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DISSERTATION RESEARCH:

Cenozoic mammals and the biology of extinction

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Introduction

Background

Why species go extinct and at different rates remains one of the most fundamental questions in paleobiology. It is expected that for the majority of geological time, extinction is biologically non-random [78, 101, 105, 111, 112, 123, 124]. Determining which biological factors or traits influence extinction risk and how is vital for understanding the differential diversification of life during the Phanerozoic. Periods of background extinction represent the majority of geologic time, remain relatively predictable and change slowly, and provide a great opportunity to study how traits are related to survival [105, 132]. The Law of Constant Extinction [149] posits that extinction risk of taxa within a given adaptive zone is age independent (memoryless), however the generality of this statement is possibly suspect [92, 93, 129, 137]. By analyzing survival patterns within adaptive zones during periods of background extinction, it should be possible to determine if extinction is best modeled as age independent or dependent.

A simple purely stochastic expectation where extinction is not selective is that abundant and widespread taxa are less likely to go extinct than rare and restricted taxa [131]. For example, species with larger geographic ranges tend to have lower extinction rates than species with smaller geographic ranges [100, 105, 107, 123, 136]. However, this common pattern does not explain why certain taxa may be less prone to extinction than others. In this example, how range size is formed varies between clades and thus remains a black box for most taxa [104] and so it is impossible to determine if differential extinction is caused purely by chance versus the product of selection. By focusing on traits related to environmental preference, the traits which may underly why a taxon is abundant or widespread and which are mostly likely under selection, the strength of selection related to extinction may be elucidated.

Species do not exist in a vacuum but must interact with their environment. Environmental availability and stability are crucial for both the establishment and persistence of species. Environment here is defined following Simpson [140] as the set of all possible biotic and abiotic interactors. The set of interactions experienced by a taxon is called the adaptive zone. The quantification of all or most community interactions is difficult in a paleontological context, though has been accomplished for small temporal windows and at limited spatial scales [84, 122, 133]. By focusing on spatially co-occurring taxa instead a more general subset of the environment can be studied at a longer

geological duration. This is similar to the demarcation of biomes as opposed to food webs [151]. By tracking the number, membership, and similarity of communities over time and how this relates to taxon ecology it should be possible to estimate spatial heterogeneity in selection pressure.

It is under this framework that I propose to study how ecological traits associated with environmental preference have affected both Cenozoic mammal spatio-temporal dynamics and extinction risk. Cenozoic mammals represent an ideal group and time period as it is the fossil record is well sampled, well resolved both temporally and spatially, and the ecology and phylogeny of these taxa are generally understood [81, 83, 109, 114, 143].

The funds from this grant will allow for significant enhancement of these projects through the inclusion of a third and rarely integrated continent: South America. The fossil records of North American and Europe are frequently the subject of large spatial and temporal scale analyses of diversification [79, 80, 83, 97, 108–110, 114, 128, 148] and these two continents are frequently used as proxies for global mammalian diversification even though there are known differences between them [114, 148]. The continent of South America, though well sampled for certain time periods, is rarely included and integrated into large spatial and temporal scale analyses [120, 147]. My goal is to include the South American along with the North American and European mammal fossil records in order to better understand the different selective pressures on mammal distributions and survival.

Study system

Mammals are motile organisms which can track their preferred environmental context over time and space. Three important traits that describe the relationship between mammals and their environmental context are body size, dietary category, and locomotor category [89, 90, 110, 115, 116, 143, 144]. Each of these traits describe different aspects of a taxon’s adaptive zone such as energetic cost, population density, expected home range size, set of potential prey items, and dispersal ability among others.

Dietary category roughly describes the trophic position of a taxon and its distance from primary productivity. The dietary categories used here are coarse groupings of similar ecologies: carnivores, herbivores, omnivores, and insectivores. Mammalian herbivores and carnivores have been found to have a greater diversification rate than omnivores [126] which may indicate that these traits are better for survival. However diversification can be caused by either an increase in speciation relative to extinction or a decrease in extinction relative to speciation. Which scenario occurred, however, is (currently) impossible to determine from a phylogeny of only extant organisms [127] which means that analysis of the fossil record is required. If survival is found to be similar between all dietary categories, this may mean that the differential diversification patterns observed by Price et al. [126] are due to differences in speciation and not extinction.

