5
<i>Sigmodon fulviventer</i>	4	21.07	5.73	31.79	18.7	5.62	6.8	0.21	39.7	0.4	338.5	0.5
<i>Sigmodon hispidus</i>	3	22.48	5.95	35.05	19.1	5.75	7.2	0.21	44.6	0.4	449.3	0.5
<i>Sigmodon ochrognathus</i>	4	20.01	5.58	30.43	17.7	5.40	6.3	0.21	31.1	0.4	260.6	0.5
<i>Sigmodontomys alfari</i>	4	22.55	6.63	34.03	18.2	5.30	5.0	0.15	17.5	0.3	459.3	0.4
<i>Sooretamys angouya</i>	3	20.09	4.94	35.09	17.1	5.62	6.1	0.18	23.4	0.4	466.7	0.5
<i>Thaptomys nigrita</i>	4	15.41	4.70	23.03	12.6	3.36	4.7	0.20	11.6	0.4	121.8	0.3
<i>Thomasomys aureus</i>	4	22.41	6.60	37.10	19.8	6.90	6.4	0.17	35.3	0.3	468.3	0.4
<i>Thomasomys daphne</i>	4	16.29	4.51	25.08	12.9	3.95	4.6	0.18	14.7	0.3	124.4	0.4
<i>Thomasomys notatus</i>	4	16.84	4.60	28.41	14.7	4.20	5.5	0.19	20.4	0.3	198.0	0.3
<i>Transandinomys talamancae</i>	4	17.38	4.81	27.98	14.1	4.05	4.8	0.17	13.6	0.3	202.3	0.3
<i>Wiedomys pyrrhorhinos</i>	3	16.52	5.22	28.34	14.3	4.24	6.4	0.23	37.4	0.3	182.5	0.4
<i>Zygodontomys brevicauda</i>	3	17.62	4.77	27.97	14.2	4.00	5.1	0.18	15.4	0.3	209.1	0.4
Tylomyinae												
<i>Nyctomyssumichrasti</i>	5	18.49	5.08	29.66	16.6	4.55	5.3	0.18	19.3	0.4	220.1	0.5
<i>Ototylomys phyllotis</i>	3	24.10	5.44	39.55	19.3	6.90	7.3	0.18	59.0	0.3	365.2	0.5
<i>Tylomys nudicaudus</i>	5	23.55	8.57	42.72	22.2	7.88	7.2	0.17	49.2	0.3	556.3	0.4
Muridae												
Deomyinae												
<i>Acomys cahirinus</i>	7	15.47	4.13	26.07	12.8	3.96	4.9	0.19	15.0	0.3	127.6	0.4
<i>Acomys cinereaceus</i>	4	15.24	4.05	25.92	12.1	3.76	4.7	0.18	12.9	0.3	132.2	0.4
<i>Acomys dimidiatus</i>	1	16.61	4.77	28.10	14.0	4.01	5.2	0.19	22.8	0.3	153.7	0.3
<i>Acomys ignitus</i>	4	13.20	4.07	27.13	12.9	3.83	5.5	0.20	19.0	0.3	138.8	0.4
<i>Acomys percivali</i>	4	15.52	3.97	27.18	13.1	4.16	5.2	0.19	17.7	0.3	133.8	0.4
<i>Acomys russatus</i>	4	16.46	4.11	27.78	13.7	4.56	5.7	0.20	23.8	0.3	158.1	0.5
<i>Acomys spinosissimus</i>	4	14.80	3.99	25.17	12.3	4.05	4.5	0.18	11.3	0.3	113.4	0.5
<i>Acomys wilsoni</i>	4	14.85	3.54	27.14	13.3	4.18	5.6	0.21	21.7	0.3	123.9	0.4

Table E.7—continued.

	#	AJL	AIL	ASL	ASW	AML	ABL	BI	BV	NI	NV	LII
<i>Deomys ferrugineus</i>	4	21.74	4.92	34.03	14.5	5.47	6.0	0.18	27.5	0.3	327.3	0.5
<i>Lophuromys f. flavopunctatus</i>	3	18.57	5.04	27.34	12.8	4.47	5.6	0.21	21.6	0.3	152.9	0.3
<i>Lophuromys f. zaphiri</i>	1	22.29	6.17	29.93	15.3	4.96	6.1	0.20	29.2	0.3	181.0	0.4
<i>Lophuromys f. zena</i>	4	18.22	4.89	27.84	13.6	4.42	5.9	0.21	24.7	0.2	159.1	0.4
<i>Lophuromys sikapusi</i>	4	19.01	5.06	30.14	15.0	4.82	6.0	0.20	29.5	0.3	187.6	0.3
<i>Uranomys ruddi</i>	4	18.56	5.19	25.87	13.6	4.26	5.1	0.20	15.0	0.3	163.5	0.3
Gerbillinae												
<i>Ammodillus imbellis</i>	1	15.51	3.66	28.99	14.0	4.32	8.8	0.30	71.1	0.2	135.6	0.3
<i>Brachionomys przewalskii</i>	1	14.16	3.77	22.94	13.3	3.41	8.0	0.35	76.0	0.4	109.2	0.5
<i>Desmodillus braueri</i>	6	11.74	2.87	19.61	11.5	2.89	7.2	0.36	61.5	0.3	58.6	0.4
<i>Desmodillus auricularis</i>	8	19.75	5.08	33.66	18.5	4.04	13.5	0.40	328.8	0.3	284.4	0.4
<i>Dipodillus campestris</i>	4	15.09	3.92	25.47	13.0	3.52	7.5	0.29	47.9	0.3	126.8	0.4
<i>Dipodillus dasyurus</i>	4	15.19	3.45	25.24	13.4	3.47	8.1	0.32	66.4	0.3	135.5	0.4
<i>Dipodillus harwoodi</i>	4	13.28	3.31	23.45	12.2	3.43	7.1	0.30	46.8	0.3	108.5	0.4
<i>Dipodillus lowei</i>	2	15.78	4.02	28.95	13.4	4.05	7.6	0.26	71.7	0.3	187.8	0.4
<i>Dipodillus mackilligini</i>	1	16.02	4.16	25.31	13.0	3.63	9.0	0.35	89.7	0.3	120.5	0.4
<i>Dipodillus magharebi</i>	6	17.71	4.58	29.01	15.5	4.01	8.2	0.28	77.4	0.3	252.5	0.4
<i>Dipodillus simoni</i>	4	12.95	3.27	22.86	12.6	3.22	7.0	0.30	43.0	0.3	89.9	0.4
<i>Dipodillus stigmonyx</i>	4	12.95	3.17	22.73	11.7	3.10	7.7	0.34	61.7	0.3	76.9	0.5
<i>Gerbiliscus afra</i>	4	23.05	5.54	37.74	20.4	6.06	10.7	0.28	188.1	0.3	456.3	0.5
<i>Gerbiliscus boehmi</i>	4	25.82	6.04	40.61	21.6	6.56	10.7	0.26	169.0	0.3	672.2	0.3
<i>Gerbiliscus b. brantsii</i>	4	23.54	5.24	36.50	19.3	5.75	11.3	0.31	206.7	0.3	426.7	0.5
<i>Gerbiliscus b. humpatensis</i>	2	24.44	5.71	39.20	19.8	6.32	10.8	0.27	198.5	0.3	484.1	0.5
<i>Gerbiliscus b. perpallidus</i>	4	20.74	4.65	34.44	17.8	5.44	10.0	0.29	141.8	0.3	319.2	0.5
<i>Gerbiliscus guineae</i>	4	22.62	5.55	37.20	18.1	5.44	9.9	0.27	126.2	0.3	471.5	0.4
<i>Gerbiliscus inclusus</i>	4	24.52	6.54	37.04	19.3	5.94	10.7	0.29	172.1	0.3	502.0	0.4
<i>Gerbiliscus kempti</i>	4	24.25	6.39	38.34	19.3	5.89	9.8	0.26	133.7	0.3	508.4	0.4
<i>Gerbiliscus leucogaster</i>	4	21.83	4.86	34.47	18.3	5.24	10.0	0.29	144.0	0.3	383.2	0.4
<i>Gerbiliscus nigricaudus</i>	4	22.64	5.44	38.19	18.6	5.47	10.1	0.26	140.4	0.3	477.8	0.3
<i>Gerbiliscus philipsi</i>	4	23.87	5.46	38.35	19.7	5.75	11.1	0.29	157.0	0.3	501.5	0.4
<i>Gerbiliscus robustus</i>	4	23.55	4.41	41.00	20.5	6.06	11.0	0.27	166.2	0.3	549.4	0.5
<i>Gerbiliscus validus</i>	4	25.80	6.12	38.78	21.1	6.15	10.9	0.28	168.0	0.3	528.5	0.4
<i>Gerbillurus paeba</i>	4	15.49	3.74	27.71	14.1	3.82	8.3	0.30	67.2	0.3	155.2	0.4
<i>Gerbillurus setzeri</i>	4	16.41	3.30	27.32	15.0	3.98	10.5	0.38	159.0	0.3	139.2	0.4
<i>Gerbillurus tytonis</i>	4	16.33	4.08	27.13	14.3	3.82	9.4	0.35	121.3	0.3	146.1	0.4
<i>Gerbillurus vallinus</i>	4	15.41	3.56	27.52	14.7	3.72	10.2	0.37	149.6	0.3	146.1	0.4
<i>Gerbillus agag</i>	4	14.72	3.47	28.30	14.7	3.87	8.9	0.31	100.8	0.3	146.4	0.5
<i>Gerbillus amoenus</i>	4	12.93	3.23	23.27	12.5	3.13	7.1	0.31	61.8	0.3	85.9	0.4
<i>Gerbillus andersoni</i>	4	15.61	3.71	27.99	15.2	3.86	8.5	0.30	88.2	0.3	157.8	0.5
<i>Gerbillus aquilus</i>	4	16.01	3.83	28.17	15.2	3.59	8.9	0.32	119.6	0.3	138.1	0.4
<i>Gerbillus cheesmani</i>	4	15.59	3.40	27.63	15.2	3.57	9.1	0.33	114.3	0.3	136.8	0.4
<i>Gerbillus famulus</i>	4	13.81	3.38	25.18	13.0	3.03	8.2	0.33	96.7	0.3	112.8	0.4
<i>Gerbillus floweri</i>	4	18.11	4.21	32.05	17.2	4.02	9.0	0.28	120.6	0.3	238.5	0.4
<i>Gerbillus garamantis</i>	1	13.82	3.28	23.41	12.5	3.11	6.9	0.29	56.2	0.3	92.2	0.4
<i>Gerbillus gerbillus</i>	6	15.06	3.74	26.39	14.6	3.34	8.3	0.32	71.0	0.3	131.1	0.4
<i>Gerbillus gleadowi</i>	4	15.08	3.58	28.00	14.6	3.72	8.6	0.31	97.9	0.3	160.1	0.4
<i>Gerbillus henleyi</i>	4	11.49	2.75	21.40	11.7	2.82	7.0	0.33	53.0	0.3	68.4	0.4
<i>Gerbillus hesperinus</i>	4	15.59	3.80	28.46	15.4	3.90	8.1	0.29	80.4	0.3	190.9	0.3
<i>Gerbillus hoogstraali</i>	4	14.97	3.64	26.70	14.3	3.46	8.0	0.30	80.3	0.3	132.1	0.4
<i>Gerbillus latastei</i>	4	15.53	3.65	28.03	14.9	3.73	9.0	0.32	103.3	0.3	163.7	0.4
<i>Gerbillus mauritaniae</i>	4	12.57	2.90	20.41	11.1	2.85	6.4	0.31	40.6	0.3	60.9	0.5
<i>Gerbillus mesopotamiae</i>	4	14.76	3.88	26.44	14.3	3.48	8.0	0.30	75.8	0.3	159.3	0.4
<i>Gerbillus muriculus</i>	4	11.50	2.70	20.57	10.5	2.98	6.4	0.31	37.0	0.3	57.1	0.4
<i>Gerbillus nanus</i>	6	13.48	3.09	25.28	13.1	3.31	8.1	0.32	85.4	0.3	108.8	0.4
<i>Gerbillus nigeriae</i>	2	14.79	3.92	25.17	12.7	3.49	7.0	0.28	na	0.3	124.9	0.5
<i>Gerbillus occiduus</i>	1	15.91	3.84	30.26	16.6	3.71	9.1	0.30	107.1	0.3	199.4	0.4
<i>Gerbillus perpallidus</i>	4	17.59	4.29	29.20	15.7	3.92	8.8	0.30	93.1	0.3	201.2	0.4
<i>Gerbillus poecilops</i>	4	16.25	4.38	27.90	14.8	3.41	8.6	0.31	89.5	0.3	176.7	0.4
<i>Gerbillus pulvinatus</i>	4	15.91	3.66	26.30	14.4	3.37	8.5	0.33	85.5	0.3	174.4	0.4
<i>Gerbillus pusillus</i>	4	12.31	3.00	22.13	11.0	2.91	6.5	0.30	38.9	0.3	73.0	0.4
<i>Gerbillus pyramidum</i>	4	19.03	4.86	32.41	17.8	4.22	10.0	0.31	127.9	0.3	263.1	0.3
<i>Gerbillus tarabuli</i>	4	17.96	4.57	29.86	15.8	3.76	9.3	0.31	110.8	0.3	189.6	0.4
<i>Meriones crassus</i>	4	20.33	4.56	34.08	18.7	4.68	13.3	0.39	344.9	0.3	290.3	0.4
<i>Meriones grandis</i>	4	27.53	7.20	41.70	22.6	5.67	12.8	0.31	280.9	0.3	605.9	0.4
<i>Meriones hurrianae</i>	4	20.24	5.02	34.05	19.7	5.13	10.6	0.31	178.3	0.3	312.7	0.4
<i>Meriones l. erythrourus</i>	1	22.85	5.60	38.78	21.6	5.09	14.2	0.37	407.2	0.2	401.9	0.4
<i>Meriones l. libycus</i>	4	22.61	5.42	40.53	21.6	5.50	14.6	0.36	452.5	0.3	438.8	0.4
<i>Meriones meridianus</i>	4	18.35	5.13	33.02	18.2	4.60	12.3	0.37	263.4	0.3	278.9	0.3
<i>Meriones persicus</i>	4	27.54	7.41	46.26	25.2	6.00	12.4	0.27	287.4	0.3	805.7	0.4
<i>Meriones rex</i>	4	22.95	5.92	37.61	20.9	5.49	11.8	0.31	226.9	0.3	522.6	0.5
<i>Meriones shawi</i>	4	22.05	5.53	37.79	21.2	5.16	13.2	0.35	302.7	0.3	444.0	0.4
<i>Meriones tamariscinus</i>	4	23.91	6.46	39.85	21.8	5.55	10.9	0.27	196.5	0.3	573.0	0.4
<i>Meriones tristrami</i>	4	23.06	6.28	37.65	20.2	4.92	10.8	0.29	177.6	0.3	470.5	0.4
<i>Meriones unguiculatus</i>	8	18.94	4.60	33.76	19.7	4.44	10.9	0.32	178.2	0.3	332.6	0.4
<i>Meriones vinogradovi</i>	4	23.85	6.31	37.55	20.4	5.09	11.6	0.31	205.3	0.3	421.5	0.4
<i>Pachyuromys duprasi</i>	9	18.53	4.79	32.01	18.2	4.50	15.6	0.49	453.1	0.3	233.0	0.4

Table E.7—continued.

