

# Morphological novelty evolves by bursts in a continental radiation of skinks

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## Abstract

Animals come in all shapes and sizes. From mundane to bizarre, their features are the result of millions of years of evolution and mutation accumulating differences and adjusting designs. As a result of differing selective pressures and drift phenotypes evolve and diverge. However

15 there is little consensus about the evolutionary mode of most traits and if novel morphologies evolve from prolonged (Darwinian gradualist) or episodic (Simpsonian jump) divergences. Here we use novel exon-capture and linear morphological datasets to investigate the tempo and mode of morphological evolution in Australo-Melanesian Tiliquini skinks. By collecting a morphological dataset that encompasses the lizard body plan we are able to identify that

20 most traits evolve conservatively but infrequent evolutionary bursts result in morphological novelty. These phenotypic discontinuities occur via rapid rate increases along individual branches, inconsistent with both gradualistic and punctuated equilibrial evolutionary modes. Instead, this ‘punctuated gradualism’ has resulted in the rapid evolution of blue-tongued giants and armored dwarves in the ~20 million years since colonizing Australia. These results

25 outline the evolutionary pathway towards new morphologies and highlight the heterogeneity of evolutionary tempo and mode.

# Introduction

Great variations in organismal morphology are expected to accumulate over long periods of time and reflect the varied requirements of different species (Foote 1997; Deline *et al.* 2018). Some organisms are very small and some are very large, others are brightly colored and others cryptic, and through drift and selection, traits respond and diverge from common forms. But despite the dramatic variation we see in nature, when we look closely, measures of these differences (variance, disparity, *et al.*) almost always fail to exceed the expectation of a neutral model where the accumulation of variation is the result of a random evolutionary walk through time (Brownian Motion) (Lynch 1990; Hansen & Houle 2004). In other words, Earth's flora and fauna realize only a fraction of all possible shapes and sizes (Hall 1996). This diversity undershoot suggests bounds on phenotypes as a result of genetic, functional, or developmental constraints [CITE]. If this is the case, then how do novel morphologies arise? And what does the mode of morphological evolution look like if not gradual?

When traits are assumed to evolve under an unbiased random walk (Brownian Motion), trait variance ( $v$ ) is proportional to evolutionary rate ( $\sigma^2$ ), and the accumulation of variance is dictated by elapsed time ( $t$ ; so  $v=\sigma^2 t$ ). This exploration of trait space (diffusion) is characterized by trait change along branches drawn from a normal (Gaussian) distribution, and assumes a flat adaptive landscape (Hansen & Martins 1996; Arnold *et al.* 2001). Given observed trait limits, correlations among traits, and the "clumpiness" of extant morphological diversity, this seems an unlikely expectation (Felsenstein 1988; Deline *et al.* 2018). In practice, morphological evolution is often concentrated on one or a small number of major axes. The primary axis serves as a 'line of least resistance' (Schluter 1996) providing a pool of variation on which selection can act. However evolution is not limited to the major axis, and trajectories along minor axes may also pave a path towards new phenotypes. These competing processes have been termed "elaboration" (*along* major axis) and "innovation" (*away* from major axis) (Endler *et al.* 2005; Guillerme *et al.* 2023). However their relative contributions towards organismal macroevolution and the evolution of novel forms has been largely overlooked (Guillerme *et al.* 2023).

Almost 80 years ago G.G. Simpson suggested this occurred by rapid "jumps" to new adaptive zones across an uneven landscape (Simpson 1944). One potential path across this landscape requires relaxing our assumption that traits evolve consistently across lineages—changing the *mode* of evolution. Proposed alternative evolutionary models such as pulsed or punctuated processes account for rapid jumps in just such a way—by deviating only in the evolutionary *mode*—leaving variance to accumulate as under BM. Another pathway however requires relaxing our assumption that traits evolve via constant rates through time—changing the *tempo* of evolution. This is often implemented in Variable Rates or Multi-Regime models of trait evolution. Traditionally, jumps have been difficult to identify without fossil data. This is due in part to the limited information content at internal nodes of a phylogenetic tree, however, even in fossil studies debate has continued about gradual versus pulsed/punctuated evolution (Hunt 2008; Hunt *et al.* 2015). Recent advances in phylogenetic comparative methods however, provide the tools to distinguish between gradual and punctuated evolutionary modes, and suggest that pulsed evolution and rate heterogeneity may be common processes (Uyeda *et al.* 2011; Venditti *et al.* 2011a; Landis *et al.* 2013; Baker *et al.* 2016; Landis & Schraiber 2017; Bastide & Didier 2023).

When studying the morphological evolution of any empirical group differences in evolutionary mode and tempo are potentially compounded by mosaic evolution—which suggests that processes may vary widely across individual traits and the modules they make up. So when looking for macroevolutionary shifts towards new phenotypes, changes may be temporally, phylogenetically, or regionally (across the body) heterogenous. **Something about how major/minor axes of variation may change across groups.** Just a century ago these complications seemed impossible to address: “To select a few of the great number of structural differences for measurement would be almost certainly misleading; to average them all would entail many thousands of measurements for each species or genus compared” (Matthew 1914). Modern comparative methods however, have made these comparisons possible. Here we investigate the relative roles these sources of variation play, by focusing on the Tiliquini skinks. Tiliquines consist of ~62 species with varied ecologies, high levels of sociality (Chapple 2003; Gardner *et al.* 2008), and highly imbalanced biogeographic richness. The majority of species (~48 spp.) are endemic to Australia where their distributions span the continent’s highest alpine peaks and most inhospitable deserts. To survive in such varied climes, tiliquines have diverged into herbivorous giants that roam the treetops, spiky socialites that live communally in rock crevices or complex burrows, and elongate long-lived slow-movers that wander across open lands. These ecotypes have diagnosable morphologies, and the modest species richness of the group allows high-dimensional macroevolutionary study to be computationally tractable. Additionally, tiliquines are ideally suited for studies of the tempo and pace of morphological evolution because they have been suggested to represent a plesiomorphic grade with highly derived morphotypes nested deeply within the phylogeny (Gardner *et al.* 2008; Thorn *et al.* 2021).

But to what degree are these morphological deviations *remarkable*, and what tempo and mode have they evolved by? To answer these questions we started by generating an exon-capture dataset for Tiliquini skinks and reconstructing the phylogenetic relationships of this group. To look at morphological evolution we collected an extensive phenotypic dataset of 21 linear measurements which summarize broad axes of variation across the head, body, limbs, and tail. Finally we incorporate these data into a multivariate framework for comparing evolutionary rates and disparity of traits (and the modules they compose) relative to a neutral BM model of evolution. From this we are able to show that (1) most traits show heterogeneous—not neutral or incremental—evolutionary histories, (2) evolutionary bursts are temporally and phylogenetically distributed but uncommon, and (3) these jumps result in morphological novelty that can exceed uncorrelated trait expectations.

## Methods

Walkthroughs of the data, code, analyses, and results are available in the *Supplementary Material*, on GitHub at [www.github.com/IanGBrennan/Tiliquini](https://www.github.com/IanGBrennan/Tiliquini), and from the Dryad Digital Repository: [http://dx.doi.org/10.5061/dryad.\[NNNN\]](http://dx.doi.org/10.5061/dryad.[NNNN]) (to be updated)

## Data Collection

110 We assembled an exon-capture dataset across 77 Tiliquini skinks representing 48 of 62 currently recognized species, with a focus on Australian taxa (45 of 48 spp.). This sampling covers all 8 genera, as well as many recognized subspecies ([Table S1](#)). We included outgroup representatives from all subfamilies and most tribes, generated as part of broader look at squamate phylogenetics (Burbrink *et al.* 2020). Nuclear exons were targeted and sequenced  
115 using the Anchored Hybrid Enrichment approach (Lemmon *et al.* 2012), and resulted in 379 loci (average coverage 367 loci, min = 362, max = 375) totaling ~600 kbp per sample (Fig.[S2](#)). Rough alignments were compiled using MAFFT (Katoh & Standley 2013) and refined using MACSE (Ranwez *et al.* 2018), alignment parameters are specified in the supplementary materials. Per locus information content is summarized in Fig.[S3](#).

120 We collected 21 linear measurements for 61 Tiliquini skink species from 650 museum samples (average 10 per spp., min.=2, max.=134). These linear measurements aimed to capture the gross morphology of the lizard body plan and are distributed across the head, body, limbs, and tail (Fig.[S4](#)). From the initial 21 measurements some were further divided (e.g. snout-vent length) or dropped to arrive at a set of 19 non-overlapping morphological  
125 traits that are summarized in the Supplemental Material ([Morphological Measurements](#)).

## Phylogenetic Analyses

We reconstructed individual genealogies for our exon-capture data (n=379) under maximum-likelihood in IQ-TREE 2 (Minh *et al.* 2020), allowing the program to assign the best fitting model of molecular evolution using ModelFinder (Kalyaanamoorthy *et al.* 2017), then perform 1,000 ultrafast bootstraps (Haeseler *et al.* 2013). We then estimated the species tree using the shortcut coalescent method ASTRAL III (Zhang *et al.* 2017), with IQTREE gene trees as input. For comparison we estimated a locus-partitioned concatenated species tree in IQTREE. To estimate divergence times among taxa we applied a series of fossil and secondary calibrations in MCMCTree (Rannala & Yang 2007) as outlined in [Table S2](#). We  
130 started by concatenating all exonic loci and partitioning them into two partitions, first and second codons together, and third codons separately, then used *baseml* (Reis & Yang 2011)  
135 to get the approximate likelihoods before running *mcmcTree* on the gradient and Hessian (in.BV file) for four replicate analyses. We compared mcmc files for stationarity and convergence, combined them using logCombiner, and used this combined mcmc file to summarize  
140 divergence times on our tree (*print* = -1 in .ctl file).

## Phenotypic Analyses

Our interest is in identifying the tempo and mode of evolution that produces morphological novelty and so we focus on the dynamics of morphological diversification in the Tiliquini radiation. Our approach is based on a novel dataset that summarizes the lizard body plan.  
145 We started by generating mean trait values per species and removed the effect of absolute size by transforming our trait values into log-shape ratios. To identify independently evolving morphological modules we designed module models that ranged from highly specialized (head, limbs, body, and tail traits evolve independently) to highly integrated (null model in which all traits belong to a single module), see Supplementary Material for details. We

150 compared model likelihoods and estimated correlation coefficients using *EMMLi* (Goswami & Finarelli 2016) and used the preferred model to designate module-specific datasets.

To identify the evolutionary mode of individual morphological traits we fit a series of models ranging from a basic unbiased random walk to entirely punctuated. These allowed phenotypes to evolve through incremental change (Brownian Motion—BM), incremental change 155 around an optimum (Ornstein Uhlenbeck), decreasing change with time (Early Burst)—akin to an adaptive radiation scenario, two “pulse” or “jump” models which allow change in instantaneous bursts (Jump Normal, Normal Inverse Gaussian), and a Variable Rates model in which rates of change vary across individual branches of the tree—similar to the relaxed clock model of timetree estimation. For consistency we fit the BM, OU, EB, JN, and NIG 160 models in *pulsR* (Landis & Schraiber 2017). We fit the VR model in *BayesTraits V3* (Venditti *et al.* 2011b) and processed the output using the standalone *PPPostProcess* software. We compared model fit by AIC scores. *BayesTraits* implements an MCMC algorithm so to estimate a maximum likelihood for the VR model we transformed the input tree by the 165 estimated median rate scalar, then fit the observed data to the transformed tree using BM in *pulsR*. We obtained an AIC value by penalizing the likelihood for each scaled branch of the transformed tree with mean scalar  $r$  greater than two, in addition to the estimation of the rate parameter and root state. We then calculated AICw for each model and identified a preferred model if its AICw was greater than twice the next best model.

To understand the temporal and phylogenetic heterogeneity of evolution we estimated 170 ancestral states for each trait under the rate heterogeneous VR model by optimizing Brownian Motion on the VR rate-transformed trees in *phytools* (Revell 2012). We extrapolated trait values linearly along branches given start and end values at nodes and a constant evolutionary rate. We did this from the root to the tips in 0.1 million year windows across all branches (using the function *trait.at.time*). To summarize the standing morphological 175 variation across the same temporal windows we calculated disparity as both the variance and the average squared Euclidean distance among all pairs of contemporaneous taxa (using *extract.variance*). Similarly we extracted the mean evolutionary rate in 0.1 million year windows for each trait and module (using *extract.stat*). To determine if our observed patterns follow a null expectation of the accumulation of disparity through time we simulated univariate and uncorrelated and correlated multivariate datasets for each trait and module applying 180 parameter estimates from observed data for theta, sigma, and covariance. We carried out the same disparity and rate through time extraction methods in 0.1 million year windows. To understand the relative contribution of niche expansion and niche packing to the accumulation of disparity through time we compared slopes of the accumulation of variance of 185 observed traits and modules to simulated data. We plotted the trends in variance, rate, and slopes using custom functions found in the scripts included in the supplement.

Lastly, to summarize the major avenues of morphological change we ran PCA on (1) all traits jointly and across (2) individual modules and (3) clades separately, then fit linear models to the first 2 PC axes (always accounting for  $\geq 90\%$  of variance). This allowed us to 190 identify the major axes of elaboration (PC1) and innovation (PC2) following the language of Endler *et al.* (2005) and Guillerme *et al.* (2023). Tracking the angle (slope of regression) and extent of trait change between individual nodes enabled us to qualitatively identify periods of primarily innovation or elaboration on a branch-by-branch basis.

# Results

## 195 Phylogenetic Analyses

Concatenated (Fig.S7) and coalescent species trees (Fig.1) return broadly similar topologies with the exception of a handful of extremely short internal branches (Fig.S8). These discordant branches fall within the anomaly zone (Linkem *et al.* 2016) in which concatenation is likely to be misled by the contribution of a large number of anomalous gene trees.

200 In support of this, these nodes as represented in our coalescent species tree generally have low gene concordance factors (gCFs) and equivocal site concordance factors (sCFs), but are strongly supported by individual topology tests (see Supplementary Materials [Topology Tests](#)). Of these contentious nodes, two have taxonomic implications. *Lissolepis* is not recovered as monophyletic, with *L. coventryi* estimated as sister to *Liopholis*, and *L. luctuosa* more closely related to the remaining tiliquines (*Cyclodomorphus*, *Tiliqua*, *Bellatorias*, 205 *Egernia*). We also find *Cyclodomorphus* to be non-monophyletic, with the *C. gerrardii* group more closely allied with *Tiliqua* than with the *C. maximus* group.

Branches that define many of the inter-generic relationships among Australian tiliquines are the result of rapid speciation events. Most of these branches are shorter than a million 210 years long, and several of which are less than 500k years long. These rapid divergences contrast with the deep splits between Australian tiliquines and their sister taxon *Corucia* (30 mya), as well as the preceding split from *Tribolonotus* (60 mya) (Fig.1,S1).

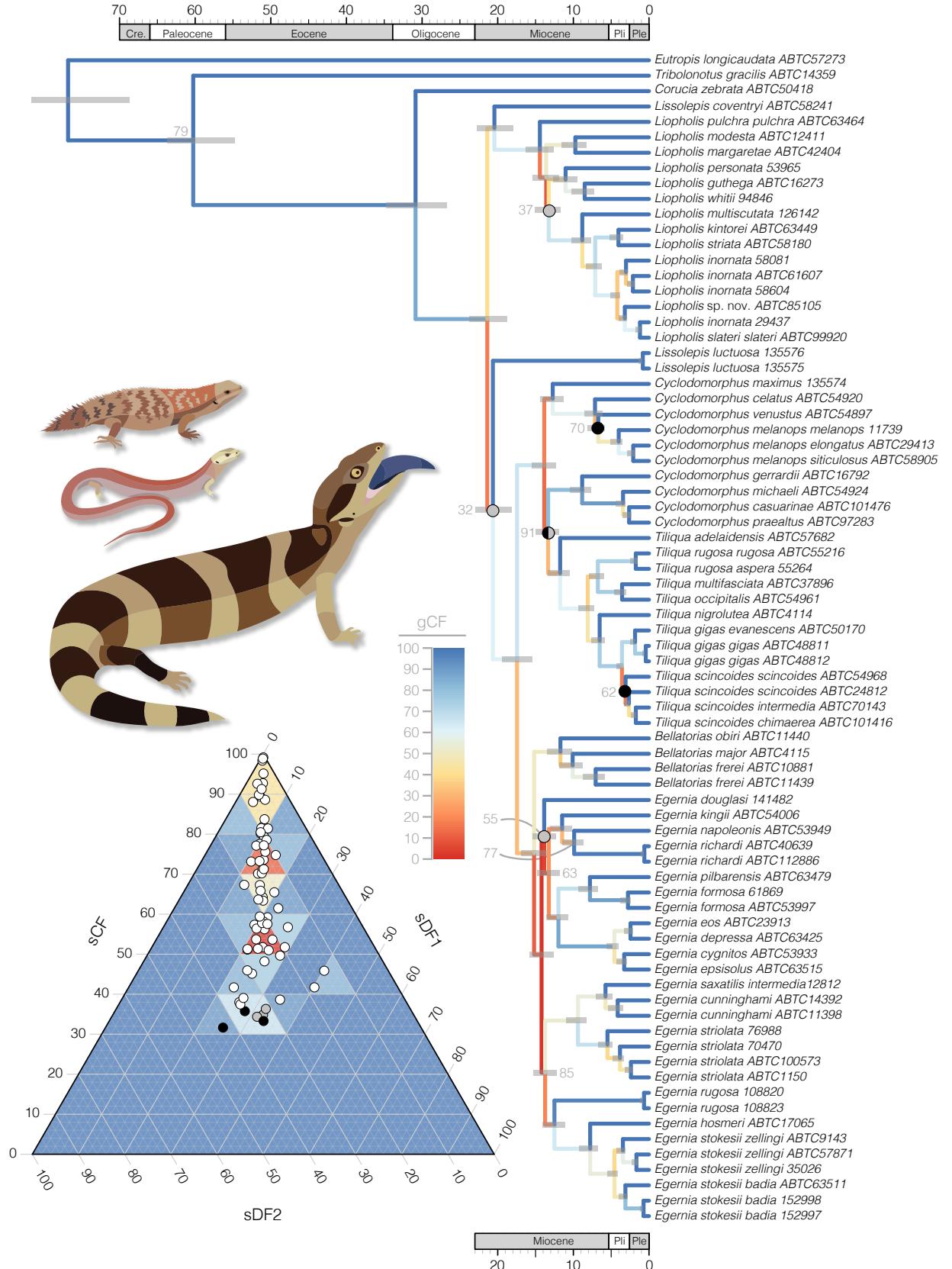


Figure 1: Species tree caption below.

Figure 1. The species tree estimated with ASTRAL and time-calibrated with MCMCTree shows late Oligocene or early Miocene divergences of most major Australian Tiliquini skinks, in contrast  
 215 to a Paleocene divergence from *Tribolonotus* and early Oligocene divergence from the monotypic *Corucia*. Local posterior supports for all nodes are 100, except where indicated by grey numbers. Branches are colored according to gene concordance factors (gCF)—the proportion of gene trees which decisively support the given bifurcation—as estimated by iqtree. The ternary plot bottom left shows the distribution of site concordance factors (sCF) for all nodes in the presented tree.  
 220 sCFs provide another way of interpreting uncertainty by showing relative support for alternative resolutions of a given bifurcation (sDF1, sDF2). sCF values plotted in black on the ternary plot and corresponding tree highlight nodes where  $sCF < sDF1$  or  $sCF < sDF2$ , meaning the bifurcation presented on the tree is not supported by the majority of sites in the concatenated alignment. sCF values plotted in grey on the ternary plot and corresponding tree highlight nodes where  $sCF \approx sDF1 \approx sDF2$ , suggesting an unresolved polytomy.  
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## Phenotypic Analyses

Modularity and integration model selection in *EMMLi* identified a four module model with separate within module correlations (intramodule integration varies among modules) and separate among module correlations (intermodule integration varies among modules) as the  
 230 best fit to our data.

