

THE EVOLUTIONARY HISTORY OF THE FELIFORMIA: CONTINGENCY,
CONSTRAINT, DISPARITY

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DISSERTATION ABSTRACT

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Constraint is a fundamental concept in evolutionary theory. The possibilities are not endless for what shape an organism can take, nor ecology of one generation to the next. Cat-like carnivorans (Feliformia) offer a unique opportunity in investigating aspects of evolutionary constraint, given several of their constituent clades are purported to experience this phenomenon in terms of limited evolutionary potential, but also in the presence of some clades with extreme durophagous (bone-crushing) and sabertooth morphology. I investigated the evolutionary history of feliforms by considering their phylogeny, ecology and cranial morphology. I recover results that suggest there are three distinct ecospace within which feliforms reside. The first is occupied by those small in overall size, covering a wide dietary and ecological spectrum, up to but not including hypercarnivory. These broad ecologies are facilitated by a narrow band of similar cranial shapes, evocative of “one to many mapping”. The second ecospace is occupied by soft-flesh specialists, such as felids (cats) and nimravids. These hypercarnivores possess distinct (non-overlapping) crania from the first ecospace, optimized for bite force and large gape angles. The evolutionary end member of this ecospace are those taxa possessing sabertooth morphology and the most disparate cranial shapes of all. The third ecospace is that of hyaenids, with a diverse ecological breadth optimized for dental toolkit and body mass, channeled by postcranial cursorial adaptations. The evolutionary end member of this ecospace are those taxa possessing

durophagous morphology. In all three ecospace, constraint exists in what cranial morphology and ecological transitions are possible. Large size nor hypercarnivory are achievable within the small feliform ecospace, and thus require transitions into the other two zones. Soft-flesh specialization is a road of no return that does not facilitate ecospace transitions. The hyaenid ecospace does not facilitate transitions into the 'soft flesh' ecospace, nor by extension sabertooth morphology. These limitations are a result of phylogenetic baggage and functional challenges, but fruitfully channel extreme cranial shapes (soft-flesh specialist) and diverse ecologies (hyaenids) that couldn't exist without these constraints.

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For those of whom the old bones come alive and join the pageant of the living.

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Chapter I

Introduction

Variation supplies the raw material by which natural selection operates, “variation supposes, while selection disposes.” However, numerous studies have acknowledged the importance of understanding that, unlike Darwin’s original formulation, variation generated by organisms is not isotropic (Olson and Miller, 1958; Vermeij, 1973; Gould, 2002; Goswami et al., 2011).

Possibilities are not limitless, as evident by the non-equal occupation of morphospace and ecology of all lineages. What obstructs the opportunities for some lineages and perhaps facilitates diversity and disparity for others remain central questions in biology and evolutionary theory (Dobzhansky, 1951; Hutchinson, 1959; Gould, 2002).

Hypotheses have existed since Galton (1869) that there may be minimally stable states or positions in both morphology and ecology, where evolution proceeds less like a rolling billiard ball of isotropic generational variation, and more analogous to a polyhedron that flips facets of stable ecomorphology. In other words, maybe a reasonable amount of isotropic variation is created in each generation, but only a limited amount is tenable in being a successful organism. From these proposals rose ideas of channelized evolution (Haeckel, 1866; Eimer, 1890; Hyatt, 1897; Goldschmidt, 1940) that held promise in predicting the course of shape and niche change if the framework could be understood. Evolutionary history or deep homology may play a truly integral part in determining what shapes and occupations an organism can achieve, either through lack of genetic raw material or variation, or developmental correlation of parts that will not allow certain changes to happen. However, these same correlations may also provide an axis of exploitation, where a greater magnitude of change may be possible within a certain trajectory

compared to equally probable random change in any direction (Goswami et al., 2014). This fruitful channeling could then be viewed as a positive aspect of constraint leading to more extreme shapes and, by extension, ecologies than would be possible under Darwin's initial hypothesis.

Areas of limited variation are often ascribed to specialists. With the concept of one-to-one mapping of ecology to shape, one would expect that fewer niches or a more limited ecology would correlate with less morphological variation. Among the carnivoran clades, low amounts of cranial-dental variation have been described in literature for "cat-like" feliform carnivores such as felids and nimravids (Radinsky, 1981a, 1982; Van Valkenburgh, 1991; Holliday and Stepan, 2004). This reduced raw material is argued to relate to increased specialization towards a hypercarnivorous diet, one dominated by a predominance of vertebrate prey. Felids and nimravids both exhibit simplified dentition that efficiently slices soft flesh but lacks the grinding surfaces found in more omnivorous carnivores (Evans and Pineda-Munoz, 2018). The loss of grinding surfaces on teeth seems to be an evolutionary road of no return, resulting in an ecomorphological constraint that did not allow these specialists to evolve additional ecologies (Solé and Ladevèze, 2017; Brocklehurst, 2019).

Consequently, feliforms offer a unique opportunity to investigate aspects of evolutionary constraint, not only for the perceived lack of variation inherent to their specialist clades, but also the extreme morphologies acquired by extinct sabertooth and bone-crushing members. Was constraint an aspect of feliform evolution that limited possibilities for certain lineages, or did that same constraint fruitfully channel the extreme morphologies that did evolve? Additionally, since all clades did not enter into the hypercarnivorous and presumably specialized realms of cats, nimravids and hyenas, what gave these latter groups the push to get there in the first place?

I investigated the evolutionary history of feliforms by considering their phylogeny, ecology and cranial morphology across the following chapters. In Chapter II, I construct a hypothesis of feliform evolutionary relationships using total-evidence Bayesian techniques. This methodology allowed me to incorporate molecular (nuclear and mitochondrial genome), dental and osteological morphology and stratigraphic occurrence data in a single analysis. This phylogeny serves as a framework for all following analyses, while also assessing relationships of several purported feliform taxa for the first time, e.g., percrocotids, and holistically estimating major clade originations and relative speciation and extinction rates by combining the fossil and living record.

Chapter III assesses ecological evolution of feliforms in terms of their diet, dental toolkit and body mass. I used hypotheses of adaptive radiation, as facilitated by tectonic and climatic events, as a framework to assess different clades' ecological trajectory. However, I compared models of adaptive radiation to other potential processes to best explain the patterns observed in feliform natural history. These models included random walk, trended evolution, optimal body mass and toolkit per dietary category, and clade-based regime shifts. Using the results of Chapter II, I was also able to incorporate phylogenetic uncertainty for all analyses by virtue of sampled trees over the course of the Bayesian analysis tree search.

Chapter IV explores the generating forces of feliform cranial shape through 3D geometric morphometric analysis. I assessed which feliform clades possess the greatest cranial disparity, such do clades with broad ecological occupation have greater variance compared to specialists? I consider multiple plausible sources of cranial disparity such as allometry as a line of least evolutionary resistance, integration of the developmental units of the cranium, the geologic time a clade has existed to evolve disparate shapes, and dietary ecology.

Chapter V synthesizes the above analyses into a narrative of feliform evolution and offers predictions for all terrestrial carnivorans. This narrative finds support for constraint in the evolutionary history of feliforms with a finite number of possible ecospace. Certain transitions are not possible from one ecospace to another, but these same constraints fruitfully channel the extreme endmembers of cranial evolution and ecology that otherwise are inaccessible to other groups, i.e., sabertooth and durophagous morphology. Similar patterns are further observed for caniforms and suggestive of a general process at work in the evolution of terrestrial carnivores.

Chapter II

Phylogeny of the Feliformia

Introduction

Current hypotheses of feliform relationships are derived from primarily molecular- or morphological-only datasets (though see Barrett et al., 2021). Molecular hypotheses (e.g. Nyakatura and Bininda-Emonds, 2012; Pajjmans et al., 2017; Zhou et al., 2017; Slater and Friscia, 2019; Hassanin et al., 2021) differ extensively from morphological ones (e.g. Wesley-Hunt and Flynn, 2005; Spaulding and Flynn, 2012), such as the placement of the Hyaenidae (hyenas) as distantly related to the Felidae (cats) in molecular phylogenies, while most closely related to the Felidae in morphological phylogenies. An additional issue is the cited morphological studies, including the preliminary total-evidence analysis of Barrett et al. (2021), sample extinct taxa from across the Feliformia, but contain typically one representative operational taxonomic unit (OTU) per family, usually extant. These living OTUs are commonly derived members of their respective families and thus may generate long-branch attraction in phylogenetic hypotheses (Bergsten, 2005). Another explanation for this discrepancy is that differing topologies in molecular trees result from the inability to include most extinct taxa, while all multifamily morphological trees are depauperate in the extant and fossil taxa that they do contain. Furthermore, several extinct clades of feliform (e.g., Percrocutidae, Lophocyonidae, Machairodontinae) have rarely been included in broad feliform phylogenetic analyses, so their placement is poorly known. Combined, these challenges have resulted in uneven knowledge of feliform relationships. Extant or recently extinct clades with molecular data have returned

consistent relationships, but necessarily devoid of the diversity of extinct clades, while taxa known only from morphology suffer from lack of analyses, limited taxon sampling or both.

Is there a contradiction in the evolutionary relationships of feliforms depending on what datasets one employs, or is this an artifact of methodology and taxon sampling? Here I present a broad investigation of the phylogenetic relationships of feliform taxa by examining the relationships of all major families, and numerous OTUs within each family, with extensive morphological and molecular datasets. I address the conflict of past analyses by employing total-evidence techniques (Lee et al., 2009; Pyron, 2011; Ronquist et al., 2012) which use a Bayesian framework to create a probabilistic model of evolution, inclusive of molecular data, fossil data, and stratigraphic information in a single analysis. Specifically, I implement a total-evidence analysis with a Sampled Ancestor, Birth-Death Skyline with Serial Sampling (SABDSKY) model (Stadler et al., 2013; Gavryushkina et al., 2014) which allows the identification of direct ancestors and changing speciation, extinction and sampling rates through time. This analysis yields a dated phylogeny of extinct and living taxa combining data previously studied in separate morphology-only and molecular-only analyses. Furthermore, this analysis places several taxa/clades in novel arrangements allowing de novo assessment of historical patterns of morphological and ecological evolution.

Methods

Taxa Selection

I chose feliform taxa that captured the cranial disparity and ecological diversity of their given clade, while providing even taxonomic coverage. All feliform taxa with published aDNA (n=7)

were also incorporated into this analysis to provide greater resolution on phylogenetic relationships along with molecular data from all extant taxa. The fossil record of feliform carnivorans is not symmetric across clades, with collections and literature favoring large-bodied taxa, e.g. felids, hyaenids and nimravids. However, I included well-preserved small-bodied fossil viverrids, herpestids and stem feloids/viverroids whenever possible. The final phylogenetic analysis includes 124 taxa, plus five caniform outgroups, with approximately two-thirds of all taxa being extinct.

Molecular Data

I downloaded three nuclear loci and complete mitochondrial genomes from Genbank for the forty-five extant and seven extinct (aDNA) taxa of the analysis (Appendix A). However, where complete mitochondrial genomes were unavailable, I used individual mitochondrial genes. I aligned Nucleotide sequences one gene at a time using MAFFT v.7 online server (Kato et al., 2019), with the G-INS-I and 'Leave gappy regions' parameters selected. All sites containing missing data were removed. This necessitated the loss of codon-position information for all save one mitochondrial gene (ND4L). I deleted the stop codons and manually optimized these aligned sequences in UGENE v. 35.1 (Okonechnikov et al., 2012) to maintain codon positions when possible and trimmed excess bases of tail data that had no comparative sequences. I then concatenated the aligned sequences in SequenceMatrix (Vaidya et al., 2011) and analyzed them for partitioning schemes utilizing PartitionFinder version 2.1.1 (Lanfear et al., 2016) on XSEDE (Townsend et al., 2014) through the CIPRES Science Gateway v. 3.3 (Miller et al., 2011). I designated twenty data blocks for the dataset, such that only genes IRBP and ND4L were separated into three blocks based on codon positions. The remainder I gave a single block per

molecular sequence. I defined linked branch lengths and investigated all evolutionary models available to BEAST 2 (40 models) using a ‘greedy’ partitioning strategy to compare partitions and differential substitution models under the Bayesian information criterion (BIC). A 10-partition scheme was best supported (Appendix B, Table 1).

Table 1. Best supported substitution models recovered in PartitionFinder2 using the Bayesian information criterion (BIC).