	#	AJL	AIL	ASL	ASW	AML	ABL	BI	BV	NI	NV	LII
<i>Psammomys obesus</i>	9	24.33	5.93	39.01	23.3	6.11	13.0	0.33	318.9	0.3	499.7	0.5
<i>Rhomomys o. sodalis</i>	4	25.22	6.66	39.67	23.5	6.27	12.5	0.32	262.7	0.3	565.9	0.5
<i>Rhomomys o. ssp</i>	5	25.17	5.89	38.07	22.0	6.08	12.7	0.34	294.6	0.3	488.0	0.5
<i>Seketamys calurus</i>	8	19.12	4.12	32.87	16.7	4.38	11.2	0.34	193.2	0.3	242.9	0.5
<i>Tatera indica</i>	8	23.93	5.92	40.97	21.7	5.72	11.5	0.28	217.3	0.3	604.4	0.4
<i>Taterillus arenarius</i>	4	17.60	4.37	32.14	16.1	4.17	9.1	0.28	96.8	0.3	218.7	0.3
<i>Taterillus conicus</i>	4	18.83	4.65	32.67	16.1	4.71	9.0	0.28	82.5	0.3	262.8	0.3
<i>Taterillus emini</i>	4	17.82	4.80	31.97	15.9	4.63	8.7	0.27	79.5	0.2	257.5	0.4
<i>Taterillus gracilis</i>	4	17.42	4.22	32.20	15.9	3.90	8.8	0.27	90.0	0.3	226.9	0.3
<i>Taterillus harringtoni</i>	4	18.18	4.36	33.23	16.8	4.52	9.8	0.29	114.7	0.3	277.8	0.3
<i>Taterillus lacustris</i>	4	18.00	3.93	32.09	16.0	4.80	8.7	0.27	87.3	0.3	242.1	0.4
<i>Taterillus pygargus</i>	4	19.01	4.79	33.84	17.1	4.62	9.1	0.27	98.1	0.3	283.1	0.4
Lophiomyinae												
<i>Lophiomys i. imhausi</i>	2	41.30	8.86	59.61	36.2	13.10	9.9	0.17	113.0	0.4	2713.7	0.7
<i>Lophiomys i. thomasi</i>	2	37.92	9.22	55.95	33.4	13.24	10.6	0.19	119.0	0.5	1959.5	0.2
Murinae												
<i>Abeomelomys sevia</i>	4	19.74	5.44	32.44	15.9	5.79	4.9	0.15	17.7	0.4	219.5	0.4
<i>Aethomys chrysophilus</i>	4	20.56	5.39	35.38	17.7	5.78	6.7	0.19	40.0	0.4	346.5	0.4
<i>Anisomys imitator</i>	4	42.07	11.28	66.28	32.3	10.21	8.2	0.12	84.4	0.4	3735.7	0.3
<i>Apodemus agrarius</i>	4	15.50	4.46	25.83	12.1	3.82	4.9	0.19	18.8	0.4	122.8	0.4
<i>Apodemus mystacinus</i>	4	17.85	4.83	29.24	13.9	4.48	5.3	0.18	22.2	0.4	209.0	0.4
<i>Apodemus semotus</i>	4	14.68	3.91	25.50	12.1	3.89	4.5	0.18	13.1	0.3	136.7	0.4
<i>Apodemus speciosus</i>	2	16.03	4.41	25.29	12.6	3.79	4.6	0.18	13.6	0.3	140.7	0.3
<i>Apodemus sylvaticus</i>	4	14.63	3.62	23.77	11.8	3.62	4.7	0.20	15.3	0.3	108.3	0.4
<i>Apomys datae</i>	4	23.07	6.34	36.67	17.1	6.66	5.6	0.15	27.8	0.3	405.9	0.4
<i>Apomys hylocoetes</i>	4	16.73	4.41	28.34	12.8	5.22	4.5	0.16	15.9	0.3	182.6	0.4
<i>Archboldomys luzonensis</i>	4	16.48	4.65	25.98	12.3	4.40	4.3	0.17	14.9	0.3	132.0	0.4
<i>Arvicathis neumanni</i>	2	19.73	4.75	29.87	15.6	5.61	6.2	0.21	35.8	0.4	277.0	0.4
<i>Arvicathis niloticus</i>	4	20.49	5.28	30.57	15.5	6.19	6.6	0.22	37.4	0.3	253.0	0.5
<i>Bandicota bengalensis</i>	3	30.91	10.09	41.22	24.8	7.94	8.8	0.21	110.8	0.3	794.9	0.5
<i>Batomys salomonensi</i>	4	25.42	7.40	39.49	19.9	7.25	5.4	0.14	26.5	0.3	757.5	0.4
<i>Berylmys bowersi</i>	4	34.80	8.85	53.87	27.1	9.12	9.0	0.17	120.0	0.3	1546.7	0.5
<i>Bullimus bagobus</i>	6	38.02	9.15	60.40	28.9	9.43	12.7	0.21	278.9	0.3	1988.7	0.5
<i>Bunomys chrysocomus</i>	4	24.44	6.51	38.16	18.1	5.88	7.0	0.18	48.5	0.3	467.6	0.4
<i>Carpomys phaeurus</i>	1	23.69	6.77	36.36	19.7	6.07	6.3	0.17	39.0	0.3	465.0	0.4
<i>Chiromyscus chiropus</i>	4	22.95	5.57	37.08	17.4	6.73	6.3	0.17	32.3	0.3	417.8	0.5
<i>Chiropodomys gliroides</i>	4	15.83	4.30	23.86	13.6	3.44	4.6	0.19	14.6	0.3	115.3	0.4
<i>Chrotomys gonzalesi</i>	2	26.82	8.11	36.03	19.3	5.85	6.6	0.18	37.6	0.3	339.0	0.4
<i>Colomys goslingi</i>	4	19.16	5.22	31.44	14.7	5.01	5.6	0.18	22.6	0.3	293.1	0.3
<i>Conilurus penicillatus</i>	4	25.88	6.10	39.53	20.6	7.53	7.2	0.18	54.3	0.4	637.8	0.4
<i>Cremonomys cutchicus</i>	4	19.13	4.94	30.40	13.6	4.98	5.7	0.19	25.5	0.3	235.8	0.4
<i>Crunomys melanius</i>	2	16.35	4.89	27.82	12.4	3.79	5.5	0.20	18.9	0.3	175.8	0.4
<i>Dacnomys millardi</i>	4	35.83	9.44	55.49	25.7	11.25	8.0	0.14	62.0	0.3	1594.9	0.4
<i>Dasymys i. medius</i>	3	23.19	6.95	32.45	17.5	6.49	6.6	0.20	35.0	0.4	433.3	0.5
<i>Dasymys i. nudipes</i>	1	27.04	8.14	38.02	18.6	7.38	6.5	0.17	40.3	0.3	715.0	0.4
<i>Golunda ellioti</i>	3	19.10	4.10	29.46	14.2	5.70	6.4	0.22	32.9	0.3	201.8	0.7
<i>Grammomys d. dolichurus</i>	3	16.62	4.63	29.11	14.1	4.31	6.2	0.21	38.4	0.3	202.8	0.4
<i>Grammomys d. sardaster</i>	1	15.91	4.32	28.22	14.1	4.34	5.4	0.19	21.7	0.3	160.0	0.4
<i>Grammomys ibeanus</i>	4	18.81	5.28	29.22	14.1	4.33	5.4	0.19	27.1	0.3	201.6	0.3
<i>Grammomys macmillani</i>	4	15.58	4.15	26.29	12.8	3.81	5.3	0.20	20.7	0.4	155.9	0.4
<i>Hapalomys delacouri</i>	1	19.71	5.11	29.05	15.9	5.06	6.4	0.22	48.6	0.3	154.5	0.6
<i>Heimyscus fumosus</i>	4	14.99	4.06	23.65	10.5	3.45	4.7	0.20	12.8	0.3	113.4	0.3
<i>Hybomys univittatus</i>	4	18.66	4.72	30.78	14.6	5.02	5.6	0.18	26.2	0.4	309.7	0.4
<i>Hydromys c. chrysogaster</i>	1	32.71	9.74	53.35	28.1	7.95	8.3	0.16	78.9	0.4	1381.0	0.5
<i>Hydromys c. fowlavatus</i>	2	34.70	10.27	57.39	28.7	8.98	9.0	0.16	110.8	0.3	1581.5	0.3
<i>Hydromys c. ssp</i>	1	35.48	9.42	55.07	27.1	8.74	9.0	0.16	103.6	0.3	na	na
<i>Hylomyscus parvus</i>	4	14.93	4.11	22.65	11.0	3.28	4.2	0.19	10.9	0.4	96.4	0.4
<i>Hylomyscus stella</i>	4	15.60	4.43	24.04	11.4	3.38	4.3	0.18	12.0	0.3	114.2	0.3
<i>Hyomys goliath</i>	4	48.48	12.65	73.91	39.2	16.12	10.3	0.14	146.8	0.4	7968.6	0.7
<i>Leggadina forresti</i>	3	12.94	3.51	18.73	9.7	3.46	4.3	0.23	12.5	0.3	57.9	0.4
<i>Lemniscomys barbarus</i>	4	17.67	4.07	29.43	13.8	4.90	6.6	0.22	37.9	0.3	237.2	0.5
<i>Lemniscomys striatus</i>	3	18.57	4.53	29.36	13.7	4.86	6.0	0.20	30.3	0.3	259.7	0.4
<i>Leopoldamys sabanus</i>	4	33.61	7.83	53.26	23.7	9.39	8.4	0.16	74.5	0.3	1335.5	0.5
<i>Leptomyss elegans</i>	4	21.97	5.99	35.30	15.3	6.01	6.1	0.17	33.8	0.3	375.8	0.4
<i>Limnomyss sibuanus</i>	4	18.60	5.07	30.62	14.3	4.48	6.5	0.21	41.3	0.3	264.5	0.3
<i>Lorentzimys nouhuysi</i>	3	13.48	3.86	20.01	11.1	2.43	3.7	0.18	7.6	0.4	72.2	0.4
<i>Macruromys major</i>	4	31.21	8.42	51.22	24.0	6.37	6.6	0.13	46.3	0.4	1624.9	0.5
<i>Malacomys longipes</i>	4	21.48	5.49	36.56	16.0	4.93	5.5	0.15	26.9	0.3	392.0	0.4
<i>Margaretamys elegans</i>	4	25.14	6.40	41.34	19.2	6.28	6.6	0.16	47.6	0.3	533.4	0.4
<i>Mastacomys fuscus</i>	1	26.57	6.13	41.80	23.3	8.50	8.1	0.19	56.7	0.5	912.5	0.4
<i>Mastomys erythroleucus</i>	4	19.13	5.17	29.39	14.4	4.41	5.5	0.19	23.1	0.3	219.7	0.3
<i>Maxomys bartelsii</i>	4	23.36	5.75	36.63	15.7	5.02	6.0	0.16	32.0	0.3	397.4	0.4
<i>Maxomys surifer</i>	4	22.34	5.64	39.94	18.0	5.70	6.4	0.16	32.0	0.3	539.1	0.4
<i>Melasmotherix naso</i>	4	18.21	4.13	30.85	12.9	4.40	6.2	0.20	26.1	0.3	167.9	0.4
<i>Melomys cervinipes</i>	4	20.28	5.04	33.05	17.3	6.34	5.7	0.17	31.2	0.4	338.7	0.4
<i>Melomys rufescens</i>	2	19.68	4.86	30.87	15.2	5.92	5.1	0.16	19.5	0.4	280.5	0.4

Table E.7—continued.

	#	AJL	AIL	ASL	ASW	AML	ABL	BI	BV	NI	NV	LII
<i>Mesembriomys gouldii</i>	3	41.47	9.73	60.61	29.0	11.05	9.9	0.16	183.2	0.3	3060.5	0.4
<i>Micralamys namaquensis</i>	3	17.22	3.94	28.05	14.1	4.95	5.4	0.19	21.8	0.3	221.4	0.5
<i>Micromys minutus</i>	4	10.82	2.71	20.27	10.5	2.58	4.1	0.20	8.0	0.4	73.2	0.4
<i>Millardia gleadowi</i>	4	16.64	3.96	25.12	11.9	4.18	5.8	0.23	28.2	0.3	127.7	0.4
<i>Millardia kathleenae</i>	2	20.60	5.44	32.16	14.1	5.40	7.0	0.22	49.3	0.3	223.7	0.2
<i>Mus booduga</i>	5	12.26	3.44	18.65	9.5	3.03	4.0	0.21	7.4	0.3	57.0	0.4
<i>Mus cervicolor</i>	4	14.15	3.81	20.83	10.8	3.11	4.3	0.21	9.4	0.3	70.7	0.4
<i>Mus cookii</i>	4	15.64	4.55	23.63	11.4	3.72	4.4	0.19	11.1	0.3	90.9	0.4
<i>Mus minutoides</i>	9	10.87	2.67	17.90	9.1	2.86	3.6	0.20	6.2	0.3	52.1	0.5
<i>Mus m. bactrianus</i>	1	12.03	2.66	19.59	9.6	2.85	3.8	0.19	6.5	0.4	63.4	0.5
<i>Mus m. ssp</i>	2	11.67	2.96	19.99	10.1	2.86	4.1	0.20	8.4	0.3	64.0	0.4
<i>Mus m. yamashinai</i>	1	11.69	2.99	19.20	10.0	3.15	4.0	0.21	9.3	0.3	53.4	0.4
<i>Mus pahari</i>	4	15.74	3.92	25.28	12.1	3.72	4.7	0.18	12.5	0.3	145.5	0.4
<i>Mus saxicola</i>	4	18.40	4.67	25.57	12.4	4.05	5.1	0.20	14.1	0.3	130.6	0.4
<i>Mus spretus</i>	4	12.56	3.41	20.39	10.5	3.20	4.2	0.21	8.5	0.3	77.7	0.4
<i>Mus terricolor</i>	4	12.26	3.07	18.03	9.0	2.82	4.0	0.22	7.7	0.3	50.1	0.4
<i>Myomys dybowskii</i>	4	21.30	4.89	33.63	15.7	7.27	6.7	0.20	44.5	0.4	378.8	0.4
<i>Myomyscus Brockmani</i>	4	16.71	4.23	27.40	12.7	4.31	5.0	0.18	18.5	0.3	171.9	0.4
<i>Niviventer c. confucianus</i>	3	20.07	4.82	35.47	16.1	6.29	6.2	0.18	36.7	0.3	261.9	0.4
<i>Niviventer c. lotipes</i>	1	21.93	5.24	36.34	15.6	5.74	6.0	0.17	33.0	0.4	418.9	0.5
<i>Niviventer cremeriventer</i>	4	20.73	5.35	34.26	15.6	5.33	5.1	0.15	23.3	0.3	374.2	0.5
<i>Niviventer excelsior</i>	2	21.07	4.63	36.03	16.4	5.89	5.8	0.16	32.1	0.3	331.8	0.4
<i>Notomys alexis</i>	4	16.53	3.45	26.65	13.1	4.37	6.7	0.25	40.8	0.3	133.8	0.5
<i>Notomys cervinus</i>	4	17.53	3.89	26.95	13.7	4.47	6.4	0.24	37.9	0.3	151.1	0.4
<i>Notomys fuscus</i>	4	15.76	3.69	29.17	14.8	4.39	6.8	0.23	49.3	0.3	171.2	0.4
<i>Oenomys h. editus</i>	2	20.78	4.59	33.30	15.9	6.16	6.3	0.19	40.9	0.4	374.1	0.5
<i>Oenomys h. hypoxanthus</i>	2	21.45	4.99	33.54	15.1	6.34	6.1	0.18	40.2	0.3	386.0	0.6
<i>Otomys angoniensis</i>	4	23.70	4.84	36.99	18.6	8.28	8.2	0.22	86.5	0.5	1086.9	0.8
<i>Otomys denti</i>	4	21.48	5.21	36.21	17.7	7.62	7.9	0.22	84.1	0.5	846.0	0.7
<i>Parotomys brantsii</i>	4	23.53	5.04	35.17	18.7	7.32	11.7	0.33	292.9	0.5	394.0	0.7
<i>Parotomys littledalei</i>	5	23.80	5.07	34.99	18.2	7.04	11.5	0.33	255.6	0.4	456.8	0.7
<i>Paruromys dominator</i>	4	35.94	8.71	55.60	26.3	8.80	9.0	0.16	115.4	0.3	1847.4	0.4
<i>Pogonomys loriae</i>	2	22.88	5.67	33.91	18.3	5.82	5.1	0.15	21.7	0.3	377.6	0.5
<i>Pogonomys macrourus</i>	4	20.27	5.85	30.24	16.4	5.13	5.3	0.17	23.0	0.3	215.4	0.4
<i>Praomys jacksoni montis</i>	1	19.36	5.11	28.11	13.8	4.31	4.8	0.17	17.6	0.3	219.1	0.4
<i>Praomys jacksoni ssp</i>	3	18.18	5.11	30.91	13.9	4.39	5.4	0.17	22.4	0.3	219.6	0.3
<i>Praomys misonnei</i>	4	19.88	5.39	31.41	14.1	4.57	5.0	0.16	21.4	0.3	259.6	0.3
<i>Praomys tullbergi</i>	3	20.43	5.66	30.60	14.1	4.44	5.1	0.17	19.6	0.3	257.0	0.3
<i>Pseudohydromys ellermani</i>	3	13.66	4.56	21.67	9.7	1.61	3.9	0.18	7.1	0.4	73.9	0.4
<i>Pseudomys australis</i>	5	18.90	4.80	30.50	15.4	5.51	6.0	0.20	33.6	0.4	249.3	0.5
<i>Pseudomys hermannsburgensis</i>	4	12.64	2.82	21.57	10.5	3.40	5.1	0.24	22.7	0.3	66.9	0.4
<i>Rattus exulans</i>	4	18.50	4.77	29.14	14.0	4.67	5.9	0.20	33.7	0.3	213.1	0.4
<i>Rattus norvegicus</i>	3	29.04	7.81	44.99	21.8	6.48	8.2	0.18	70.1	0.3	989.7	0.4
<i>Rattus praetor</i>	4	29.78	8.22	45.24	21.9	7.00	7.5	0.17	65.5	0.3	1158.9	0.3
<i>Rattus rattus</i>	4	24.99	6.52	39.81	18.6	5.68	7.8	0.20	77.3	0.3	592.8	0.4
<i>Rattus sordidus</i>	4	22.36	6.10	33.20	17.2	6.70	7.7	0.23	75.7	0.4	341.3	0.5
<i>Rattus tiomanicus</i>	4	27.41	7.88	40.33	19.1	6.53	7.9	0.20	74.0	0.3	647.1	0.4
<i>Rattus verecundus</i>	4	21.45	4.89	34.77	15.7	5.65	5.7	0.16	31.1	0.3	316.5	0.5
<i>Rattus villosissimus</i>	4	26.88	7.58	37.67	18.8	6.69	8.5	0.23	92.2	0.3	498.6	0.4
<i>Rhabdomys pumilio</i>	4	16.13	4.29	26.31	13.0	4.37	6.1	0.23	30.0	0.4	167.1	0.4
<i>Rhynchosomys isarogenensis</i>	4	27.97	6.32	41.26	16.0	2.14	6.4	0.15	29.8	0.2	310.3	0.3
<i>Stenocephalemys albipes</i>	4	19.89	5.18	30.24	14.5	5.18	5.3	0.18	24.3	0.3	246.5	0.4
<i>Stochomys longicaudatus</i>	4	22.91	6.47	36.95	18.0	6.31	5.9	0.16	30.3	0.4	581.4	0.4
<i>Sundamys muelleri muelleri</i>	4	34.69	9.68	50.65	24.8	8.97	8.0	0.16	95.7	0.3	1477.4	0.4
<i>Tarsomys apensis</i>	3	22.15	6.04	35.93	17.4	5.65	6.4	0.18	42.8	0.3	387.3	0.4
<i>Uromys caudimaculatus</i>	4	47.66	12.22	71.89	34.9	12.19	8.5	0.12	115.5	0.3	3894.0	0.4
<i>Vandeleuria oleracea</i>	4	11.75	3.11	19.46	10.1	2.83	3.8	0.20	8.5	0.3	60.4	0.5
<i>Zelotomys h. ssp</i>	1	21.30	6.51	27.66	14.8	5.01	4.9	0.18	21.3	0.3	285.6	0.2
<i>Zelotomys h. vinaceus</i>	3	20.45	6.30	28.02	15.1	4.79	5.3	0.19	20.4	0.3	269.6	0.3
<i>Zelotomys woosnami</i>	4	19.97	5.97	29.07	14.5	4.74	5.7	0.19	23.1	0.3	243.4	0.4
<i>Zyzomys argurus</i>	4	17.99	4.61	29.55	13.3	4.67	4.9	0.17	22.4	0.3	171.3	0.4
Nesomyidae												
Cricetomyinae												
<i>Beamyshindei</i>	4	21.59	5.78	33.00	15.2	4.76	5.8	0.18	23.1	0.3	269.2	0.3
<i>Cricetomys gambianus</i>	3	40.09	9.02	59.24	27.3	10.02	9.2	0.16	108.7	0.4	2654.4	0.5
<i>Saccostomus campestris</i>	4	19.05	5.13	29.77	14.6	4.30	6.3	0.21	33.1	0.4	237.8	0.4
Delanomyinae												
<i>Delanymys brooksi</i>	4	9.29	2.30	16.35	8.9	2.33	4.1	0.25	7.4	0.3	34.3	0.5
Dendromurinae												
<i>Dendromus insignis</i>	4	12.83	3.29	22.70	10.9	3.59	5.2	0.23	16.1	0.3	105.4	0.5
<i>Dendromus mesomelas</i>	1	11.16	2.87	21.27	10.4	3.24	4.9	0.23	14.2	0.3	68.4	0.4
<i>Dendromus nyasae</i>	4	12.49	3.13	21.23	10.3	3.21	4.8	0.22	12.6	0.3	77.1	0.5
<i>Malacothrix typica</i>	4	13.71	3.04	23.13	12.6	3.67	4.7	0.20	20.2	0.3	104.3	0.5
<i>Steatomys krebsi</i>	1	14.30	3.58	20.52	10.4	3.33	5.2	0.25	18.9	0.3	74.7	0.4
<i>Steatomys p. athi</i>	1	13.62	3.50	22.44	11.2	3.17	5.7	0.26	26.9	0.3	115.8	0.4
<i>Steatomys p. kalaharicus</i>	1	13.48	3.90	22.51	11.7	3.18	6.2	0.28	29.9	0.3	114.6	0.3