Locomotor categories describe the motility of a taxon, the plausibility of occurrence, and dispersal ability. Dispersal ability is important for determining both the extent of a taxon’s geographic range and ability to track changing environments [87, 98, 106] which then affects both extinction risk and community similarity. Here, mammals are categorized as either arboreal, ground dwelling, or scansorial. With the transition from primarily closed to open environments, it is expected that arboreal taxa during the Paleogene will have a greater expected duration than Neogene taxa while

the opposite will be true for ground dwelling taxa. In comparison, taxon duration of scansorial taxa is expected to remain relatively similar between the two time periods because it represents a mixed environmental preference that may be viable in either closed or open environments.

An organisms body size, here defined as mass, has an associated energetic cost in order to maintain homeostasis which in turn necessitates a supply of prey items. Many life history traits are also associated with body size: reproductive rate, metabolic rate, home range size, among others [88, 89, 125, 143]. Body size may affect upon extinction risk because as body size increases, home range size increases [89] and if individual home range size scales up to reflect a species geographic range, this would mean that extinction risk would decrease. This expectation may be flawed and a plausible alternative scenario is that as body size increases, reproductive rate decreases [111], populations get smaller [154], and generations get longer [121] all of which increase extinction risk. A negative relationship between mammal body size and taxon duration has been observed [91, 114] though this is inconsistent between continents [114, 148]. By expanding to include a third continent, South America, and analyzing specific level data I hope to elucidate how differences in taxonomic diversity at a continental level might affect body size mediated extinction rate.

Preliminary results and proposed work

Community connectedness

Community connectedness will be analyzed in a network theoretic context where taxa and localities are connected in a bipartite network [138, 151, 152]. This strategy allows for occurrences to be analyzed whole-sale without use of a possibly arbitrary similarity metric [138]. This framework also allows for the use of measures of community structure such as the map equation [134, 135] which estimates the number of modules of a network based on it's topology. A module in this context is a set of taxa and localities which are more connected to each other than to other modules, effectively a biome or province.

This approach has been used in the study of communities at the Permo-Triassic boundary [138] and bivalves at the Cretaceous-Tertiary boundary [152]. Here, I propose to apply this approach to the mammalian record for the entire Cenozoic.

In this application, a bipartite network is where a taxon and a particular spatial area are defined as nodes. An occurrence of a species at a particular area creates a link between that species node and that area node. Links are defined only as taxon-locality occurrences, so species cannot be connected to species and spatial nodes cannot be connected to spatial nodes. For the temporal unit of interest, a biogeographic network is made between all observed taxa and occupied spatial units.

In the context of this study, taxa are defined as species and a spatial unit is a uniform latitude-longitude grid unit. Because of the high spatio-temporal resolution of the mammalian fossil record for North America and Europe [81, 97, 110, 119], temporal units are 2 million year (My) bins and spatial units are from a 2x2 grid.

The four measures of community structure used here are relative number of unique taxa per locality, relative taxon provincial occupancy, relative number of taxa per province, and code length. Code

length is an information theoretic measure of how most efficiently to divide a network into modules and is a measure of total spatial similarity [134, 135]. Biogeographic networks for taxa in the dietary and locomotor categories described above will be similarly analyzed.

In addition to these four measures of community structure, I will measure phylogenetic similarity of the taxa at a locality. Phylogeny may play an important role in community structuring where closely related taxa may be “repulsed” due to competitive exclusion or “clumped” because of environmental filtering [153].