No. of partitions	Partition	Model
1	<i>ND4L_1stpos, COX3, ATP6, COX2, COX1</i>	HKY+I+G+X
2	<i>ND4, CYB, ND1, ATP8, ND5, ND3</i>	GTR+I+G+X
3	<i>TTR, CHRNA_1</i>	SYM+G
4	<i>IRBP_1stpos</i>	TRN+G+X
5	<i>IRBP_2ndpos</i>	TRNEF+I
6	<i>IRBP_3rdpos</i>	HKY+G+X
7	<i>ND2</i>	HKY+I+G+X
8	<i>ND4L_2ndpos</i>	HKY+I+G+X
9	<i>ND4L_3rdpos</i>	HKY+I+G+X
10	<i>ND6</i>	HKY+G+X

Morphology Data

I scored all taxa from personal observation of specimens or literature as listed in Appendix C for 325 morphological characters derived from prior carnivoran/feliform phylogenetic analyses (Van Valkenburgh et al., 1990; Werdelin and Solounias, 1991; Salles, 1992; Bryant, 1996; Peigné, 2003; Rothwell, 2003; Gaubert et al., 2005; Wesley-Hunt and Flynn, 2005; Tseng and Wang, 2007; Christiansen, 2008a; Salesa et al., 2010; Sakamoto and Ruta, 2012; Salesa et al., 2012; Spaulding and Flynn, 2012; Christiansen, 2013; Robles et al., 2013a; Barrett, 2016; Morales et al., 2019; Barrett, 2021; Barrett et al., 2021) and several novel characters. When possible, multiple individuals of a given taxon were scored to assess polymorphic conditions. Characters and their associated descriptions can be found in Appendix D, while the resultant morphology character matrix is Appendix E. I assessed six competing schemes of morphological character partitioning and evolution by Bayes Factor via a Generalized Stepping Stone (GSS; Fan et al., 2011) analysis (Table 2). These schemes partitioned characters based upon anatomical association (cranial/post-cranial), number of states a character contains (n-states), or a combination of the two. I additionally wrote custom evolutionary rate matrices for specific multistate characters (Appendix F) that included ordered, multipath and Dollo (irreversible) characters to compare to null unordered character evolution. Each scheme was assessed by GSS with 10 steps, a chain length of five million and 50% burnin.

Table 2. Summary of marginal log-likelihoods and Bayes factor (BF) support for differential substitution models and partitioning schemes of the morphology data. Log BF values are reported as the support of the best model (model 6) over the inline model. P=partition used, * = best supported model.

Scheme	n-state partition	Cranial/Post-cranial part.	Complex Evo. models	Marginal log-likelihood	Log BF vs Best Model
1		P		-16804.22	4058.26
2		P	P	-14672.40	1926.44
3	P	P		-12984.09	238.13
4	P			-12974.56	228.60
5	P	P	P	-12752.54	6.58
6*	P		P	-12745.96	-

Total-evidence Analysis

I jointly estimated tree topology, branch lengths and evolutionary parameters in a Bayesian framework using BEAST2, version 2.6.3 (Bouckaert et al., 2014) with a Sampled Ancestor, Birth-Death Skyline with Serial Sampling (SABDSKY) model as a tree prior (Stadler et al., 2013; Gavryushkina et al., 2014). A SABDSKY model allows analyzed taxa to be direct ancestors (zero length branches) to other taxa, while serial skyline models facilitate changes in extinction, speciation or sampling rates through time, factors which are likely non-trivial to the approximately 50 million year history of feliform evolution (Liow and Finarelli, 2014; Pires et al., 2017). I assessed the number of speciation and extinction rate shifts (sampling standard deviation was found to approximately zero, thus rejecting the presence of rate variation and justifying the use of a single sampling parameter) by first arbitrarily testing ten evenly spaced

shifts at 5 Ma increments. I visualized/assessed the proposed shifts in Tracer version 1.7.1 (Rambaut et al., 2018) and the ‘bdskytools’ R package (Plessis, 2016). From these results, I reduced the number of shifts to six with boundaries correlating to the rate inflection points in Figure 1. Speciation (R_e) and extinction (δ) were given uniform priors [0,10], while sampling was given a uniform [0,1]. The origin parameter was given a lognormal distribution, offset of 47.4 Ma (being the FAD of the oldest taxon in the analysis), mean=1.0, standard deviation=1.25 and ‘mean in real space’ parameter selected.

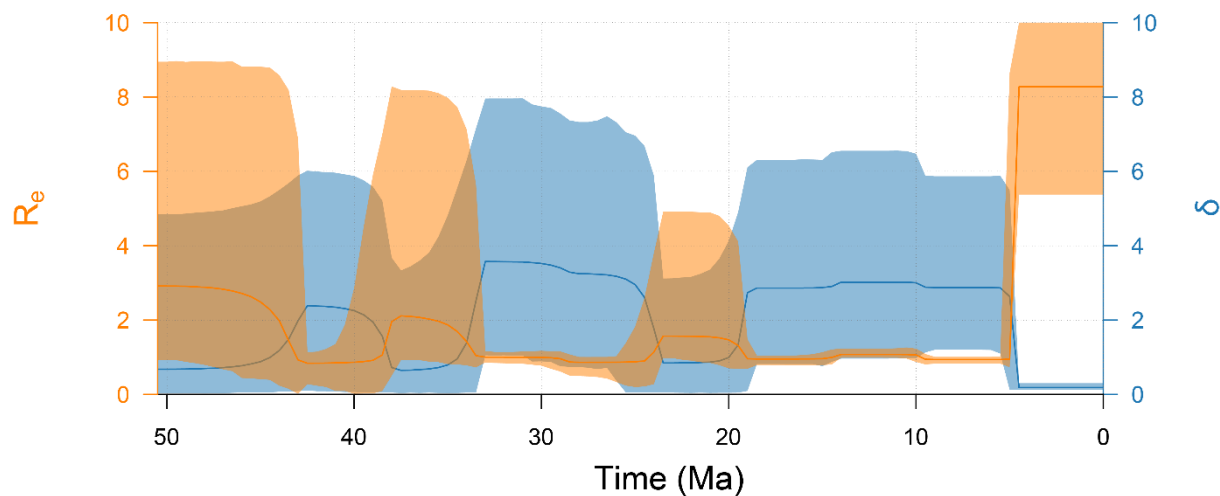


Figure 1. Skyline plot of assessed changes in speciation (R_e) and extinction (δ) rates through time of the Feliformia.

I set each morphological partition to evolve under the Lewis Mk_v model, or those best supported by the GSS analysis, scheme 6. All partitions were set to accommodate ascertainment bias and ambiguities in the character matrix with a substitution rate that varied across characters

according to a Gamma distribution shared by all partitions. I modelled the shared morphological clock with an uncorrelated relaxed clock model with log-normal distributed rates. For molecular data, I applied a single lognormal relaxed clock model with partitions and evolutionary models following the results of the PartitionFinder2 analysis. I derived the distributions (with provided justifications) of tip dates from the information in Appendix G.

Early runs of the analysis displayed a lack of convergence between the morphological and molecular data, thus I constructed a reasonable time-scaled starting tree in R version 4.0.3 (R Core Team, 2020) using the ‘DatePhylo’ function in the ‘strap’ package (Bell and Lloyd, 2014). I set a relatively uninformed “equal” set of branch lengths, calculated across a feliform tree derived from relationships in literature (e.g. Turner et al., 2008; Christiansen, 2013; Slater, 2015; Slater and Friscia, 2019; Barrett, 2021; Barrett et al., 2021) using the First Appearance Data (FAD) as described in Appendix G. These branches I further scaled using the ‘minBranchLength’ function in ‘paleotree’ (Bapst, 2012) with a setting of 1.5 to approximate divergence dates of major clades following molecular hypotheses as listed in the aforementioned literature. I finally specified a minimal set of topology constraints separating the ingroup from the outgroup taxa, as well as relationships within the outgroup Caniformia as ascertained from phylogenetic analyses in the prior listed literature.

I ran Markov Chain Monte Carlo (MCMC) chains for 100 million generations, sampling trees and parameters every 10,000 generations, until satisfactory sampling of parameters had been reached as assessed by Tracer v. 1.7.1. Thus, I discarded 10% burn-in and estimated topology and posterior probabilities from the remaining generations in the form of a maximum clade credibility (MCC) tree with median node heights.

I assessed morphological synapomorphies via TNT v. 1.5 (Goloboff and Catalano, 2016) on the MCC tree of the above analysis. TNT only reports synapomorphies supported by both ACCTRAN and DELTRAN optimization and thus forms a conservative assessment of shared derived character states.

Results

The MCC tree is presented in Figure 2. Overall, broad (family-level) relationships are consistent to those recovered in molecular analyses, with felids and prionodontids sister to the viverroids (e.g. Zhou et al., 2017; Slater and Friscia, 2019; Hassanin et al., 2021). Similarly, relationships within families containing extant taxa largely follow those of molecular analyses, though differences do exist. Euplerids follow relationships of Hassanin et al. (2021), but differ in the placement of the fossa, *Cryptoprocta ferox*, relative to previously referenced studies. The Herpestinae (solitary mongooses) lineage differs amongst all cited studies, while the clade Mungotinae (eusocial mongooses) is recovered in the same arrangement amongst all cited studies. The poor resolution of the Herpestinae is reflected in the relatively poor support metrics amongst these studies and the present one, indicating need for future work with this clade. Similarly, certain feline relationships differ amongst all studies, while pantherine felids were recovered in the same arrangement. The recovered internal relationships of the remaining extant clades were identical to those of the literature previously cited.

(PP) for each clade. The Nimravidae exhibits a basal split consisting of the Hoplophoninae and Nimravinae of Barrett (2021), though the taxa *Dinictis* and *Pogonodon* are recovered as basal members of the Hoplophoninae (0.74 PP), while *Maofelis* and unnamed specimen MA-PHQ 348 as basal members of the Nimravinae (0.12 PP). The remaining differences in relationships of the Nimravidae are to regions of the tree where both the present study and Barrett (2021) recovered poor resolution.

The African palm civet, *Nandinia binotata*, is recovered in a novel relationship nested amongst the Stenoplesictidae (0.53 PP), late Oligocene stem feloids. This clade further includes *Proailurus*, *Stenogale* and *Palaeoprionodon*, similar to previous morphology only studies, minus the inclusion of *Nandinia* (Wesley-Hunt and Flynn, 2005; Spaulding and Flynn, 2012; Solé et al., 2014, 2016).

The felids are split amongst the Machairodontinae (0.94 PP, seven synapomorphies) and Felinae + Pantherinae (1.0 PP, eight synapomorphies) with *Pseudaelurus validus* as stem to both (1.0 PP). The Machairodontinae contains the Smilodontini, Homotherini and a series of stem “Metailurini” taxa which diverged from the remaining living felids at approximately 15.17 Ma, comparable to other molecular-only analyses, ranging from 14-22 Ma (Paijmans et al., 2017; Slater and Friscia, 2019; Barnett et al., 2020). The Homotherini of the present study contains *Homotherium*, *Xenosmilus* and *Amphimachairodus* taxa (0.54 PP, three synapomorphies) diverging from the Smilodontini at 10.78 Ma, much shallower than the molecular aDNA analysis of Paijmans et al. (2017) at ~18 Ma, though comparable to Slater and Friscia (2019), 11.78 Ma. The *Homotherium* species *H. latidens* and *H. serum* were also assessed to have an extremely shallow divergence (~0.46 Ma), supporting a conspecific relationship previously hypothesized in analyses with narrower taxonomic scope (Antón et al., 2014; Paijmans et al., 2017). The

Smilodontini of the present study contain *Smilodon* and *Megantereon* (0.99 PP, seven synapomorphies). As previously mentioned the remaining machairodontines form a grade of stem “metailurins”, resembling the relationships presented in Christiansen (2013) most closely. However, the taxa *Nimravides* and *Machairodus* were recovered as well supported (0.72-0.86 PP) stem members of Smilodontini + Homotherini clade, while the remainder recovered poorer support at the base of the Machairodontinae.

Extinct lions, *Panthera atrox* and *Panthera leo spelaea*, are recovered in the same relationships of previous molecular studies, with the Eurasian cave lion sister to the North American lion and the living African lion stem to both, but at slightly deeper divergence dates, 1.58-2.31 Ma (Barnett et al., 2009, 2016). The North American cheetah-like cat, *Miracinonyx*, was recovered as sister to *Puma concolor* (1.0 PP), diverging approximately 3.63 Ma, comparable to past molecular analyses (Barnett et al., 2005; Slater and Friscia, 2019).

Hyaenids experienced perhaps the most disparate changes in relationships compared to past analyses which generally described an evolutionary trajectory of ‘civet-like’ to extremely durophagous forms (Werdelin and Solounias, 1991; Turner et al., 2008; Coca-Ortega and Pérez-Claros, 2019). The present study recovers up to three independent lineages evolving durophagous morphology. However, similar to Werdelin and Solounias (1991), the civet- and mongoose-like *Protictitherium*, *Plioviverrops* and *Tungurictis* were recovered in basal positions. Tip ward of these taxa, the first durophagous clade is recovered of *Tongxinictis* and *Allohyaena* (0.5 PP). This is followed by the divergence of the ‘ictithere’, Hyaenotheriini + Ictitheriinae of Semenov (2008), taxa including *Ictitherium viverrinum*, *Hyaenictitherium hyaenoides* and *Hyaenotherium wongii* (0.96 PP, four synapomorphies). Subsequently to diverge is the second clade of durophagous morphs, including *Belbus*, *Palinhyaena*, and *Lycyaena* (0.58 PP).