Table E.7—continued.

	#	AJL	AIL	ASL	ASW	AML	ABL	BI	BV	NI	NV	LII
<i>Steatomys p. ssp</i>	1	12.83	3.23	20.70	10.5	3.10	5.2	0.25	19.4	0.3	75.4	0.4
<i>Steatomys p. tongensis</i>	1	12.83	3.24	18.24	9.9	3.06	5.3	0.29	17.0	0.4	62.3	0.3
Mystromyinae												
<i>Mystromys albicaudatus</i>	4	22.72	6.52	32.73	16.8	5.79	6.9	0.21	46.2	0.3	369.9	0.4
Nesomyinae												
<i>Brachytarsomys albicauda</i>	4	29.90	7.72	44.31	24.8	8.18	8.5	0.19	58.2	0.3	887.4	0.5
<i>Brachyuromys betsileensis</i>	4	22.26	6.21	33.06	19.7	6.36	7.7	0.23	61.0	0.4	428.2	0.5
<i>Elurus minor</i>	4	17.02	4.52	28.67	14.5	3.95	5.2	0.18	21.3	0.3	218.2	0.4
<i>Elurus tanala</i>	4	24.96	6.83	39.13	18.4	5.66	6.5	0.17	39.6	0.3	588.2	0.4
<i>Gymnuromys roberti</i>	4	23.33	6.44	37.67	19.2	5.50	6.4	0.17	35.3	0.3	553.9	0.4
<i>Hypogeomys antimena</i>	1	na	na	na	na	na	na	na	na	na	na	na
<i>Macrotarsomys bastardi</i>	4	15.90	4.20	26.42	13.2	3.65	5.9	0.22	32.3	0.3	164.8	0.3
<i>Monticolomys koopmani</i>	2	15.83	4.01	26.30	13.5	3.59	6.2	0.24	27.7	0.3	127.5	0.4
<i>Nesomys rufus</i>	4	26.63	6.73	43.71	22.7	6.61	8.0	0.18	77.8	0.4	879.5	0.5
<i>Voalavo gymnocaudus</i>	4	15.72	4.24	24.50	12.8	3.60	4.3	0.18	11.9	0.3	117.2	0.4
Petromyscinae												
<i>Petromyscus collinus</i>	8	13.95	3.48	23.03	10.9	3.13	4.8	0.21	13.3	0.3	92.7	0.5
Platacanthomysinae												
<i>Typhlomys c. chapensis</i>	1	15.69	4.92	25.39	12.9	4.06	4.0	0.16	13.1	0.4	115.4	0.3
<i>Typhlomys c. cinereus</i>	3	14.31	4.79	21.70	11.7	3.50	3.6	0.17	8.8	0.4	78.7	0.4
Spalacidae												
Myospalacinae												
<i>Eospalax f. kansus</i>	2	30.02	9.16	39.94	28.4	9.05	10.4	0.26	160.3	0.6	859.4	0.5
<i>Myospalax aspalax</i>	2	25.59	6.34	37.02	23.3	9.11	8.9	0.24	117.3	0.6	695.5	0.6
Rhizomysinae												
<i>Cannomys badius</i>	4	38.11	11.48	43.94	33.4	10.59	11.2	0.25	269.3	0.5	1664.0	0.6
<i>Rhizomys pruinosus</i>	4	47.53	13.75	67.45	49.1	14.17	14.3	0.21	682.2	0.4	5743.0	1.1
Tachyoryctinae												
<i>Tachyoryctes splendens</i>	4	35.05	13.05	44.68	31.3	8.55	11.0	0.25	224.0	0.4	1788.5	0.4
Spalacinae												
<i>Spalax ehrenbergi</i>	4	29.80	11.07	37.92	27.5	6.53	8.3	0.22	99.6	0.4	783.4	0.3
Sciuroomorpha												
Gliridae												
Graphiurinae												
<i>Graphiurus oocularis</i>	3	18.84	5.74	31.84	16.8	3.25	8.9	0.28	104.0	0.3	316.3	0.4
Leithiinae												
<i>Eliomys melanurus</i>	4	19.21	5.51	31.34	17.5	4.59	9.5	0.30	152.0	0.3	195.5	0.4
<i>Eliomys quercinus</i>	4	20.47	5.96	32.45	19.0	5.31	9.4	0.29	137.2	0.4	236.5	0.3
Sciuridae												
Xerinae												
Xerini												
<i>Atlantoxerus getulus</i>	4	28.39	7.21	43.02	26.0	8.55	11.0	0.26	220.7	0.5	613.8	0.5
<i>Xerus erythropus</i>	4	37.04	9.13	56.80	30.4	11.74	13.9	0.24	336.3	0.6	1522.1	0.5
<i>Xerus inauris</i>	4	34.64	7.99	55.54	33.8	10.94	13.5	0.24	434.1	0.6	1872.1	0.5
<i>Xerus princeps</i>	3	37.98	9.76	58.96	34.7	10.84	14.7	0.25	483.3	0.5	1992.1	0.5
Marmotini												
<i>Ammospermophilus harrisi</i>	4	23.28	6.23	38.38	22.0	6.72	9.6	0.25	157.6	0.5	368.7	0.4
<i>Ammospermophilus interpres</i>	4	22.94	5.75	36.40	20.9	5.76	9.4	0.26	151.3	0.6	314.5	0.4
<i>Ammospermophilus leucurus</i>	4	21.70	5.83	37.30	21.2	6.37	9.4	0.25	158.0	0.5	331.8	0.4
<i>Ammospermophilus nelsoni</i>	4	23.93	5.13	39.00	22.9	7.23	10.4	0.27	206.9	0.6	343.3	0.5
<i>Spermophilus fulvus</i>	4	40.68	8.87	53.89	36.5	13.23	11.1	0.21	290.5	0.5	1901.1	0.5
<i>Spermophilus mexicanus</i>	4	31.86	8.38	49.19	29.1	9.46	10.8	0.22	188.9	0.5	1117.7	0.4
<i>Spermophilus mohavensis</i>	4	25.60	6.05	36.63	23.1	7.39	9.3	0.25	142.7	0.4	404.1	0.4
<i>Spermophilus pygmaeus</i>	4	29.23	7.37	38.59	25.1	8.58	8.7	0.22	102.0	0.6	711.5	0.4
<i>Spermophilus spilosoma</i>	4	23.94	5.77	36.55	21.8	6.98	9.7	0.27	139.3	0.6	397.6	0.5
<i>Spermophilus tereticaudus</i>	4	24.53	5.77	35.92	22.7	7.45	9.1	0.25	134.1	0.5	320.4	0.4
<i>Spermophilus variegatus</i>	4	42.52	10.39	62.38	38.6	12.31	13.7	0.22	398.6	0.6	2616.7	0.4

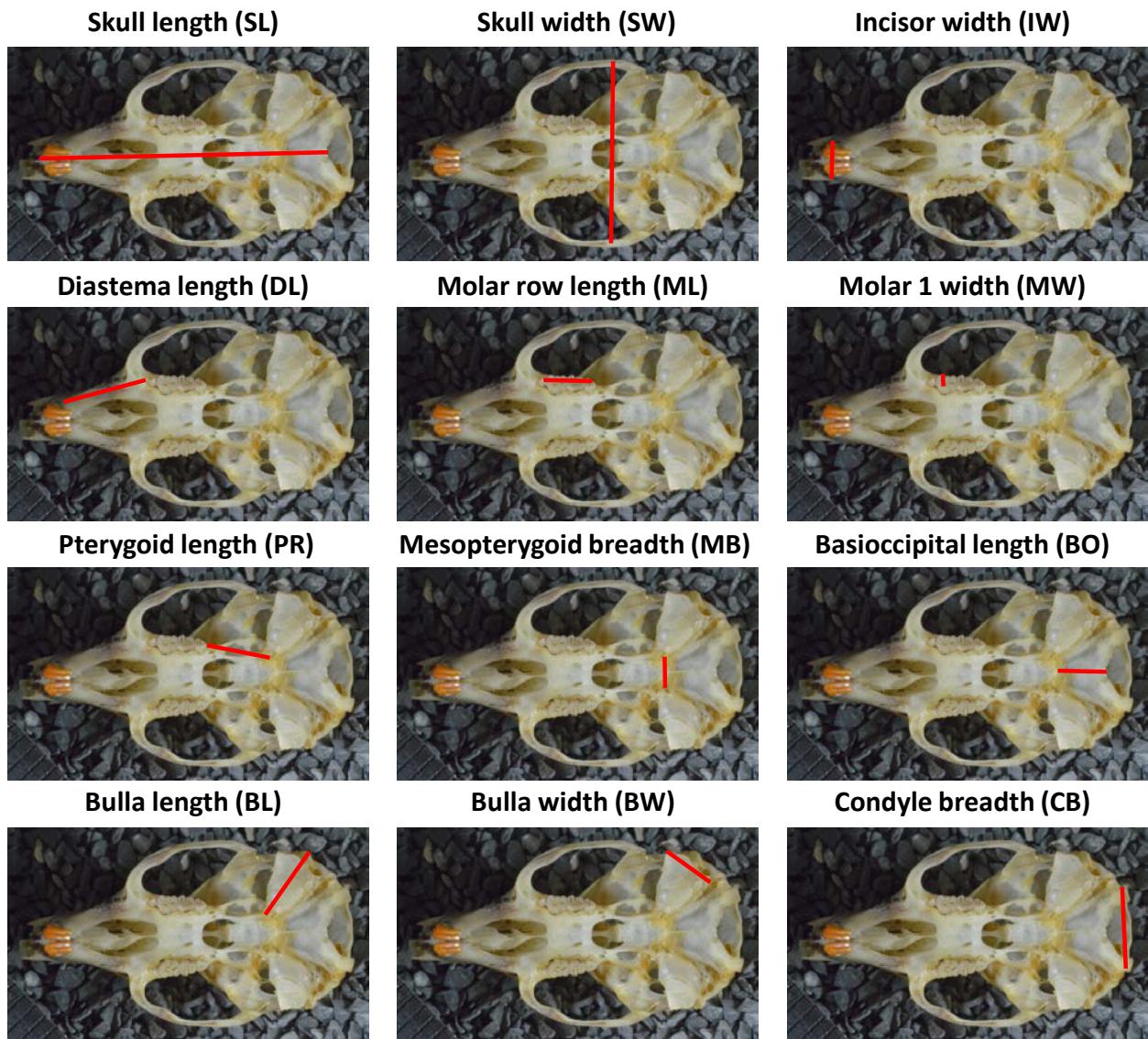


Figure E.1. Visual depictions of linear distances extracted from the ventral views of crania as described in Table E.4. Distances are displayed on the cranium of the western jumping mouse (*Zapus princeps*; AMNH 124327).