Thirteen of nineteen morphological traits are best fit by variable rate or pulsed models (Fig.S6). The abundant preference for heterogeneous evolutionary models encouraged us to focus on the evolution of traits and modules under the Variable Rates model for all further analyses. The major axis of morphological variation (elaboration; PC1) across the  
 235 Tiliquini and across each genus is primarily explained by tail length (Fig.S20—S22). The major axis of morphological innovation (PC2) varies when considering the clade as a whole (interlimb length) or individual genera (primarily size and/or interlimb length). We visualize this through varied slopes between our first two PC axes, highlighting different paths to phenotypic novelty (Fig.2).

With few exceptions, trait variance accumulated more slowly through the first 40 million years of tiliquine evolution than under the BM null model, for both individual traits (Fig.S16) and modules (Fig.3). Comparing the slopes of these accumulation curves highlights periods of significant morphological conservatism (tail module 20–15 mya) and expansion (body and limb modules 18–14 mya; tail module 3 mya–present). Periods of expansion generally—but  
 240 not always—coincide with periods of increased mean evolutionary rates (Fig.3). Discretizing morphological change as primarily elaborative or innovative allows us to identify that both processes happen at clade and species-level scales (Fig.2).

Averaging rates however, hides pulses of extreme rate variation (Fig.4). We identified pulses by isolating branches with at least twice the background evolutionary rate (mean  
 245 scalar  $r \geq 2$ ) that were shifted in at least 70% of the sampling posterior. Across all 19 focal traits, roughly 13% branches exhibited a significant rate pulse, with more than 3% showing major shifts in evolutionary rate (mean scalar  $r > 10$ ) (Fig.S14). Major shifts were primarily concentrated in head width, interlimb length, tail length and width, and upper arm length. In modules, nearly 16% of branches exhibited significant rate pulses,  
 250 with 2% showing major shifts, concentrated in tail and body modules. Many rate increases are concentrated in the *Cyclodomorphus*–*Tiliqua* clade, with particularly rapid rates among

*Cyclodomorphus michaeli*, *casuarinae*, and *praealtus*. Body and tail traits also commonly show rate pulses in the crevice dwelling *Egernia stokesii* and *depressa* clades.

Simulations under uncorrelated and correlated Brownian Motion show differences in the accumulation of trait combinations. This highlights how evolution can be biased along particular axes (Fig.5, S5). Empirical traits generally conform to BM expectations, however extreme phenotypes exceeding BM predictions have evolved in the feet of *Tiliqua* and tails of some *Egernia* (Fig.5, S9–S13).

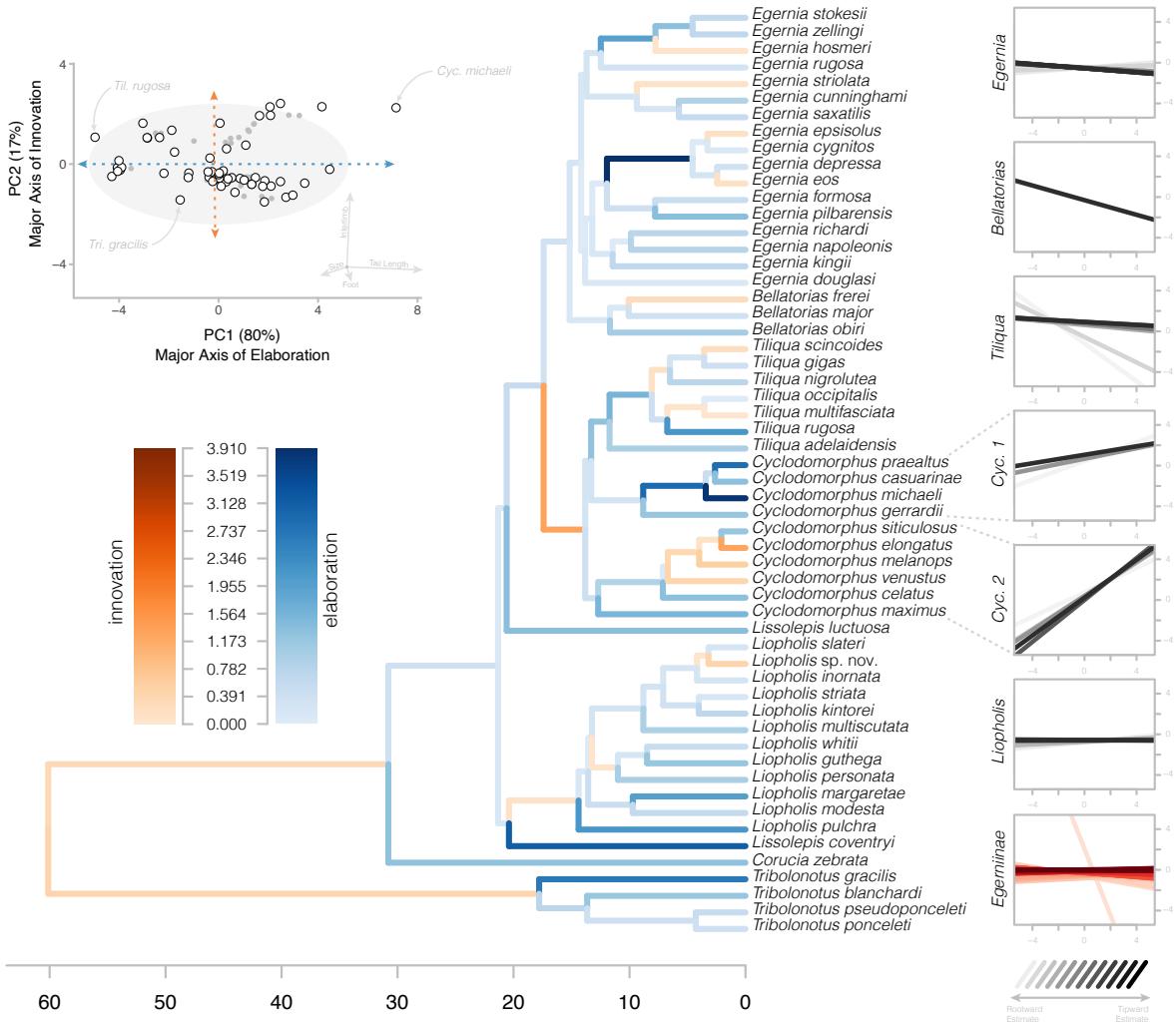


Figure 2: Major and minor axes of morphological change allow us to identify moments of elaboration (along PC1-blues) and innovation (along PC2-oranges) in Tiliquini skinks. Top left—biplot of first two principal components show the distribution of observed species (white circles with black outlines) and estimated ancestors (grey circles) along the major axis of elaboration and innovation. Colored branches on the tree at center indicate the primary direction of morphological change from ancestor to descendant node. Blue branches indicate principally elaborative change, while orange branches indicate principally innovative change. At right we visualize the varied relationships between these axes among groups. For each clade (genera and group as a whole) we plot the evolution of the relationship between elaborative and innovative axes through time from the root of the clade (lightest regression) to the tips (darkest regression). Regression plots highlight the varied patterns of subclades, including strong conservatism of *Liopholis* and novelty of *Cyclodomorphus*.

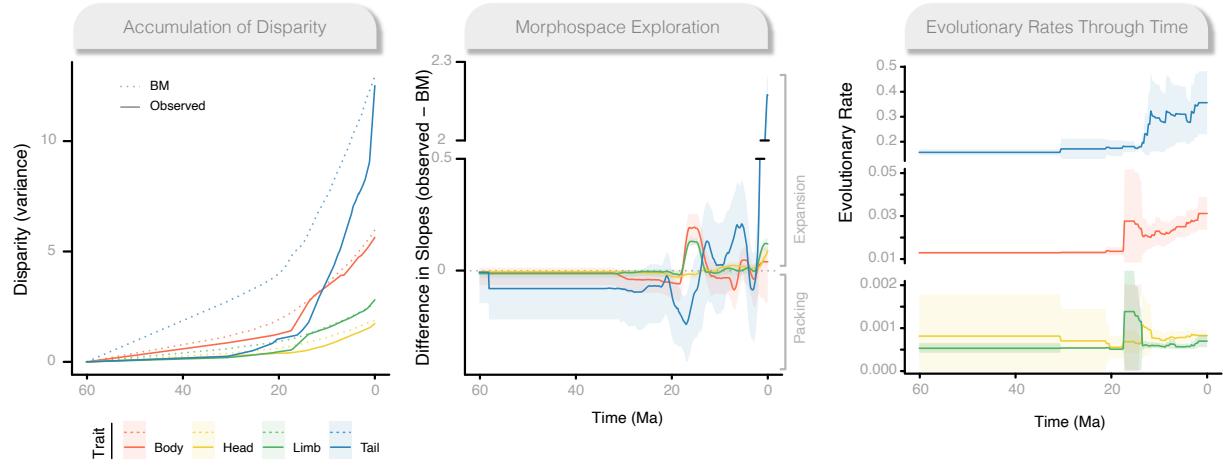


Figure 3: Evolutionary trajectories vary widely across modules and through time. (left) Accumulation of multivariate disparity (as variance) through time for each module (solid lines) compared to Brownian Motion (dotted lines). (center) The comparison of slopes of each module to BM highlights periods of morphological expansion (values greater than 0) and conservatism (values less than 0). (right) Evolutionary rates across modules are highly heterogeneous (see three different scales for y axis), showing periods of temporal variability, as well as high variances within modules and among traits (Fig.S15–S17).

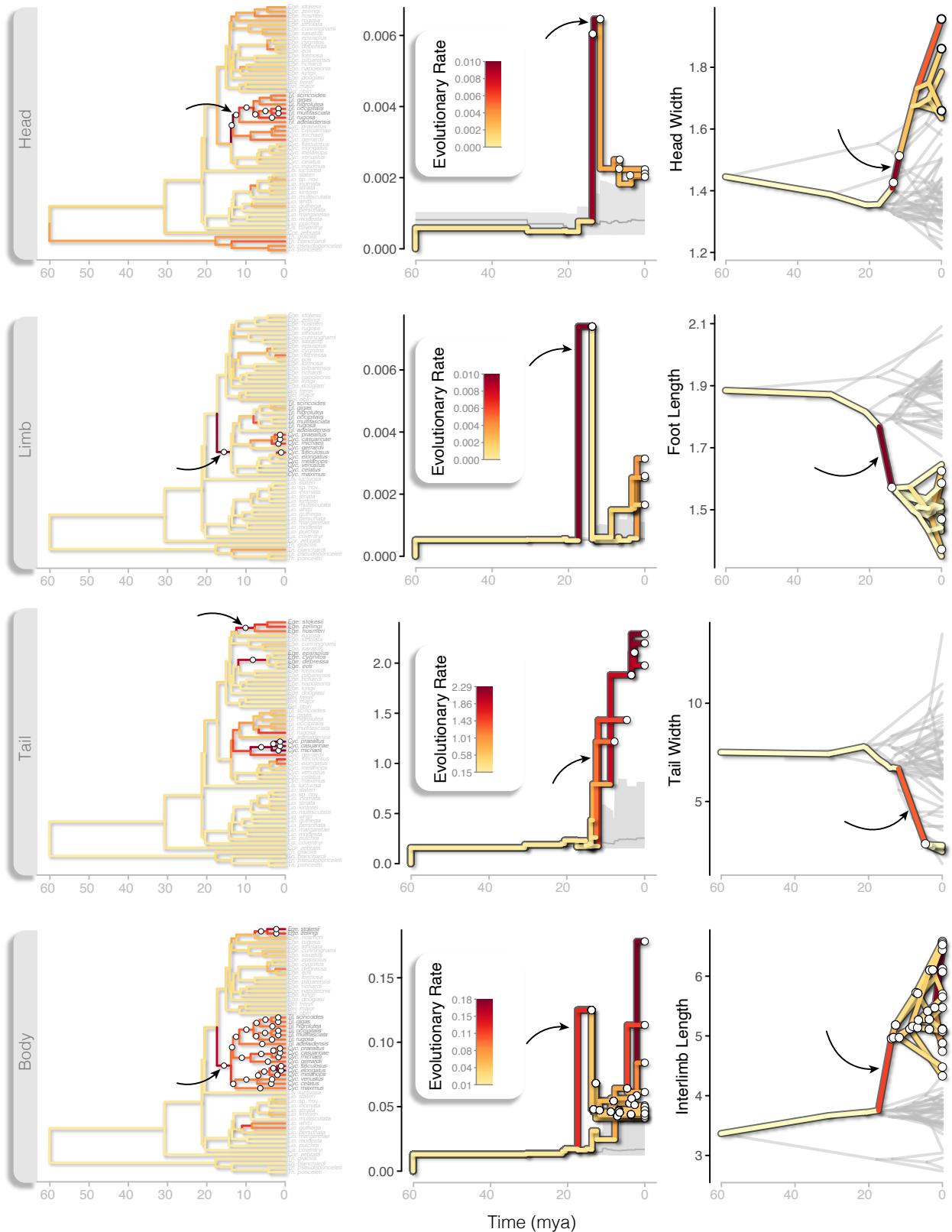


Figure 4: Rates caption below.

Figure 4. Bursts in rates of phenotypic evolution are distributed across the Tiliquini tree and exhibit strong departures from background rates. Rows represent morphological modules. In all plots branch colors correspond to estimated multivariate evolutionary rates, with significant rate changes noted by white circles at nodes or along branches. (left column) Tiliquini species trees highlighting the location of multivariate rate pulses. (center column) Branch rate trajectories plotted from the root node to nodes that show significant rate shifts. Solid grey envelope contains 95% quantiles of background evolutionary rates (estimated rate scalar  $r < 2$ ) with the mean plotted in dark grey. (right column) Phenograms of an individual trait from each module showing the evolution of extreme phenotypes driven by bursts in evolutionary rate. In each row, a black arrow highlights a single branch of interest across all three plots.

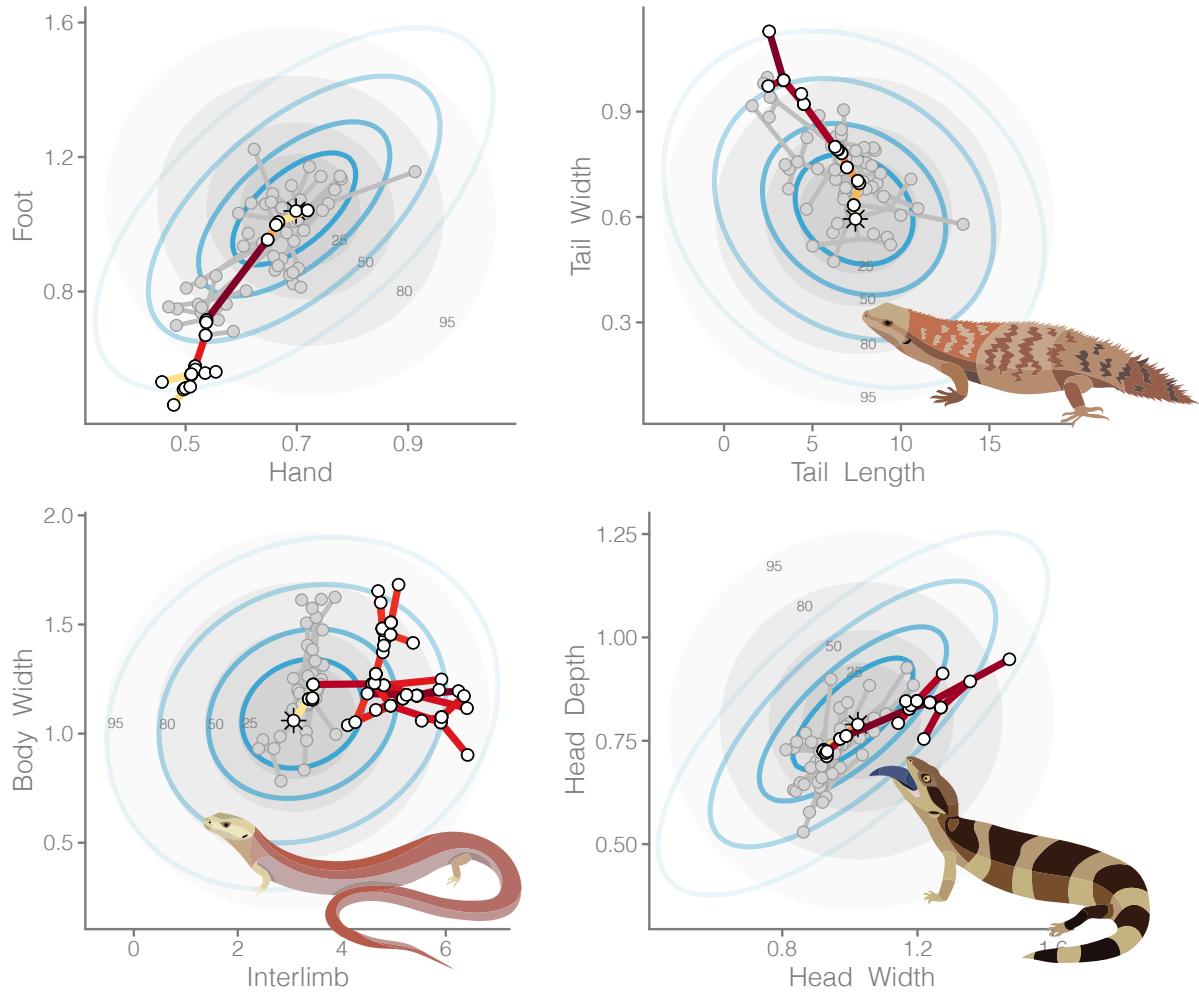


Figure 5: Novel morphologies exceed expectations of uncorrelated trait evolution. Bivariate plots show a phylomorphospace (species points connected by a phylogeny) of the Tiliquini. Each plot isolates a single clade within the group to highlight morphological extremes. Branches of the highlighted clade are colored according to evolutionary rates, with remaining species and branches in grey. In the background are ellipses containing 25/50/80/95% of traits simulated under empirical rates for uncorrelated (grey) and correlated (blue rings) Brownian Motion. Highlighted clades are (clockwise from top left: *Tiliqua*; *Egernia stokesii*–*E. hosmeri*, *Tiliqua rugosa*–*T. gigas*, *Cyclodomorphus*–*Tiliqua*).

## Discussion

275 The variety of organismal forms has been a bottomless well of inspiration for scientists and the public, and an almost infinite source of data for macroevolutionary biologists to investigate the timing and accumulation of morphological diversity. Whether morphological disparity has accumulated early (Foote 1997), uniformly (Imfeld & Barker 2022), or via intermittent pulses (Uyeda *et al.* 2011; Landis & Schraiber 2017; Deline *et al.* 2018) remains a contested topic at varied evolutionary scales. Here we investigate the morphological evolution of the lizard body by looking across time, phylogeny, and body regions to better understand the modes by which traits evolve. We provide evidence for Tiliquini skinks that most traits evolve conservatively, but morphological novelty accumulates through extreme punctuations—jumps into new trait space. These jumps are uncommon (0.003–0.05 jumps/my), do not follow an established morphological order (Sallan & Friedman 2012), and can be nested to develop new trait combinations.

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### Phylogenomics of the Tiliquini

Skinks are a tremendously species rich group that make up more than 25% of all lizard diversity (1700+ species). The largest and most impressive skinks belong to the tribe Tiliquini which are primarily distributed across Australia with a small number of species found in Indonesia, Papua New Guinea, and the Solomon Islands. Despite their importance as models of reptilian sociality (Chapple 2003; Gardner *et al.* 2016) and as an emerging fossil system (Thorn *et al.* 2019, 2023; Thorn *et al.* 2021) phylogenetic hypotheses for the Tiliquini have relied on a handful of molecular markers and limited species sampling (Chapple *et al.* 2004; Chapple & Keogh 2006; Gardner *et al.* 2008). Our exon capture dataset provides a well supported estimate of the relationships among all eight Tiliquini genera and 80% of described species. In agreement with previous estimates we recover the Tiliquini as members of the Lycosominae alongside the Sphenomorphini, Eugongylini, and Mabuyini (Fig.S1), suggesting an Asian origin for the subfamily (**Burbink2020?**).