However, this clade's precise position within the greater Hyaenidae is not robustly supported with adjacent nodes yielding only 0.37-0.54 PP values. The final major clade (0.58 PP) of the Hyaenidae contains the crown group plus a sister-group of cursorial meat and bone specialists and durophagous taxa (*sensu* Coca-Ortega and Pérez-Claros, 2019). The non-crown clade contains the taxa *Chasmaporthetes*, and a novel *Adcrocuta* + *Pachycrocuta* clade (0.94 PP, five synapomorphies). *Pachycrocuta* has been closely connected to the *Hyaena* genus, both taxonomically and cladistically (see Liu et al., 2021), but the present study finds a more distant relationship. The crown clade contains the living and recently extinct taxa (i.e. *Crocuta crocuta spelaea*) in the relationship of molecular hypotheses (Koenfli et al., 2006; Slater and Friscia, 2019; Westbury et al., 2020; Hassanin et al., 2021), diverging from a common ancestor at ~7.7 Ma. Basal to these taxa lie the entirety of the 'percrocudid' (*sensu* Werdelin and Solounias, 1991) species of this study. Percrocudids have long been attributed to a separate family (Schmidt-Kittler, 1976; Chen and Schmidt-Kittler, 1983; Werdelin and Solounias, 1991), based upon derived dentition and their early geologic occurrence. However, the present study recovers them nested far within the Hyaenidae, immediately basal to the living taxa (0.68 PP, nine synapomorphies). The taxa *Dinocrocuta gigantea* and *Percrocuta carnifex* are recovered in a sister-group relationship (0.97 PP), while the remaining *Percrocuta* taxa form a grade below the extant species.

The last feliform family assessed was the Lophocyonidae, whose highly supported internal relationships (0.96-1.0 PP, seven synapomorphies) are found to be identical to those of Morales et al. (2019). However, placement of this clade within the Viverroidea was not well resolved by the present analysis. The aforementioned analysis of Morales et al. (2019) hypothesized a relationship sister to the hyaenids, to the exclusion of viverrids, but did not include herpestid

taxa. The present study recovered lophocyonids between viverrids and the hyaneid + euplerid + herpestid clade, but posterior probability of placement only ranged from 0.09-0.27 PP for adjacent nodes. This high uncertainty is likely related to the equally uncertain placement of other historically enigmatic feliform taxa: *Herpestides antiquus*, *Kichechia zamanae* and *Kanuites lewisae* (0.05-0.25 PP) in this analysis.

Discussion

The recovered feliform phylogeny presents new insights into relationships of several clades, as well as aspects of overall diversification and rates of speciation for the clade. Compared to the most recent Nimravidae analysis (Barrett, 2021), *Maofelis* and MA-PHQ 348 were recovered as stem Nimravines, sister to the European taxa *Dinailurictis*, *Quercylurus* and *Eofelis*. This is not unreasonable, given all these Eurasian taxa share an apomorphic triple rooted P3, though the support for this clade is low, 0.25 PP. Likewise, the clade of *Dinictis* and *Pogonodon* was also recovered in a different part of the tree, as stem hoplophonines, but in contrast, this relationship had substantial support, 0.74 PP. These differences in topology to Barrett (2021) may relate to the differential model choice (FBD versus BDSKY) of the two analyses, given the morphology character matrices contain identical scorings for the shared characters. Of course, the present analysis also contains one hundred more characters than Barrett (2021), which may have reconstructed different models of character evolution even when most of these characters were non-parsimony informative for nimravids. Regardless, the results of this analysis suggest that the stem members of each nimravid subfamily are somewhat unstable, needing additional characters and/or newly discovered taxa to aid in their resolution. However, the current phylogeny is informative on the oldest occurrences of purported nimravids. These specimens are from the

Irдинmanhan Asian land mammal age of China, and represented by fragmentary upper canines (Chow, 1958; Ding et al., 1977; Zheng et al., 1978). Problematically, these canine fragments are referred to *Eusmilus* (a genus otherwise not known until the late Eocene), based upon their degree of compression and presence of serrations. These teeth are more derived than the geologically younger (late Eocene) *Maofelis cantonensis* (Averianov et al., 2016) for which a whole cranium is known. The present phylogenetic analysis suggests that an Irдинmanhan or older age (i.e., ≥ 43 Ma) for the basal nimravid node is highly improbable (Median = 41.33 Ma; 95% credible interval = [38.76, 43.94] Ma). Combined, these early records are more likely those of machaeroidine oxyaenodonts, another group of sabertooth carnivores known more securely from the Irдинmanhan of China (Zack, 2019a; Zack et al., 2022).

A notable long branch of this study's phylogeny is located on the stem of the Feloidae. This region of the tree has received little phylogenetic work in literature, with groups such as the palaeogalids and stenoplesictids rarely incorporated in evolutionary trees. Palaeogalids are small viverroid-like feliforms first known from the late Eocene of North America, whereby they achieve a Holarctic distribution in the Oligocene and early Miocene (Wang and Zhang, 2015). The exact phylogenetic placement of this family has long been disputed, but the only analysis thus far places the clade at the base of the Feliformia (Wang and Zhang, 2015). However, given the geologic age of the earliest nimravids and lack of temporal context in the aforementioned analysis, a future Bayesian tip-dated phylogeny may shed light on the placement of this clade. Furthermore, a recently described *Palaeogale* specimen (JODA 13221) from the Turtle Cove Member of the John Day Formation features a complete cranium with intact and fully ossified auditory bullae (Famoso and Orcutt, 2022). Basal nimravids and all stenoplesictids lack a fully ossified auditory bulla, which implies that palaeogalids independently acquired this condition, as

seen in Miocene nimravids, or may nest higher within crown Feliformia. Inclusion of the John Day specimen in any subsequent phylogenetic analysis will go far in unraveling the evolutionary history of this group. Stenoplesictids also offer a fruitful avenue of investigation given numerous publications describing their anatomy, but lacking in phylogenetic analysis (e.g. Hunt, 1989, 1998a; Peigné, 1999; Peigné and De Bonis, 1999; Hunt, 2001a; Hans-Volker et al., 2007). A sample of stenoplesictids was analyzed in the presented phylogeny, suggesting that the living African palm civet *Nandinia* may represent the last surviving descendant of this once hypo- to hypercarnivorous clade. *Nandinia* has been found has the most-basal member of the extant Feliformia in several molecular analyses (Flynn et al., 2005; Nyakatura and Bininda-Emonds, 2012; Paijmans et al., 2017; Zhou et al., 2017; Slater and Friscia, 2019; Hassanin et al., 2021), with frequent commentary on its apparently plesiomorphic partially-ossified auditory bullae in morphological analyses (Hunt, 1987, 1989, 1998a; Wible and Spaulding, 2013). The inclusion of *Nandinia* in the Stenoplesictidae fits well with the molecular divergence estimates of the current and prior studies, as well as the bullar condition of representative stenoplesictids of the latest Oligocene (Hunt, 1998a; Peigné and De Bonis, 1999). Thus, the evolution of an ossified bulla amongst feliforms may have occurred on three independent occasions: nimravids, palaeogalids and crown Feliformia minus stenoplesictids.

Machairodontines were recovered with two, not three, well-supported tribes. However, it is probably no coincidence that the purported third tribe, Metailurini, was also the only tribe lacking aDNA data. Felids are generally believed to be conservative in their hypercarnivorous morphology (Holliday and Stepan, 2004; Van Valkenburgh, 2007; Chamoli and Wroe, 2011), creating challenges in the available diversity of morphological characters when the identified fossil material is limited in most taxa to craniodental remains. The most recent machairodontine

analysis (Werdelin and Flink, 2018) was also unable to recover these traditional tribes, even with a slightly expanded ingroup compared to this study's phylogeny (18 versus 14). However, the presented phylogeny did provide support for some disputed machairodontine hypotheses. The genus *Nimravides* has been suggested to be a taxon stem to Pantherinae + Felinae which convergently became sabertoothed given its relatively less derived dental morphology, geologic age and geographic context (Werdelin et al., 2010; Piras et al., 2018). This hypothesis cannot be ruled out by the tree of Werdelin and Flink (2018), given its unstable position as a stem feline or machairodontine depending on the settings of that study. However, this analysis supports the taxon as a machairodontine (0.94 PP) located near the base of the subfamily, before the split of smilodontins and homotherins. *Nimravides* is a New World taxon, with at least one species (*Nimravides catocopsis*) suggested to be a member of the Old World homotherin *Machairodus* lineage (Antón et al., 2013). The presented results cast doubt on that hypothesis. However, no Old World *Machairodus* taxa were included in this analysis, so assessment of immigration events and tribe allocation for *Machairodus* taxa will require an expanded taxa set, though recent phylogenetic analyses suggest Old World *Machairodus* may not be a homotherin either (Christiansen, 2013; Werdelin and Flink, 2018). Additionally, *Promegantereon* was not recovered as a stem smilodontin, a relationship historically hypothesized, but not demonstrated via phylogenetic analysis (Christiansen, 2013; Werdelin and Flink, 2018). Instead, this taxon was recovered in a poorly supported clade (0.24 PP) at the base of the machairodontines reminiscent of hypothesized metailurins (see Christiansen, 2013). Much like *Nimravides*, this region of the machairodontine tree would benefit from the addition of further taxa. Recent revisions and anatomical descriptions offer abundant content to include a potential clade or grade of taxa thought to be convergent on felines and pantherines (Werdelin and Lewis, 2001; Spassov and

Geraads, 2015; Li and Spassov, 2017; de Bonis et al., 2018; Piras et al., 2018). One final area of the felid tree that would benefit from increased scrutiny, is the ancestry and descendant relationships of *Pseudaelurus* and *Hyperailurictis* with other felids. Numerous stem felids have historically been lumped into the *Pseudaelurus* genus, but renewed interest in a hypothesis of differential lineages of felid evolution has gained ground in recent years. Old World *Pseudaelurus* has been hypothesized to be a stem member of the Machairodontinae, while New World *Hyperailurictis* stem to all felids, or even a basal felid offshoot that gave rise to an endemic *Nimravid*es (Kretzoi, 1929; Werdelin et al., 2010; Browne and Reynolds, 2015; Piras et al., 2018). However, even with the wealth of fossil material and publications on these early felids (e.g. Hunt, 1998a; Rothwell, 2001, 2003; Robles et al., 2013b), no analysis has given them broad context to support the splitting of these stem taxa into distinct lineages. Future work will go a long way towards our understanding of the evolution of the felids, how many lineages converged upon sabertooth, feline and pantherine morphologies, and biogeographic history of the entire family.

Perhaps the most novel result of this phylogeny is the recovery of percrocitids as derived hyaenids (1.0 PP). As previously mentioned, the derived dentition of these taxa has been the main evidence for their exclusion from the hyaenids. Specifically, in the dp4 a metaconid that is medially located within the trigonid complex and clearly separated from the talonid has been argued to be synapomorphic for hyaenids, while an inline, posteriorly placed metaconid connected with the talonid is the pattern among percrocitids (Schmidt-Kittler, 1976; Chen and Schmidt-Kittler, 1983; Werdelin and Solounias, 1991). However, in the work of Schmidt-Kittler (1976) it is suggested that this percrocitid condition could be the result of rapid evolution towards a hypercarnivorous morphology, losing the crushing talonid in favor of the slicing

trigonid. In the same work, the author describes the percrocutid condition in a variety of other feloids and nimravids (see Xiong, 2019 for a more detailed discussion) suggesting that it may have evolved multiple times. In fact, this morphology is present in the aardwolf, *Proteles*, and formed the basis for its removal to a separate Protelidae, inclusive of *Percrocuta* and *Dinocrocuta* (Baryshnikov and Averianov, 1993; Averyanov and Baryshnikov, 1996). The presented phylogeny used this character as part of its analysis, but still recovered all percrocutids as derived hyaenids, a hypothesis proposed, but untested in Xiong (2019) based upon basicranial morphology in *Dinocrocuta*. Furthermore, these taxa were recovered basal to the living hyaenids, but this relationship is challenged by the well-supported hypothesis that *Proteles* is the most basal living hyaenid (Zhou et al., 2017; Slater and Friscia, 2019; Westbury et al., 2020; Hassanin et al., 2021). Thus, any phylogenetic analysis relying on morphology (especially dental characters) to connect extinct taxa to the extant will be hampered by *Proteles*' near total lack of postcanine dentition and derived insectivorous lifestyle. This is reflected in the nodal support of the extant taxa to the most closely related "percrocutid" (0.46 PP). However, support does increase through progressive root-ward nodes (0.58-0.75 PP). This resolution of relationships does suggest rapid evolution of the aardwolf world's insectivory given its most recent common ancestors were well adapted for a durophagous lifestyle.

Several internal nodes of the Hyaenidae were recovered with low to moderate support. For example, the relationship between the civet- and mongoose-like taxa *Protictitherium* and *Plioviverrops* only received 0.36 PP. This may be related to the species chosen if these genera are well represented in the fossil record, but later occurring than other congeners (Turner et al., 2008; Gracia, 2015). Addition of more of the currently thirteen recognized species of these genera (Turner et al., 2008) will likely increase support and resolution of this region of the

hyaenid tree by reducing long branch attraction and maximizing inclusion of transitional morphology. This general suggestion of increased taxon sampling will likely benefit all poorly or moderately supported nodes of the presented phylogeny, especially given the large diversity of extinct hyaenids, approximately one-third of which was sampled for this study (Werdelin and Solounias, 1991; Turner et al., 2008). One of these regions that still contains several evolutionary and taxonomic questions is that of the ‘ictitheres’. Representing a diverse group (~13 taxa) of jackal or wolf-like taxa, ‘ictitheres’ may represent a unique clade characterized by a combination of five synapomorphies: a more anteriorly located bullar partition, the presence of second molars in both upper and lower dentition, enlarged m1 talonid and m2 surface area, an alisphenoid canal, and the lack of an enlarged frontal sinus (Semenov, 1989, 2008). However, all of the above features are ancestral for viverroids (save the bullar partition character) and thus unable to diagnose a clade with a recent common ancestor distinct from living hyaenids. Indeed, *Ictitherium viverrinum*, namesake of the ‘ictitheres’, was recovered in a position within typical ‘hyaenotheres’ (sensu Semenov, 1989), casting doubt within this analysis of a monophyletic clade for these canid-like taxa.