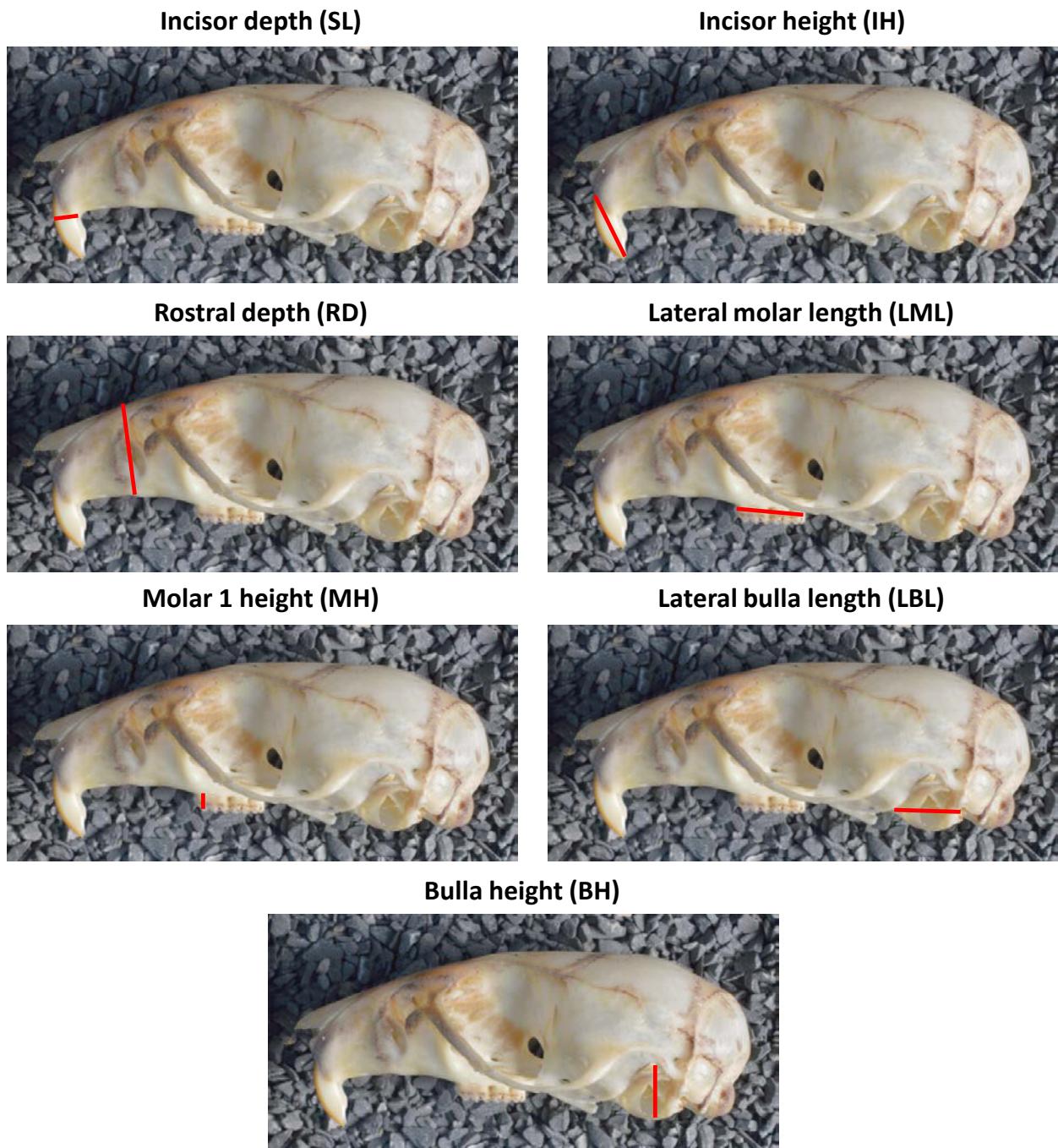


Figure E.2. Visual depictions of linear distances extracted from the lateral views of crania as described in Table E.5. Distances are displayed on the cranium of the common cane mouse (*Zygodontomys brevicauda*; MVZ 113383).

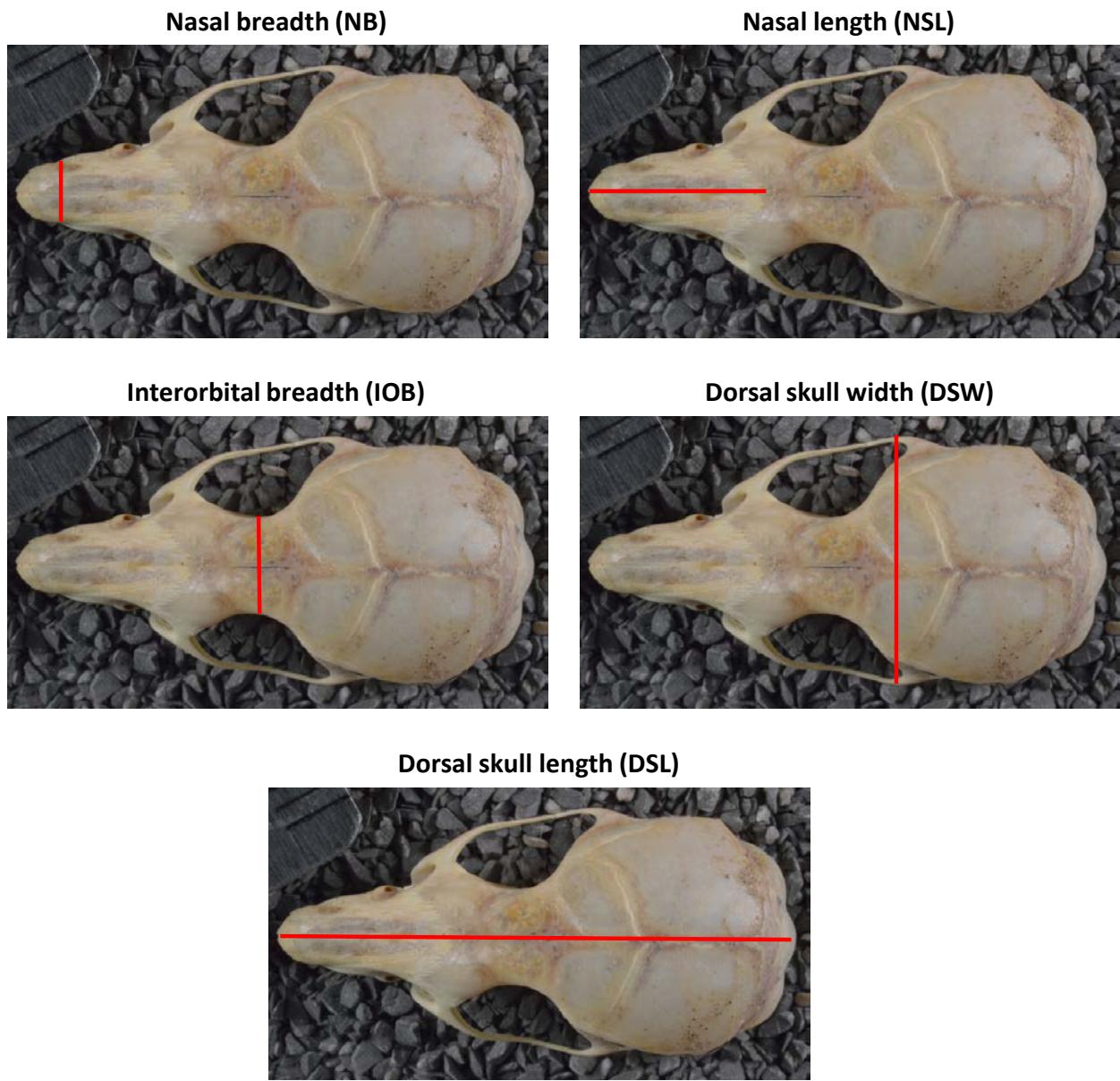


Figure E.3. Visual depictions of linear distances extracted from the dorsal views of crania as described in Table E.5. Distances are displayed on the cranium of Spegazzini's grass mouse (*Akodon spegazzinii*; UF 27623).

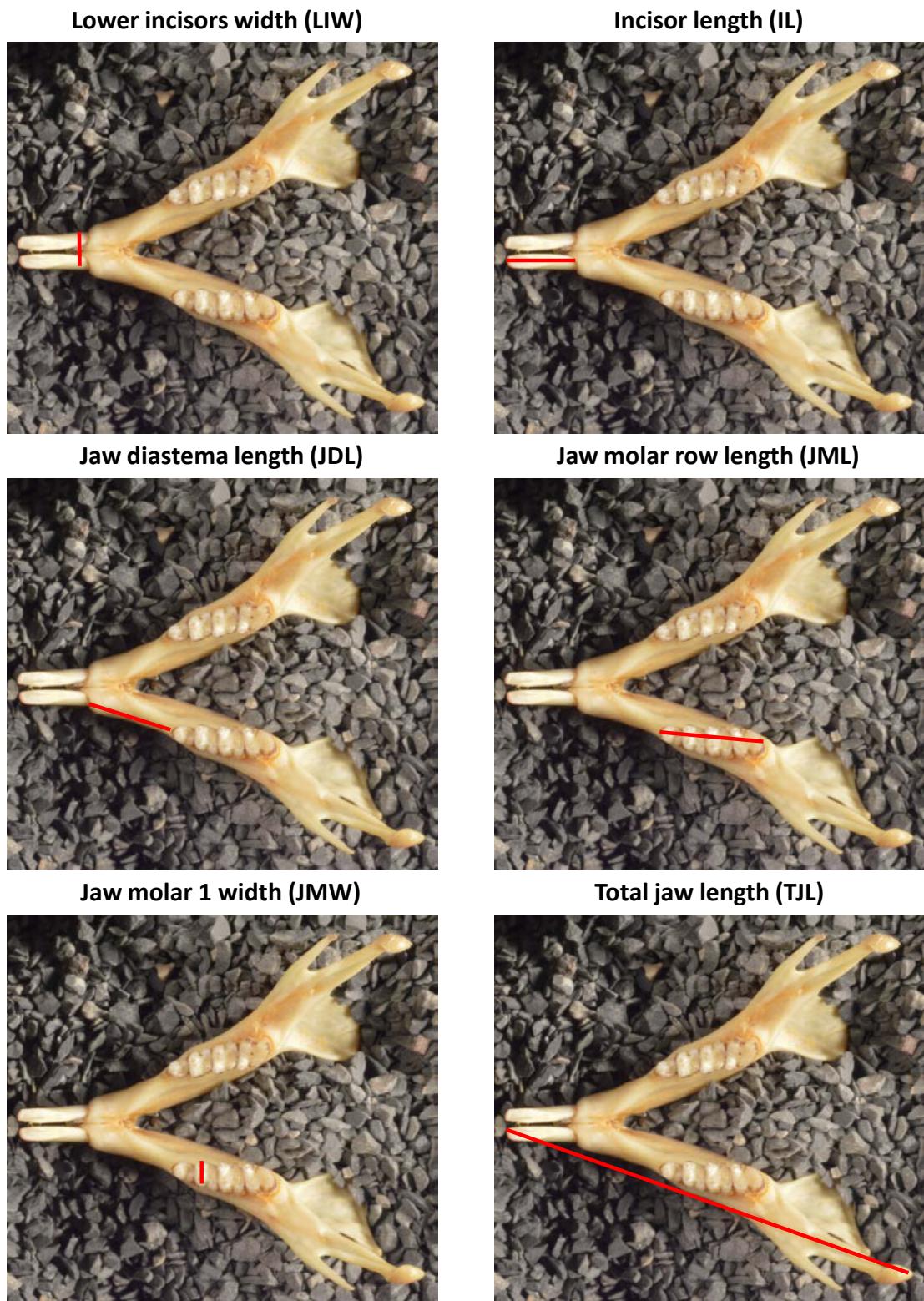


Figure E.4. Visual depictions of linear distances extracted from the occlusal views of mandibles as described in Table E.6. Distances are displayed on the mandible of the Texas antelope squirrel (*Ammospermophilus interpres*; USNM 18154).

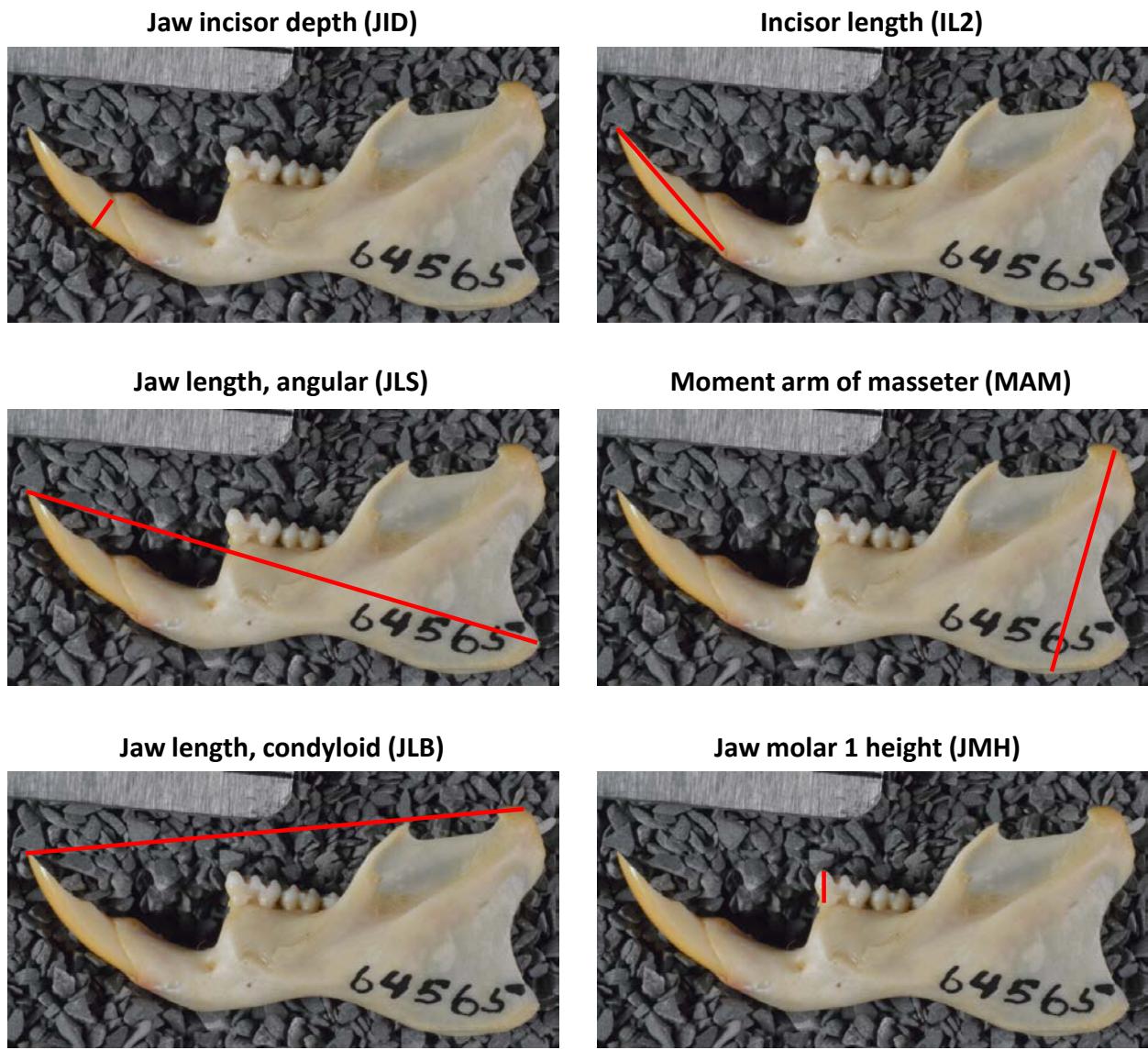


Figure E.5. Visual depictions of linear distances extracted from the lateral views of mandibles as described in Table E.6. Distances are displayed on the mandible of the big eared climbing rat (*Ototylomys phyllotis*; FMNH 64565).



Figure E.6. Composite chronogram of 591 rodent OTUs with collected morphological data. Molecular phylogeny modified from Fabre et al. (2012) and Steppan et al. (in prep). Some of the major taxonomic groups are indicated.