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Living tiliquines are divided into three clades, comprising the enigmatic Crocodile Skinks *Tribolonus*, the monotypic Solomon Islands endemic *Corucia*, and an Australian radiation. Splits among these groups are old (~60 & ~30 mya), and followed by the rapid Miocene divergence of all Australian Tiliquini genera (23–15 mya). These rapid speciation events result in short internal branches that prove difficult to resolve on a per-locus basis (Fig.1,S18). However, most of these difficult nodes are resolved by leveraging our 400 loci in ASTRAL, investigating summary statistics, and applying topology tests. Our new phylogenetic hypotheses of these nodes has necessitated that we propose taxonomic changes for two genera, which we provide in the attached Appendix. Some splits remain intractable however. The branching patterns among major *Egernia* clades, and the series of splits among *Lissolepis luctuosa*, *Liopholis*, and the remaining Australian tiliquines have splits so short (300–400ky) that they exist at the limits of phylogenetic reconstruction. Regardless of resolution of these difficult branches, the radiation of Australian Tiliquini into divergent ecologies and morphologies happened rapidly and in concert across open landscapes, closed forests, deserts, and mountain peaks.

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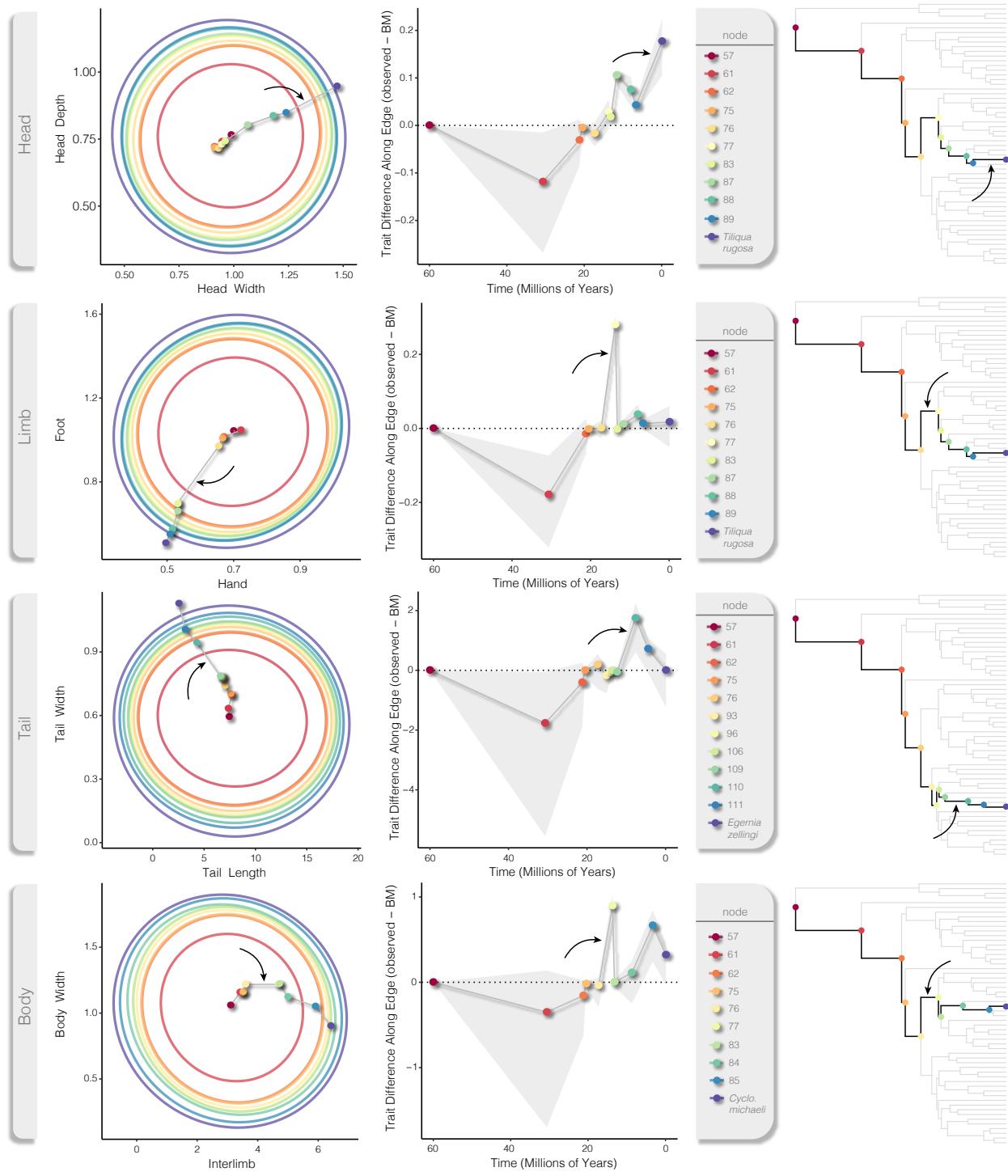


Figure 6: Phenotypic jumps caption below.

315 Figure 6. Phenotypic jumps are visible as greater than expected trait changes along branches, as estimated under the Variable Rates model and compared to Brownian Motion. Rows correspond to morphological modules, noted in grey at far left. Both circular and line plots show the evolutionary trajectory of focal traits from the root of the Tiliquinii tree (node 57, dark red) to a single tip (dark

purple) that has exhibited one or more rate bursts. (left) Large colored rings represent the simulated distribution of trait values under uncorrelated Brownian Motion at each node along the root-to-tip trajectory. Small colored points represent observed and ancestral trait values as estimated under Variable Rates as they traverse the path root-to-tip connected by a grey line. (center) The line plot indicates the trait difference of nodes as (observed - simulated) values with 95% quantiles shown in light grey. Nodes that fall above the dotted line (0) show greater than expected trait change along the branch that leads to that node, visible as greater distances between points in the plots at left. Nodes falling below the dotted line show less trait change than expected. Trees at right serve as a guide for the root-to-tip path of each example, with nodes colored accordingly. Black arrows in each row indicate the greatest jump in phenotype compared to expectations. References to node numbers can be seen in Fig. S19.

### 330 Evolving Novel Phenotypes by Bursts

Earth's incredible biodiversity of forms and functions have evolved over hundreds of millions of years. Growing evidence suggests that much of this diversity accumulated via short periods of rapid phenotypic change, not by incremental divergence (Uyeda *et al.* 2011; Landis & Schraiber 2017; Novack-Gottshall *et al.* 2022; **Leslie2022?**). If this is true and pulsed morphological evolution is common, then it is important to understand how it contributes to the development of morphological novelty and diversity. To do this we identified how pulses are distributed through time, across the phylogeny, and among morphological axes.

Much of modern macroevolutionary thinking relies on Simpson's (1944) idea of adaptive zones. The varied adaptive landscape accumulates diversity as lineages traverse into new adaptive zones that are centered around fitness peaks. Lineages move into new zones by evolutionary jumps—rapid movement across suboptimal space. In comparative studies the idea of a multipeak morphological landscape is often described by multi-optima OU models (Hansen 1997; Beaulieu *et al.* 2012; Burin *et al.* 2023). While these models account for the clustering of species around discrete trait values (evolutionary ‘clumpiness’) they do not explain well the process of movement across the landscape to occupy new peaks. Our analysis of the lizard body plan provides evidence that pulses in evolutionary rate and coincident phenotypic change are common across many morphological traits (preferred in 13 of 19 traits). This suggests that large distances of suboptimal trait space can be quickly traversed to reach new morphological realms. When comparing modeled empirical data to gradualist simulations, jumps are observable as large trait changes along individual branches (Fig. 6). However, the accumulation of morphological disparity does not appear to be dictated solely by rare jumps, or to occur explicitly at speciation, as in the punctuated equilibrium model of Gould & Eldredge (1972). Instead, we find broad support for a model in which the background process of evolution by a random walk (Brownian Motion) is punctuated by bursts in evolution that result in jumps to new adaptive zones. We consider this process more akin to the “punctuated gradualism” model of Malmgren *et al.* (1983). While we recognize that our inferred process is not entirely consistent with Malmgren *et al.* (1983) who proposed punctuations between evolutionary stasis and gradualism, we suggest that these distinctions may instead be indicative of similar processes occurring at different scales along the micro-to-macroevolutionary continuum. At both scales, a heterogeneous mode driven by an increase in evolutionary rates facilitates the evolution of novel and divergent morphologies (Fig. 4)—in the case of these lizards, this occurs against a background morphological diffusion process. In

this way we attempt to find common ground for both Darwinian and Simpsonian evolution.

In the Variable Rates model branch-specific shifts are indicative of an increase in evolutionary rate but remain a parameter of a random walk (Brownian) process. So, increasing the evolutionary rate suggests an increase in the *evolvability* and ultimately the potential variance of a lineage. An alternative interpretation for the identification of rate bursts could instead be a directional (biased) trend towards distinct trait values. A recently designed method for addressing this—the *fabric* model of *BayesTraits V4* (Pagel *et al.* 2022)—proposes that excess rate estimates could instead be absorbed by a biased walk to new trait space. Importantly, this does not fundamentally change the outcome that evolution has swerved into a new morphological lane, but it does suggest a difference in the evolutionary mode. Whereas a rate pulse suggests a rapid, random exploration of trait space that lands in a new zone, directional trends elicit a guided evolutionary walk (e.g. via selection) towards a new area of trait space. Because a guided walk is directional the evolutionary rate need not be rapid. Regardless, the jump in trait value along a branch, and evolution of a new phenotype remains the same. This provides an appealing explanation for scenarios where selection might be particularly effective, such as in small populations or those with high trait variances.

Importantly, inferred phenotypic jumps happen along both the primary morphological axis—where they exaggerate existing variance (elaboration)—**and** along minor morphological axes—where they develop novel trait combinations (innovation). Along both major and minor axes relatively uncommon but major discontinuities result in unusual and novel morphologies, as seen in birds (Cooney *et al.* 2017) and fish (Ronco *et al.* 2021). In Tiliquinis, the most obviously novel phenotypes belong to the Bluetongue lizards *Cyclodomorphus* and *Tiliqua*. Bluetongues concurrently underwent dramatic shifts in limb and body modules, extending the length of the body and shortening the limbs. Subsequent jumps in head and tail modules resulted in further temporally staggered morphological bursts. Nested morphological pulses gave rise to broad heads and bodies, and stumpy tails in *Tiliqua*. However, some of the most dramatic changes have happened on the shortest timescales. In the *Cyclodomorphus michaeli* clade (*C. casuarinae*, *C. michaeli*, *C. praealtus*) which we estimate at less than 4 million years old, we identify jumps in tail, limb, and body traits. These result in the rapid shortening of the interlimb, tail, and leg lengths in *C. praealtus*, and lengthening of these traits in *C. casuarinae* and *C. michaeli*. Interestingly, these changes are potentially driven not by functional morphological reasons but instead by physiological ones. *C. praealtus* lives at high elevations where shortened extremities may be advantageous to maintain thermal mass following Allen’s Rule (Alho *et al.* 2011).

Occasionally independent evolutionary trajectories arrive at similar adaptive zones, a process usually called morphological convergence. We identify convergence in the spiny crevice-dwelling clades of *Egernia* (*E. stokesii* and *E. depressa*). These clades have undergone rapid shortening and widening of the tail from non-armored, long-tailed ancestors (Fig. 4). Amazingly, these clades have both arrived at this novel phenotype via rate increases of roughly ten times the background rate. The repeated evolution of a distinct phenotype like highly modified tails suggests strong selective pressures shaping some morphological axes (Ramm *et al.* 2020). Another example of the strength of selection concerns the only clade of primarily crepuscular and nocturnal tiliquines the *Liopholis kintorei-inornata* group. This clade is broadly distributed across arid and semi-arid Australia, living in burrows they dig in

loose soil or sand. However, the transition of these skinks towards a nocturnal lifestyle does not appear to have driven exceptional morphological differentiation from other *Liopholis*,  
410 except for the size of their eyes. The transition in diel activity is coincident with a jump in eye diameter and even the evolution of vertical pupils in the Night skink *Liopholis striata* (Fig.S14). Despite the evolution of novel morphologies by phenotypic bursts, truly exceptional morphologies are rare. In a few cases, such as the feet of some *Tiliqua* and the tails of  
415 some *Egernia*, contemporary trait values fall outside what we expect under a uncorrelated random walk model. These instances provide the strongest cases for active selection driving the evolution of phenotypes (Fig.5).

## Conclusions

Animal bodies are made up of many morphological traits which in their myriad combinations contribute to Earth's amazing biodiversity. This diversity has diverged from common forms  
420 on deep temporal scales, however our understanding of this process has begun to question the popularity of commonly invoked Darwinian gradualism as its driver. Our study of gross lizard morphology provides evidence instead that trait evolution is heterogeneous, and is structured phylogenetically, temporally, and across the body-plan. This adds to a growing body of evidence that morphological traits diverge through evolutionarily discontinuous processes.  
425 These discontinuities contribute substantially towards the evolution of novel morphologies, and we suggest that this is likely a common process in morphological diversification across animals that helps reconcile Darwinian and Simpsonian evolution.

# Appendix

## Taxonomic Implications and Changes

- 430 As a result of our phylogenetic investigation, some taxonomic issues must be addressed and others will unfortunately remain outstanding until more focused sampling can be achieved. We comment on both cases below. **The order of the following comments can easily be shifted**

435 (1) Paraphyly of *Lissolepis*: Phylogenetic estimation and topology testing do not support the monophyly of *Lissolepis*. The type species of *Lissolepis* is *L.luctuosa* (Peters 1866), and despite *L.coventryi* (Storr 1978) forming a clade with *Liopholis*, these taxa are morphologically distinct. We feel that to acknowledge the distinctiveness of *L.coventryi* the best course of action is to erect a new genus to contain this species.

440 *Paluarius* gen. nov. Brennan ...

*Egernia* Storr 1978

*Lissolepis* Gardner 2008

Type species: *Egernia coventryi* Storr 1978

Diagnosis and definition: Currently a monotypic genus comprising a single medium sized (̄x = 80 mm; max = 100 mm) skink with four well developed limbs each with five digits and fourth toe much longer than third. Lower eyelid movable and without a transparent ‘window’. Parietal and nasal scales both narrowly separated. Ear aperture small and with two anterior lobules. Distinguished from *Lissolepis* by broad geographic separation (southwest WA for *Lis.*; extreme southeast SA and coastal VIC for *Pal.*), continuous striped (*Paluarius*) rather than spotty (*Lissolepis*) dorsal patterning, shorter and blunter head (head length 15% of SVL in *Pal.*, 20% in *Lis.*), fewer midbody scale rows, longer postnasal crease that runs to the top of the nasal scale, and smaller size (80–100 mm vs. 100–129mm).

455 Etymology: This skink lives among swamps, heaths, and marshes in far southeastern Australia. In allusion to its preferred habitat, from latin ‘palus’—swamp and ‘-arius’—where things are kept, together meaning ‘keeper of the swamp’.

Contents: *Paluarius coventryi* comb. nov. (Storr 1978)

460 (2) Paraphyly of *Cyclodomorphus*: Phylogenetic estimates and topology testing do not support the monophyly of *Cyclodomorphus* (). The type species of *Cyclodomorphus* is *C. casuarinae* (Dumeril & Bibron 1839), which along with the species *gerrardii*, *michaeli*, and *praealtus* form a clade with *Tiliqua*. We propose a new generic name to contain the taxa more closely related to *C. maximus* than to *C. gerrardii*.

*Caeruleulus* gen. nov. Brennan ...

*Cyclodus* Dumeril & Bibron 1839

465 *Hinula* Gunther 1867

*Lygosoma*

*Tiliqua*

*Omolepida* Gray 1845

*Cyclodomorphus* Fitzinger 1843

470 Type species: *Omolepida maxima* Storr 1976

Diagnosis and definition: A genus of moderate to large, elongate skinks characterized by long interlimb (trunk) lengths and relatively short limbs, each with five digits. Many scalation characters are shared with *Cyclodomorphus*, and so make distinguishing the two difficult. Starting from the snout, nasals are in contact with one another and broadly contact  
475 the frontonasal which widely separates the prefrontals. There are no subocular scales, but three supraocular scales, the anterior two of which contact the frontal. Eyelid movable and no transparent ‘window’. Parietal scales are widely separated by an interparietal scale. Ear opening small, with small anterior lobules (usually 2).

Etymology: From the Latin ‘caeruleus’ for blue and the diminutive ‘-ulus’, meaning ‘little  
480 blue one’, alluding to their blue tongues and smaller size relative to the larger ‘bluetongue’ relatives *Tiliqua*.

Contents: *Caeruleulus branchialis* comb. nov. (Gunther 1867); *Caeruleulus celatus* comb.  
485 nov. (Shea & Miller 1995); *Caeruleulus maximus* comb. nov. (Storr 1976); *Caeruleulus melanops elongatus* comb. nov. (Shea & Miller 1995); *Caeruleulus melanops melanops* comb. nov. (Stirling & Zietz 1893); *Caeruleulus melanops siticulosus* comb. nov. (Shea &  
490 Miller 1995); *Caeruleulus venustus* comb. nov. (Shea & Miller 1995).

Comment: Wells (2007) proposed splitting *Cyclodomorphus*, reallocating *C. gerrardii* to *Hemisphaeriodon* and creating a new generic name for the *Cyclodomorphus maximus* clade. In following the best practices in herpetological nomenclature outlined by Kaiser et al. (2013)  
495 and adopted by the Australian Society of Herpetologists in their Position Statement on Taxonomy (2022) we do not recognize the name proposed by Wells (2007) and instead provide *Caeruleulus* as the generic name for this clade of tiliquine skinks.

(3) *Cyclodomorphous melanops*: Our limited sampling suggests species-level divergences  
495 among the three subspecies of *C. melanops* (~4mya, 2mya), however unpublished mtDNA data shows more complicated genetic history among these taxa and the closely related *C. venustus*, *C. celatus*, and the currently unsampled *C. branchialis*. In light of these results we take the conservative stance of retaining the subspecies as is, and suggest a more focused  
500 study with greater sampling would provide better understanding of this morphologically conservative clade.

(4) *Egernia stokesii*: Similarly, the divergence between *E. stokesii* subspecies *E.s.badia* and *E.s.zellingi* are comparatively deep (~4.5mya), and subspecies are recovered as reciprocally monophyletic. However, our sampling lacks representatives of the nominate subspecies  
505 *E.s.stokesii*. Unpublished mtDNA data does not appear to distinguish between subspecies *E.s.stokesii* and *E.s.badia*, and so we refrain from making taxonomic changes without having *E.s.stokesii* included in our analyses.

(5) Paraphyly of *Liopholis inornata*: Our sampling of *L. inornata* and sister taxa *L. slateri* and *L. sp. nov.* from Purnululu highlight a complicated phylogenetic history. As currently understood, *L. inornata* is a wide ranging species found across much of arid WA, SA, NSW, and QLD. This range overlaps entirely with *L. slateri* with which it could potentially be confused, but remains allopatric from *L. sp. nov.* Purnululu. We highlight this clade as a group which needs a much more thorough population genetic assessment to resolve.

## **Supplementary Material**

Supplementary material included below consists of additional figures, tables, and extended methods to complement the main text.