Finally, the last region of the recovered phylogeny that would benefit from increased sampling and investigation is that of stem viverroids. Of those analyzed, the lophocyonids formed the most cohesive group with highly supported internal relationships, but poorly constrained broader placement within Viverroidea. Lophocyonids are feliforms that evolved to be herbivorous browsers with highly complex lophate dentition (Morales et al., 2019). This dental complexity provides numerous morphological characters to resolve intraclade relationships, but basicranial morphology is unknown, creating challenges in determining the most recent common ancestor within the viverroids. Additional taxa such as *Lophocyon paraskevaidisi* (Koufos et al., 1995)

with known rostrum and near complete dentaries may help refine these relationships, but knowledge of the bullar condition from future specimens would likely contribute much more in broader relationships given the synapomorphic disparity of viverroid families for this feature (Hunt, 1987, 1989, 1991). Conversely, a taxon which does present known bullar morphology, could not be confidently resolved. *Kanuites lewisae* has a mosaic of basicranial features found in both herpestids and viverrids. *K. lewisae* possesses the viverrid oblique bullar partition, but herpestid + euplerid carotid artery caudal entotympanic posterior entrance (Werdelin, 2019). Furthermore, the temporal occurrence of *K. lewisae* (14.0-13.4 Ma) is as expected for both stem herpestids and viverrids. However, one illuminating feature that may be determined from CT scanning is the condition of the fossa for the tensor tympani in the petrosal, character 34. In both herpestids and euplerids this fossa forms a delicate tube, compared to a general depression or absence in all other feliforms. This feature may then help resolve the placement of this relatively well-known taxon and inform on greater mosaic evolution of a set of families known for their convergence (Gaubert et al., 2005).

Kichechia zamanae was also tentatively placed in the viverroids. Despite substantial fossil material, this hypothesized basal paradoxurine resolved outside both the Viverridae and Herpestidae. Without known basicranial morphology, clade allocation relies upon dental morphology. However, the prominent bunodont cusps of this taxon are known from other viverrid and herpestid taxa such as *Hemigalus*, *Bdeogale* and possibly *Atilax*, while the prominent cusps of the m1 trigonid and talonid including hypoconid and entoconid is ancestral for all viverroids. Additionally, the temporal occurrence of 20.0-17.0 Ma for this taxon is deeper than the inferred split of the Paradoxurinae and Viverrinae (sensu Gaubert and Veron, 2003) at 15.7 Ma. As already discussed, the main issue with placement of all of this study's stem

viverroids is lack of information on non-convergent morphological features (i.e., basicranial anatomy). Unfortunately, what remains is homoplastic or ancestral dental morphology that creates uncertainty in the precise placement of *Kichechia zamanae* and likely the other stem viverroids such as *Herpestides* and *Kanuites*.

The phylogenetic history of the Feliformia is relatively recent compared to the deeper Eocene roots of many Caniformia clades (e.g. Hunt, 1996; Nyakatura and Bininda-Emonds, 2012; Paterson et al., 2020) with diversification receiving three main pulses, the end Eocene, end Oligocene, and possibly a third within the last five million years (Figure 1). Even so, feliforms acquired broad morphology and ecology, from likely folivores, to durophages, and sabertooth morphs, the latter of which is not found within caniforms. Furthermore, feliforms, in contrast to caniforms, can be recognized by a distinctive auditory bulla morphology (often distinct per family) and a pattern of ontogenetic development that remains stable over a significant time interval in the middle and late Cenozoic. This basicranial morphology is fruitful ground for assessment of phylogenetic relationships as in the present study, even in the face of rapid evolution and dentognathic convergence of many clades. The present phylogeny used this information to generate a novel set of relationships among extinct taxa, while combining advances in molecular phylogenetic methods to produce the most expansive hypothesis to date. While not comprehensive, this phylogeny does inform on the relationships of “percrocitids” as derived hyaenids, the ancestry of the living African palm civet, *Nandinia* within the stenoplesictids, the origin of the earliest nimravids, and details of machairodontine tribal evolution. From these inferences, a benchmark for subsequent analyses is possible, but perhaps more importantly, a framework within which to assess aspects of the timing and rates of feliform trait evolution across a time-scaled phylogeny, one that includes thousands of posterior sampled

trees to incorporate phylogenetic uncertainty. To put it simply, we have barely begun to scratch the cat tree.

Chapter III

Ecological Evolution in the Feliformia

Introduction

The uneven distribution of niche occupation across the tree of life has been a central question of evolutionary biologists (Dobzhansky, 1951; Hutchinson, 1959). Adaptive radiations, in which a key adaptive feature allows a clade to speciate rapidly, have often been used to explain the dominance of members of a single lineage in a particular ecological role (Simpson, 1944, 1953; Schluter, 2000). Opportune events are thought to create high rates of evolution for a clade early in its history, evolutionary rates that quickly diminish as an ecospace is saturated. This pattern is typified by “early burst” models of evolution (Harmon et al., 2010), one among many growing analytical tools to assess evolutionary patterns. However, recent literature suggests early burst evolution is primarily observed within higher taxonomic levels while other forces operate upon lower ones, such as selection towards optimal phenotypic values or Brownian motion over geologic time (Slater, 2015; Law et al., 2018a; Slater and Friscia, 2019).

Yet, even within an adaptive radiation there appears to be limitations on what niches are filled/created. For example, why are there not more grazing ecologies amongst bovids and cervids following their late Miocene radiations, particularly with the spread of C4 grasslands (Cantalapiedra et al., 2013)? Horses famously developed traits that facilitated their grazing ecology through the Cenozoic (Matthew, 1926), including tall-crowned teeth (hypsodonty) with complex grinding surfaces, and a single toe (monodactyly) on an elongate limb. Though these traits may not be directly caused by expanding Cenozoic grasslands (Hansen, 1997; McHorse et

al., 2019), the comparative dearth of bovids and cervids with similar morphology and grazing ecology raises the question of why these clades did not radiate into this ecospace.

One possible explanation for biased ecospace exploitation relates to diet. It has been shown that there is a dietary transition bias associated with mammals, likely related to physiological challenges of switching to certain food types and energetic constraints of a given diet and body mass (Carbone et al., 1999; Price et al., 2012; Pineda-Munoz et al., 2016; Reuter, 2021). For example, the transition from herbivore to omnivore is far more common than omnivore to carnivore, and non-specialized insectivory is only feasible for an organism up to approximately 21 kg (Carbone et al., 2007). This latter point relates to a general decrease in dietary breadth at larger body size, where energetic constraints prevent exploitation of certain resources beyond a given size (McNab, 1986). Furthermore, phylogenetic baggage may not allow specific morphologies to efficiently utilize a given portion of ecospace, or at all. Even if a hypothetical phenotype can be produced it may not be actualized through functional restrictions, such as non-overlapping whorls in the shells of bivalves to produce a working hinge between the valves (Raup, 1966).

Amongst carnivorans, Law (2021) found patterns in head-body elongation ratios showed best-support for clade-based optimality shifts, and not models grounded in ecological traits, such as diet, locomotion or hunting behavior. Overall, living carnivorans have similar values in body shape, but certain clades possess clade-based radiations into stout (hyaenids and ursids) or elongate forms (weasels, genets and seals). This is suggestive of contingent opportunities leading to access of new ecospace with its own optimal trait value, and not that of rapid/broad occupation of ecospace that quickly decelerates. Conversely, Slater and Friscia (2019) found support for early burst patterns across living Carnivora for certain dental traits associated with

food processing, but not for body mass nor metrics of mechanical advantage in craniodental morphology. Together, this supports a decoupling, or differential selection, of size and shape evolution across Carnivora, and the importance of phylogenetic history

In this study, I test for the presence of adaptive radiations in body size and dental toolkit amongst living and fossil feliforms. The carnivoran clade Feliformia is an example of a group that has experienced a presumed bias in ecospace exploitation (Van Valkenburgh, 2007). Specifically, felids and nimravids seem to acquire their characteristic ‘cat-like’ morphology (e.g. foreshortened face, reduced dentition specializing in soft-flesh, retention of supinating/pronating forelimbs) in the earliest fossil forms and remain relatively unchanged until the present, or until their extinction, in the case of nimravids (Werdelin et al., 2010; Barrett, 2021). Why felids and nimravids did not come to occupy additional ecospace (save sabertooth ecomorphology), such as omnivory or even durophagy (bone-cracking as in hyenas) has remained a question many evolutionary biologists and paleontologists have asked (Radinsky, 1982; Holliday and Stepan, 2004; Van Valkenburgh, 2007; Chamoli and Wroe, 2011). The present study seeks to assess the evolutionary patterns of the Feliformia, and well-represented fossil clades. Were felids and nimravids examples of adaptive radiations that quickly occupied their adaptive zones, and if so, how did this differ from other feliform groups, such as hyenas, which occupied a far greater set of dietary and morphological ecologies? Furthermore, do small feliforms exhibit constraint in their evolution or facilitation because of the metabolic and functional discussion above? Below, I assess the patterns of living and extinct feliform ecological evolution with comparisons to differential evolutionary models. These include adaptive radiation, stabilizing selection, clade-based shifts and stochastic evolution. Finally, I offer a process-based framework for these patterns as a narrative of feliform evolutionary history.

Methods

Data Collection

I collected morphological measurements from fossil and living feliform specimens, as well as published values, from museums and literature as listed in Appendix C. Measurements were taken using Mitutoyo digital calipers to 0.01mm precision. Where possible, only wild-caught specimens were measured, though dental measurements were taken from some zoo animals for certain taxa to increase sample sizes. From these measurements, I calculated four ecomorphological traits (Figure 3, Table 3) that have been shown to describe morphology associated with food acquisition and processing in previous studies (Frischia et al., 2007; Meachen-Samuels and Van Valkenburgh, 2009; Slater, 2015; Slater and Friscia, 2019). Body masses (in grams) for living taxa were taken from the panTHERIA database (Jones et al., 2009), while I estimated body masses for fossil taxa from lower m1 lengths, using Van Valkenburgh's (1990) family-specific regression equations. Fossil hyenas posed their own unique problems, for the small number of living taxa do not express the entire ecological or morphological diversity of extinct members of the family (Werdelin and Solounias, 1991). For these extinct ecomorphs I used the ecological classification of Coca-Ortega and Pérez-Claros (2019) and analogous family-specific regression equations (e.g. canid, viverrid, bone-crushing hyaenid) of Van Valkenburgh (1990). Finally, for certain extinct taxa, robust reconstructions of body mass are available (Christiansen and Harris, 2005; Wheeler and Jefferson, 2009; Palmqvist et al., 2011), in which case, I used these values with source cited in Appendix C. I then converted mass estimates to a linear scale by taking their cube roots and subsequently natural log-transformed them for analysis. This was done to avoid negative values and conflict with R functions throughout the analysis.

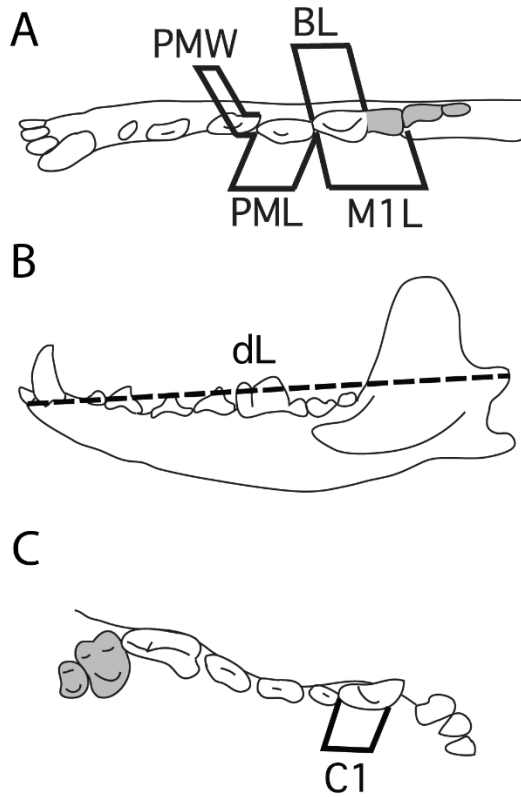


Figure 3. Measurements taken for ecomorphological traits. A: occlusal view of dentary and teeth. B: lateral view of dentary. C: occlusal view of upper dentition. PMW, lower fourth premolar width; PML, lower fourth premolar length; BL, blade length of lower first molar (trigonid); M1L, lower first molar length; dL, dentary length; C1, upper canine length. Modified from Slater and Friscia (2019: Fig. 1).

Table 3. Ecomorphological traits of analysis with abbreviations and constituent measurements.