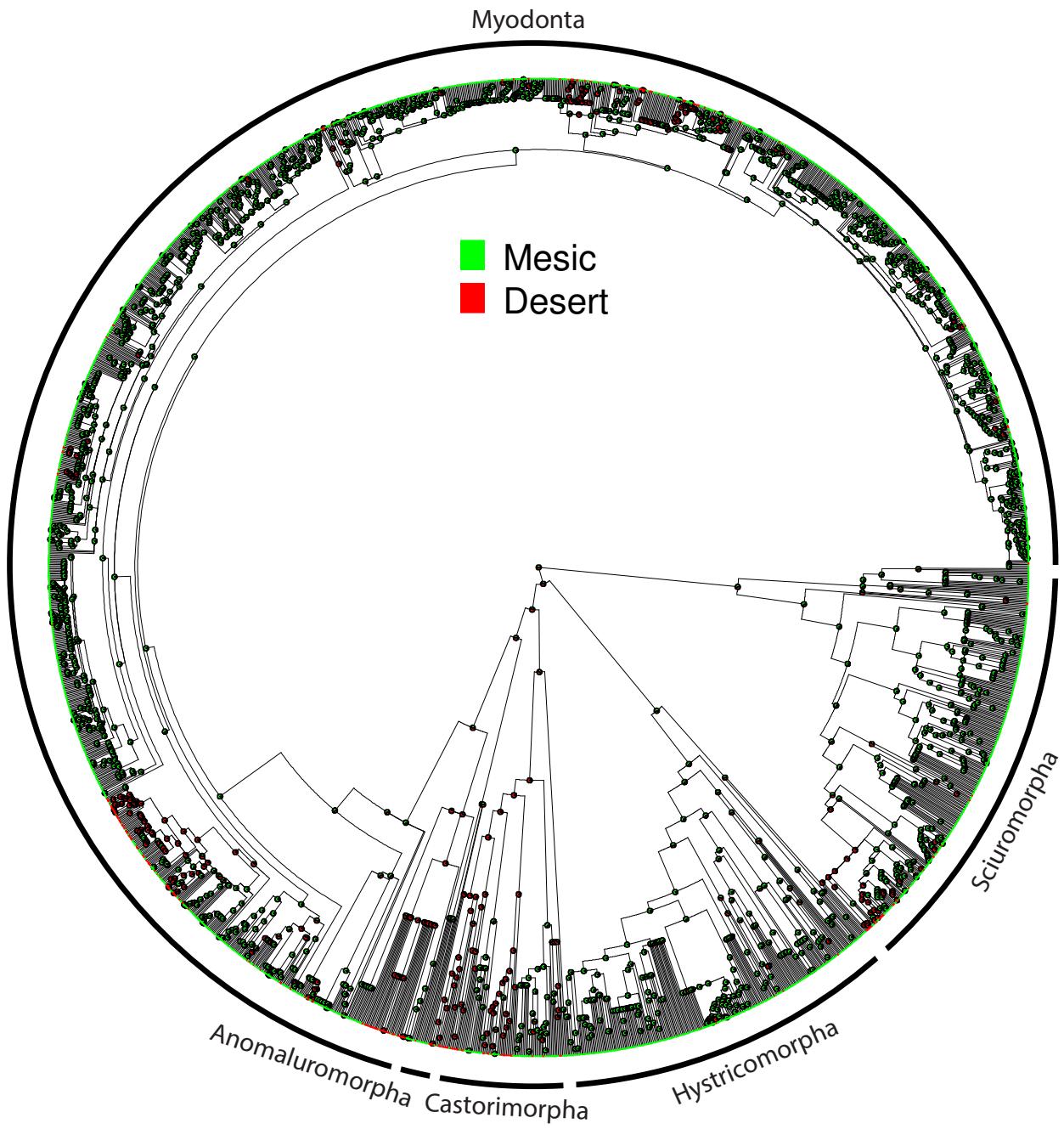


Figure E.7. Maximum likelihood ancestral state reconstruction of habitat in 2,277 species of extant rodents. Red tips/nodes indicate desert species and green tips/nodes indicate mesic species based on IUCN habitat information for the tips.

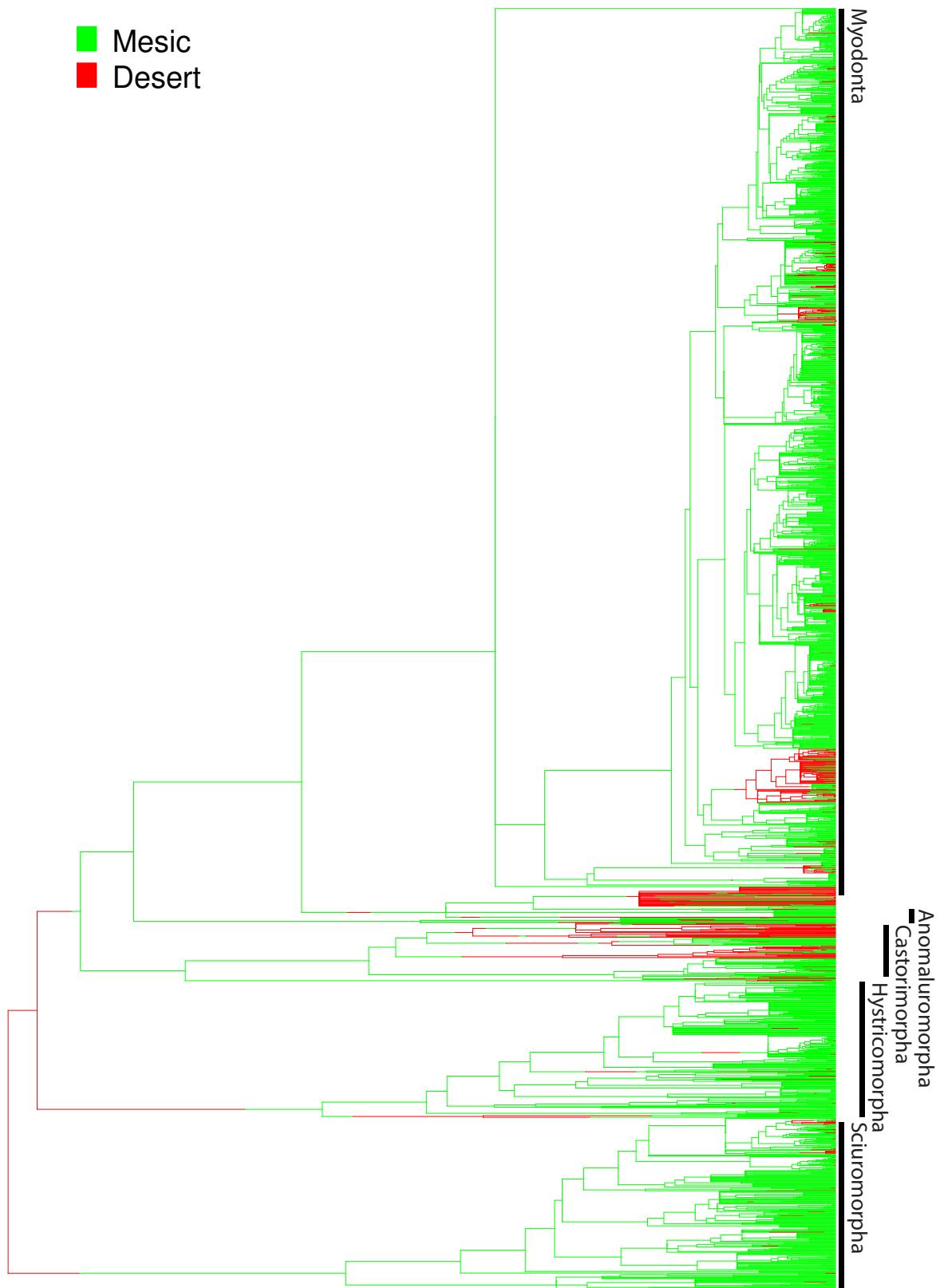


Figure E.8. One of 1,000 stochastic character maps used for ancestral character state estimation in the BI framework. See Figure E.7 legend for more information.

APPENDIX F

SUPPORTING MATERIAL FOR CHAPTER 7

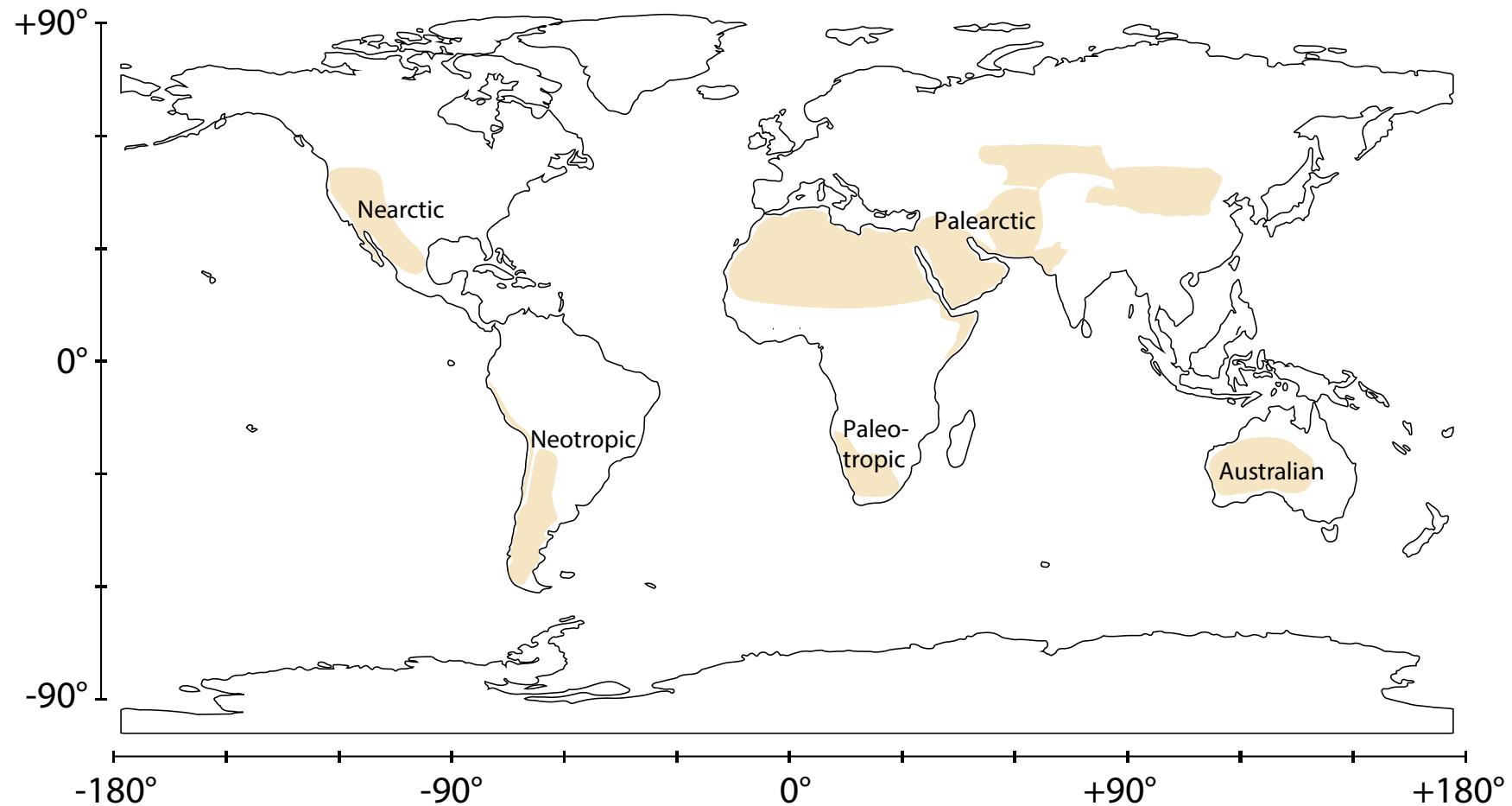


Figure F.1. Map of the 5 desert rodent regions defined in Shenbrot et al. (1999). The map and regions are not drawn to scale. Regions are defined based on the distribution of rodent species only and not on the full extent of the deserts.

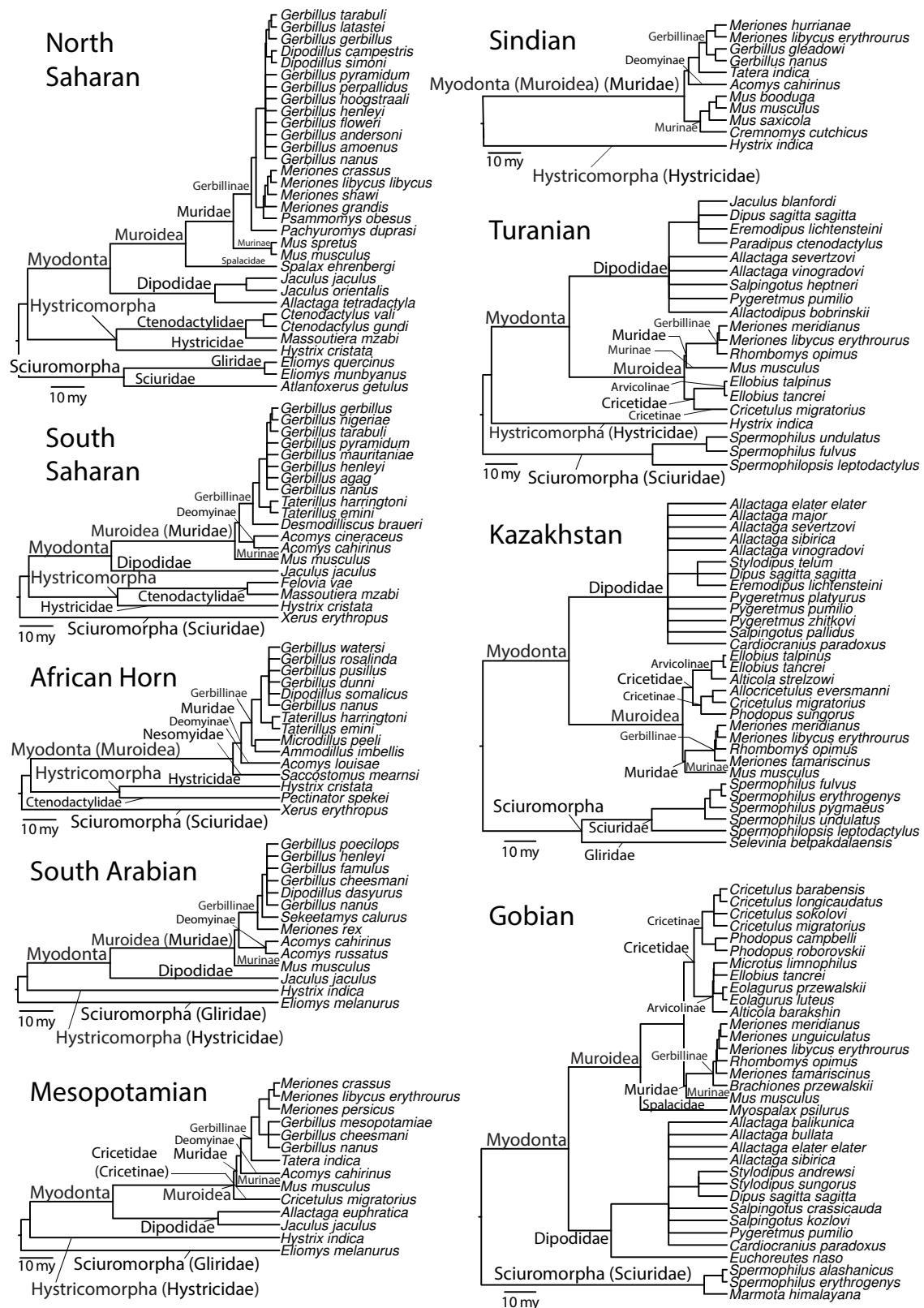


Figure F.2. Assemblage phylogenies of 9 sampled desert rodent provinces in the Palearctic desert region. Sub-trees extracted from a supermatrix chronogram of rodents modified from Fabre et al. (2012) and Steppan et al. (in prep). Some of the major taxonomic groups are indicated.