**Table S1.** Taxon sampling for this project.

Genus	Species	Subspecies	Specimen Registration	ABTC No.	Locality	State	Country	Latitude	Longitude
Bellatorias	<i>frerei</i>	—	AMS R.113970	10881	Bunya Mountains	QLD	Australia		
Bellatorias	<i>frerei</i>	—	AMS R.96317	11439	Heathlands	QLD	Australia		
Bellatorias	<i>major</i>	—	SAMA R.33412	4115	Whian Whian SF	NSW	Australia		
Bellatorias	<i>obiri</i>	—	AMS R.100018	11440	Jabiluka	NT	Australia		
Corucia	<i>zebrata</i>	—	—	50418	Levaleva Choiseul Island	—	Solomon Islands		
Cyclodomorphus	<i>melanops</i>	<i>elongatus</i>	MAGNT R20662	29413	Finke Gorge NP	NT	Australia		
Cyclodomorphus	<i>casuarinae</i>	—	SAMA R.22957	54924	Mount Victoria	NSW	Australia		
Cyclodomorphus	<i>celatus</i>	—	SAMA R.63333	101476	—	TAS	Australia		
Cyclodomorphus	<i>gerrardi</i>	—	SAMA R.22873	54920	Burns Beach	WA	Australia		
Cyclodomorphus	<i>maximus</i>	—	SAMA R.34884	16792	Paluma	QLD	Australia		
Cyclodomorphus	<i>melanops</i>	<i>siticulosus</i>	WAM R168816	135574	Middle Osborn Island	WA	Australia		
Cyclodomorphus	<i>melanops</i>	<i>melanops</i>	SAMA R.52374	58905	St. Francis Island	SA	Australia		
Cyclodomorphus	<i>praelectus</i>	—	SAMA R.34056	11739	Mount Stuart Homestead	WA	Australia		
Cyclodomorphus	<i>venustus</i>	—	—	97283	Bogong High Plains	VIC	Australia		
Egernia	<i>cunninghami</i>	—	SAMA R.18869	54897	Port Germein Dump	SA	Australia		
Egernia	<i>cunninghami</i>	—	AMS R.112873	11398	Yetman	NSW	Australia		
Egernia	<i>depressa</i>	—	AMS R.118939	14392	Kanangra Walls	NSW	Australia		
Egernia	<i>depressa</i>	—	SAMA R.22856	53933	Python Pool	WA	Australia		
Egernia	<i>douglasi</i>	—	WAM R120631	63425	Mardathuna	WA	Australia		
Egernia	<i>eos</i>	—	ABTC 141482	141482	Beverley Springs Homestead	WA	Australia		
Egernia	<i>episolus</i>	—	WAM F98079	23913	Ainsley Gorge	WA	Australia		
Egernia	<i>formosa</i>	—	WAM F90897	63515	Woodstock	WA	Australia		
Egernia	<i>formosa</i>	—	SAMA R.29267	53997	Yalgoo	WA	Australia		
Egernia	<i>hosmeri</i>	—	WAM F103993	611869	Woodstock Station	WA	Australia		
Egernia	<i>kingii</i>	—	SAMA R.36707	17065	Mount Isa	QLD	Australia		
Egernia	<i>napoleonis</i>	—	SAMA R.29444	54006	Mount Clarence	WA	Australia		
Egernia	<i>pillaensis</i>	—	SAMA R.23080	53949	Dennmark	WA	Australia		
Egernia	<i>richardi</i>	—	WAM R1.32519	63479	Burrup Peninsula	WA	Australia		
Egernia	<i>richardi</i>	—	SAMA R.26315	40639	Koonalda Station	SA	Australia		
Egernia	<i>rugosa</i>	—	SAMA R.63272	112886	Merderyrah Sandpatch	SA	Australia		
Egernia	<i>rugosa</i>	—	—	108820	Charleville	QLD	Australia		
Egernia	<i>saxatilis</i>	<i>intermedia</i>	SAMA R.44004	108823	Charleville	QLD	Australia		
Egernia	<i>stokesii</i>	<i>zellingi</i>	SAMA R.42897	12812	The Grampians	VIC	Australia		
Egernia	<i>stokesii</i>	<i>zellingi</i>	SAMA R.45053	9143	Stonehenge	QLD	Australia		
Egernia	<i>stokesii</i>	<i>zellingi</i>	SAMA R.44127	35026	Toopawarina Hill	SA	Australia		
Egernia	<i>stokesii</i>	<i>badia</i>	WAM R.35193	57871	Pernatty Station	SA	Australia		
Egernia	<i>stokesii</i>	<i>badia</i>	WAM R152997	63511	Walycatchem	WA	Australia		
Egernia	<i>stokesii</i>	<i>badia</i>	WAM R152998	92933	Waiga Rock	WA	Australia		
Egernia	<i>striolata</i>	—	AMS R.126116	92934	Waiga Rock	WA	Australia		
Egernia	<i>striolata</i>	—	SAMA R.53262	1150	Denham	NSW	Australia		
Egernia	<i>striolata</i>	—	SAMA R.55661	70470	Telowie	SA	Australia		
Egernia	<i>QM_J86594</i>	—	Moorrinya NP	76988	Moorrinya NP	QLD	Australia		
Egernia	<i>QM_R38916</i>	—	100573	57273	Durkai SF	QLD	Australia		
Eutropis	<i>longicaudata</i>	—	—	—	—	—	Malaysia		

Genus	Species	Subspecies	Specimen Registration	ABTC No.	Locality	State	Country	Latitude	Longitude
<i>Liopholis</i>	<i>guthega</i>	—	SAMA R37781	16273	Kosciusko NP	NSW	Australia		
<i>Liopholis</i>	<i>inornata</i>	—	MAGNT R20673	29437	Finke Gorge NP	NT	Australia		
<i>Liopholis</i>	<i>inornata</i>	—	SAMA R45219	58081	Mootatunga	SA	Australia		
<i>Liopholis</i>	<i>inornata</i>	—	SAMA R49140	58604	Eyre Peninsula	SA	Australia		
<i>Liopholis</i>	<i>inornata</i>	—	NMV D65868	61607	Buninyonia Springs	WA	Australia		
<i>Liopholis</i>	<i>kintorei</i>	—	WAM R131047	63449	—	WA	Australia		
<i>Liopholis</i>	<i>margaretae</i>	—	SAMA R51590	42404	Annata	SA	Australia		
<i>Liopholis</i>	<i>margaretae</i>	—	SAMA R24815	53965	Mount Remarkable NP	SA	Australia		
<i>Liopholis</i>	<i>modesta</i>	—	SAMA R39172	12411	Retreat	NSW	Australia		
<i>Liopholis</i>	<i>montana</i>	—	SAMA R37768	16389	Mount Gingera	ACT	Australia		
<i>Liopholis</i>	<i>multiscutata</i>	—	SAMA R63458	126142	—	SA	Australia		
<i>Liopholis</i>	<i>pulchra</i>	—	WAM R132054	63464	D'Entrecasteaux NP	WA	Australia		
<i>Liopholis</i>	<i>sp. nov.</i>	—	WAM R156715	85105	Purnululu NP	WA	Australia		
<i>Liopholis</i>	<i>slateri</i>	—	—	99920	Finke River	NT	Australia		
<i>Liopholis</i>	<i>striata</i>	—	SAMA R45402	58180	Anpeinna Hills	SA	Australia		
<i>Liopholis</i>	<i>whitii</i>	—	SAMA R53588	94846	Spring Mount	SA	Australia		
<i>Lissolepis</i>	<i>coventryi</i>	—	SAMA R45916	58241	Nelson	SA	Australia		
<i>Lissolepis</i>	<i>luctuosa</i>	—	WAM R90386	135575	Walpole	WA	Australia		
<i>Lissolepis</i>	<i>luctuosa</i>	—	WAM R90226	135576	Lake Wilson	WA	Australia		
<i>Tiliqua</i>	<i>adelaidensis</i>	—	SAMA R42426	57682	Burra	SA	Australia		
<i>Tiliqua</i>	<i>gigas</i>	—	AMS R.124720	48811	Usino	Manus	Papua New Guinea		
<i>Tiliqua</i>	<i>gigas</i>	—	AMS R.124720	48812	Usino	Manus	Papua New Guinea		
<i>Tiliqua</i>	<i>multifasciata</i>	—	AMIS R.129710	50170	Gulegule Normanby Island	Milne Bay	Papua New Guinea		
<i>Tiliqua</i>	<i>nigrolutea</i>	—	SAMA R49974	37896	Purni Bore	SA	Australia		
<i>Tiliqua</i>	<i>occipitalis</i>	—	SAMA R33410	4114	Clarkefield	VIC	Australia		
<i>Tiliqua</i>	<i>rugosa</i>	—	SAMA R28391	54961	Iron Knob	SA	Australia		
<i>Tiliqua</i>	<i>rugosa</i>	—	SAMA R18978	55216	Bremer Bay	WA	Australia		
<i>Tiliqua</i>	<i>scincoides</i>	intermedia	SAMA R20587	55264	Cowell	SA	Australia		
<i>Tiliqua</i>	<i>scincoides</i>	intermedia	QM J51107	24812	Cape Flattery	QLD	Australia		
<i>Tiliqua</i>	<i>scincoides</i>	—	WAM R112258	101416	Latdalam	—	Indonesia		
<i>Tiliqua</i>	<i>scincoides</i>	—	SAMA R28511	54968	Minnipa	SA	Australia		
<i>Tiliqua</i>	<i>gracilis</i>	—	SAMA R53937	70143	Tunnel Creek Gorge	WA	Australia		
<i>Tribolonotus</i>		—	AMIS R.122119	14359	Karkar Island	—	Papua New Guinea		

520 **Table S2.** Fossil calibrations as implemented in MCMCTree. The root (Mabuyini + Tiliquini) and the Tiliquini crown are  
 calibrated with Cauchy distributions based on estimates from previous studies. These leave 2.5% of the distribution each above  
 and below the minimum and maximum ages noted below. The calibration for the crown of Australian Tiliquini is bounded on  
 the lower end by the Dworramoor Local Fauna of Riversleigh which includes *Tiliqua pusilla* and *Egernia gillespieae*, and on the  
 upper end by *Proegernia palankarinensis* and *P. mikebuli*. The prior allows 2.5% below the minimum bound and 20% above  
 the maximum bound. The remaining calibrations are all soft minimums with 2.5% below the minimum.  
 525

Node	Fossil Information	Calibration	Split	Source
A	Soft Secondary	'>0.5<0.8'	Root (Mabuyini + Tiliquini) [C	ITE Burbrink et al. 2021; Thorn et al. 2021]
B	Soft Secondary	'>0.37<0.62'	Crown Tiliquini ( <i>Tribolonotus</i> + all others) [	CITE Thorn et al. 2019; Thorn et al. 2021]
C	<i>Tiliqua pusilla</i> <sup>†</sup> , <i>Egernia gillespieae</i> <sup>†</sup> , <i>Proegernia palankarinensis</i> <sup>†</sup> , <i>P. mikebuli</i> <sup>†</sup>	'B(0.15,0.26,0.025,0.2)'	Crown Australian Tiliquini [	CITE Martin et al. 2004; Thorn et al. 2019]
D	<i>Egernia gillespieae</i> <sup>†</sup>	'>0.15'	( <i>Corucia</i> + all others)	[CITE Thorn et al. 2019]
E	<i>Tiliqua cf. scincoides</i> <sup>†</sup>	'>0.036'	Crown <i>Egernia</i>	[CITE Mackness & Hutchinson 2000]
F	<i>Egernia cf. hosmeri</i> <sup>†</sup>	'>0.036'	<i>Tiliqua gigas</i> + <i>Tiliqua scincoides</i>	[CITE Mackness & Hutchinson 2000]
			<i>Egernia hosmeri</i> + <i>Egernia stokesii</i>	[CITE Mackness & Hutchinson 2000]

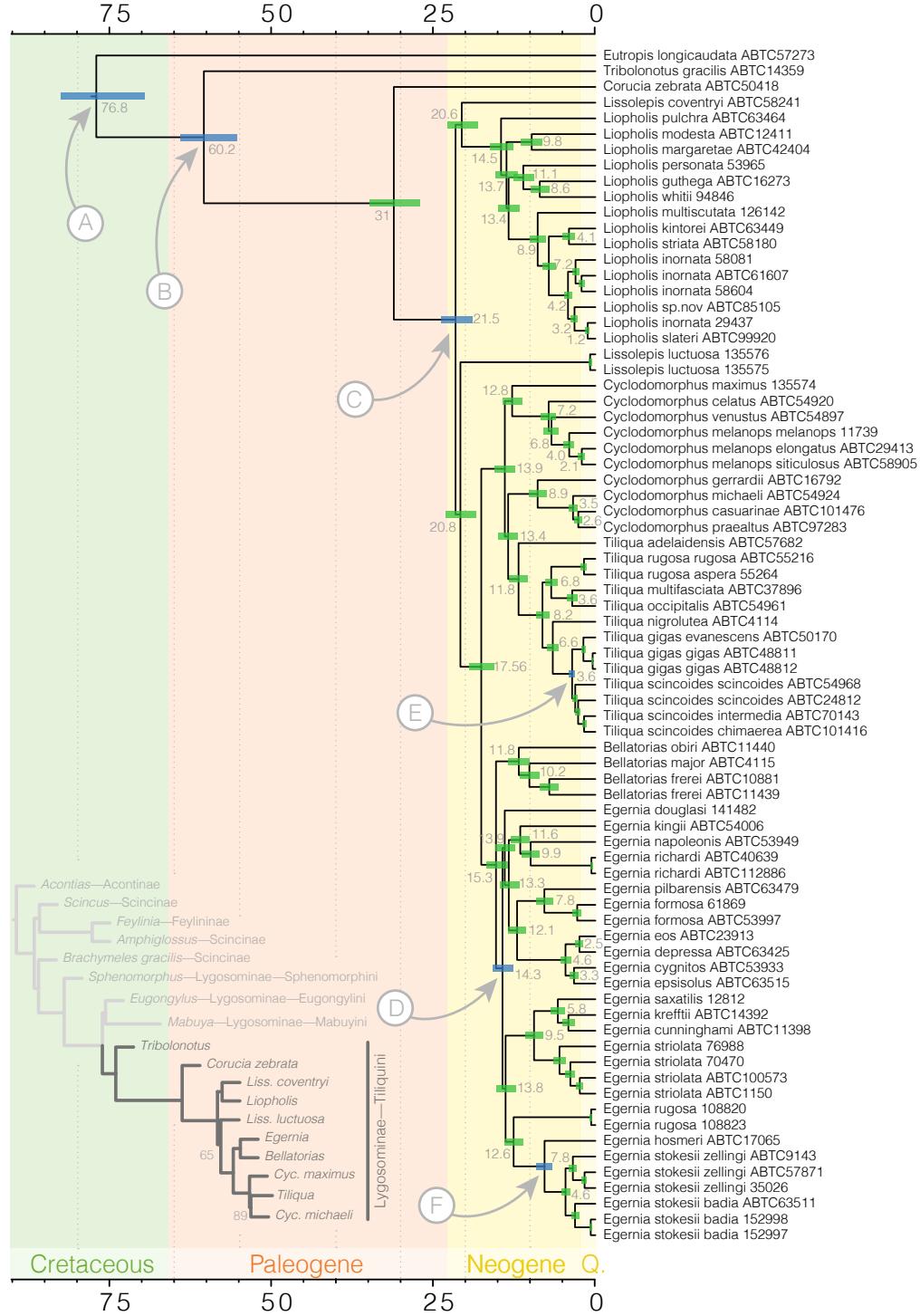


Figure S1: Tiliquini species tree estimated with ASTRAL from IQTREE genetrees and time-calibrated with MCMCTree. Shaded bars at nodes indicate 95% confidence estimates on ages. Nodes labelled by letters A–F correspond to fossil calibrations listed in Table S2. Inset tree depicts the scincid phylogeny estimated from AHE data showing the placement of the Tiliquini among the Lygosominae.

## Alignment Specifications

Input MAFFT/MUSCLE alignments were refined with MACSE using the following call:

```
$ java -jar /Applications/macse_v2.03.jar \
    -prog refineAlignment -align [rough alignment path] \
    -optim 1 -local_realign_init 0.1 -local_realign_dec 0.1 \
    -fs 10 -stop 10
```

## Investigating Data Completeness and Informativeness

Below we visualize data completeness and informativeness on a per sample and per locus basis, as well as provide some insight into our data cleaning and sample selection.

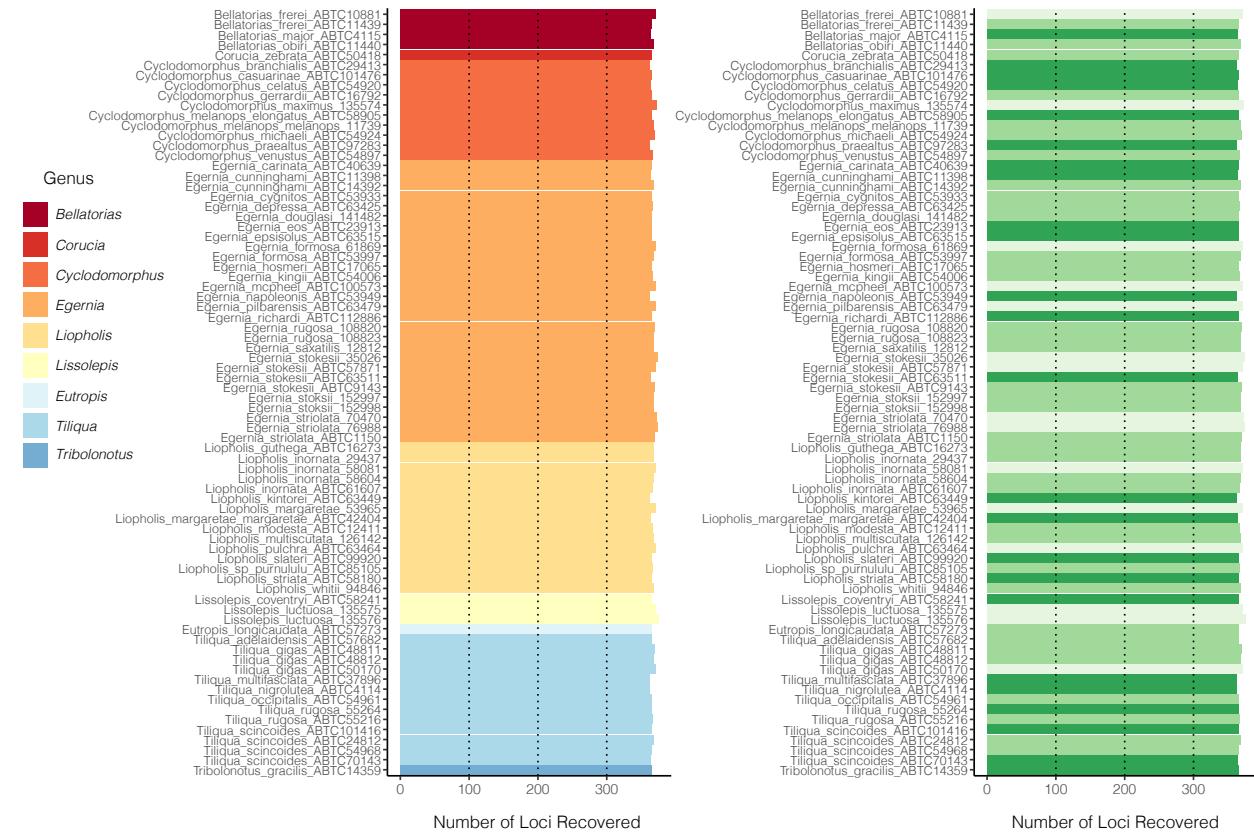


Figure S2: Number of loci recovered per sample for all Tiliquini and outgroup taxa included in the molecular data. Samples are colored by Genus (left) and coverage (right).