Abbreviation	Meaning
C1	Compression of the upper canine, measured at the dentine-enamel junction as the mediolateral width divided by anteroposterior length
P4S	Robustness of the lower fourth premolar, measured as the maximum mediolateral width divided by maximum anteroposterior length
RBL	Relative blade length of the lower carnassial, measured as the anteroposterior ratio of trigonid length to overall m1 length
M1BS	m1 blade size relative to jaw length, measured as m1 trigonid length divided by length of dentary from anterior symphysis to posterior most portion of articular process
$\ln\sqrt[3]{mass}$	The natural logarithm of the cube root of mass, in grams

I classified each feliform species to one of five dietary/ecological categories (hypocarnivore, mesocarnivore, hypercarnivore, durophage, or sabertooth) using linear discriminant analysis (LDA) implemented in the ‘MASS’ (Venables and Ripley, 2002) package for R v. 4.0.3 (R Core Team, 2020). The training set consisted of the four ecomorphological traits listed in Table 3 (C1, P4S, RBL, M1BS) measured for 134 extant taxa (Appendix H). Non-feliform species were included because fossil feliforms exhibit more extreme adaptations to hypo- and mesocarnivory than is realized in the extant radiation. Extant caniform data was supplemented with extinct species from Slater and Friscia (Slater and Friscia, 2019). The first three dietary categories were

assigned to extant taxa using the cutoffs of Van Valkenburgh (Van Valkenburgh, 2007) and the Elton Traits dataset (Wilman et al., 2014) checked against the recent carnivoran ecological analysis of Hopkins et al. (2021). Hypercarnivorous feliforms were considered as having $\geq 70\%$ vertebrate material in the diet, mesocarnivore = 50-69% and hypocarnivore $\leq 40\%$ vertebrate material, modified from $\leq 30\%$ vert. of Van Valkenburgh (2007). *Crocota*, *Hyaena*, and *Dinocrocota* were assigned to durophages, as were “transitional and fully developed bone-crackers” from Coca-Ortega and Pérez-Claros (2019). *Dinocrocota* has much literature justifying a durophagous ecology (Tseng, 2009; Tseng and Binder, 2010), while the *Percrocota* taxa of this study do not and were thus classified using the canonical variates analysis of Coca-Ortega and Pérez-Claros (2019). Scimitar- and dirk-tooth taxa were assigned as sabertooth in the training set, while transitional scimitar- or dirk-tooth taxa were assigned by the LDA. Due to the fragmentary nature of much fossil material, I performed a series of discriminant analyses, iteratively reducing the number of variables to maximize species coverage. Classifications for highly fragmentary taxa were consistent with expectations based on congeners. The predicted categories for extinct taxa are available in Appendix H.

Analytical Methods

To understand the dynamics of body mass and carnassial evolution, I fit models of continuous trait evolution to a random sample of 500 trees from the post-burnin posterior distribution of the phylogenetic analysis of Chapter II. Constant-rate Brownian motion, temporally accelerating/decelerating rate (early burst), and trended random walk models were fitted using the ‘fitContinuous’ function in geiger (Pennell et al., 2014). I additionally fit two multipeak Ornstein-Uhlenbeck (OU) models. The first was an ecological OU model using the mvMORPH package (Clavel et al., 2015), while the second was a phylogenetic regime shift model using the

bayou package (Uyeda and Harmon, 2014). I limited the assessed OU evolutionary models to those possessing constant α (strength of pull) and σ^2 (evolutionary rate) terms; even though variable rate models do exist, simulations have shown unreliable inference for these models with phylogenies with a limited number of tips (Beaulieu et al., 2012). Measurement error was accounted for by including trait standard error in all evolutionary models. Because sample sizes were small for some species, I supplemented values for living taxa from Slater and Friscia (2019), while for poorly sampled extinct taxa I assigned each species a standard error of 0.0345, following Harmon et al. (2010). This was also the case for body mass standard error for all species, given that information is not included in the panTHERIA database. Relative model fit was assessed by computing small sample corrected Akaike Weights, AICcW. This was done for the entirety of the Feliformia, and subset analyses for the Felidae, Nimravidae, Hyaenidae and small feliforms.

Bayou uses a reversible-jump Markov chain Monte Carlo (MCMC) to fit multipeak OU models to estimate the placement and magnitude of regime shifts along lineages. This differs from the mvMORPH OU model by not assessing convergent evolution, but each shift is considered a unique adaptive regime (Uyeda and Harmon, 2014). Priors (Table 4) differed amongst the clades analyzed given the morphological breadth observed for body mass and RBL values.

Table 4. Priors for bayou analyses. Model parameter α = strength of pull, σ^2 = evolutionary rate, θ = optimal value. *= Calculated using ‘cdpois’ option in bayou. RBL = relative blade length of the lower m1.

Model Parameter	Feliformia body mass	Feliformia RBL	Felidae body mass	Felidae RBL	Nimravidae body mass	Nimravidae RBL
α	Half-cauchy with scale factor 1	Half-cauchy with scale factor 1	Half-cauchy with scale factor 1	Half-cauchy with scale factor 1	Half-cauchy with scale factor 1	Half-cauchy with scale factor 1
σ^2	Half-cauchy with scale factor 0.1	Half-cauchy with scale factor 0.1	Half-cauchy with scale factor 0.1	Half-cauchy with scale factor 0.1	Half-cauchy with scale factor 0.1	Half-cauchy with scale factor 0.1
θ	Normal distribution with standard deviation = 1.3*sd of mass data, mean = mean of mass data	Beta distribution with shape 1 = 5 and shape 2 = 1	Normal distribution with standard deviation = 0.75*sd of mass data, mean = mean of mass data	Beta distribution with shape 1 = 5 and shape 2 = 1	Normal distribution with standard deviation = 0.5, mean = mean of mass data	Beta distribution with shape 1 = 5 and shape 2 = 1

Table 4. Continued for Feliformia, Felidae and Nimravidae.

Model Parameter	Feliformia body mass	Feliformia RBL	Felidae body mass	Felidae RBL	Nimravidae body mass	Nimravidae RBL
Number of shifts per branch	Fixed at one	Fixed at one	Fixed at one	Fixed at one	Fixed at one	Fixed at one
Branch-wise shift probability	Uniform	Uniform	Uniform	Uniform	Uniform	Uniform
Number of shifts	Conditional Poisson distribution* with mean = $0.1 \times \text{number of edges on phylogeny}$ and maximum = number of tips of phylogeny	Conditional Poisson distribution* with mean = $0.1 \times \text{number of edges on phylogeny}$ and maximum = $2 \times \text{number of edges of phylogeny} - 2$	Conditional Poisson distribution* with mean = $0.1 \times \text{number of edges on phylogeny}$ and maximum = number of tips of phylogeny	Conditional Poisson distribution* with mean = $0.1 \times \text{number of edges on phylogeny}$ and maximum = $2 \times \text{number of edges of phylogeny} - 2$	Conditional Poisson distribution* with mean = $0.1 \times \text{number of edges on phylogeny}$ and maximum = number of tips of phylogeny	Conditional Poisson distribution* with mean = $0.1 \times \text{number of edges on phylogeny}$ and maximum = number of tips of phylogeny
Location of shift along branch	Uniform	Uniform	Uniform	Uniform	Uniform	Uniform

Table 4. Continued for Hyaenidae and small feliforms.

Model Parameter	Hyaenidae body mass	Hyaenidae RBL	Small feliform body mass	Small feliform RBL
α	Half-cauchy with scale factor 1	Half-cauchy with scale factor 1	Half-cauchy with scale factor 1	Half-cauchy with scale factor 1
σ^2	Half-cauchy with scale factor 0.1	Half-cauchy with scale factor 0.1	Half-cauchy with scale factor 0.1	Half-cauchy with scale factor 0.1
θ	Normal distribution with standard deviation = 0.3, mean = mean of mass data	Beta distribution with shape 1 = 5 and shape 2 = 1.5	Normal distribution with standard deviation = 0.75*sd of mass data, mean = mean of mass data	Normal distribution with standard deviation = 0.75*sd of RBL data, mean = mean of RBL data
Number of shifts per branch	Fixed at one	Fixed at one	Fixed at one	Fixed at one
Branch-wise shift probability	Uniform	Uniform	Uniform	Uniform
Number of shifts	Conditional Poisson distribution* with mean = 0.1*number of edges on phylogeny and maximum = number of tips of phylogeny.	Conditional Poisson distribution* with mean = 0.1*number of edges on phylogeny and maximum = 2*number of edges of phylogeny -2.	Conditional Poisson distribution* with mean = 6 and maximum = number of tips of phylogeny.	Conditional Poisson distribution* with mean = 0.1*number of edges on phylogeny and maximum = 2*number of edges of phylogeny -2.
Location of shift along branch	Uniform	Uniform	Uniform	Uniform

I ran two independent MCMC chains with 1.5 million generations, each sampled every 1,000 generations for the full Feliformia phylogeny. These family-level phylogenies ran for 500,000 generations, with sampling at every 500. Convergence was assessed using Gelman and Rubin's R statistic via the 'gelman.R' function in bayou (Uyeda and Harmon, 2014). R values <1.1 were considered to have reached convergence, and samples prior to this were discarded as burn-in. Effective sample sizes were greater than 200 for all analyses, and frequently over 1,000. Only evolutionary shifts with a posterior probability (PP) above 0.5 using parameters averaged from the two chains were considered in subsequent analyses. To compare the results of the bayou model to that of the likelihood-based geiger and mvMORPH models, I converted the bayou output using the 'bayou2OUwie' function (Uyeda and Harmon, 2014). Clades identified via bayou for adaptive shifts were then assessed by a comparable OUM model in mvMORPH. The relative AICc weights of all models were then compared for best fit.

Results

Feliformia

The distribution of ecological variables can be seen in Figure 4. An Ornstein–Uhlenbeck (OU) for multiple dietary optima is the best-fitting evolutionary model for both body mass and RBL for the Feliformia, (Table 5, median AICcW = 0.49 for body mass and 1.0 for RBL). Body mass sees a general increase in optimal value progressing from hypocarnivore to sabertooth ecology, with the largest jump between hypercarnivore and durophagous. Carnivores are predicted to switch to hunting of large vertebrate prey at around 14.5-21 kg (Carbone et al., 2007), with prey of equal or larger mass than their own at a subsequent 21.5-25 kg (Carbone et al., 1999). The

hypercarnivore optimum is here inferred to be 11.32 kg. This was smaller than that observed by Slater (Slater, 2015) for living and extinct canids (median = 20.7 kg). A smaller optimal mass of 1.28 kg was estimated for hypocarnivory, but a larger mass of 16.55 kg for mesocarnivory (Table 5). However, both durophagous and sabertooth ecologies returned comparable and very large optimal body masses, with 173.62 kg for the former, and 179.11 kg for the latter.

The α -parameter of OU models describes the strength of attraction to the associated optima, with higher values indicating a stronger pull. This value can be reparametrized in terms of phylogenetic half-life, $t_{1/2} = \ln(2)/\alpha$, which describes the time required for adaptation to a new selective regime to outpace implied constraints of an ancestral regime (Hansen, 1997). The phylogenetic half-life of the median estimated α -parameter for body mass is approximately 10 million years (My). This implies strong and rapid selective pressure towards an optimal body mass given a dietary category.

Relative blade length of the m1 is also best explained by an adaptive peak model (median AICcW = 1.0, Table 5). This model predicts a median optimal relative blade length of 0.50 for hypocarnivorous feliforms, while mesocarnivorous feliforms are attracted to a slightly greater relative blade lengths of 0.54. Hypercarnivorous, durophagous, and sabertooth feliforms are all attracted to relative blade lengths of approximately 1.0. These latter two dietary ecologies in fact returned optimal values greater than 1.0. Though biologically impossible, the assessed OUM model could not be constrained for possible optimal ranges, and thus suggests even stronger attraction to total slicing component of the m1 than is observed in hypercarnivorous feliforms that do not have durophagous or sabertooth morphology.