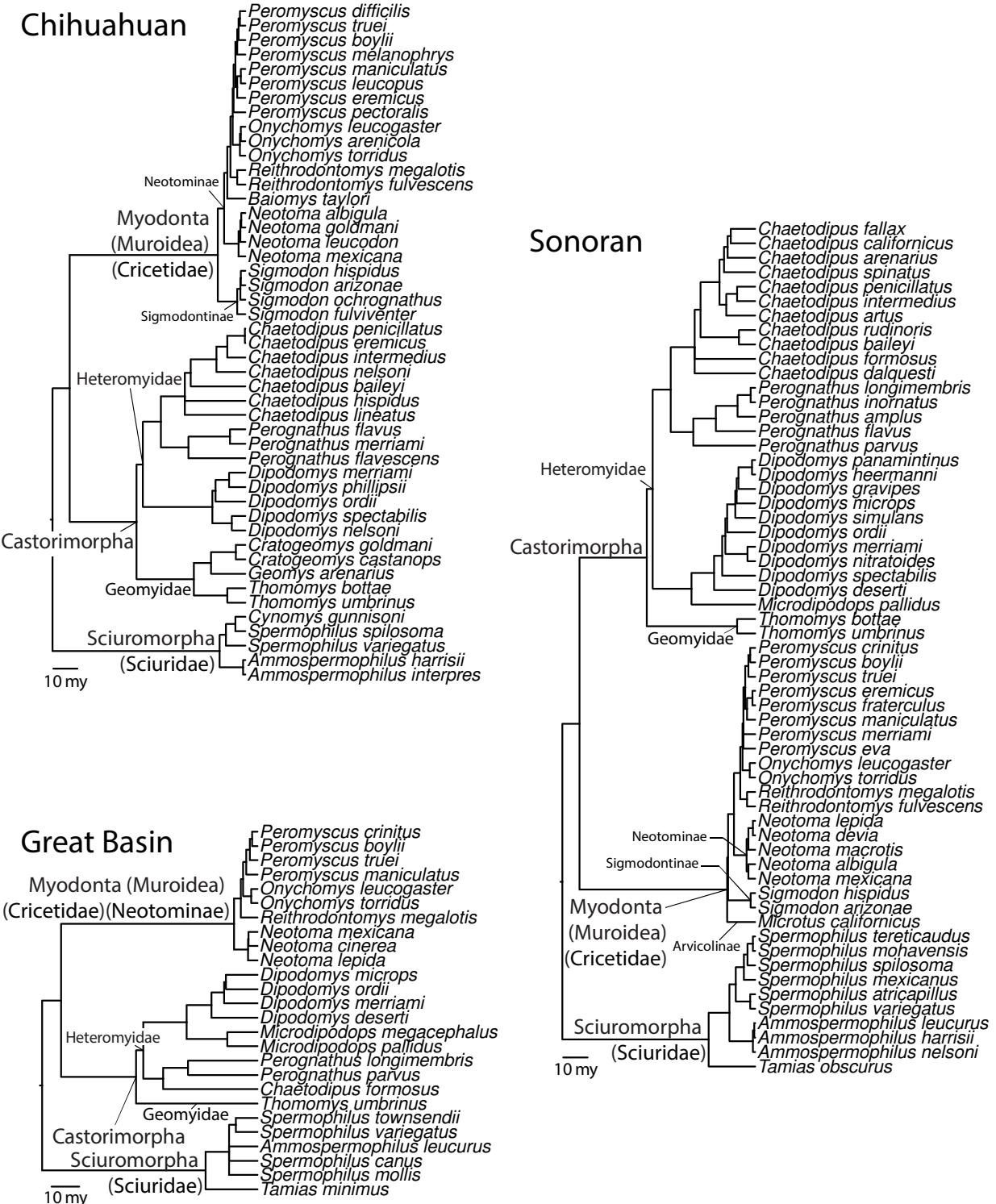


Figure F.3. Assemblage phylogenies of 3 sampled desert rodent provinces in the Nearctic desert region. See Figure F.2 for more information.

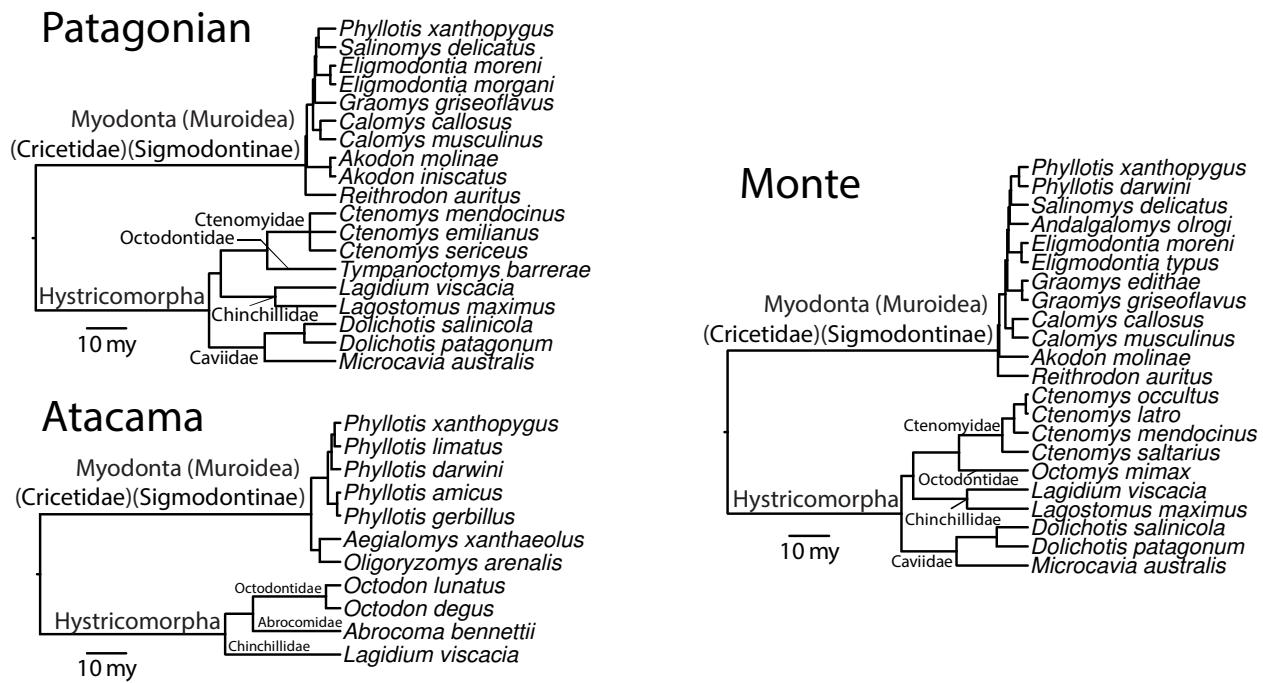


Figure F.4. Assemblage phylogenies of 3 sampled desert rodent provinces in the Neotropic desert region. See Figure F.2 for more information.

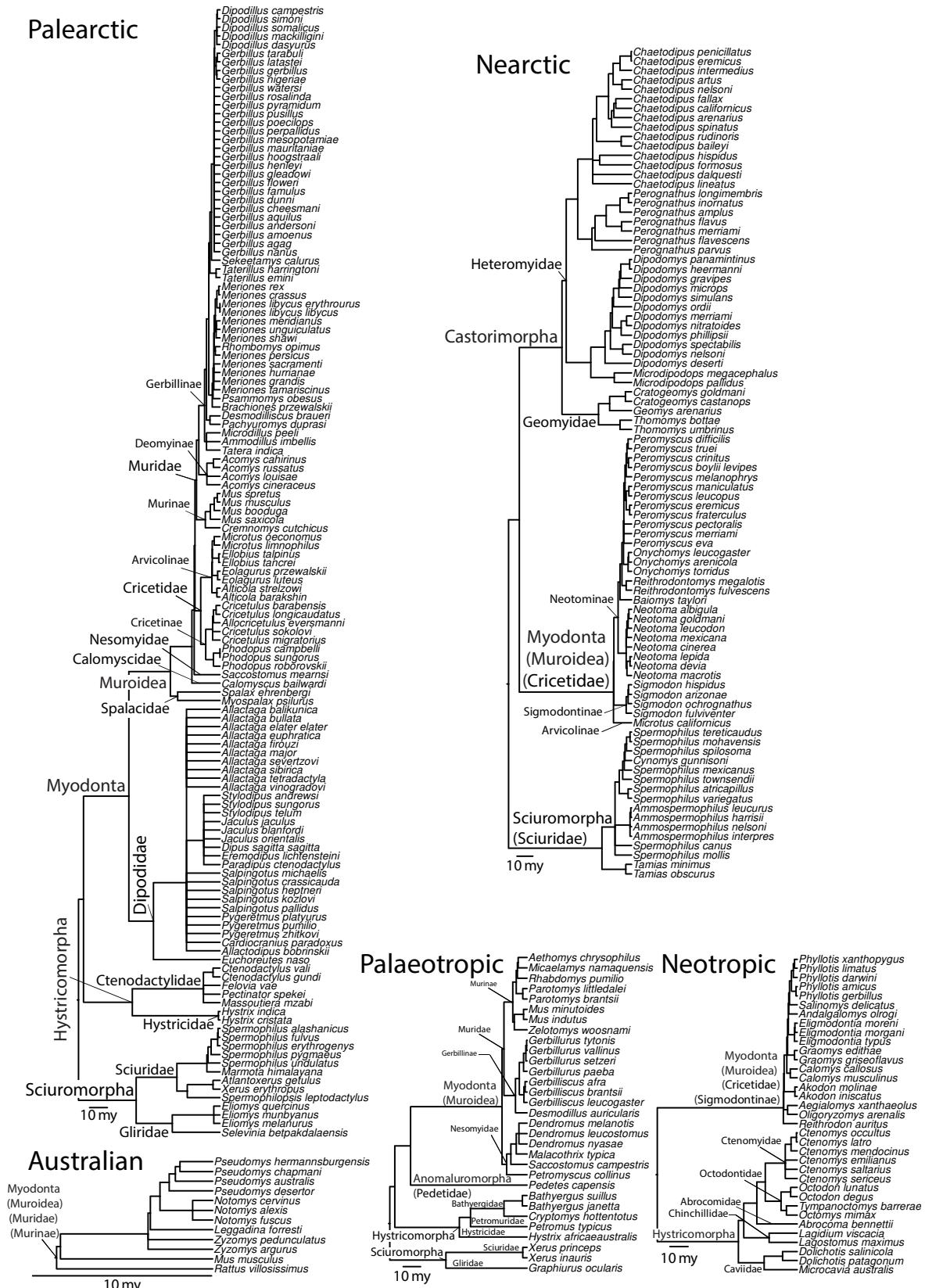


Figure F.5. Assemblage phylogenies of 5 desert regions defined in Shenbrot et al. (1999) with species added based on IUCN species distribution data. See Figure F.2 for more information.

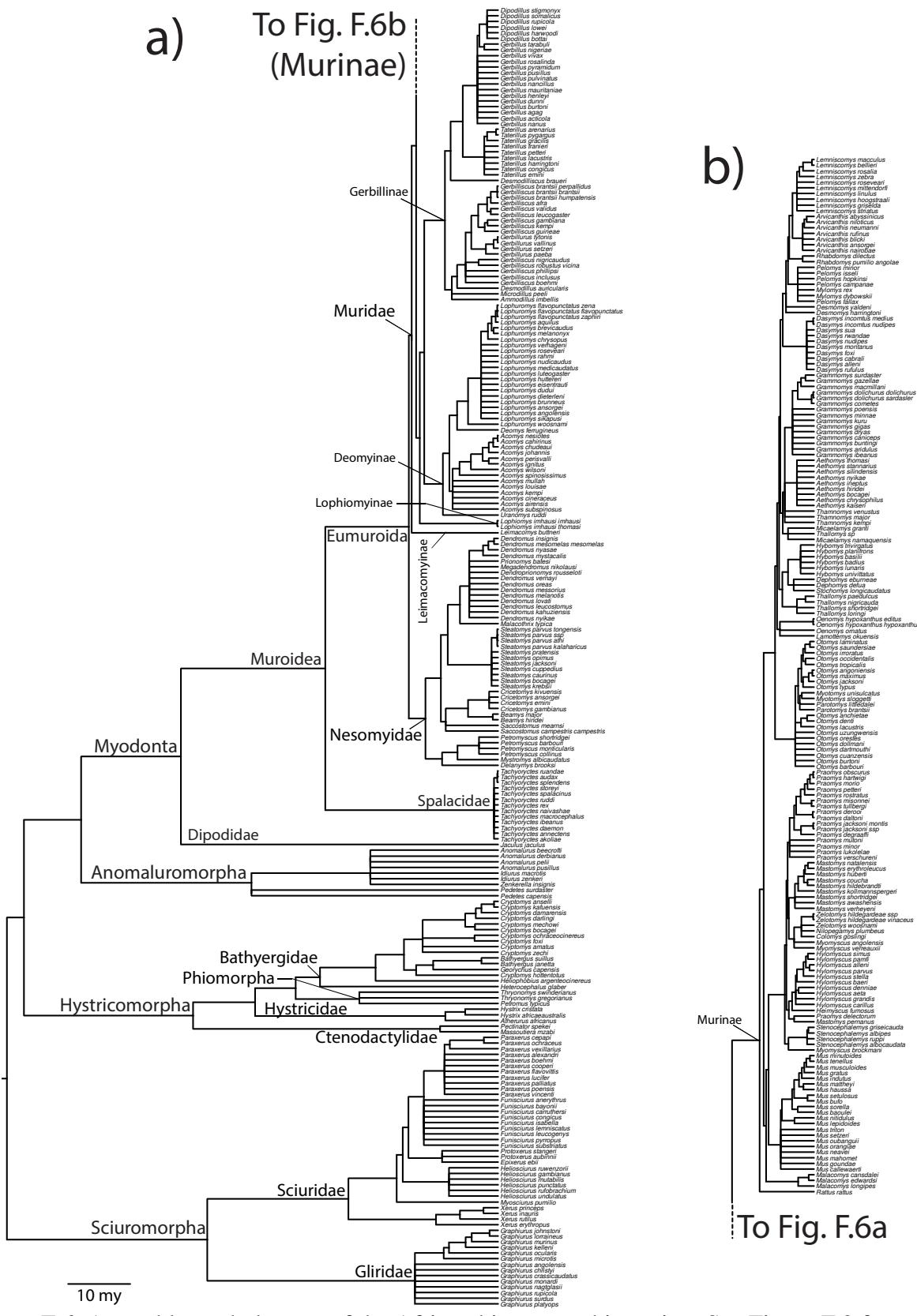


Figure F.6. Assemblage phylogeny of the African biogeographic region. See Figure F.2 for more information.

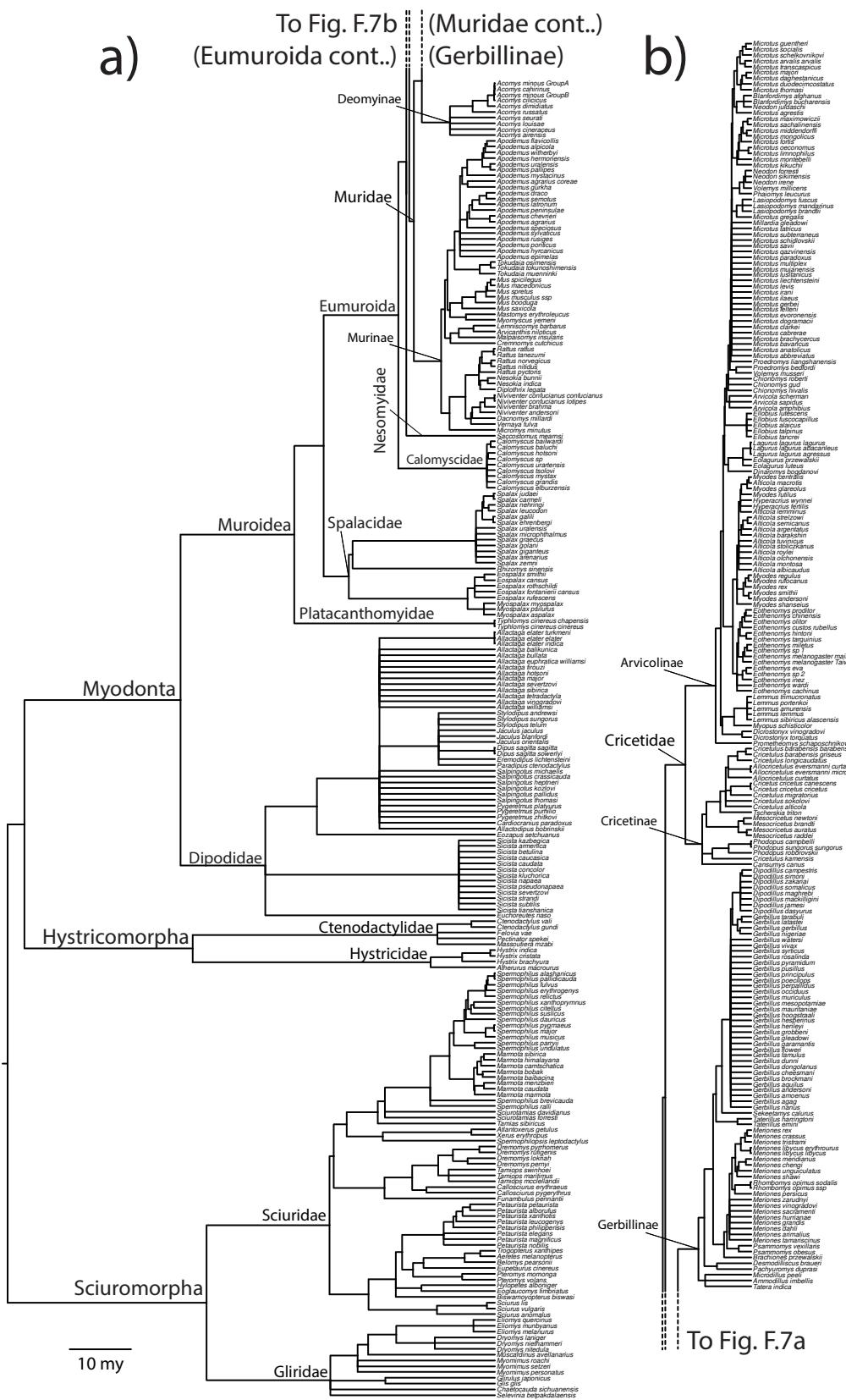


Figure F.7. Assemblage phylogeny of the Eurasian biogeographic region. See Figure F.2 for more information.