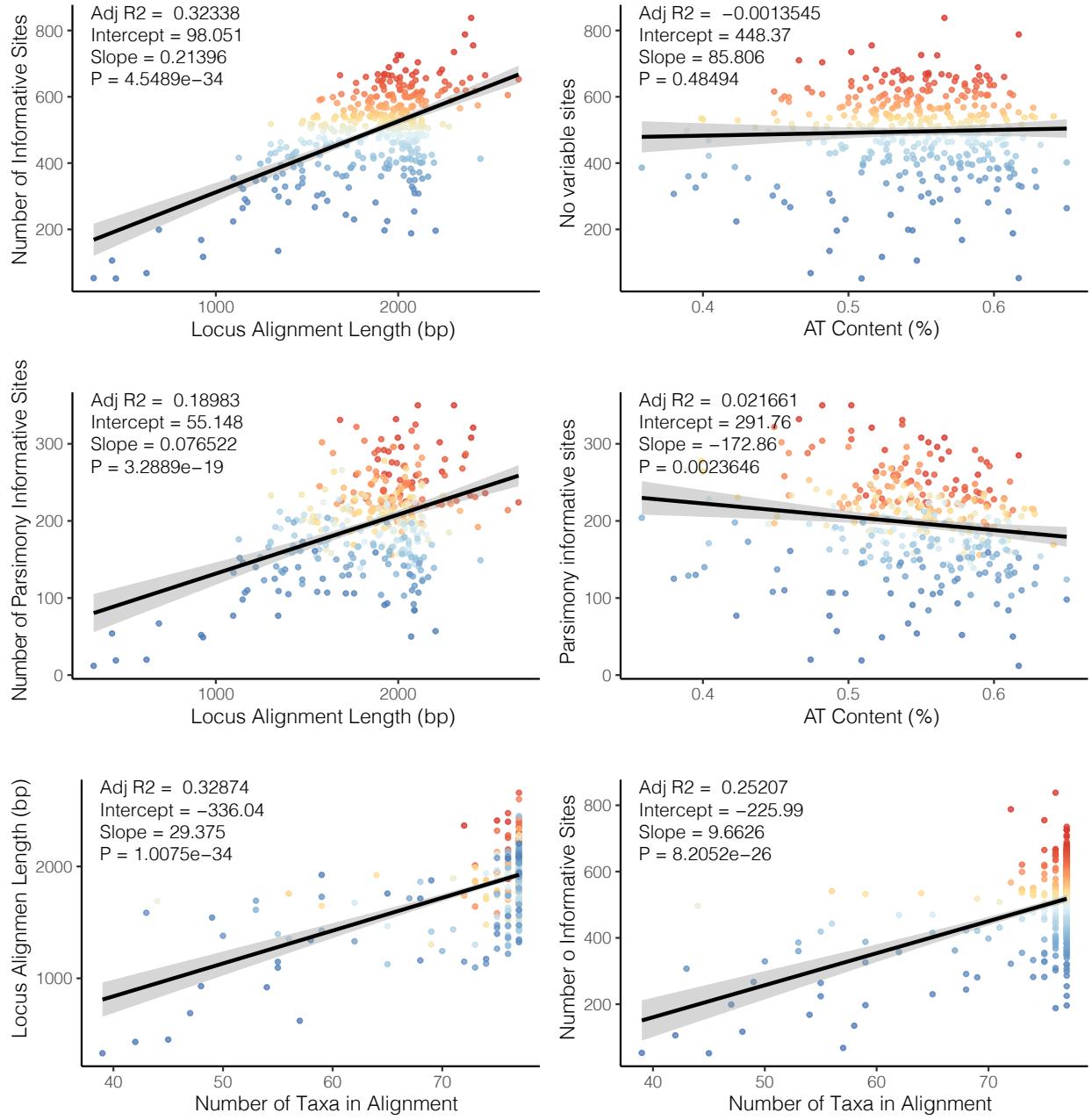


Figure S3: Plots of individual locus completeness and informativeness. Points are colored according to number of informative (variable) sites (blue—few, red—many). Top row shows the number of variable sites in each alignment as a function of alignment length and AT content. The middle row shows the number of parsimony informative sites as a function of alignment length and AT content. The bottom row shows alignment length and number of variable sites as a function of completeness.

## Morphological Measurements

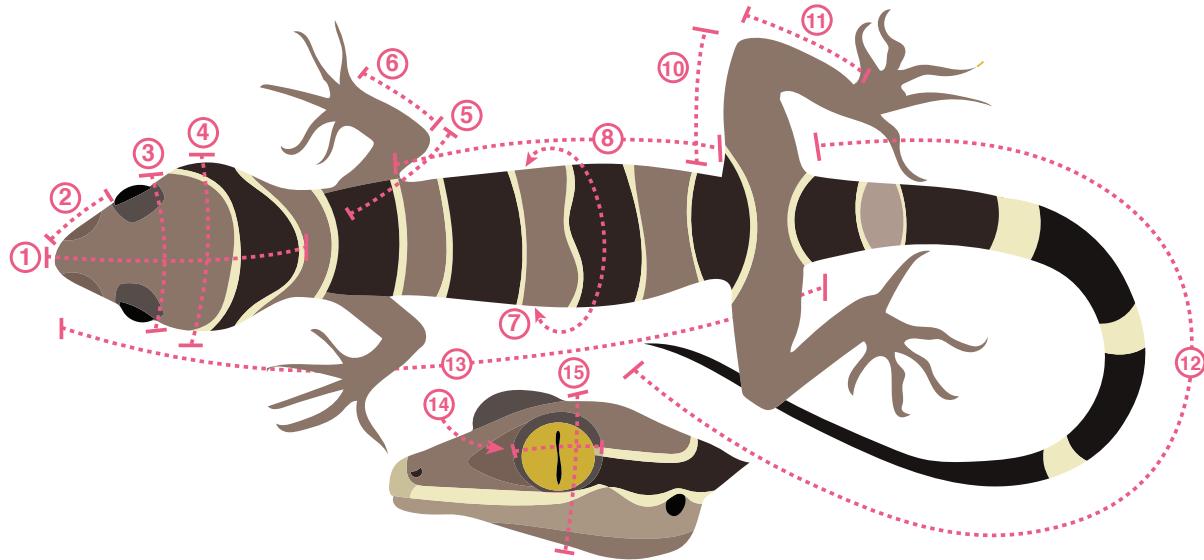


Figure S4: The 21 linear measurements collected.

Initial morphological measurements used for data investigation:

Measurement	Abbreviation	Method
Snout-vent length	SVL	From the tip of the snout to the vent.
Snout-axilla length	SAL	From the tip of the snout to the midpoint of the crease between the fore-limb and the body on the ventral surface.
Inter-limb length	ILL	Midpoint of the crease on the ventral surface where the fore-limb connects to the body, to the midpoint of the crease on the ventral surface where the hind-limb connects to the body.
Body width	BW	From one lateral side of the body to the other, where possible at the midpoint of the ILL.
Pelvic width	PW	From the midpoint of the crease on the ventral surface where the left hind limb connects to the body, to the midpoint of the crease on the ventral surface where the right hind limb connects to the body.
Pelvic height	PH	From the top of the dorsal surface where the PW was measured, to the bottom of the ventral surface where the PW was measured.
Head width	HW	Widest part of the head from one dorsal-lateral edge to the other edge.

Measurement	Abbreviation	Method
Head length	HL	From the nose tip, to the anterior of the ear.
Snout length	SN	From the nasal opening to the anterior of the eye.
Eye diameter	ED	From one side of the eye to the other.
Head depth	HD	From the top of the tallest part of the head on the dorsal surface, to the bottom of the ventral surface under the jaw.
Tail width	TW	Measured at the vent, from one dorsal-lateral edge to the other edge.
Fore-limb length	FLL	Measured fully extended from the midpoint of the crease on the ventral surface where the front limb connects to the body, to the end of longest toe (claw included).
Front foot	FFOOT	From the base of the foot to the end of the longest toe (claw included).
Lower front limb	LFL	Measured from the base of the lower fore limb to the juncture where the limb meets the front foot.
Upper front limb	UFL	Measured from the crease on the ventral surface where the fore limb connects to the body, to the end of the lower front limb.
Hind-limb length	HLL	From the midpoint of the crease on the ventral surface where the hind limb connects to the body, to the end of longest toe (claw included)
Hind foot	HFOOT	From the base of the hind foot to the end of the longest toe (claw included)
Lower hind limb	LHL	Measured from the top of the knee joint to the heel juncture where the limb meets the front foot.
Upper hind limb	UHL	Measured from the crease on the ventral surface where the hind limb connects to the body, to the end of the knee.

Final morphological traits used for phenotypic analyses:

Measurement	Shorthand	Method
Interlimb length	Interlimb	see above
Body width	Body_Width	see above
Pelvic width	Pelvic_Width	see above
Pelvic height	Pelvic_Height	see above
Head width	Head_Width	see above
Snout length	Snout_Eye	see above
Eye diameter	Eye_Diameter	see above
Head depth	Head_Depth	see above

Measurement	Shorthand	Method
Tail width	Tail_Width	see above
Tail length	Tail_Length	see above
Upper front limb	Upper_Arm	see above
Lower front limb	Lower_Arm	see above
front foot	Hand	see above
Upper hind limb	Upper_Leg	see above
Lower hind limb	Lower_Leg	see above
Hind foot	Foot	see above
Neck length	Neck	Snout_Axilla - Head_Length
Posterior skull	Pos_Skull	Head_Length - (Snout_Eye + Eye_Diameter)
Pelvic gap	Pelvic_Gap	Snout_Vent - (Interlimb + Snout_Axilla)

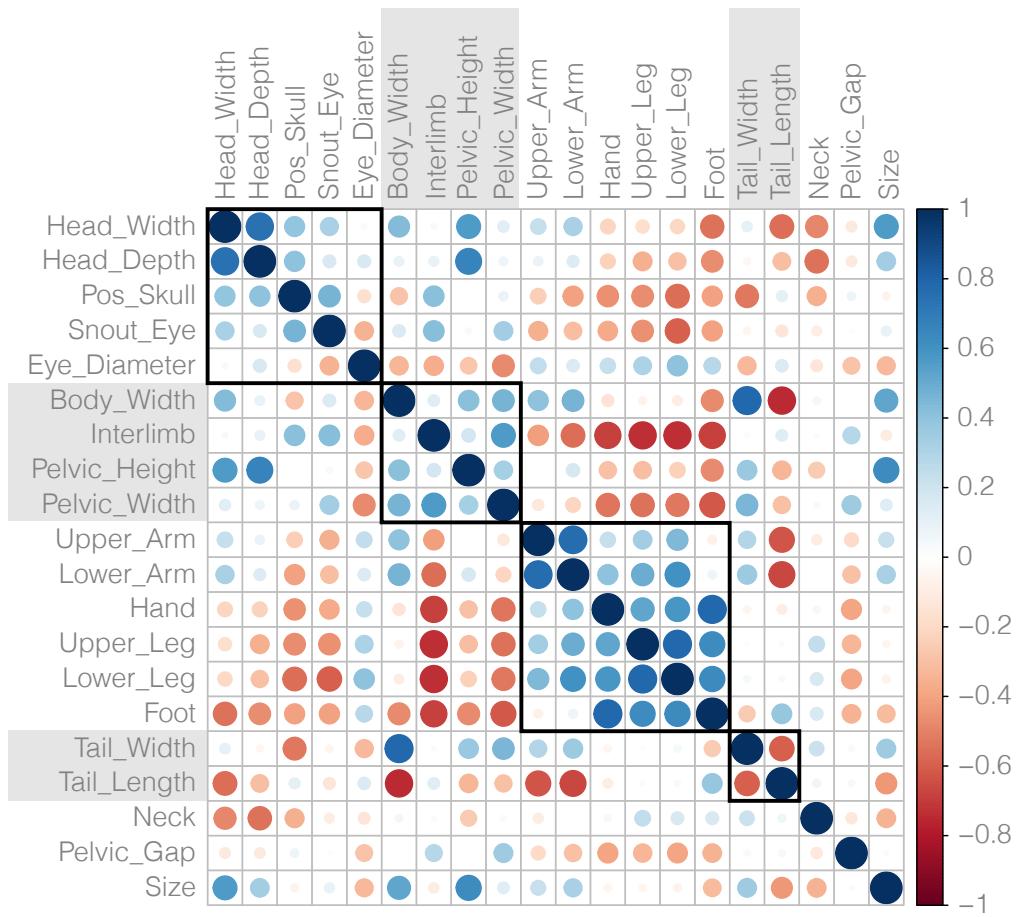


Figure S5: Correlation plot of all morphological traits after removing size via log-shape ratios. Some traits retain strong correlations despite removing the effect of size. Traits are organized according to the morphological module they belong to. Plot generated using *corrplot* [Wei & Simko 2021].

## Modelling Trait Evolution and Disparity

535 We started by generating mean trait values per species. To remove the effect of size on individual traits (allometry) we then calculated the geometric mean of all traits by species and used this to transform trait measurements into log-shape ratios. This also provided an additional trait *size*. To investigate integrated and modular evolution we estimated correlations among traits and provided this as input for the package *EMMLi* [CITE Goswami & Finarelli]. *EMMLi* also requires *a priori* hypotheses of the assignment of traits to modules. We provided five general hypotheses for model comparison with the most specialized model allowing traits of the head, limbs, body, and tail to evolve as independent modules, and the most restrictive null model lumping all traits into a single module. *EMMLi* also allowed us to compare models in which the correlation coefficient among modules and among traits within 540 modules is either similar or different (see Goswami & Finarelli Fig.2). Once we established the preferred model (head, body, limbs, tail as separate modules with differing inter- and intramodule correlations) we split our traits into module-specific datasets.

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We designed five models of modular evolution for the Tiliquini skink body plan to test integration and modularity via *EMMLi*. (1) a four-module model (*Body\_Tail\_Limbs\_Head*) 550 in which each of the major body regions is isolated as an independent module; (2) a three-module model (*BodyHead\_Tail\_Limbs*) where traits of the head and body are combined into a single module; (3) a two-module model (*BodyHeadTail\_Limbs*) in which traits of the head, body, and tail are combined into a single module; (4) a three-module model (*Body\_Head\_TailLimbs*) where tail and limb traits make up a single module; and (5) a 555 two-module model (*BodyHead\_TailLimbs*) where body and head traits are one module and tail and limb traits another.

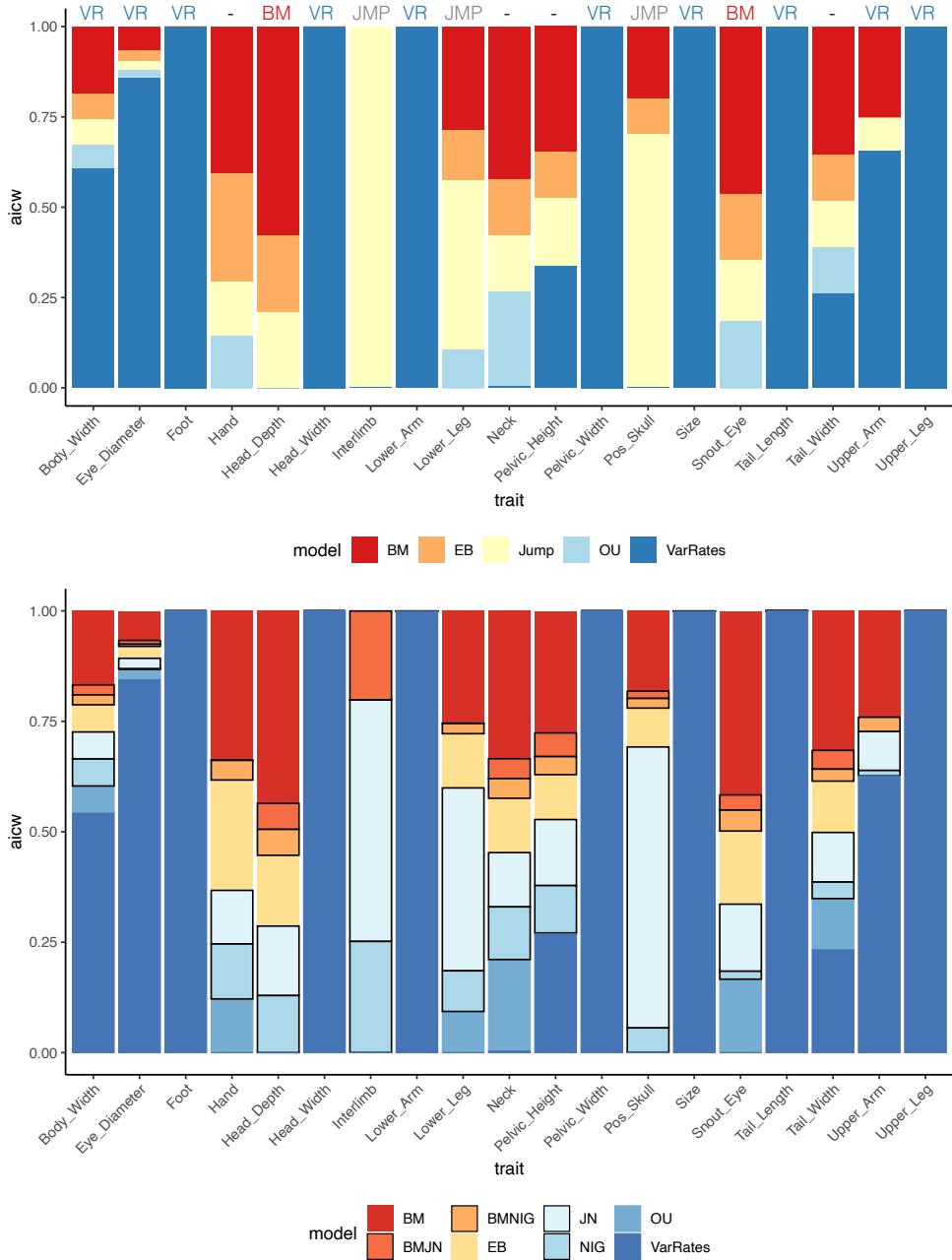


Figure S6: Comparative model fits for each of 19 morphological traits. Upper figure summarizes AICw by model type (BM, EB, ‘Jump’, OU, or VarRates), with the preferred model indicated above the column. Model preference required AICw of the best fitting model to be at least twice that of the next best fitting model. Bottom figure similarly shows model preference but with ‘Jump’ models expanded into their four alternative models (BMJN, BMNIG, JN, NIG) indicated by black outlines.

## Concatenation and the Anomaly Zone

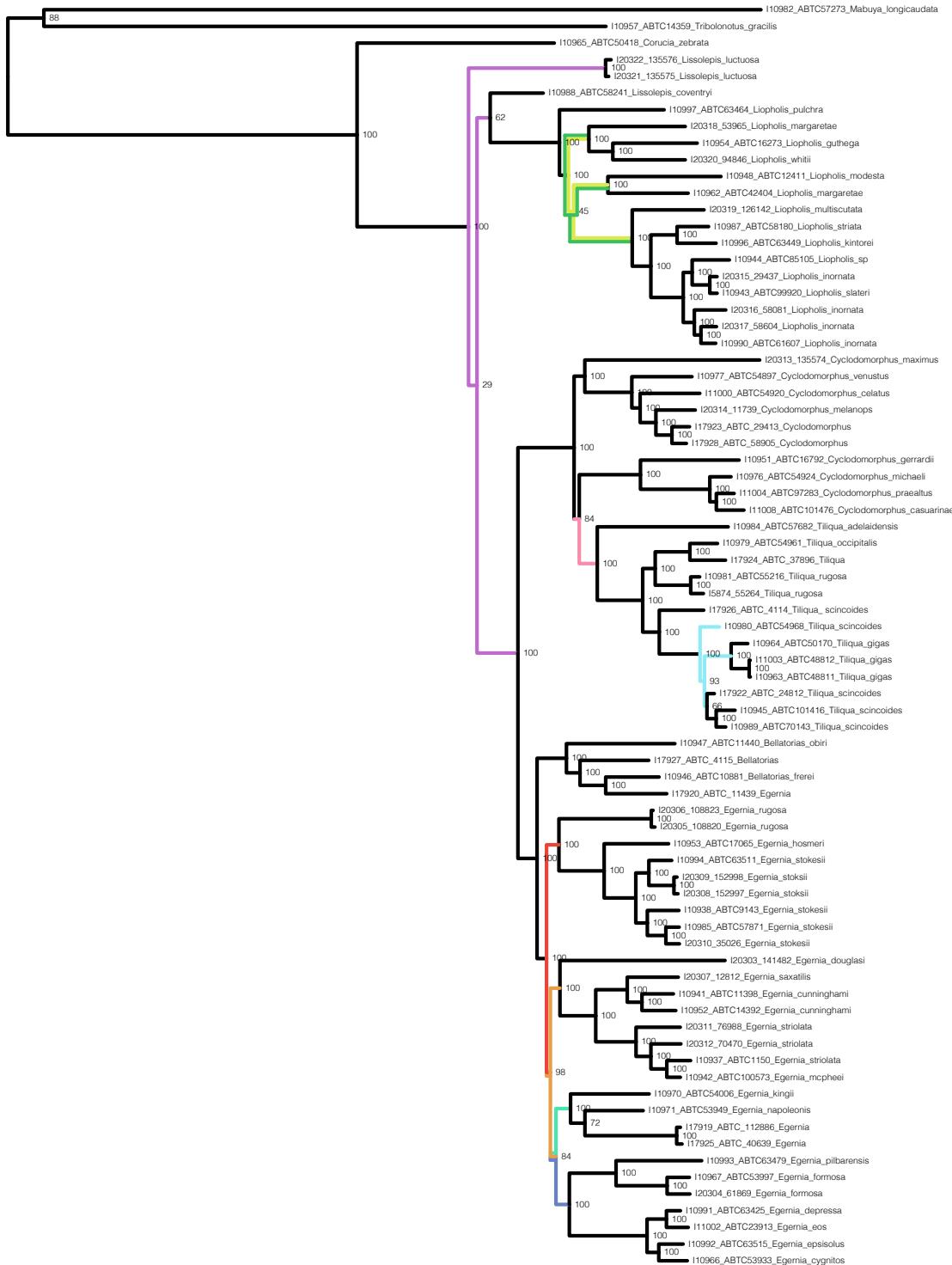


Figure S7: The Tiliquini phylogeny estimated from a concatenated and locus-partitioned alignment is likely misled by branches which fall into the anomaly zone. Colored branches correspond to the anomaly zone cladogram below and indicate edges which differ from the coalescent species tree.