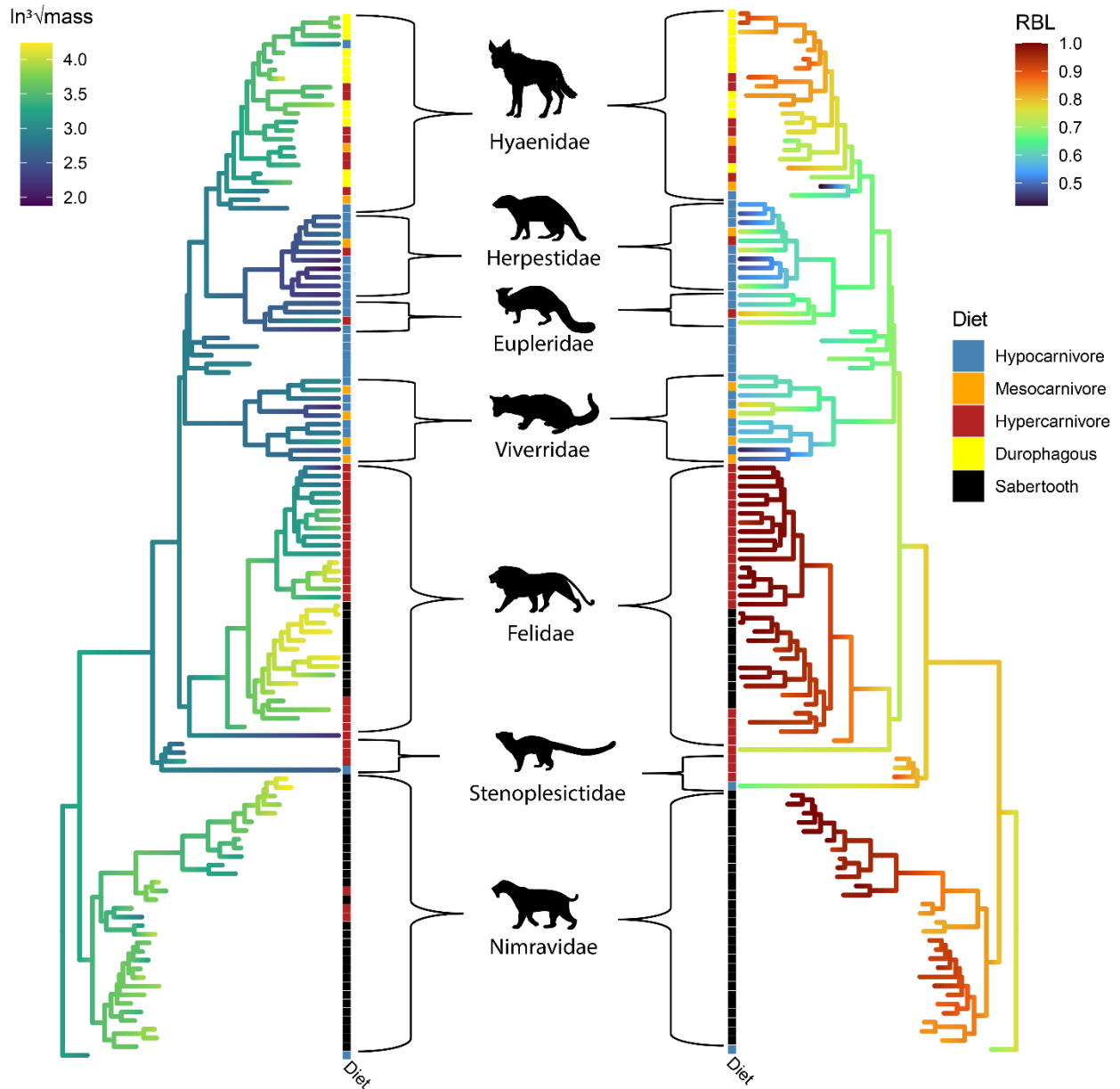


Figure 4. Distribution of ecological proxy variables used in the presented analysis, natural log of the cube root of body mass in grams, left, and the relative blade length of the lower m1, right. Ancestral states for both body mass and relative m1 blade length were estimated using the ‘fastANC’ function found in ‘phytools’ (Revell, 2012) on the MCC tree of Chapter II. Silhouettes taken from phylopic.org or created by the author.

Likewise, to optimal body mass values, the median estimated α -parameter (0.040) for relative m1 blade length implies strong selection for these values, but not as strong as bodymass, $t_{1/2}$ = 17.3 My. However, this value does approximate the divergence of major feloid clades, 15-31 Ma, suggesting the primary pull of RBL selection began at the clade's appearance and has been sustained since.

Felidae

In contrast to overall feliform evolution, felid body mass was best explained by a model of Brownian motion (AICcW = 0.62). This was approximately three times higher in weight than the next best supported model, trended evolution, AICcW = 0.20, while an early burst model received only slightly less support than this, AICcW = 0.18. Both OUM models were the poorest supported with no node returned 0.5 or greater PP for the bayou analysis.

RBL evolution was best explained by an early burst model (AICcW = 1.0). This suggests that initial high rates of evolution for a clade exponentially decay over time as a new niche becomes available, but then is quickly saturated (Blomberg et al., 2003; Harmon et al., 2010). The scalar value for this model ($r = -13.98$) describes the deceleration of evolution, as expected by a hypothesis of adaptive radiation. The very large and negative value gives a feel for the rapidity of this burst, one that is several orders of magnitude greater than found in estimates of overall feliform RBL evolution under an early burst model, and indeed in large clades of other analyses (Harmon et al., 2010).

Table 5. Median results from macroevolutionary model fits to 500 random trees from the stable Bayesian posterior of the phylogenetic analysis in Chapter II. Mass has been converted to kgs. OUM_{bayou} did not recover a shift at any location with over 0.5 PP for RBL.

Trait	Model	lnLk	AICc	AICcW	σ^2	Scalar	Hypo-carnivore	Meso-carnivore	Hyper-carnivore	Durophagous	Sabertooth
<i>lnV^{3/4}mass</i>	BM	-33.76	71.62	0.02	0.013	-	-	-	-	-	-
	ACDC	-33.32	72.85	0.13	0.019	-0.012	-	-	-	-	-
	Trend	-33.98	74.16	0.01	0.013	0.002	-	-	-	-	-
	OUM _{diet}	-22.80	62.89	0.49	0.018	0.067	1.28	16.55	11.32	173.62	179.11
	OUM _{bayou}	-31.96	76.66	0.34	0.014	0.018	-	-	-	-	-
RBL	BM	-33.76	71.62	<0.01	0.013	-	-	-	-	-	-
	ACDC	145.17	-284.12	<0.01	7.5 ⁻⁴	-0.013	-	-	-	-	-
	Trend	145.79	-285.37	<0.01	5.2 ⁻⁴	0.002	-	-	-	-	-
	OUM _{diet}	159.32	-301.29	1.0	0.018	0.040	0.50	0.54	0.97	1.02	1.09
	OUM _{bayou}	-	-	-	-	-	-	-	-	-	-

Table 6. Median Felidae results from macroevolutionary model fits to 500 random trees from the stable Bayesian posterior of the phylogenetic analysis in Chapter II. Mass has been converted to kgs. OUM_{bayou} did not recover a shift at any location with over 0.5 PP for body mass.

Trait	Model	lnLk	AICc	AICcW	σ^2	Scalar	Hypercarnivore	Sabertooth
<i>ln³mass</i>	BM	-8.00	20.43	0.62	0.014	-	-	-
	ACDC	-8.05	22.98	0.18	0.011	0.016	-	-
	Trend	-8.06	23.00	0.20	0.014	-0.002	-	-
	OUM _{diet}	-8.21	38.97	<0.01	0.017	0.030	5.63	1788.15
	OUM _{bayou}	-	-	-	-	-	-	-
RBL	BM	-7.98	20.39	<0.01	0.014	-	-	-
	ACDC	6808.59	-13610.30	1.0	7.6^{-218}	-13.98	-	-
	Trend	5213.70	-10420.50	<0.01	7.1^{-218}	-2.5^{-18}	-	-
	OUM _{diet}	297.69	-572.83	<0.01	0.016	0.112	1.0	1.0
	OUM _{bayou}	462.74	-913.09	<0.01	1.8^{-33}	0.112	-	-

Nimravidae

Similar to felids, the best supported evolutionary models for nimravid body mass and RBL was Brownian motion and early burst respectively, Table 7. However, the relative support of a Brownian motion model for body mass over the next best supported model was not as great as in the Felidae, BM AICcW = 0.52, ACDC = 0.32. Additionally, the sigma squared parameter, which can be interpreted as the net rate of evolution (Harmon et al., 2010) was the same as in both nimravid and felid analyses. This suggests similar overall rates of body mass evolution even over different persistence times for each clade (Nimravidae = 34.3 Ma, Felidae = 18.9 Ma). RBL evolution for nimravids is also best explained by an early burst model (AICcW = 1.0). The rate parameter for this model is even greater than that inferred for felid evolution ($r = -16.68$), implying a very rapid decrease in evolutionary rates beyond an initial adaptive radiation.

Hyaenidae

Hyaenid ecological evolution returned similar results to the overall Feliformia, such that body mass and RBL evolution was best supported by an OU model for multiple dietary optima (Table 8), median AICcW = 0.95 for body mass and 0.48 for RBL). Body mass also sees an increase in optimal value progressing from hypocarnivore to durophagous ecology compared to overall Feliformia. The hypercarnivore optimum for hyaenids is inferred to be 25.46 kg. This is quite similar to that observed by Slater (Slater, 2015) for canids as mentioned previously, but the additional optimal values for hypo- and mesocarnivorous hyaenids (median optima = 3.19 kg, 16.11 kg respectively) are also quite similar to that observed by Slater for living and fossil canids, (hypo. = 3.2 kg and meso. = 4.7 kg). Durophagous hyaenids returned the largest optimal mass at 64.98 kg, similar to living *Crocota* but less than that estimated in the overall feliform analysis. The phylogenetic half-life of the α -parameter for body mass returned the shortest value

of all analyses at 1.96 My. This implies extremely strong selective pressure towards an optimal body mass given a hyaenid dietary category.

Relative blade length of the m1 is also best explained by an adaptive peak model (median AICcW = 0.48, Table 8), but only moderately better supported than the next best model, early burst (AICcW = 0.27). The adaptive peak model predicts a median optimal relative blade length of 0.69 for hypocarnivorous hyaenids, while mesocarnivorous hyaenids are attracted to substantially smaller relative blade lengths of 0.44. Hypercarnivorous and durophagous hyaenids are all attracted to relative blade lengths closer to 1.0 (hyper. = 0.78, duro. = 0.86), but substantially less in value than seen in all other analyses. The α -parameter for RBL values also displayed a high attractive force (median = 0.348), $t_{1/2}$ = 1.99 My compared to body mass estimates, but slightly smaller.

Small feliforms

Unique amongst all analyses, small feliforms found best support for Brownian motion in both RBL and body mass evolution, Table 9. The relative support of these models was about twice as great as the next best models, ACDC for the former and trended evolution for the latter. The sigma squared parameter for body mass evolution (0.008) was less than that in both nimravid and felid analyses, about half as large. This suggests that body mass evolution occurs at a slower pace amongst small feliforms, though expected given their overall amount of variance in this variable. The sigma squared value for RBL evolution (0.008) is about half of that inferred for other analyzed clades, also implying relatively slower rates of evolution for the dental toolkit.

Table 7. Median Nimravidae results from macroevolutionary model fits to 500 random pruned trees from the stable Bayesian posterior of the phylogenetic analysis in Chapter II. Mass has been converted to kgs. OUM_{bayou} did not recover a shift at any location with over 0.5 PP for body mass or RBL.

Trait	Model	lnLk	AICc	AICcW	σ^2	Scalar	Hypercarnivore	Sabertooth
<i>ln³mass</i>	BM	-3.82	12.06	0.52	0.014	-	-	-
	ACDC	-3.76	14.37	0.32	0.018	-0.023	-	-
	Trend	-3.64	14.14	0.15	0.014	0.013	-	-
	OUM _{diet}	-1.19	24.64	<0.01	0.023	0.139	3.89	61.44
	OUM _{bayou}	-	-	-	-	-	-	-
RBL	BM	-3.82	12.06	<0.01	0.014	-	-	-
	ACDC	938.19	-1869.38	1.0	2.0 ⁻⁷¹	-16.677	-	-
	Trend	55.36	-103.73	<0.01	1.3 ⁻⁴	0.005	-	-
	OUM _{diet}	54.22	-98.71	<0.01	0.023	0.034	-	1.0
	OUM _{bayou}	-	-	-	-	-	-	-

Table 8. Median Hyaenidae results from macroevolutionary model fits to 500 random trees from the stable Bayesian posterior of the phylogenetic analysis in Chapter 2. Mass has been converted to kgs. OUM_{bayou} did not recover a shift at any location with over 0.5 PP for body mass or RBL.

Trait	Model	lnLk	AICc	AICcW	σ^2	Scalar	Hypo-carnivore	Meso-carnivore	Hyper-carnivore	Durophagous
<i>ln³Vmass</i>	BM	-3.38	11.36	0.03	0.012	-	-	-	-	-
	ACDC	-3.52	14.29	0.01	0.017	-0.041	-	-	-	-
	Trend	-2.79	12.85	0.01	0.011	0.021	-	-	-	-
	OUM _{diet}	7.06	12.16	0.95	0.023	0.353	3.19	16.11	25.46	64.98
	OUM _{bayou}	-	-	-	-	-	-	-	-	-
RBL	BM	-3.38	11.36	0.25	0.012	-	-	-	-	-
	ACDC	24.41	-41.41	0.27	0.003	-0.135	-	-	-	-
	Trend	23.03	-38.66	<0.01	0.001	0.006	-	-	-	-
	OUM _{diet}	34.36	-40.73	0.48	0.023	0.348	0.69	0.44	0.78	0.86
	OUM _{bayou}	-	-	-	-	-	-	-	-	-

Table 9. Median small feliform results from macroevolutionary model fits to 500 random trees from the stable Bayesian posterior of the phylogenetic analysis in Chapter 2. Mass has been converted to kgs. OUM_{bayou} did not recover a shift at any location with over 0.5 PP for body mass or RBL.