To Fig. F.8b
(Myodonta)

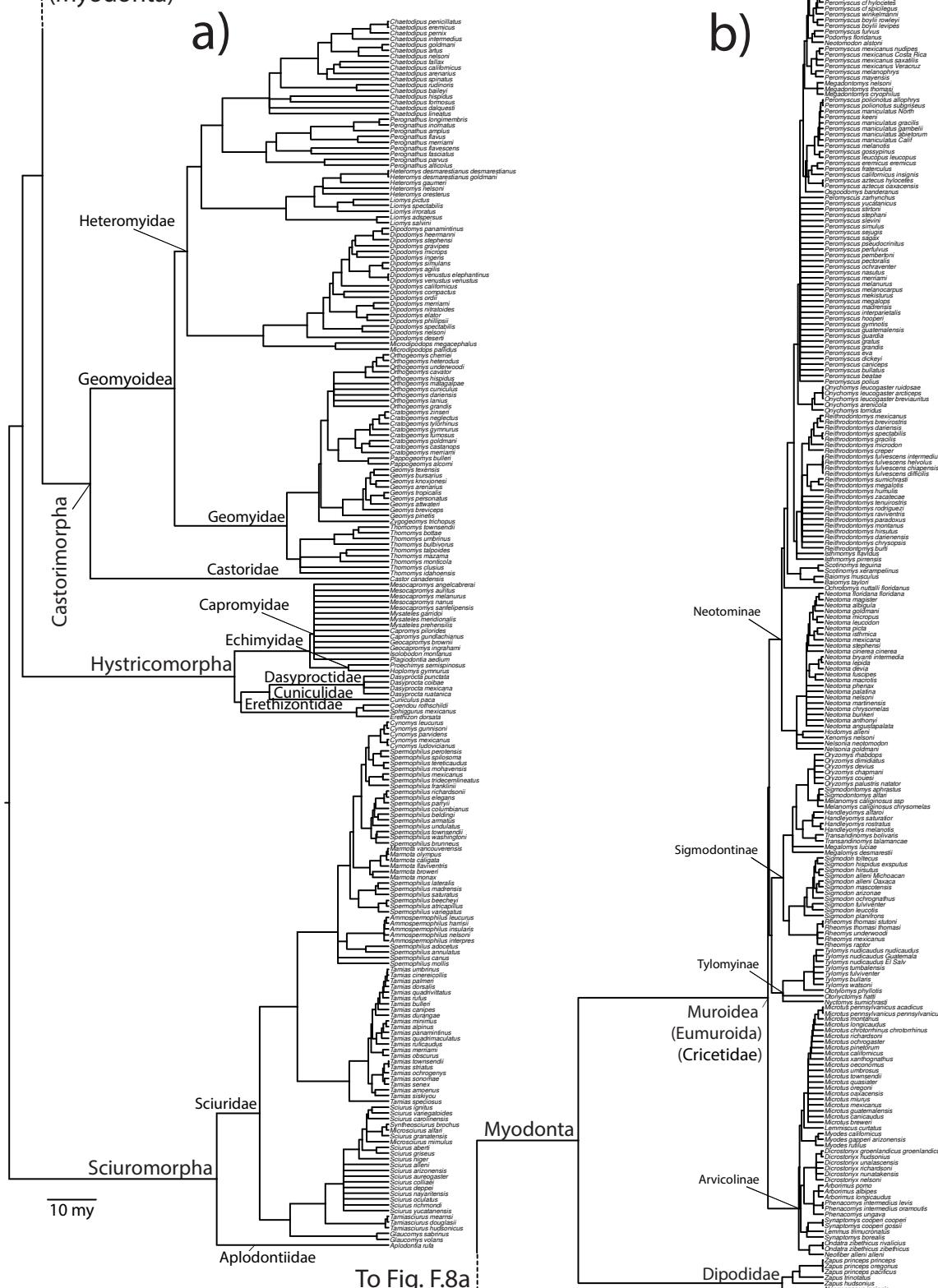


Figure F.8. Assemblage phylogeny of the North American biogeographic region. See Figure F.2 for more information.

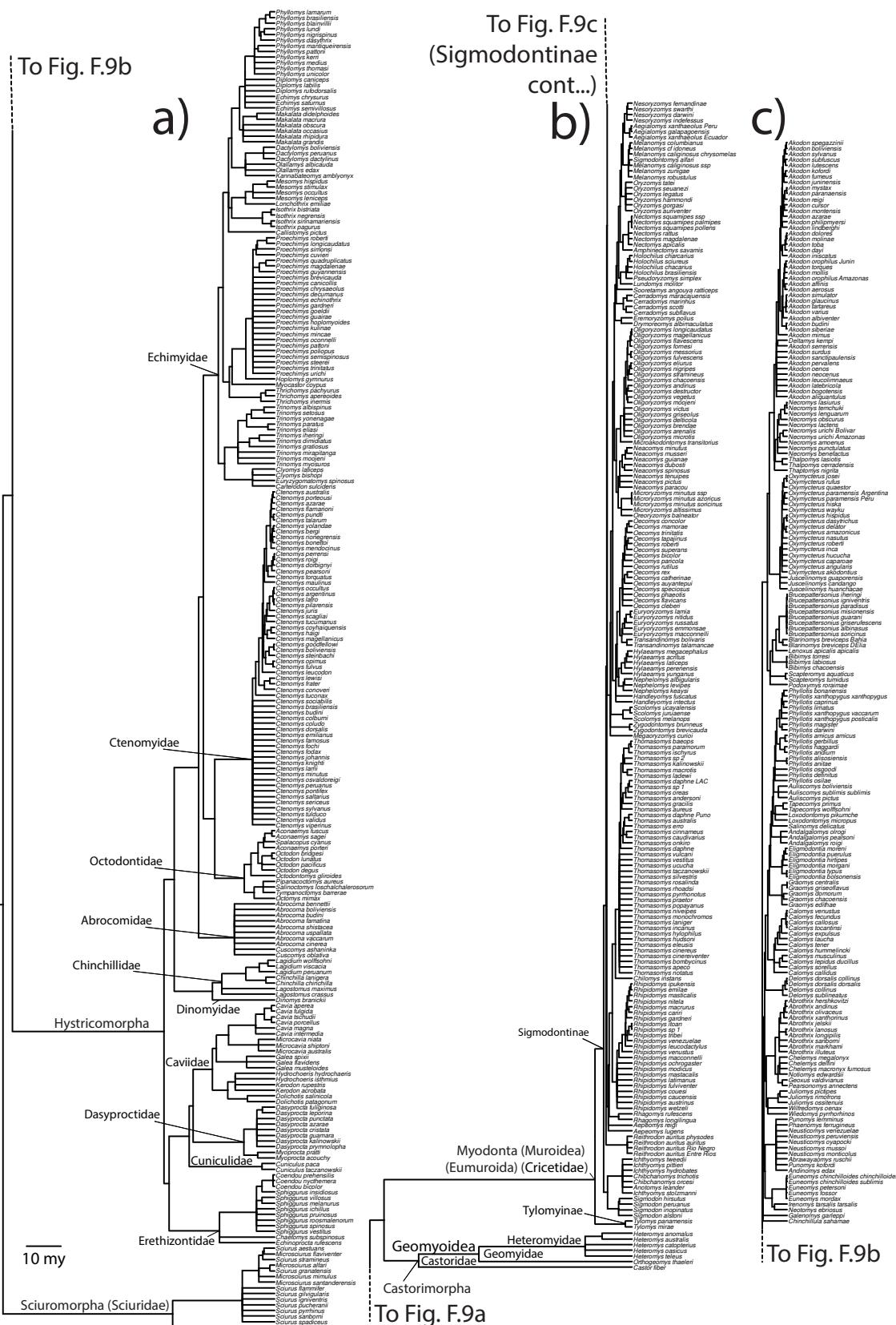


Figure F.9. Assemblage phylogeny of the South American biogeographic region. See Figure F.2 for more information.

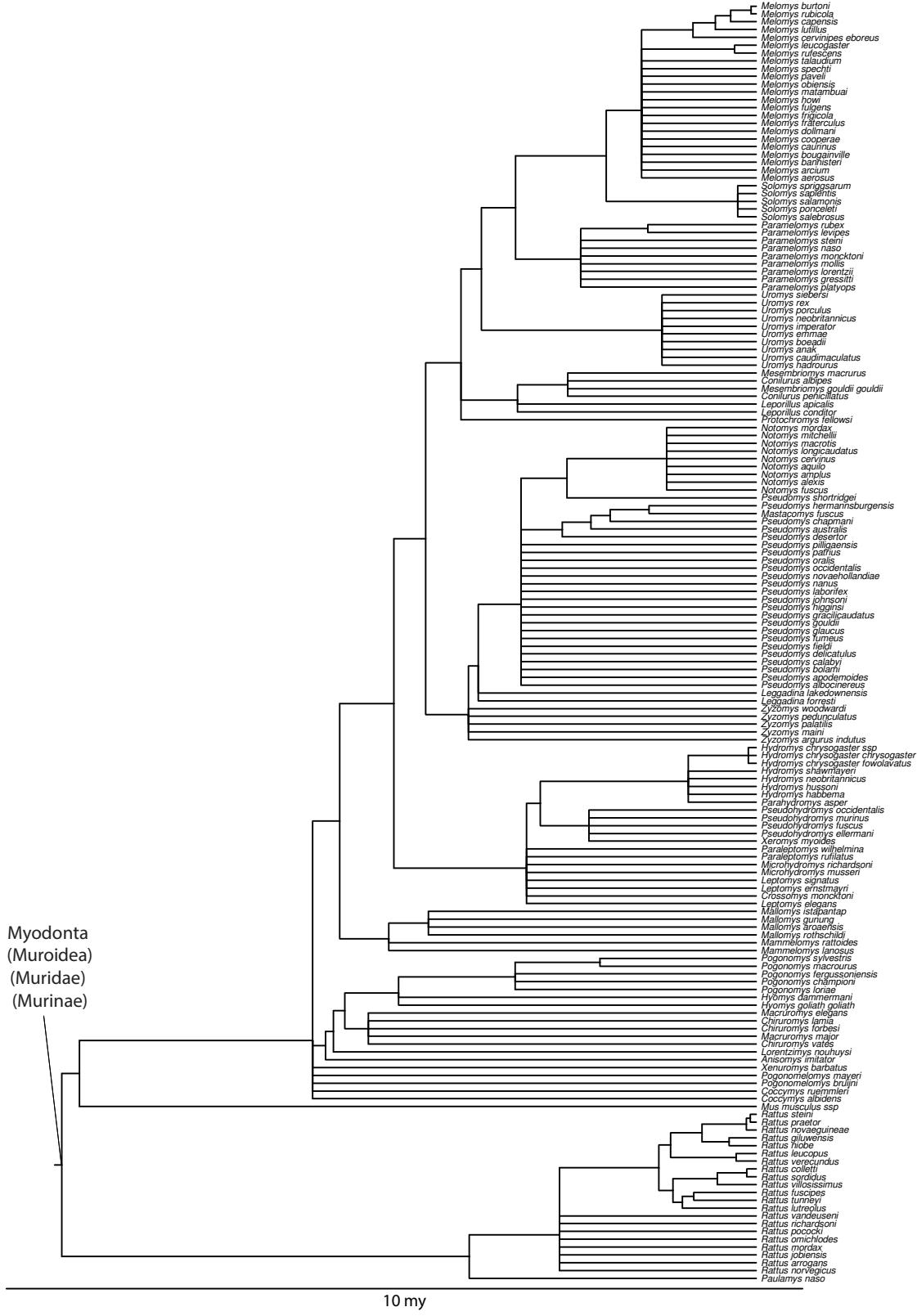


Figure F.10. Assemblage phylogeny of the Sahulian biogeographic region. See Figure F.2 for more information.

APPENDIX G

SUPPORTING MATERIAL FOR CHAPTER 8

Table G.1. Sequences used in phylogenetic analyses. Where available, GenBank accession numbers are provided. For sequences not yet submitted to GenBank, museum tag information, collector, or internal reference numbers are provided (between square brackets). Abbreviations and acronyms (for institutions and collectors) are as follows. AMCC= American Museum of Natural History Ambrose Monell Cryo Collection; CAS= California Academy of Sciences; CM= Carnegie Museum of Natural History; FMNH= Field Museum of Natural History; MVZ= Museum of Vertebrate Zoology; TK= Museum of Texas Tech University; USNM= National Museum of Natural History; RA= Ron Adkins; NA = Not Available. Unlisted abbreviations are internal reference numbers.

Table G.1—continued.

	12S	16S	ACP5	AVPR2	BZRP	BRCA1	COI	COII	CYTB	GHR	IRBP	RAG1	VWF	
<i>Gerbilus gerbillus</i>	AJ851242		[CM 113822]	FJ411204		EU349700 JF716023	DQ019082	DQ019082	[CM 113823] KF496235 JN652803 JN021420 GU356550 KF496279	DQ019049	EU349846	DQ023452	AJ402699	
<i>Gerbilus henleyi</i>														
<i>Gerbilus hesperinus</i>														
<i>Gerbilus hoogstrali</i>														
<i>Gerbilus latastei</i>														
<i>Gerbilus nancillus</i>														
<i>Gerbilus nanus</i>	AJ851244													
<i>Gerbilus nigeriae</i>	X84381	AF141257	[MVZ 192048]							KC953262 AJ430555 KF496282 JN652806 JQ753064 KF496283	KC953378 AM408333	KC953501		
<i>Gerbilus occiduus</i>														
<i>Gerbilus pallidus</i>														
<i>Gerbilus poecilops</i>														
<i>Gerbilus pyramidum</i>	AJ851245													
<i>Gerbilus tarabuli</i>														
<i>Lophiomys imhausi</i>														
<i>Lophuromys brevicaudus</i>		AY828276	[DO 111]											
<i>Lophuromys chrysopus</i>		AY828304												
<i>Lophuromys flavopunctatus</i>	U67294					AY295006	DQ019087	DQ019087						
<i>Lophuromys melanonyx</i>		AY828279												
<i>Lophuromys sikapusi</i>	AJ250349		[FMNH 137803]											
<i>Lophuromys woosnami</i>														
<i>Lophuromys zena</i>														
<i>Meriones chengi</i>														
<i>Meriones crassus</i>	AJ851251		[TK 25637]											
<i>Meriones libycus</i>	AJ851250													
<i>Meriones meridianus</i>	AJ851252			FJ411223										
<i>Meriones persicus</i>			[MVZ 19197]											
<i>Meriones rex</i>	AJ851248													
<i>Meriones shawi</i>				FJ411225										
<i>Meriones tamarsicinus</i>														
<i>Meriones tristrami</i>			[TK 25568]											
<i>Meriones unguiculatus</i>	AJ851249			FJ411228										
<i>Microtus chrotorrhinus</i>														
<i>Mus pahari</i>	AB125793		EU349629											
<i>Ondatra zibethicus</i>			[NA]	FJ411232										
<i>Pachyuromys duprasi</i>	AJ851258			FJ411234										
<i>Phloeomys sp.</i>				DQ023451										
<i>Phyllotis xanthopygus</i>						EU349644								
<i>Psammomys obesus</i>	AJ851253		[TK 40892]			KC953208								
<i>Psammomys vexillaris</i>														
<i>Rattus tiomanicus</i>														
<i>Rheomys thomasi</i>			[USNM 590331]											
<i>Rhomomys opimus</i>	AJ430590													
<i>Sekeetamys calurus</i>	AJ851246		[Ron Adkins]											
<i>Sigmodon hispidus</i>	X89788		[CN]											
<i>Tatera indica</i>	AJ430553	AM409239				AY295016								
<i>Taterillus arenarius</i>	AJ851254													
<i>Taterillus emini</i>	Z83921		[CM 102330]			KC953224	DQ019085	DQ019085	[CM 102330] AJ851263	DQ019050	KC953461	DQ023453		
<i>Taterillus gracilis</i>	AJ851256	AM409238							JF716025					
<i>Taterillus petteri</i>														
<i>Taterillus pygargus</i>	AJ851255									AJ851262				
<i>Tokudaia osimensis</i>	AJ311133		EU349640			EU349659			AB033703	EU349828	EU349878	EU349918		
<i>Uromomys ruddi</i>	X84388	Z83922	[CM 113723]			EU349642	DQ019088	DQ019088	HM635858	DQ019051	EU360812	DQ023454	AJ402714	