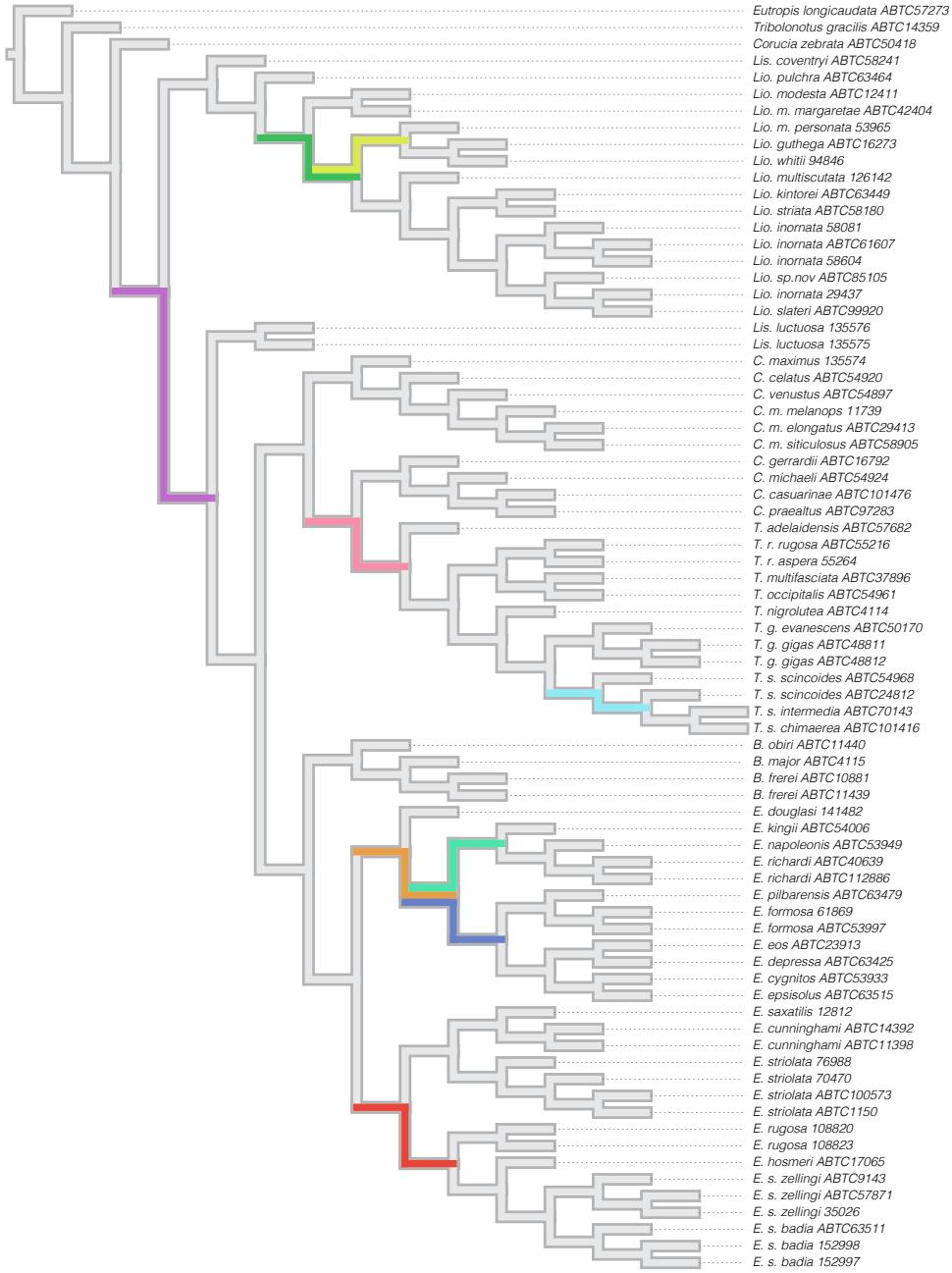


Figure S8: Colored branches indicate edges that fall within the anomaly zone and may provide misleading results under concatenation. We used *Anomaly Finder* [CITE Linkem et al. 2016], using the script from Chafin et al. 2021

## Topology Tests

We used a series of topology tests in IQTREE to investigate two nodes which bear taxonomic implications. We used the concatenated alignment and simplified phylogenies as the input. In each case the preferred topology is presented first followed by the two alternative resolutions to the bipartition. Significant differences are denoted by (-), and show decisive preference for the coalescent species tree topology in comparison to alternative resolutions, reinforcing molecular phylogenetic evidence for the paraphyly of both *Cyclodomorphus* and *Lissolepis*.

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Topology test for the paraphyly of *Cyclodomorphus* with regards to *Tiliqua*.  
Tree topologies:

1. (Egernia,(C.maximus,(T.gigas,C.michaeli)); : coalescent/concatenated species trees
2. (Egernia,(C.michaeli,(T.gigas,C.maximus)); : alternative *Cyclodomorphus* paraphyly
3. (Egernia,(T.gigas,(C.maximus,C.michaeli)); : *Cyclodomorphus* monophyly

Tree	logL	deltaL	bp-RELL	p-KH	p-SH	p-WKH	p-WSH	c-ELW	p-AU
1.	-1142007.338	0	0.97(+)	0.98(+)	1(+)	0.98(+)	0.993(+)	0.971(+)	0.981(+)
2.	-1142067.499	60.161	0.03(-)	0.02(-)	0.026(-)	0.02(-)	0.039(-)	0.0294(-)	0.021(-)
3.	-1142110.488	103.15	0(-)	0(-)	0(-)	0(-)	0(-)	2.08e-10(-)	1.79e-05(-)

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Topology tests for the paraphyly of *Lissolepis*.

Tree topologies:

1. (Outgroup,((Lis.luctuosa,E.striolata),(Lis.coventryi,Lio.\_inornata))); : coalescent species tree
2. (Outgroup,(Lis.luctuosa,(E.striolata,(Lis.coventryi,Lio.inornata)))); : concatenated species tree
3. (Outgroup,((Lis.coventryi,Lis.luctuosa),(Lio.inornata,E.striolata))); : *Lissolepis* monophyly

Tree	logL	deltaL	bp-RELL	p-KH	p-SH	p-WKH	p-WSH	c-ELW	p-AU
1.	-1326723.218	0	1(+)	1(+)	1(+)	1(+)	1(+)	1(+)	0.995(+)
2.	-1326798.358	75.141	0(-)	0(-)	0.122(+)	0(-)	0(-)	8.47e-07(-)	0.00491(-)
3.	-1327315.329	592.11	0(-)	0(-)	0(-)	0(-)	0(-)	1.9e-174(-)	3.58e-05(-)

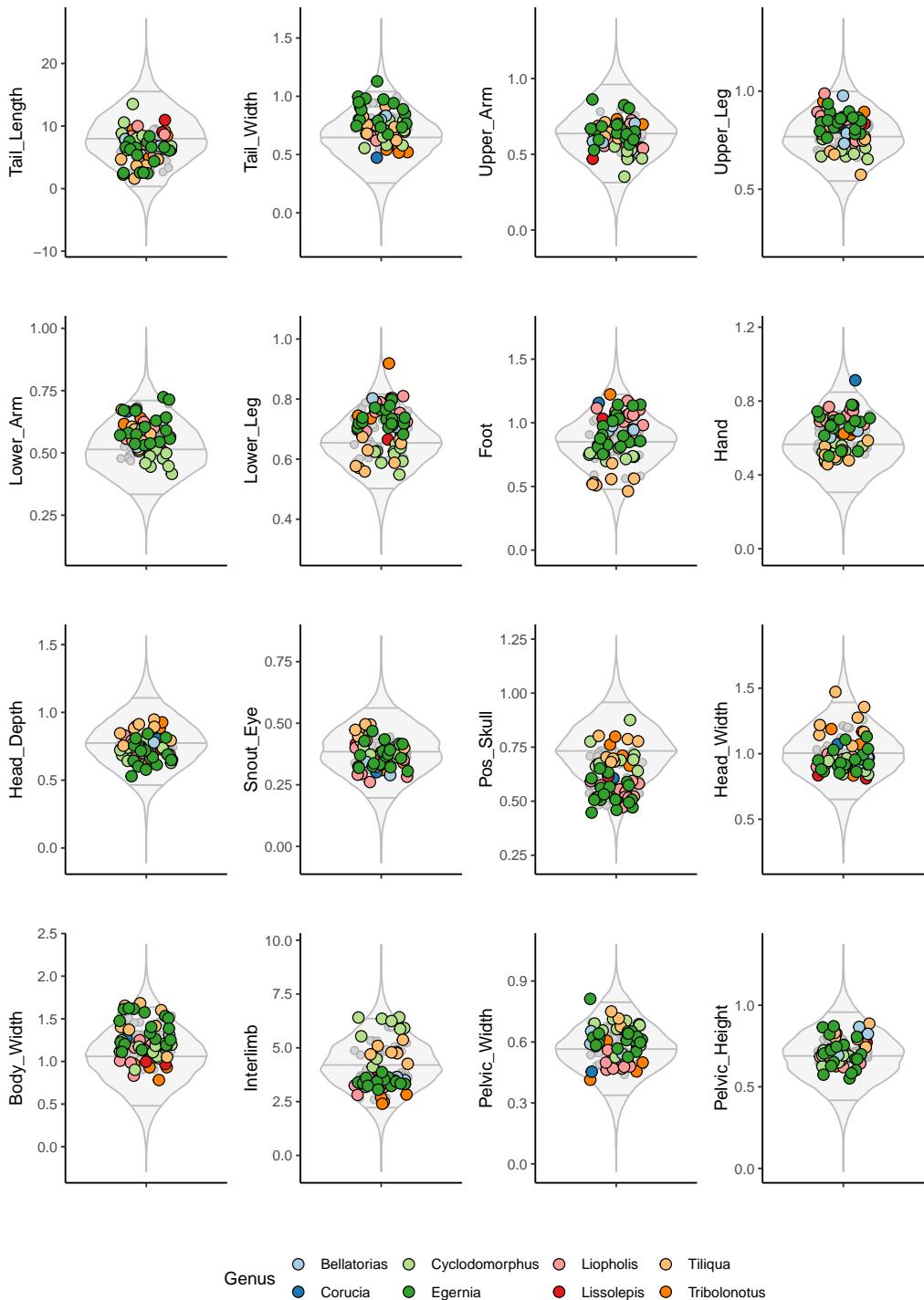


Figure S9: Empirical phenotypes generally conform to expected trait values of data simulated under uncorrelated evolution, showing limited ability of selection to exceed null expectations in Tiliquini skinks. Circles represent empirical trait values per species, colored by genus, with grey representing ancestral states. Transformed traits size corrected by log-shape ratios are plotted against 500 simulated datasets for each trait. Simulated traits are plotted as a grey violin plot summarizing the distribution of trait values, with 5%, 50%, and 95% quantiles plotted as horizontal lines. Simulations were generated with MVMORPH using as input the theta-root and sigma values estimated by MVMORPH assuming a constant-rate Brownian Motion model.

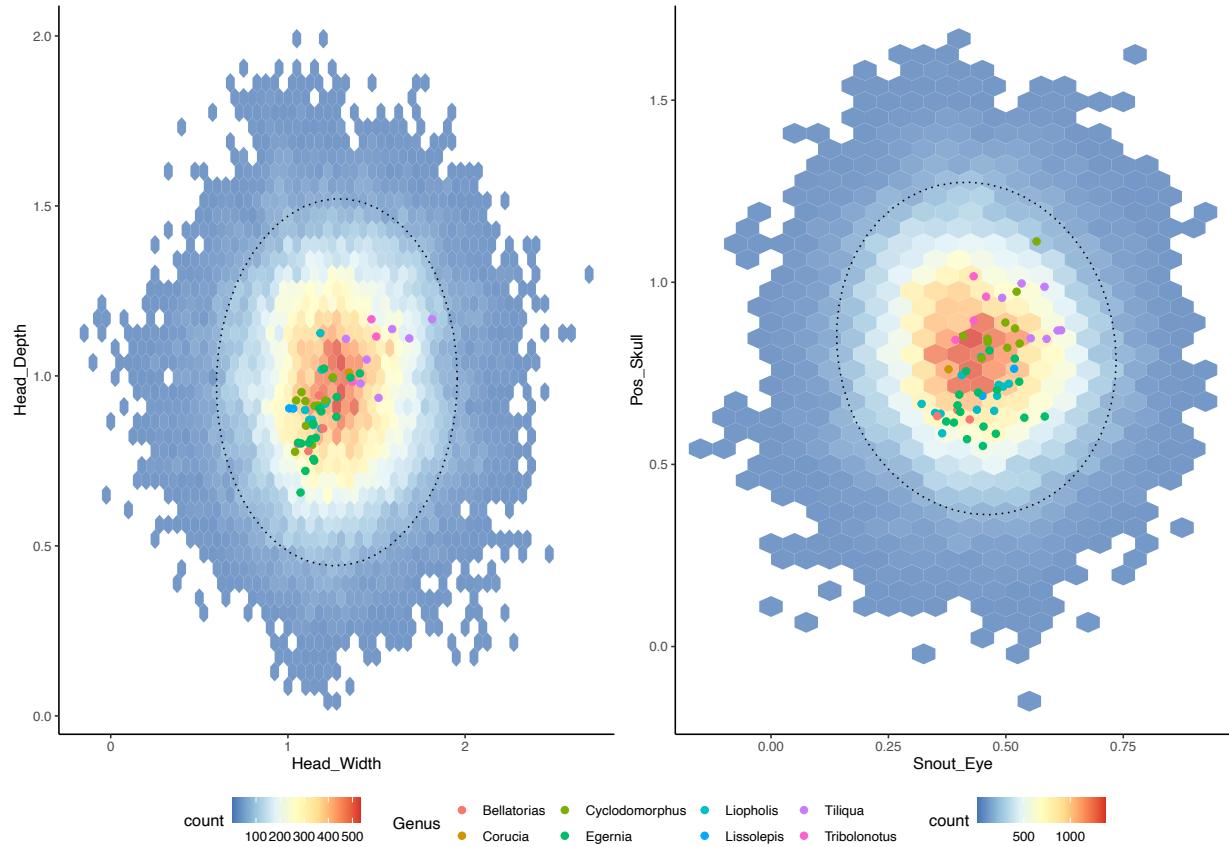


Figure S10: Empirical phenotypes generally conform to expected trait values of data simulated under uncorrelated evolution, showing limited ability of selection to exceed null expectations in *Tiliquini* skinks. Hexagonal heatplot in background shows the distribution of trait values from 500 datasets simulated under rates from empirical estimates. Warmer colors indicate greater density of simulated points. Circular points indicate empirical trait values and are colored according to the genus the belong to. The dotted ellipse contains 95% of the simulated data (95% confidence interval).

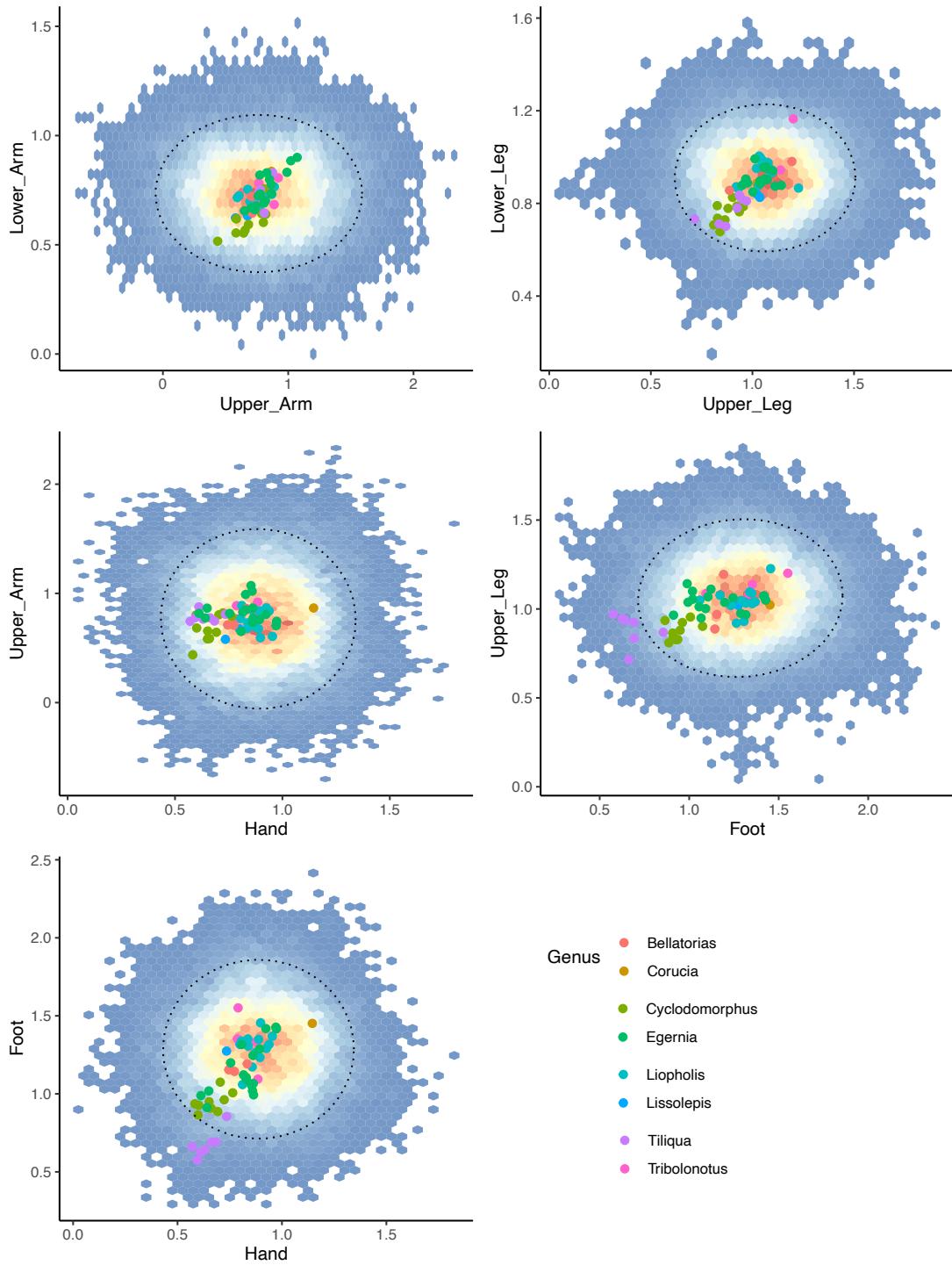


Figure S11: Empirical phenotypes generally conform to expected trait values of data simulated under uncorrelated evolution, showing limited ability of selection to exceed null expectations in *Tiliquini* skinks. Hexagonal heatplot in background shows the distribution of trait values from 500 datasets simulated under rates from empirical estimates. Warmer colors indicate greater density of simulated points. Circular points indicate empirical trait values and are colored according to the genus they belong to. The dotted ellipse contains 95% of the simulated data (95% confidence interval).