Trait	Model	lnLk	AICc	AICcW	σ^2	Scalar	Hypo-carnivore	Meso-carnivore	Hyper-carnivore
<i>ln³mass</i>	BM	-8.29	20.96	0.51	0.008	-	-	-	-
	ACDC	-8.39	23.58	0.29	0.008	-3.0 ⁻⁴	-	-	-
	Trend	-7.52	21.84	0.18	0.008	-0.011	-	-	-
	OUM _{diet}	-4.18	30.13	0.01	0.015	0.094	1.73	19.85	1.83
	OUM _{bayou}	-	-	-	-	-	-	-	-
RBL	BM	-8.29	20.96	0.46	0.008	-	-	-	-
	ACDC	30.23	-53.66	0.22	0.001	0.0134	-	-	-
	Trend	31.02	-55.25	0.30	0.001	-0.004	-	-	-
	OUM _{diet}	35.62	-49.48	0.03	0.015	0.142	0.59	0.65	0.79
	OUM _{bayou}	-	-	-	-	-	-	-	-

Discussion

Overall, feliform ecological evolution is pulled towards optima related to dietary category. However, clade-specific patterns suggest far more nuance in evolutionary history. Both nimravids and felids experienced an adaptive radiation (early burst) with entrance into hypercarnivore and sabertooth ecologies, while body mass evolution of these clades is best supported by a random walk over geologic time. The processes behind adaptive radiations are often hypothesized to relate to the development of ‘key innovations’ or contingent historical events that facilitate diversification by creating new ecological opportunities (Schaeffer, 1948; Van Valen, 1971; Gould, 1989; Sanderson and Donoghue, 1994; Hunter and Jernvall, 1995; Slater, 2015). Though it may be more straightforward to correlate the acquisition of a given morphologic feature with an adaptive radiation, the nature of contingent events implies chance opportunities such as sweepstakes dispersals or climatic change that generates a land bridge due to falling sea levels. These are events that if we were to “rewind the tape” (Gould, 1989) may not happen again. However, there are theoretical frameworks that, although unable to predict a given climatic or tectonic event, offer utility in predicting the biotic response to such a perturbation. For example, under Habitat Theory (Vrba, 1992) most speciation and extinction events are correlated to global tectonic and/or climatic changes, while common climatic fluctuations typically drive geographic habitat tracking as species move with their biome if possible. Furthermore, at times of global warming with a strong latitudinal thermal gradient, Habitat Theory predicts higher speciation rates at lower latitudes and higher extinction rates at higher latitudes. This principle is related to the habitat preference of specialist clades where resources would tend to disappear during recurrent environmental extremes. Though challenged for certain African Pliocene taxa (Bobe et al., 2002; Werdelin and Lewis, 2005; Frost, 2007; Faith and

Behrensmeyer, 2013), Habitat Theory may still provide a useful framework for global dynamics of the Cenozoic.

One assumption in the application of Habitat Theory to the fossil record is that clades, generally speaking, have maintained habit preference, or in other words, that the fundamental habit of a clade has changed minimally over geologic time. Most living feliforms, including felids, hyenas, mongooses, civets, and genets are found in tropical regions, while most terrestrial caniforms reside within temperate or seasonal climatic regions (Pickford and Morales, 1994; Hunt, 1996). This differential climatic signal is even found in the cranial shape of feliforms versus caniforms, where mean precipitation and temperature are significant predictors of cranial shape in feliforms, but not caniforms (Tseng and Flynn, 2018). The divergence time of the most recent common ancestor (MRCA) of nimravids for the phylogeny presented in Chapter II is suggested to be at approximately 41.3 Ma. Even the earliest nimravids are known to possess hypercarnivorous dentition, but based on phylogenetic analysis, and the results of the presented chapter, quickly derived this dental condition from more generalist feliforms present in the middle to early Eocene (Solé, 2014; Tomiya and Tseng, 2016; Barrett et al., 2021). The above MRCA date occurs slightly after the Middle Eocene Climatic Optimum (Zachos et al., 2001). This period of global warming is associated with an increase in hypercarnivory amongst mammals in North America (Tomiya et al., 2021), but also in the earliest Asian nimravid material (Chow, 1958; Peigné et al., 2000; Averianov et al., 2016). Nimravids likely originated in Asia, as did the earliest feliforms (Hunt, 1996, 1998a). If nimravids were also tropical specialists, the spread of this clade into North America would be predicted by Habitat Theory. As the thermal gradient extended northward during the Middle Eocene Climatic Optimum (Figure 5), nimravids would have found dispersal easier via northern passages into North America. Tropical specialists would

also benefit from increased speciation rates during this time, as seen in Figure 1, though it is unclear if this provided the impetus for the rapid development of hypercarnivory within this clade and non-carnivorans. Hypercarnivory amongst mammals appears to have experienced a process of slow assembly within the Cenozoic. One that didn't develop the familiar secant dentition and reduced tooth count until the Early to Middle Eocene in oxyaenodontan, hyaenodontan and carnivoramorphan taxa (Borths et al., 2016; Solé and Ladevèze, 2017). However, hypercarnivorous members of the above clades all seem to have rapidly acquired this dental toolkit during this epoch. Nimravids arrival in North America is also associated with rapid acquisition of sabertooth morphology compared to Asian ancestors, e.g., *Maofelis*. Compressed and serrated canines are known from the Hancock mammal quarry of Oregon (~40 Ma, Hanson, 1996), and a c.f. *Hoplhoneus* maxilla (San Diego Natural History Museum 60554) from the Pomerado conglomerate of San Diego (ca. 38-37 Ma). These first nimravids would have encountered large hyaenodont and mesonychid hypercarnivores (e.g. *Hyaenodon*, *Hemipsalodon*, *Harpagolestes*). Perhaps the rapid acquisition of sabertooth morphology allowed nimravids a way to access a greater variety of prey resources while staying relatively small in the presence of potentially competing non-carnivoramorph hypercarnivores. What's more, following the loss of sabertooth machaeroidines prior to the Middle Eocene Climatic Optimum (Zack et al., 2022), an opportunity may have presented itself for a new lineage to create or occupy a similar ecology in North America.

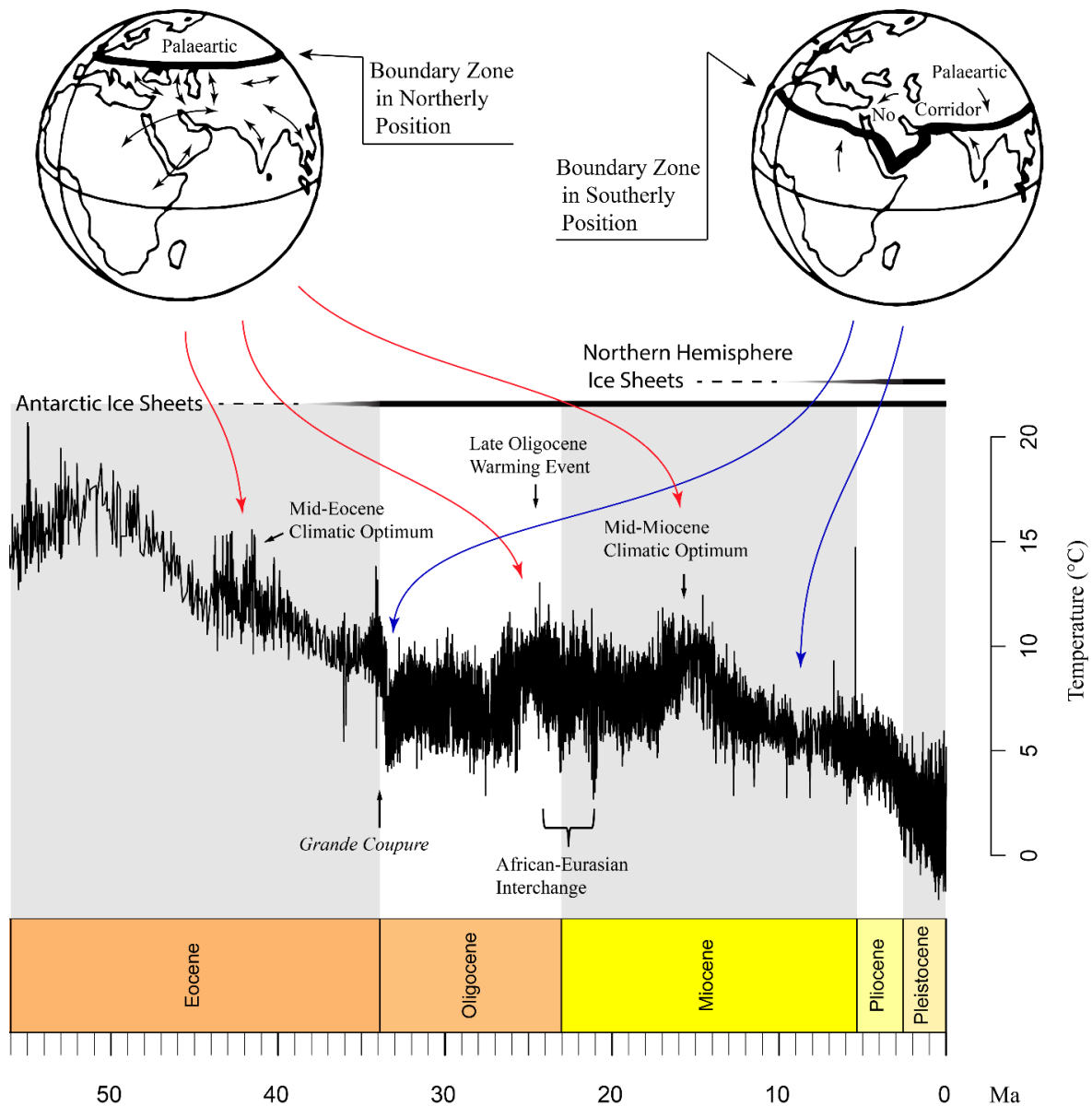


Figure 5. Latitudinal boundary shift of tropical and boreal climate zones from the Eocene to the present. Climate gradient modified from Pickford and Morales (1994), Fig. 5. Global climate data from Zachos et al. (2008), where absolute temperatures were converted from $\delta^{18}O$ using the equation of Epstein et al. (1953). Climatic events are annotated above temperature curve while biogeographic events below curve. Note global geography depicts the modern arrangement, approximately Miocene to present.

Though unanalyzed at the clade level for ecological evolution, stenoplesictids are the earliest known feloids (save perhaps palaeogalids with a Chadronian occurrence, Famoso and Orcutt, 2022) with a Late Eocene occurrence in Mongolia (Dashzeveg, 1996; Hunt, 1998a). The diversity and morphology of this clade is poorly known until the start of the Oligocene when a diversity of forms arise and spread into Europe. In fact, the earliest known feloids of the Oligocene are found at Quercy (France) at the Eo-Oligocene transition along with nimravids (Hunt, 1998a). This sudden European appearance is likely related to the *Grande Coupure*, an event with substantial faunal turnover and associated immigration of Asian taxa into Europe. The *Grande Coupure* was during a time of global cooling associated with Antarctic ice sheet formation (Zachos et al., 2001). Costa et al. (2011) summarize several theories for this event and the replacement of European taxa, but sea level drop with the formation of the Antarctic icesheet likely facilitated a land bridge to Europe to aid the dispersal of Asian taxa. Stenoplesictids are also known in Mongolia post-*Grande Coupure*, along with palaeogalids and nimravids, though there is a distinct lag (~2 Ma) between the first Oligocene geographic radiation and following feloid diversification (Dashzeveg, 1996; Hunt, 1998a). The latitude of both France and Mongolia are approximately at 45 degrees north, being substantially outside the tropics of today, combined with the rapid global cooling at the formation of Antarctic ice sheets, it would be expected under Habitat Theory to see a retraction of tropical specialists to the equator during this time, while biome generalists would be relatively unaffected. However, recent data suggests that high-latitude temperatures may have been almost as warm as those pre-Antarctic glaciation (O'Brien et al., 2020). This is hypothesized to be in part related to the lack of a northern ice sheet. Additionally, the East Asian record of mid-late Eocene and early Oligocene carnivoramorpha is quite poor (Ducrocq et al., 1995; Wang et al., 2007; Böhme et al., 2013). This suggests the taxa

that did immigrate into Europe during the *Grande Coupure* were relatively unencumbered by the global cooling at this period, either to being biome generalists or being in a high-latitude climate warmer than previously hypothesized but did not experience the boost in speciation rates associated with a warming climate as predicated under habitat theory. In fact, an increase in overall feloid diversity isn't seen for two million years after the event which does follow a rapid warm excursion immediately after the initial cold excursion of the Eo-Oligocene transition (Zachos et al., 2001).

The Oligocene saw rapid diversification of nimravid species (Barrett, 2021), but also in those of stenoplesictids and palaeogalids (Hunt, 1998a; Peigné, 1999; Peigné and De Bonis, 1999; Hunt, 2001a; Welsh, 2021; Famoso and Orcutt, 2022). Ecologically, save the living African Palm Civet (*Nandinia*), all analyzed stenoplesictids are hypothesized to be hypercarnivorous feliforms, though not derived to the degree seen in contemporary nimravids, nor in later hyaenids or felids. This suggests that the global faunal turnover of the Eo-Oligocene transition may have provided a large opportunity (contingent event) for Feliform diversification, as supported by the nimravid-specific RBL analysis of this chapter, though not yet assessed at the clade level for stenoplesictids nor palaeogalids.