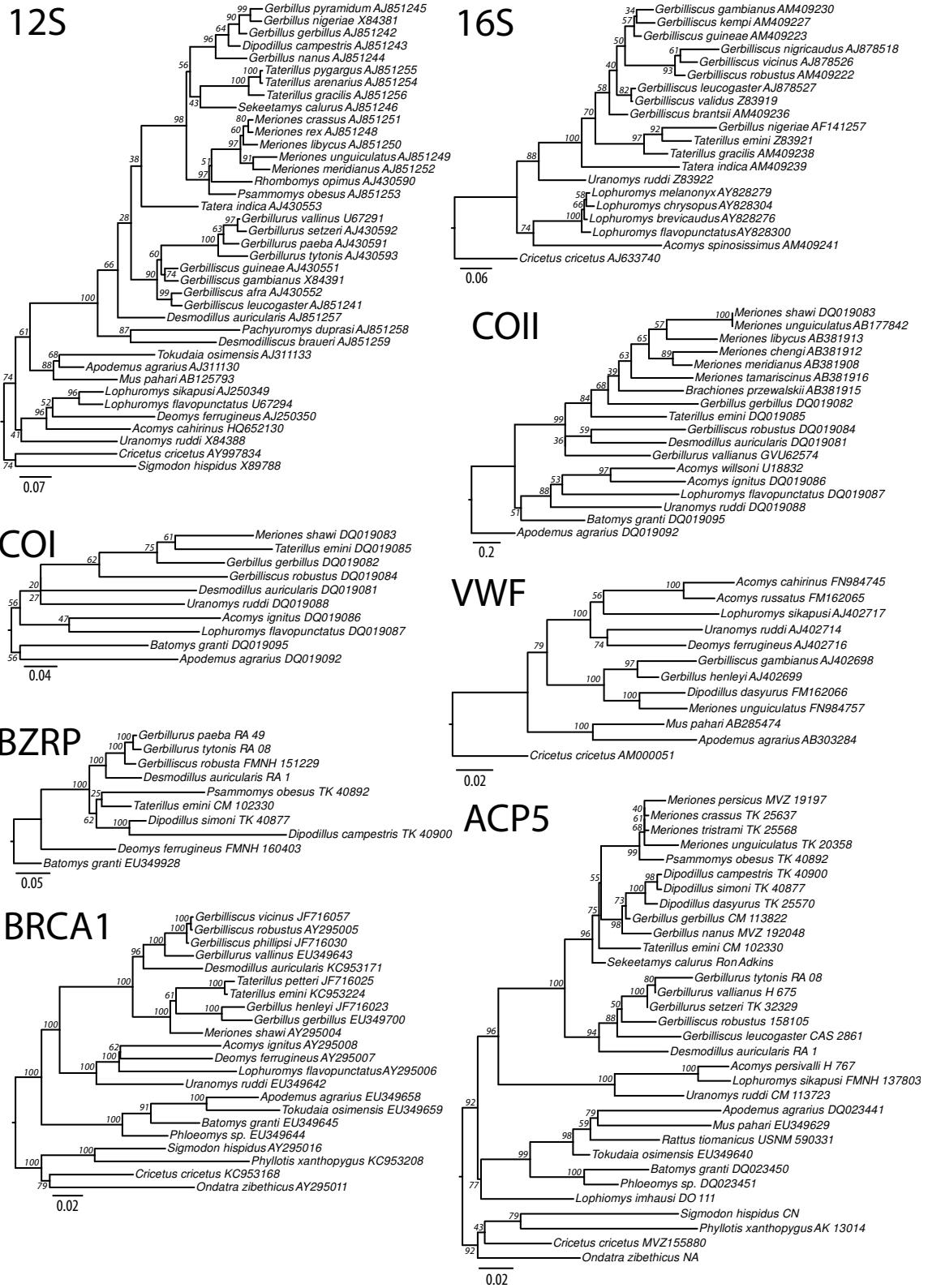


Figure G.1. Maximum-likelihood phylogenograms of the 13 loci reconstructed with the GTR + Γ + I substitution model. Values at nodes represent bootstrap support values and the scale bar represents the number of substitutions per site.

CYTB

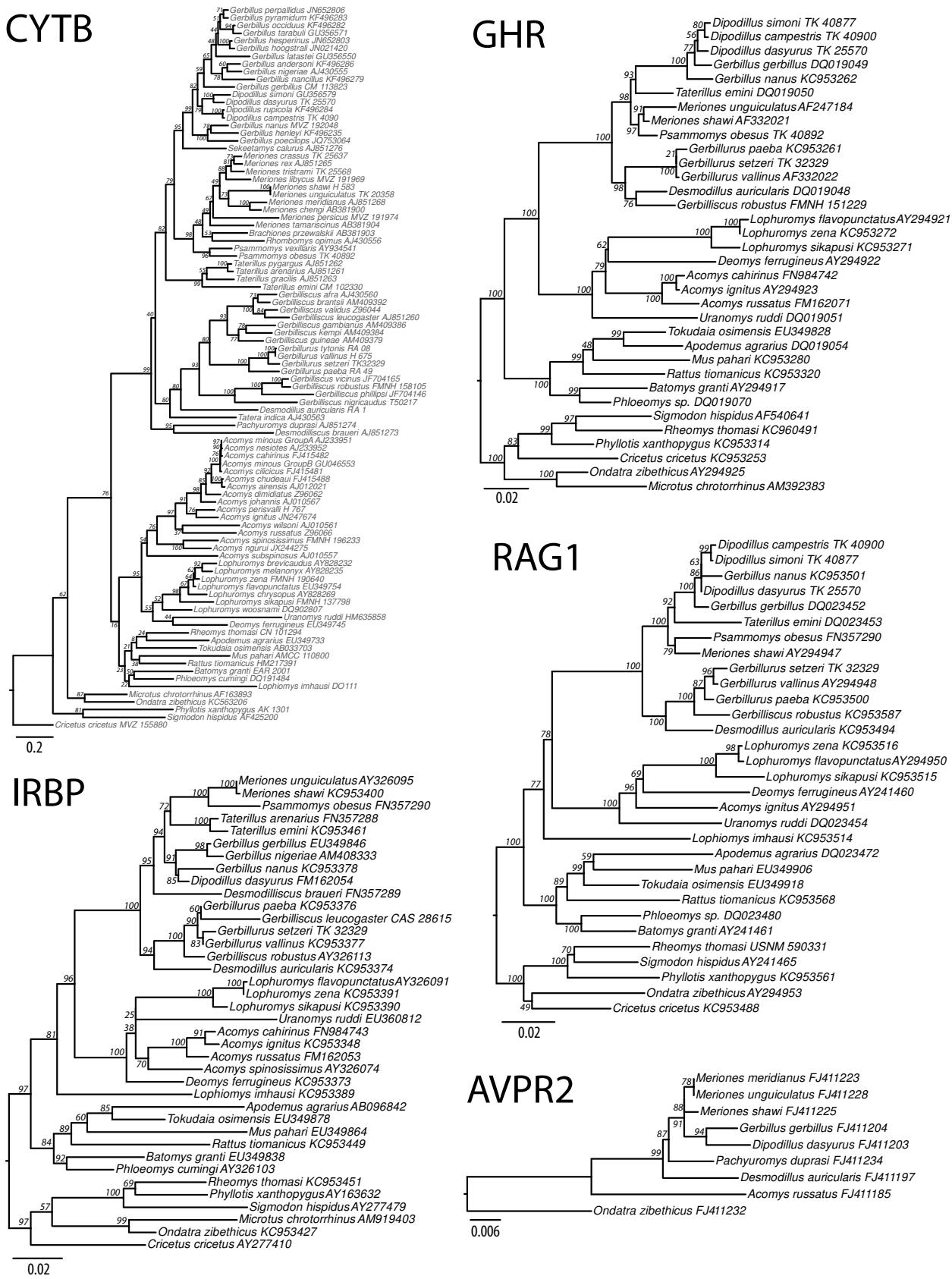
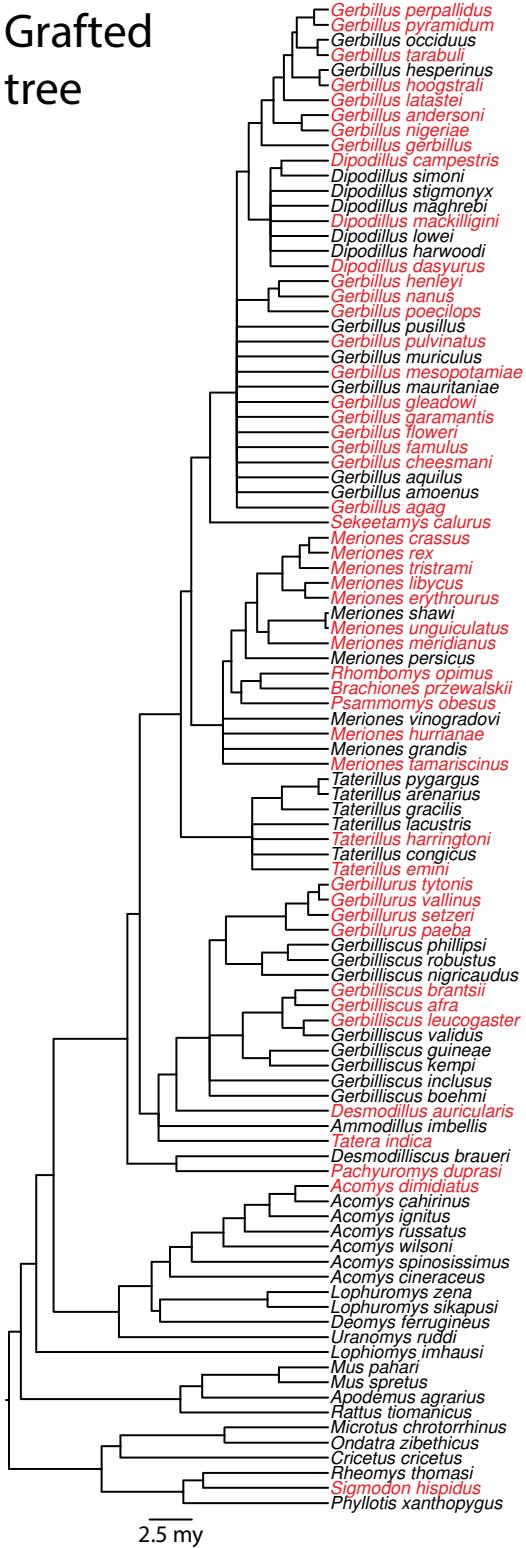


Figure G.1—continued.

Grafted tree



Pruned tree

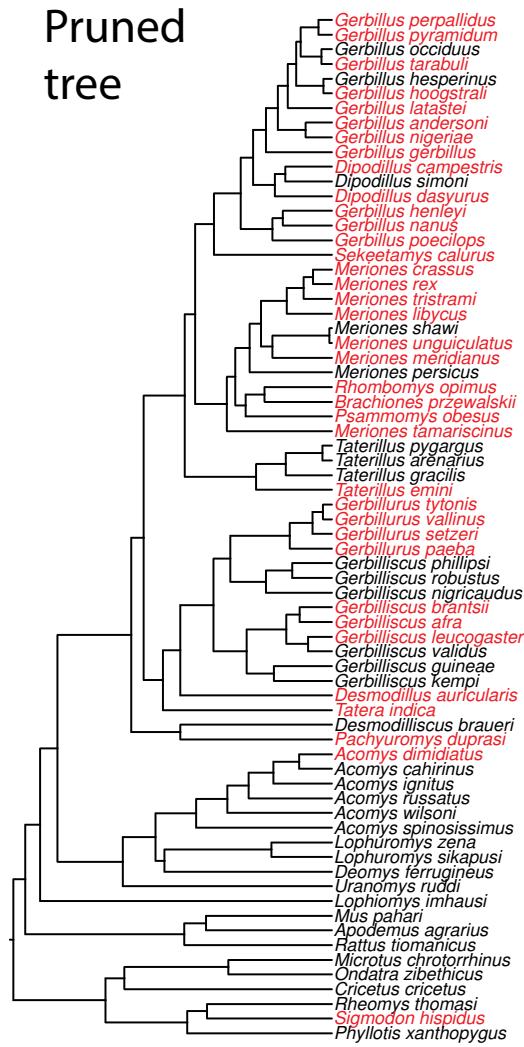


Figure G.2. Bayesian chronograms used for phylogenetic comparative analyses. Trees are the same as Figure 8.5 with species lacking morphological data pruned off (pruned tree) and subsequently species in the morphological dataset, lacking molecular data, grafted onto their closest relatives (grafted tree). Labels: red= IUCN desert species, black= IUCN mesic species.

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BIOGRAPHICAL SKETCH

EDUCATION

M.A., Ecology and Evolutionary Biology (2010) – University of Colorado at Boulder
Thesis project: The role of Wnt signaling in the evolution and development of teeth in teleost fishes
Thesis advisor: Dr. David Stock

Certificate, Neuroscience (2008) – University of Colorado at Boulder

B.A., Ecology and Evolutionary Biology (2008) – University of Colorado at Boulder
Class Rank: 5 of 111
Research: Mouth brooding behavior of African cichlids and their catfish parasites
Advisor: Dr. Alexander Cruz

B.A., Molecular, Cellular, Developmental Biology (2008) – University of Colorado at Boulder
Class Rank: 27 of 167
Honors: graduated with distinction

TEACHING EXPERIENCE

Fall 2013; Guest lecturer for Ecology, topic: Ecological Biogeography, at Florida State University, Tallahassee, FL (Biological Science Department; Instructor: Dr. Tom Miller, course # PCB 3043)

Summer 2013; Guest lecturer for Evolution, topic: Biogeography, at Florida State University, Tallahassee, FL (Biological Science Department; Instructor: Dr. Scott Steppan, course # PCB 4674)

Spring 2013; Teaching Assistant for Comparative Vertebrate Anatomy, at Florida State University, Tallahassee, FL (Biological Science Department; Instructor: Dr. Gregory Erickson, course # ZOO 3713C)

August 2010; Biological Science Teaching Workshop, at Florida State University, Tallahassee, FL (Biological Science Department; Workshop Director: Dr. Ann Lumsden)

PUBLICATION AND ACADEMIC PRESENTATIONS

Alhajeri, B.H. April 2014. The role of intrinsic and extrinsic factors in the diversification of muroid rodents. Ecology and Evolution Departmental Seminar, Florida State University, Tallahassee, Florida, oral presentation

Alhajeri, B.H., Schenk, J.J., and Steppan, S.J. August 2013. Tympanic bulla morphology and desert adaptation in rodents. Ecological Society of America, Minneapolis, Minnesota, oral presentation

Alhajeri, B.H., Schenk, J.J., and Steppan, S.J. June 2013. Ecological correlates of morphological variation in the tympanic bulla of gerbils (Rodentia, Gerbillinae): phylogeny and desert adaptation. American Society of Mammalogists, Philadelphia, Pennsylvania, oral presentation

Schenk, J.J., Alhajeri, B.H., and Steppan, S.J. July 2012. The morning after: testing ecomorphological diversification following continental colonization in muroid rodents. Evolution, Ottawa, Canada, poster presentation

Alhajeri, B.H. 2010. The role of Wnt signaling in the evolution and development of teeth in teleost fishes. Master's Thesis, University of Colorado, Boulder, CO

Alhajeri, B.H. April 2010. The role of Wnt signaling in the evolution and development of teeth in teleost fishes. Department of Ecology and Evolutionary Biology Spring Symposium, University of Colorado, Boulder, CO, oral presentation

ACADEMIC AWARDS

Golden Key Honor Society; Florida State University; nominated (2012)

PhD Fellowship to the Florida State University: Fall 2010 - Summer 2014 (Kuwait University)

MA Fellowship to the University of Colorado at Boulder: Fall 2008 - Summer 2010 (Kuwait Ministry of Higher Education)

Phi Beta Kappa Honor Society (University of Colorado at Boulder)

Golden Key Honor Society; University of Colorado at Boulder; nominated (2007)

Certificate of Academic Merit: Fall 2004 - Spring 2010 (Kuwait Ministry of Higher Education)

Dean's List: Fall 2004, 2006, Spring 2007, Fall 2007, Spring 2008 (University of Colorado at Boulder)

BA Merit Scholarship to the University of Colorado at Boulder: Fall 2004 - Summer 2008
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