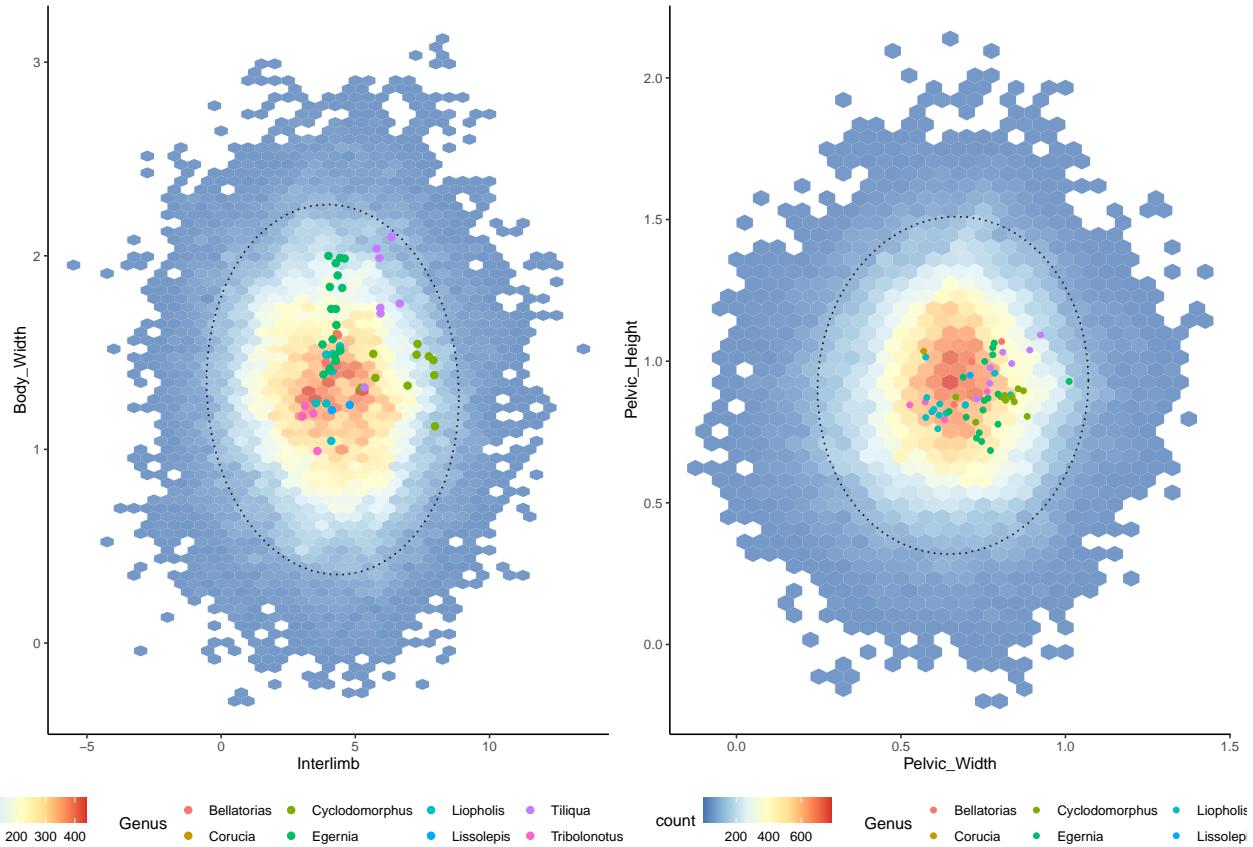


Figure S12: Empirical phenotypes generally conform to expected trait values of data simulated under uncorrelated evolution, showing limited ability of selection to exceed null expectations in *Tiliqua*ini skinks. Hexagonal heatplot in background shows the distribution of trait values from 500 datasets simulated under rates from empirical estimates. Warmer colors indicate greater density of simulated points. Circular points indicate empirical trait values and are colored according to the genus they belong to. The dotted ellipse contains 95% of the simulated data (95% confidence interval).

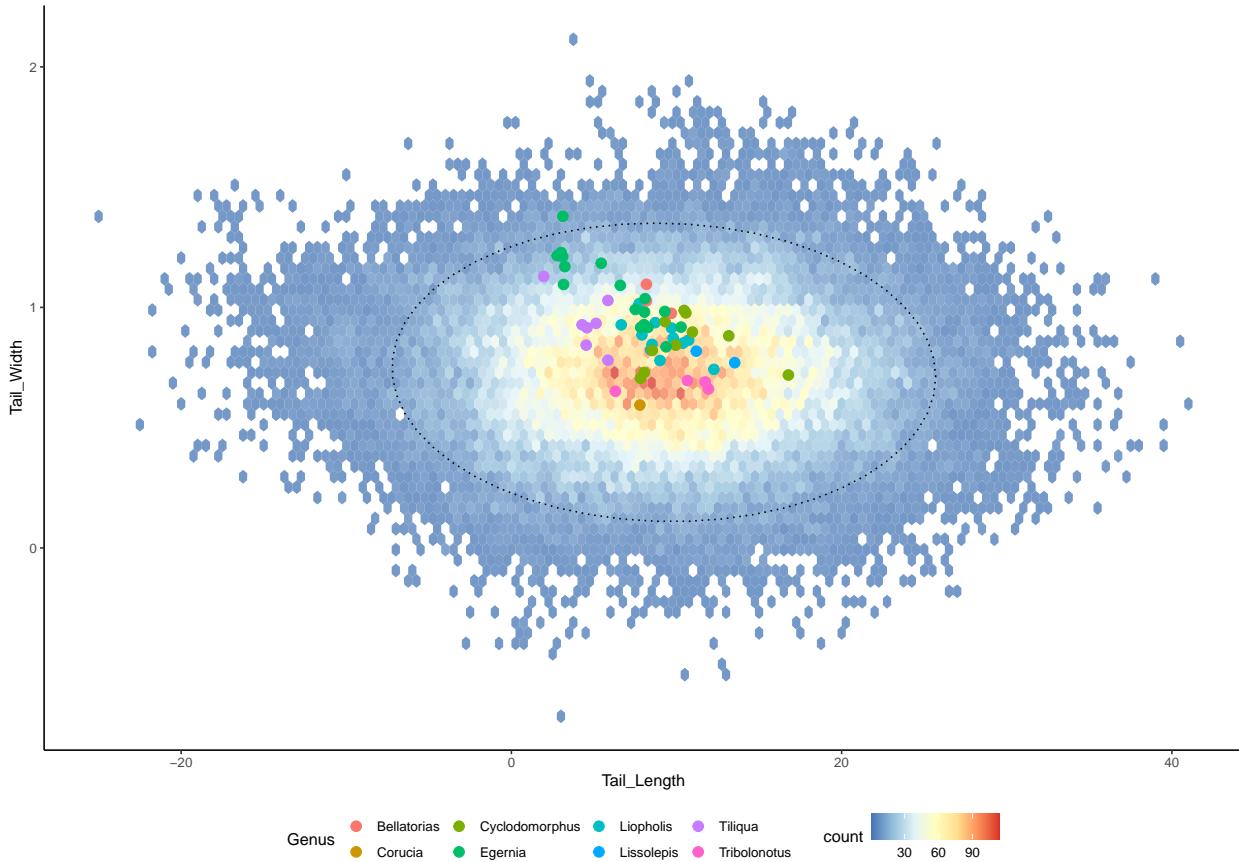


Figure S13: Empirical phenotypes generally conform to expected trait values of data simulated under uncorrelated evolution, showing limited ability of selection to exceed null expectations in Tiliquini skinks. Hexagonal heatplot in background shows the distribution of trait values from 500 datasets simulated under rates from empirical estimates. Warmer colors indicate greater density of simulated points. Circular points indicate empirical trait values and are colored according to the genus they belong to. The dotted ellipse contains 95% of the simulated data (95% confidence interval).

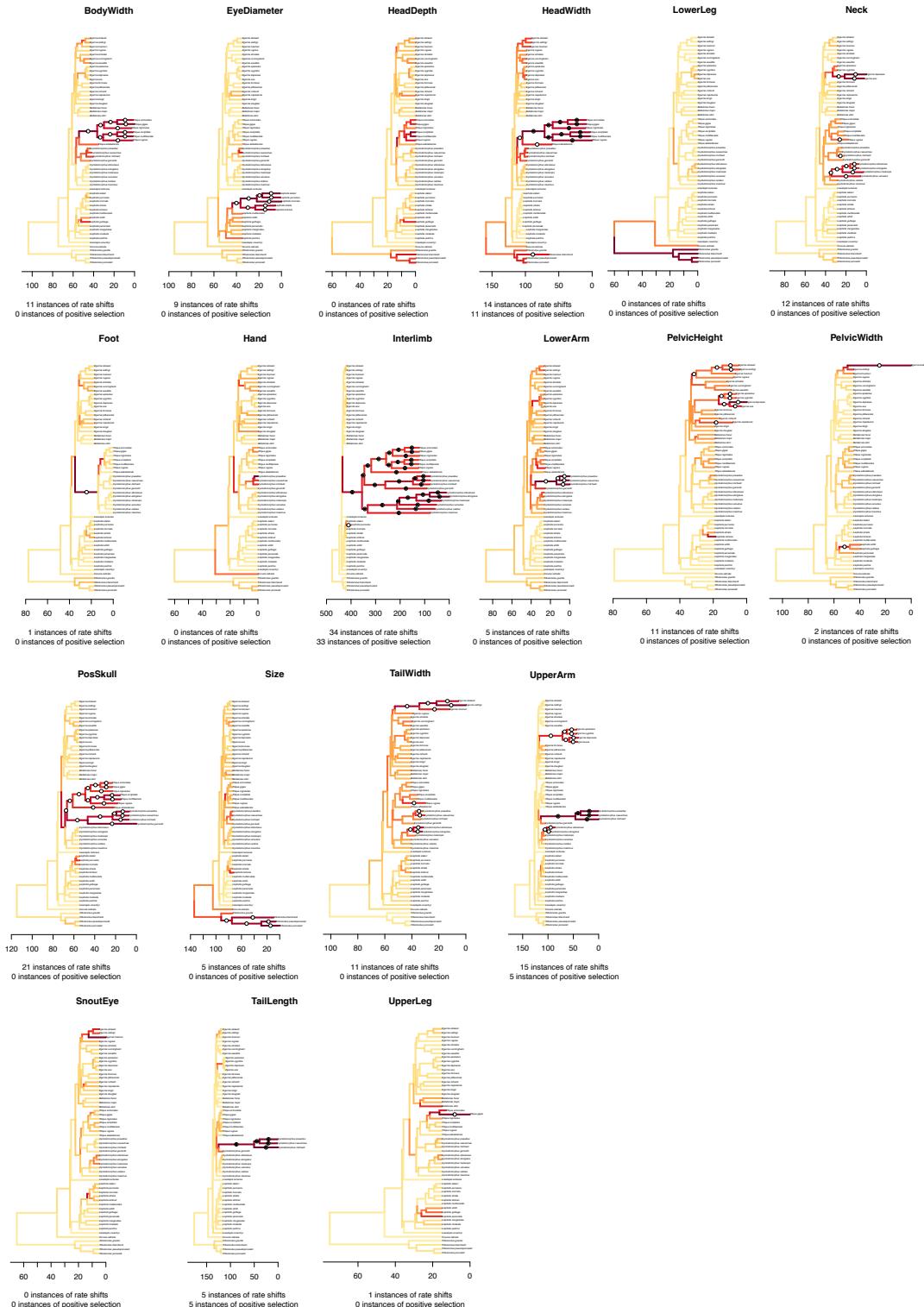


Figure S14: Pulses in rates of phenotypic evolution are common across tiliquine morphological traits. Species trees have been transformed for each trait with branch lengths adjusted relative to the estimated Variable Rates median scalar. Branches are colored according to mean estimated sigma value. Circles indicate significant rate shifts: empty circles represent shifts which appeared in > 70% of the posterior samples and in which the mean estimated scalar > 2; black circles represent shifts which appeared in >95% of the posterior samples and in which the mean estimated scalar > 2 corresponding to instances of “positive phenotypic selection” per Baker et al. 2017.

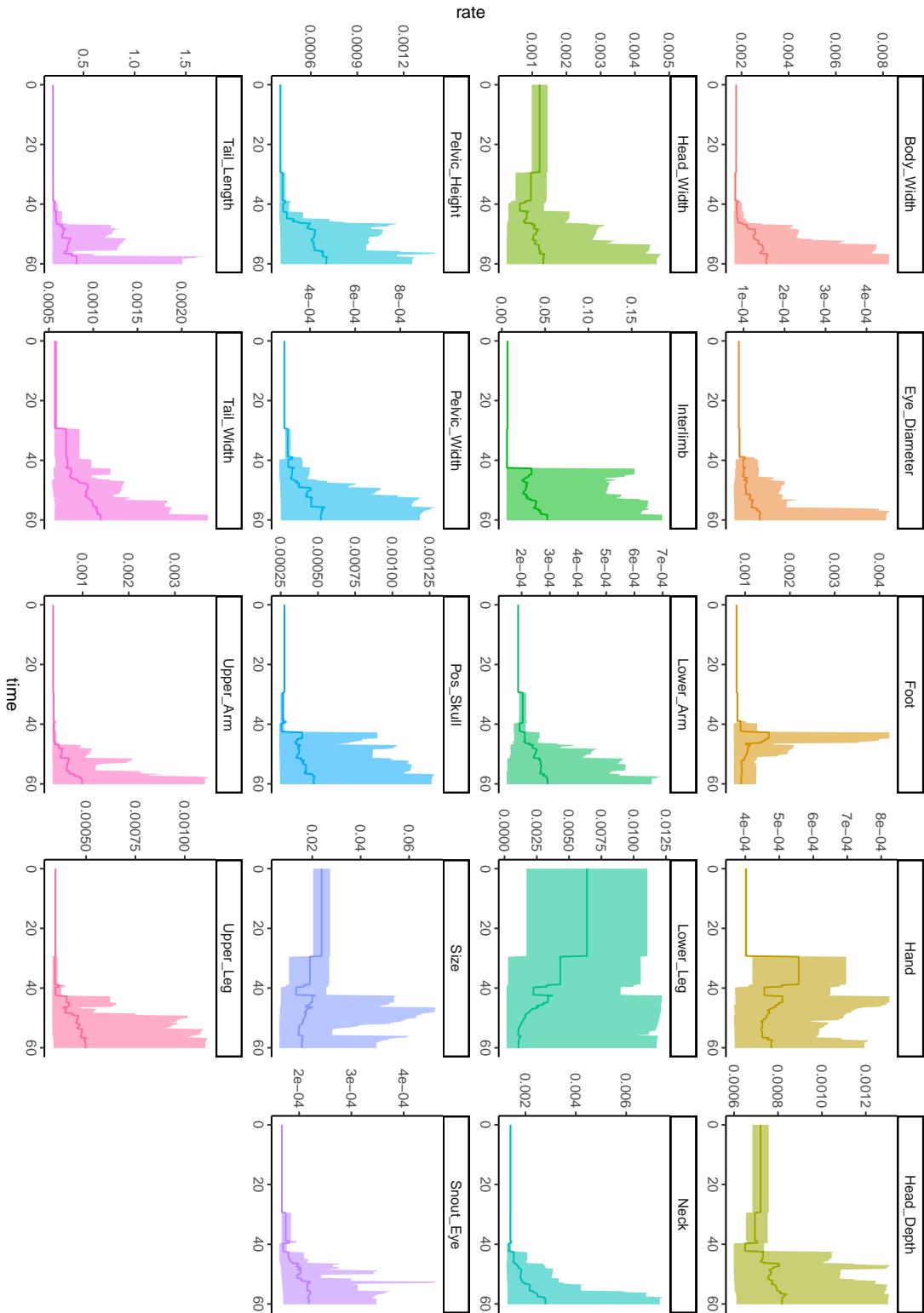


Figure S15: Mean evolutionary rates through time for all morphological traits with envelopes containing 95% quantiles.

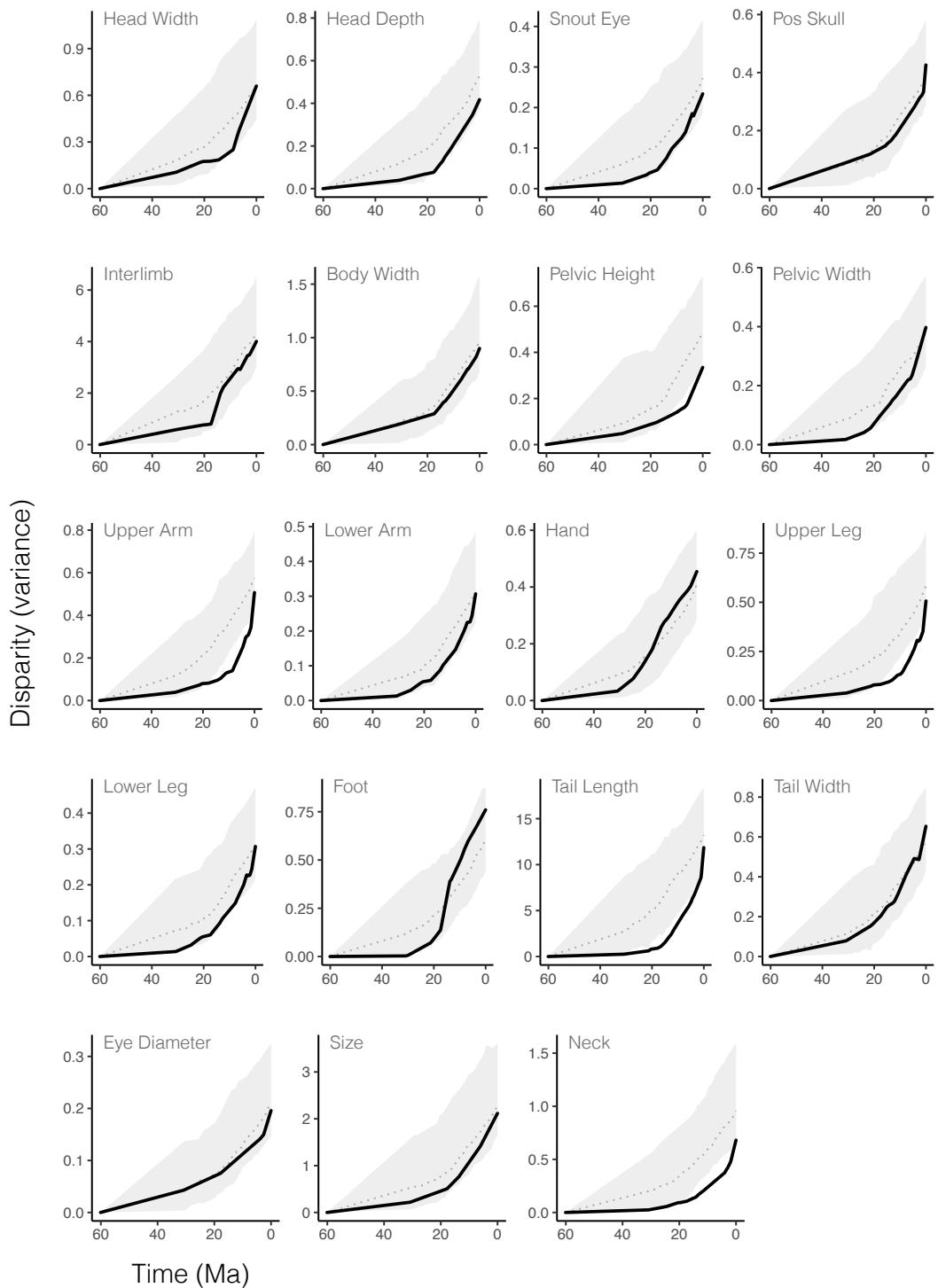


Figure S16: Disparity (variance) through time for morphological traits is often lower than expected under BM for long periods of time early in the evolution of this group. Empirical trends are shown in black with 95% quantiles of disparity for simulated datasets in grey.