While it is infeasible to infer an explicit phylogenetic hypothesis for all observed taxa on all continents, all taxa have some degree of hierarchical information. By combining multiple large scale extinct mammal phylogenies with taxonomic information, an informal phylogeny of all observed taxa can be constructed. From there measures of phylogenetic similarity can be estimated such as the phylogenetic species variability of a single locality [102] which can then be used as data in subsequent models of spatial structure.

Preliminary results are restricted to North America and Europe. Fossil occurrence information was downloaded from both the Paleobiology Database (PBDB; <http://paleodb.org/> and the Neogene Old World Database (NOW; <http://www.helsinki.fi/science/now/>). Dietary and locomotor assignments for each species were taken from the PBDB and the NOW. Currently, these results are primarily exploratory. These network measures will be analyzed as a hierarchical Bayesian time series model where, for each continent, the different ecological combinations are exchangeable samples from a common underlying continent-specific mammalian distributional pattern. Because only two continents are currently this is not stable enough to estimate of an additional hierarchical level where continents are drawn from a common underlying global mammal distributional pattern [99]. The inclusion of a third continent, South America, would allow for potentially stable estimates of a underlying common global mammal distributional pattern.

Extinction risk

Mammalian species durations will be modeled in a survival analysis framework where the effect of the above traits can be quantified as the effect upon a taxon’s duration. This form of analysis has a long history in paleobiology [86, 95, 140, 141, 150] but has fallen out of favor in recent years. Importantly, because some taxa may have originated before the Cenozoic or not have gone extinct yet, this information can be explicitly modeled as a censored duration which increases the total information included in the model. What makes survival analysis different from various linear modeling strategies such as logistic regression is that both duration and event occurrence are incorporated explicitly. In logistic regression, for example, only event occurrence is modeled, while in linear regression only duration is modeled. Importantly, this particular analytical framework has become quite mature since it’s apparent abandonment by paleontology as it is commonly used in epidemiology, engineering, and demography [113].

Many paleontological analyses of extinction selectivity and survivorship are performed at the generic level [93, 96, 100, 114, 148] there are potential biases in accurately modeling a specific level process using generic level data [129, 130, 137, 139, 150]. Differences in species and generic level extinction risk can be attributed to speciation. Namely, if a trait has no effect on extinction risk at the specific

level but decreases generic extinction risk this is most likely caused by a higher speciation rates in taxa exhibiting that trait. Because of this potentially elucidating property, I will be analyzing both species and generic level extinction risk. Importantly, this moves beyond simple analysis of diversification rates but partially decomposes the two aspects of diversification: speciation and extinction.

The current analyses are restricted to North America and Europe principally because of data availability. Fossil occurrence information was downloaded from both the PBDB and the NOW. As with the study of community connectedness described above, dietary and locomotor assignments for each species were taken from the PBDB and the NOW. Body size estimates are based on a combination of measurement data from the PBDB, NOW, and a species by species literature search. These estimates are based on the common practice of using regression equations for estimating mass from measures such as tooth area or skull length [80, 81, 110, 142, 148].

Duration was measured as the difference between first appearance (FAD) and last appearance (LAD), in millions of years. This value is most certainly a truncated version of the true species duration and so some amount of correction must be made for sighting failure [82, 145, 146].

Preliminary analyses were performed solely within a maximum likelihood framework combined with multi-model inference. Duration information was fit to either an exponential or Weibull distribution, common distributions for wait-time data used in survival analysis. The exponential distribution is a special case of the Weibull distribution where the scale (acceleration-deceleration) parameter k is set to 1, meaning that an exponential distribution corresponds to age-independent extinction and thus the Law of Constant Extinction [150]. Dietary and locomotor categories were broken up into $r - 1$ binary predictor variables, where r is the number of unique states, for a total of five binary predictors. A constant term was also estimated which corresponds to the remaining dietary and locomotor states. For North America the final predictor was natural log of body mass as while this was not included for Europe that collection effort is not completed.