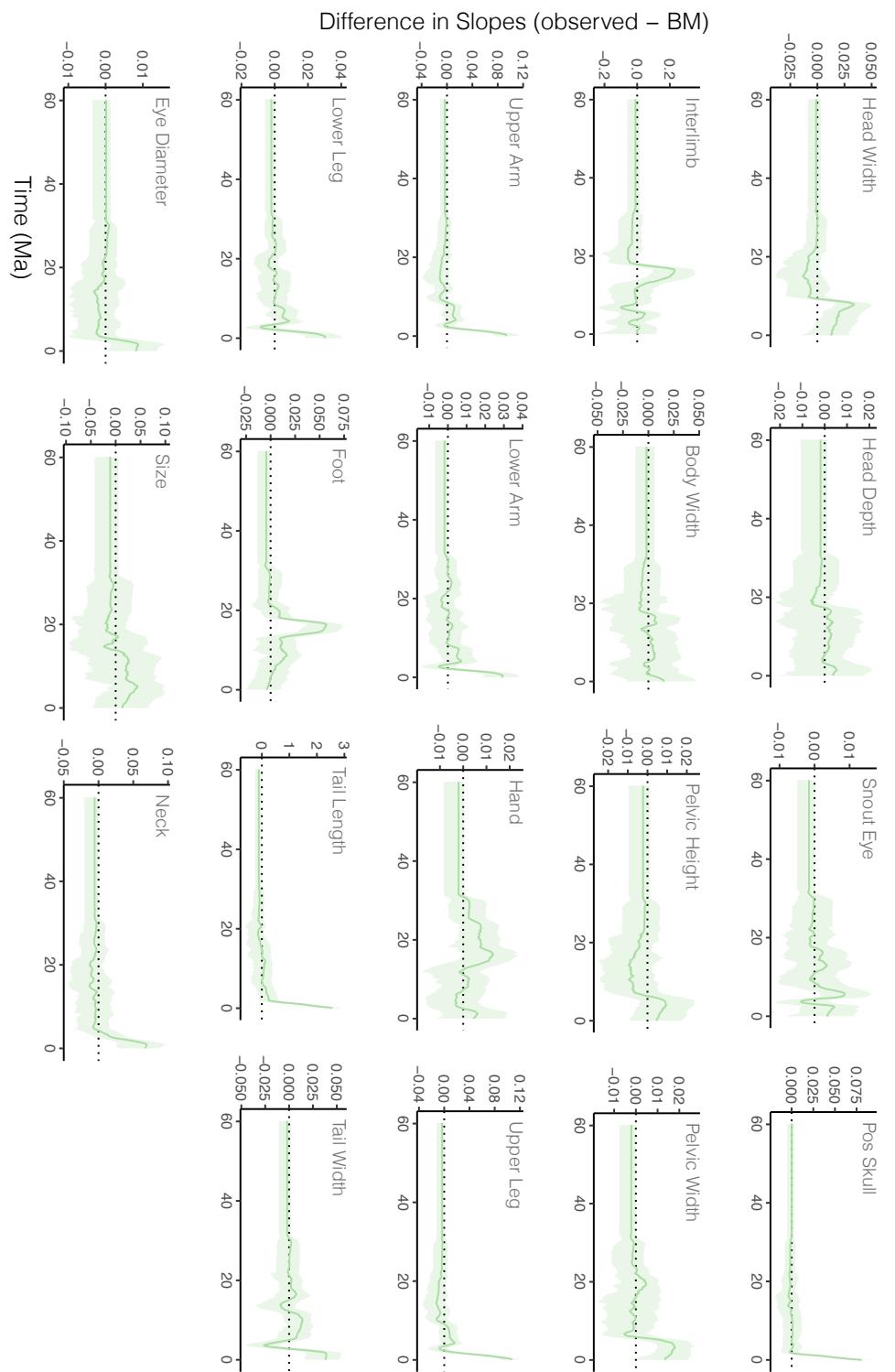


Figure S17: Individual traits show varied temporal patterns of morphological expansion and niche packing. Solid green line shows the mean trend and green envelope shows the 95% quantiles.

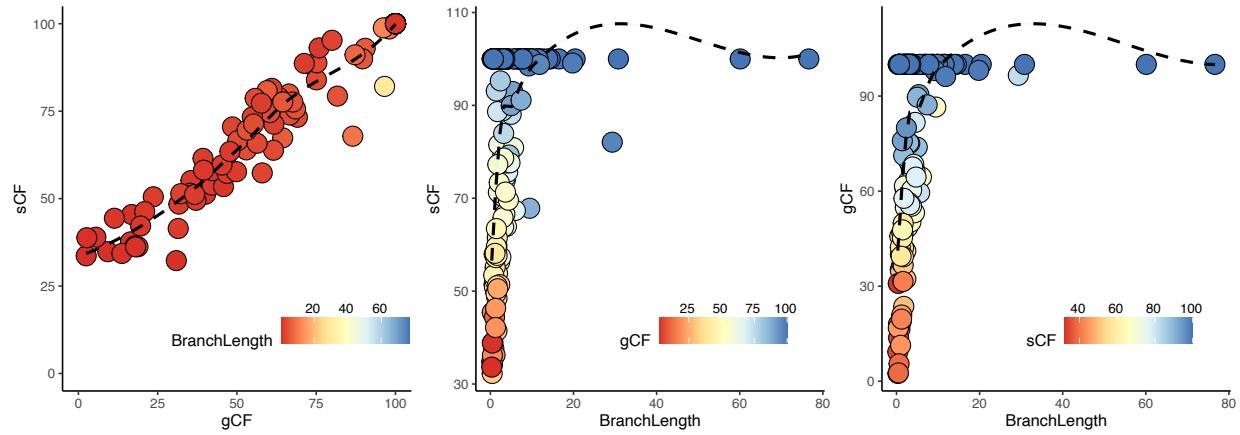


Figure S18: Concordance factors show a positive relationship with increasing branch length. Both site- and gene concordance factors increase support with increasing branch lengths (time), but show saturation ( $sCF=100$ ,  $gCF=100$ ) on branches  $\geq 10$  million years long.

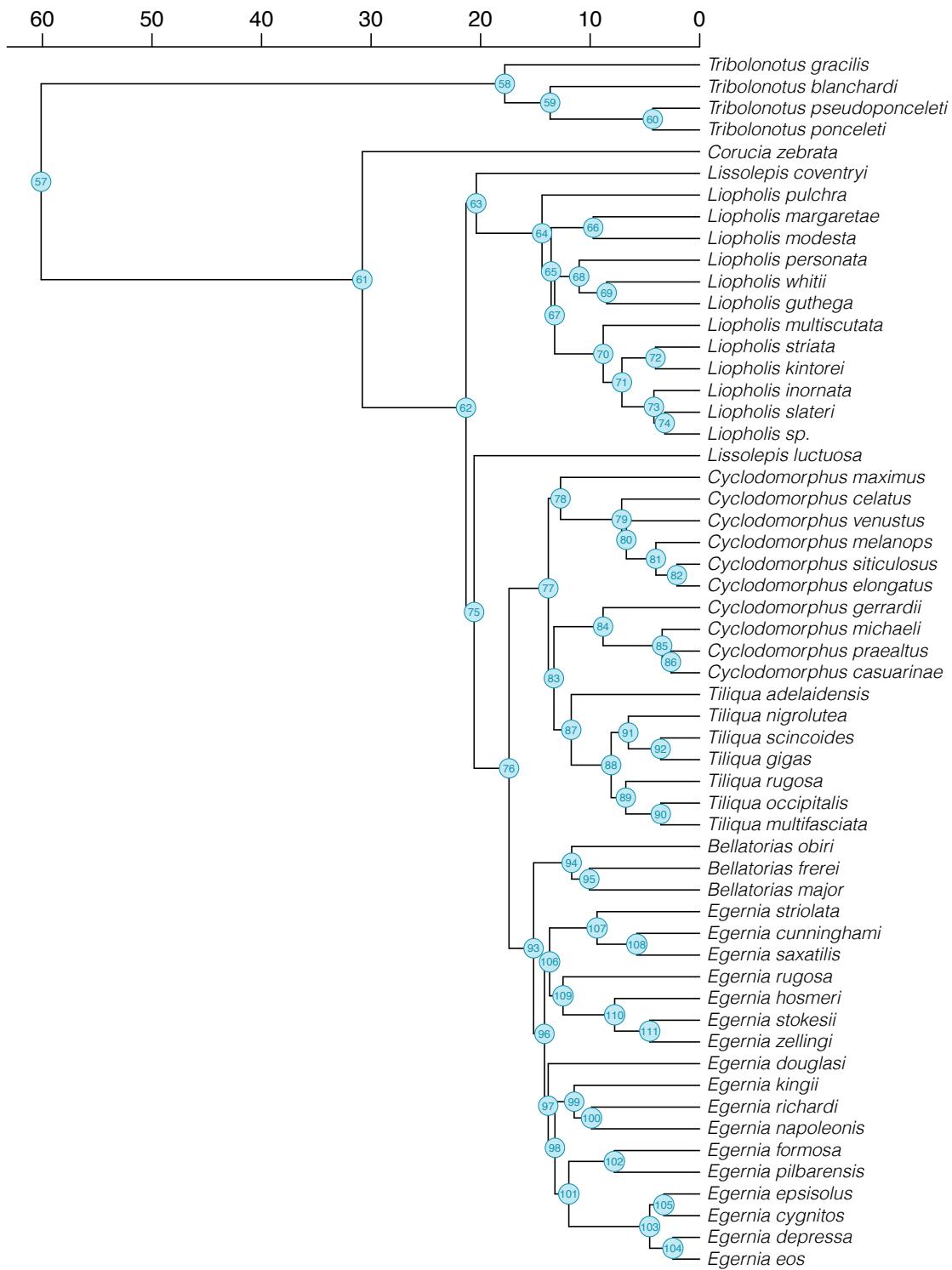


Figure S19: Node numbers of ASTRAL species tree.

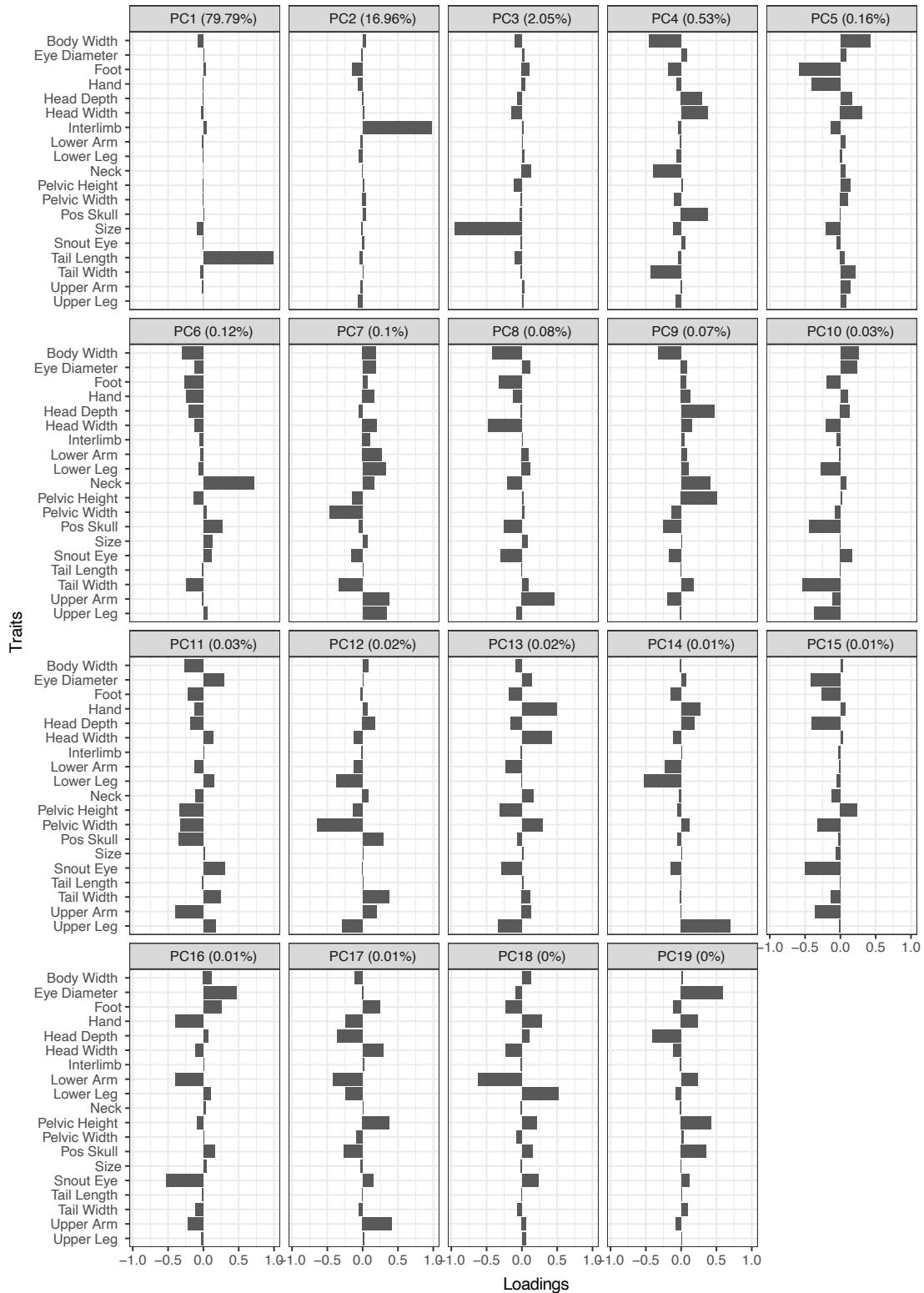


Figure S20: PCA loadings for 19 focal traits across all *Tiliquini* skinks. The first three principal components account for >98% of the variance, and are primarily explained by tail length, interlimb length, and size.

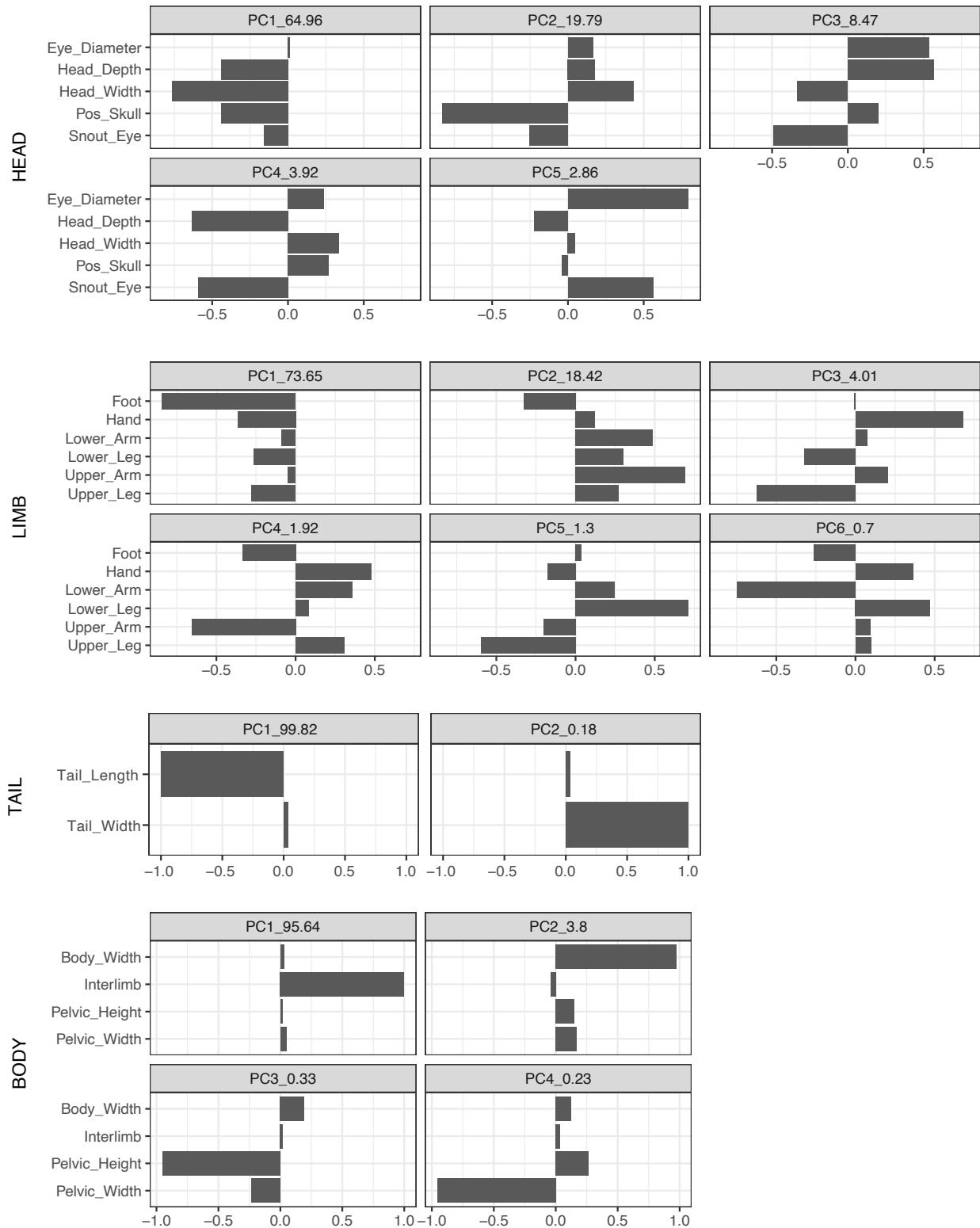


Figure S21: PCA loadings for 19 focal traits analyzed by module across all Tiliquini skinks.

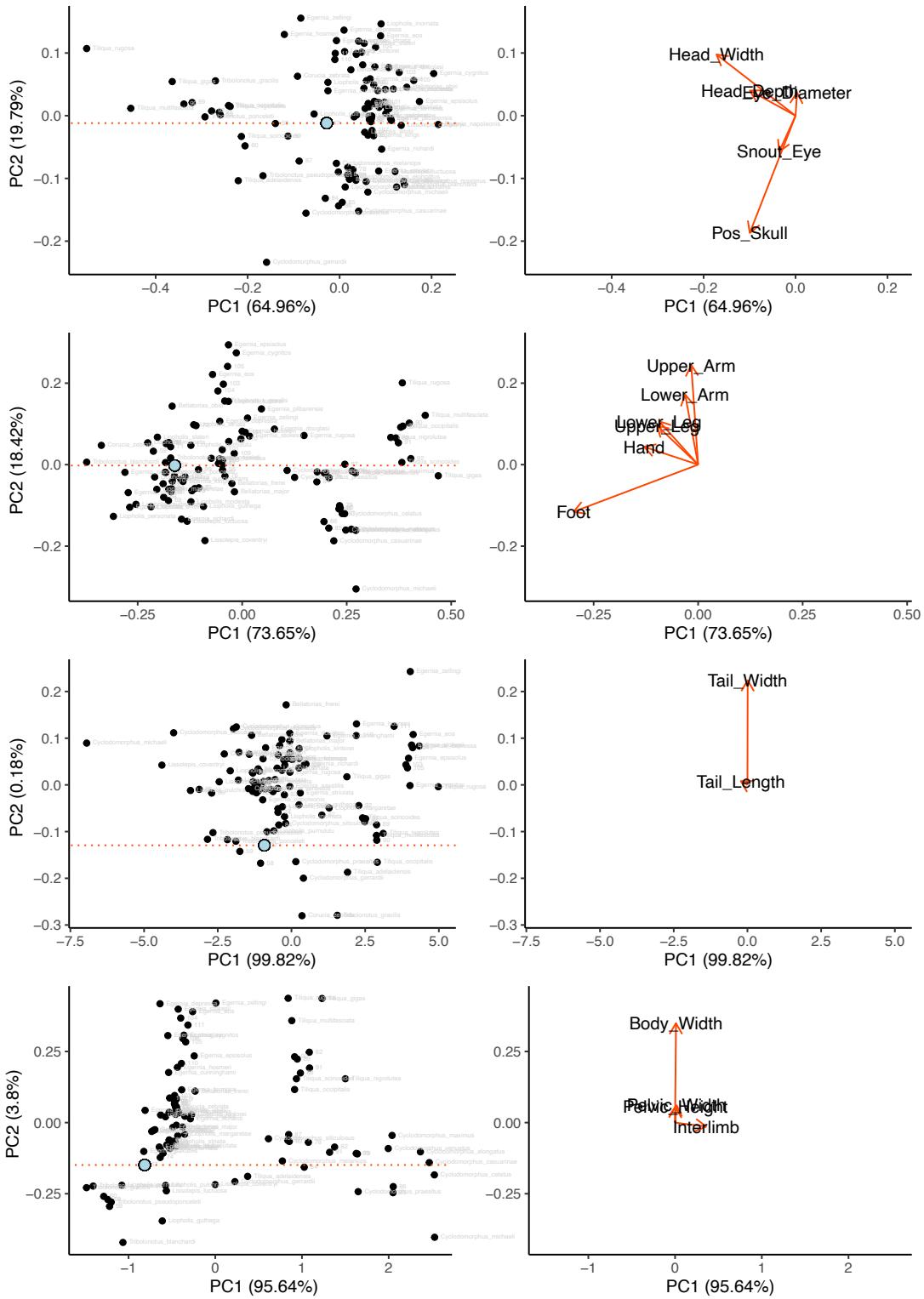


Figure S22: Biplots of the first two PC axes from analyses of modules.

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