Future modeling work will be done in a purely Bayesian framework. This shift in analytical style is to 1) better estimate the uncertainty with which estimates are made, 2) combine the analysis of the different continents in hierarchical framework in order to estimate a common underlying distribution of survival times, 3) incorporate phylogenetic distance into a prior on a frailty coefficient [85, 103], and to 4) move on a continuous model expansion framework as opposed to a discrete model choice one [99]. All of these changes will dramatically improve the interpretability and meaning of the results. Importantly, estimates under goal 2 would most likely not be stable without the inclusion the inclusion of a third continent, South America.

For example, a unique aspect of the South American record is the presence of multiple orders that are rare or completely absent from other continents of which there are multiple ungulate-like orders (e.g. Notoungulata) [94, 117, 118, 120]. These convergent orders combined with the other ungulate-like orders present in North American and Europe make it possible to estimate, in a hierarchical Bayesian framework, the order specific distributions of taxon durations but also estimate the of the underlying distribution common to all ungulate-like taxa [99].

Intellectual merit

I am proposing to analyze how mammalian species ecology affects both spatial distribution and temporal duration. By taking advantage of the extensively studied and well sampled mammalian fossil record, I have the unique opportunity to model a much more complex relationships that are both spatially and temporally explicit than is normally possible in the fossil record.

Mammalian evolution remains one of the corner stones of paleobiology [140] though has been historically restricted to North America and Europe, only. The inclusion of South America, a region heavily studied by Simpson CITATIONS, into the analysis of mammalian diversification will provide a much needed Southern Hemisphere perspective which will greatly improve the generality of these analyses.

Broader impacts

Mental health of students and researchers is a passion of mine and my time spent on campuses around the world has let me observe many of the different and complex scenarios people encounter. I recently became involved with GSMHAB, a graduate student group involved with outreach, communication, and improvement of mental health services on the University of Chicago campus. The group specifically targets graduate students which make up two-thirds of the campus' student population. Additionally, I will be serving as a peer mentor to entering first-year graduate students through the SAIL program at the university.

My past and current research are based out of natural history museum collections which has let me be involved in some wonderful outreach programs. In Seattle, I participated for my entire undergraduate experience as an expert on both marsupial mammals and fossil mammals with the "Meet the Mammals" and "Dino Day" programs at the Burke Museum of Natural History and Culture. These programs were designed specifically to reach out to children and provide them the opportunity to see and touch specimens, providing the opportunity to interact directly with the museums collections. I plan to continue to participate in similar outreach programs at the Field Museum of Natural History in Chicago in order to possibly inspire future scientists.

Additionally, because most of the literature on South American fossil mammals is in Spanish it is effectively unavailable to many researchers. One of my goals with this study is to open up this literature. I am committed to providing whatever data I gather to other researchers through services such as the PBDB so that South America will continue to be included in paleobiological studies.

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Biographical sketch

Peter D. Smits

Committee on Evolutionary Biology, University of Chicago

Professional preparation

University of Washington	Biology (Ecology and Evolution)	B.S. 2010
Monash University	Biological Sciences	M.Sc. 2012
University of Chicago	Evolutionary Biology	Ph.D. 2017 (expected)

Appointments

September 2012–present, Ph.D Candidate, Committee on Evolutionary Biology, University of Chicago.

July 2010–August 2010, Lab Assistant, Vertebrate Paleontology, Burke Museum of Natural History, University of Washington.

July 2009–August 2009, REU Intern, Mammalogy, American Museum of Natural History.

September 2006–September 2008, Lab and Field Assistant, Mammalogy, Burke Museum of Natural History and Culture, University of Washington.

Products

Related publications

- .

Unrelated publications

- .
- .
- .

Synergistic activities

Reviewer for *Systematic Biology*, *PLOS One*.

Member of student mental health panel GSMAB, University of Chicago, 2014–present.

Volunteer instructor for peer led programming class, University of Chicago, 2012–2013.

Volunteer expert at “Dino-Day” at the Burke Museum of Natural History and Culture, 2010.

Volunteer expert at “Meet the Mammals” at the Burke Museum of Natural History and Culture, 2007, 2008, 2009.

Collaborators and other affiliations

Collaborators and co-editors

Philip D. Clausen (University of Newcastle), Liliana M. Davalos (Stony Brook University), Alistair R. Evans (Monash University), Richard H. Madden (University of Chicago), Matthew R. McCurry (Monash University), Colin R. McHenry (Monash University), Christopher C. Oldfield (University of Newcastle), P. David Polly (University of Indiana–Bloomington), Michelle R. Quayle (Monash University), Richard H. Ree (Field Museum of Natural History), Heather S. Richards (University of Newcastle), Nancy B. Simmons (American Museum of Natural History), Christopher W. Wamsley (Monash University), Omar M. Warsi (Stony Brook University), Stephen Wroe (University of New England), Paul M. Velazco (American Museum of Natural History).

Graduate advisors and postdoctoral sponsors

Kenneth D. Angielczyk (Field Museum of Natural History), Michael J. Foote (University of Chicago).

Facilities, equipment, & other resources

Major equipment

Calipers, both small (12”) and large (24”), are available through the Committee on Evolutionary Biology.

Laboratory

NA

Clinical

NA

Animal

NA

Computer

All data collected from both databases and personal measurements will be stored on a personal computer owned by the Co-PI as well as in both cloud storage and external hard drives. Computer expertise is available at the University of Chicago and the Co-PI has access to large-scale computer clusters via the University of Chicago. All analysis software is free and open-source and is installed on the Co-PI's personal computer and can be installed on all additionally necessary computing clusters.

Office

The PI has dedicated office space at the Field Museum of Natural History. The Co-PI has dedicated office space provided by both the Committee on Evolutionary Biology and the Department of Geophysical Sciences.

Other

NA

Data management plan

The major data and analytical products of the proposed project are 1) anatomical measurements of specimens from museum collections, 2) organized and updated ecological information, and 3) statistical analysis code. All information gathered will be stored indefinitely on both the PI's and Co-PI's personal computers. Additionally, they will be archived on an external hard drive indefinitely in case of the loss of either personal computer.

All anatomical measurements and ecological information used in the proposed study will be provided as supplementary material for all papers produced from this research. These data will also be archived using the data storage service Dryad (<http://datadryad.org>). Finally, all measurements and ecological information will be available through the Co-PI's personal website (<http://home.uchicago.edu/psmits/home.html>).

Museums and other institutions where specimens will be measured will be named in all subsequent presentations and papers. These institutions will also be provided with all measurements made to housed specimens, as well as reprints of all related papers.

Anatomical measures, body mass estimates, and updated ecological information will be sent to the Paleobiology Database (<http://paleobiodb.org>) which is the largest repository of paleontological taxonomic, occurrence, and ecological information.

All code used in the proposed analyses will be archived using Dryad, along with the relevant data as discussed above. Code will also be made available through the Co-PI's GitHub page (<http://github.com/psmits>), a free code sharing and archiving service, as well as through the Co-PI's website (<http://home.uchicago.edu/psmits/home.html>).

The Co-PI will present the results of the proposed research at conferences and publish said results in peer-reviewed journals in the fields of evolution, paleontology, evolutionary ecology, and global conservation.

Context for improvement

The goal of the proposed research

My research (PDS) straddles the interests of both my advisor, Dr. Kenneth Angielczyk, and my co-advisor, Dr. Michael Foote. Dr. Angielczyk's research is focused on synapsids, a group of mammal-relatives, during the Permian and at the Permian–Triassic mass extinction. Dr. Foote's research is primarily focused on long-term evolutionary and spatial patterns of marine invertebrates. While I work on both spatio-temporal dynamics and extinction risk, my dissertation is independent from either of them in that it focuses on Cenozoic mammals and in the analytical framework I am applying. Because of this, my research is not an extension of any the existing projects of either of my advisors and I have not received fiscal support from either of them.

Timeline for the proposed DDIG study:

Summer 2015

Fall/Winter 2015-2016

Summer 2016

Fall/Winter 2016-2017