The end of the Oligocene saw rapid global warming that was sustained into the early Miocene. Much like the *Grande Coupure* before it, another mass immigration event occurred, the African-Eurasian interchange. This event saw the immigration of African endemic species out of Africa, such as proboscideans, while Eurasian taxa including carnivorans and ungulates into Africa. However, there is a bias in what species immigrated and subsequently diversified. For example, feliforms were the dominant carnivorans to immigrate into Africa, while caniforms are only represented by two species (Pickford and Morales, 1994). For African immigrants,

proboscideans, hyracoids and aardvarks were the only groups to find substantial success when leaving Africa, likely beginning in the latest Oligocene (Lucas and Bendukidze, 1997; Antoine et al., 2003; Sen, 2013).

Habitat Theory would predict large-scale immigration of tropical biome specialists (i.e., most feliforms) to the newly accessible landmass with the same fundamental habitat within which they currently reside, especially during a period of global warming (Figure 5). It would also predict the exclusion of boreal, or Palearctic in this case, species from Africa, possibly related to differential reproductive strategies as influenced by seasonality and day length changes. At high latitudes, temperature and day length fluctuations are the greatest signals of seasonality, while at low latitudes these same fluctuations are minor and humidity changes dominate, lending the tropics to wet/dry seasonality (Pickford and Morales, 1994). Nimravids were perhaps the first carnivorans that arrived in Africa, presumably from Asia, given the lack of known European nimravid material of this age (Frischia et al., 2020; Barrett et al., 2021; Werdelin, 2021).

However, a diversity of stenoplesictid, and stem feloid taxa also immigrated to Africa around the same time (Pickford and Morales, 1994; Morales and Pickford, 2021). This period (~25-20 Ma) correlates with an increase in speciation rate in the skyline plot of Figure 1; the divergence of hyaenids from herpestid/euplerid ancestors, the origin of felids, the origin and diversification of lophocyonids, and initial diversification of the Barbourfelini. In short, a great diversification of feliform taxa occurred resulting in the origin of most living families.

By 16 Ma, the earth would enter the Middle Miocene Climatic Optimum (Figure 5), the last excursion into a warming planet before a steady decline into the cooler and more familiar northern and southern icesheet driven system of the present (Zachos et al., 2001). With the rise in global temperatures, one would expect a correlated rise in feliform diversity under Habitat

theory. In fact, the phylogeny of Chapter II (Figure 2), recovers this as the MRCA for the extant radiation of viverrids and herpestids + euplerids, and the divergence of machairodontine felids from felines + pantherines. These values are further supported by the analysis of Slater and Friscia (2019) on a more inclusive taxon set of extant species. Globally, there is also a large increase in Mammalian diversity during the middle Miocene, including that of feliform taxa (Alroy, 1992; Pickford and Morales, 1994; Morales and Pickford, 2011; Grohé et al., 2020; Wang et al., 2020; Morales and Pickford, 2021). The present analysis found felid dietary evolution was best supported by an early burst model (Table 6); this was also the case for RBL evolution of viverrids and euplerids in Slater and Friscia (2019), inclusive of almost all living species. The latter finding for euplerids is perhaps no surprise as they are one of the most exemplary clades for contingency, with a highly supported sweepstakes dispersal to Madagascar from the African mainland (Yoder et al., 2003). Thus, it is no additional surprise that nearly all variables analyzed by Slater and Friscia (2019) found an early burst model as the best supported for euplerid evolution.

The remaining feliform clades, herpestids and hyaenids, show patterns of ecological evolution better explained by other processes. Herpestids have the most recent origin among the feliform clades, likely in Africa with a single Asian immigration event (Wesley-Hunt et al., 2010; Zhou et al., 2017). Slater and Friscia (2019) found both RBL and body mass evolution in herpestids was best supported by an OU model of evolution, suggesting there is an optimal value the clade was either constrained to, or pulled towards, and not an adaptive radiation. Furthermore, there appears to be no obvious correlation in global temperature at the extant herpestid origin (Zachos et al., 2001). Similarly, hyaenids seem drawn towards optimal body mass and dental toolkits, though the present analysis finds these values are correlated to a given dietary category. This is

the same result that was found by Slater (2015) for canid evolution, though a durophagous category was not included in that study. The analogy between canid and hyaenid evolution has been made before, where hyaenids are the Old World ecological analogs to the New World canids (Hunt, 1996; Van Valkenburgh, 2007; Tseng and Wang, 2011), and thus the results of this work offer a new line of inference on convergent evolution between these clades.

Both hyaenids and canids found remarkably similar optimal body mass (save mesocarnivory) per dietary category (Table 10). However, the inferred phylogenetic half-life for these optima differed by two orders of magnitude for hyaenids and canids, 1.96 Ma to 936 Ma respectively. For hyaenids this suggests an incredibly strong pull towards optimal values within a given category, but for canids, such weak attraction was better interpreted as a slow, sustained trend in increased body mass across all three dietary categories, an assessment supported by the next best supported model of Slater (2015), trended random walk. Relative blade length of m1 was not assessed by Slater (2015), but relative lower grinding area (RLGA) was, being another proxy for dental toolkit, and by extension diet. Higher values for this proxy indicate a greater grinding proportion (compared to slicing), and unsurprisingly optimal values from hypo- to hypercarnivory show a progressive decline in RLGA. Hyaenids show a similar pattern in reducing the grinding component with increased hypercarnivory. However, values for hypo- and mesocarnivory in hyaenids seemed backwards, such that hypocarnivory had greater optimal RBL values than mesocarnivory. This may be explained by the trigonid not necessarily being dedicated to a slicing function amongst carnivorans and instead being modified to a grinding or puncturing (in the case of arthropod food items) component like the talonid behind it. Thus, retaining a large trigonid, as in *Plioviverrops*, would be functionally advantageous. Closer inspection of the total grinding versus slicing component of the dental toolkit in hyaenids and

canids shows distinct differences. Specifically, there is a substantially greater grinding component retained in hypercarnivorous canids than hyaenids, even though the pull towards each clade’s optimal dietary value was comparably strong, $t_{1/2}$ = 1.99 Ma for hyaenids and 3.85 Ma for canids. This distinction may result from phylogenetic constraint unique to each clade, especially in the context of dental morphology and diet (Hopkins et al., 2021). This constraint has been hypothesized for durophagy in the two clades where the retention of posterior molars may have resulted in the shift of bone-crushing teeth/cusps in borophagine canids to the anterior P4 and lower m1 compared to that of non-carnassial premolars in hyaenids whom otherwise lose the posterior molars (Tseng and Wang, 2011).

Table 10. Median optimal body mass (in kg) values from model fits of 500 random trees from the stable Bayesian posterior of the phylogenetic analysis for hyaenids of the present analysis and that of canids in Slater (2015).

	Hypocarnivore	Mesocarnivore	Hypercarnivore
Hyaenidae	3.19	16.11	25.46
Canidae	3.19	4.71	20.70

A core concept of adaptive radiations has been an initial rapid diversification and phenotypic evolution that “...fit the divergent environments they exploit” (Schluter, 2000). I subsequently assessed this evolutionary pattern via early burst models of decelerating rates of phenotypic evolution. The underlying process behind these patterns is primarily explained by the work of Simpson (1944, 1953) where high rates of evolution are required to move through nonadaptive realms of the adaptive landscape to new stable realms. This view that evolution precedes through

‘quantum’ (Simpson, 1944), ‘punctuated’ (Eldredge and Gould, 1972) or only minimally stable states has existed since at least the work of Francis Galton (1869), who analogized evolution proceeding as a polyhedron flipping from one stable facet to another. Within each adaptive zone, Simpson suggested the existence of adaptive subzones giving opportunities for fine-scale ecological diversification. For example, felids and canids occupy their own unique subzones which can be grouped into a more inclusive ‘fissiped’ subzone as opposed to one of pinnipeds, and even more inclusively, all of the aforementioned can be grouped into carnivores as opposed to herbivores. Slater (2015) suggests that canids can be subdivided into canid hypo-, meso- and hypercarnivore subzones within which have their own optimal state. OU models can be viewed as evolutionary constraint, which in this context could be interpreted as a constraint in the dental morphology required to occupy a given dietary niche or subzone. The lack of an early burst signal for canids was suggested by Slater to be a result of early burst or adaptive radiations only existing at more inclusive clades. In fact, Slater and Friscia (2019) found that among extant Carnivora there was a preponderance of early burst dynamics, but primarily in only diet/dental related traits. At the family level this falls apart into far greater nuance of Brownian motion or OU models as best supported, a hierarchical distinction previously suggested in theoretical literature (Osborn, 1902; Simpson, 1944, 1953; Gould, 2002; Humphreys and Barraclough, 2014). The presented results suggest that feliform ecological evolution may best be explained as a pull towards optimal dental toolkits, and to a lesser extent body mass, per dietary category. However, these optima are filtered through contingent events, likely correlated to global climatic and/or tectonic dynamics.

Nimravids and felids explosively entered a nimravid/cat-like zone that ecologically may have prevented these clades from escaping (i.e., evolutionary ratchet, Van Valkenburgh et al., 2004)

related to phylogenetic constraints inherent to the clade. These constraints, much like tooth count in canids versus hyaenids, may have been contingent in themselves, such that the path to hypercarnivory from a hypo- or mesocarnivorous ancestor has several routes, e.g., cat/nimravid versus dog/hyaenid, and that one path may be more restrictive than the other. Canid and hyaenid hypercarnivores utilize more of the carcass than felids based on observation of living taxa (Van Valkenburgh, 1996) and dental microwear and enamel structure in fossil forms (Tseng, 2012; Desantis et al., 2015). The consumption of bone or otherwise resilient vertebrate material in addition to soft flesh may have facilitated the retention or development of robust molars in canids and bone-cracking premolars in hyaenids. Thus, the difference in what parts of vertebrate prey are consumed may be a more important distinction than how much vertebrate prey is consumed and the resulting evolutionary patterns. For canids, this could provide an escape to a more omnivorous diet and the ability to specialize in a given dietary subzone. For felids and nimravids, explosive entry into soft flesh hypercarnivory may have been irreversible, a potential generalization for mammals (Brocklehurst, 2019). Even with findings that mammal cusp number and placement are under the control of relatively limited genetic pathways allowing potentially a diverse array of dental complexity from early crown developmental (Jernvall and Jung, 2000; Kangas et al., 2004; Kavanagh et al., 2007; Harjunmaa et al., 2014), the loss of talon(ids) is seemingly inflexible to recovery (Solé and Ladevèze, 2017). Rapid felid and nimravid hypercarnivorous shifts seem to be tied to global climatic/tectonic dynamics, in turn associated with faunal turnover. These turnover events may provide contingent opportunities for soft-flesh specialist hypercarnivores to quickly exploit new resources by rapid dental toolkit specialization, but ones that constrain descendant taxa to remain within this ecospace.

The ecological evolution of hyaenids and canids saw exploration of multiple subzones, one of which was hypercarnivory. This path was still rapid given the estimated phylogenetic half-life values of the present study and that of Slater (2015), but it does not seem correlated with the type of global events that habitat theory would predict. Hyaenids may occupy a common canid-like subzone of the Neogene where optima from a hypo- or mesocarnivorous ancestor mediated the pull towards each dietary category, compared to a singular pull to extreme hypercarnivory. A possible explanation for this may lie in the postcranial *bauplan* of felids/nimravid versus canids and hyaenids. Early members of both the Canidae and Hyaneidae exhibit incipient cursorial morphology, including reduced ability to retract the distal phalanges and supinate/pronate the forelimb (Hunt Jr. and Solounias, 1991; Wang, 1993; Figueirido et al., 2015). These changes likely enhanced efficiency in covering large distances (Janis and Wilhelm, 1993), but also reduced the ability to grapple with prey, as do modern felids. Becoming increasingly face-orientated in predation, canids and hyaenids may have relied more upon the integration and optimization of body size and dental tool kit than do soft-flesh specialists and thus set them down a distinct ecospace trajectory.

A third situation is seemingly possible in the case of small feliforms, where body mass and dental toolkit evolve via random walk. This third subzone of small carnivorans and associated dietary subzones, achieves broad dietary ecologies, possibly related to their small size (Pineda-Munoz et al., 2016). Evolutionary patterns of small feliforms may correlate to the morphological refuge discussed for canids and hyaenids, in that a hypocarnivorous (and specifically insectivorous) ancestor may better facilitate evolution into varied dietary categories at small size. This bias in dietary shifts across mammalian evolution has been recovered in the work of Price et al. (Price et al., 2012) and Reuter (2021), where far greater dietary transitions occur from diets

that feature invertivory than any other. This malleability in ecology is likely facilitated by being small, where metabolic and structural burdens have minimal impact compared to mammals of larger size (Carbone et al., 1999, 2007).

The current study suggests that the hypothesis of early burst evolution being only observable at higher taxonomic levels, while stabilizing selection or Brownian motion dominates lower levels is overly simplistic. Instead, there appears to be a story of contingent opportunity mediated by global tectonic and climatic factors, but these too are filtered through phylogenetic baggage accrued through entrance into different ecological zones. Soft-flesh specialists rapidly appear at times of massive faunal turnover, from lineages with plesiomorphic carnivoramorphous postcranial morphology. However, the descendants of these lineages are constrained to remain within this ecospace with the loss of dental hardware lending itself to different diets.

Climatic/tectonic events also facilitate the diversification and appearance of other feliform clades, but the evolutionary patterns expressed differ from those of felids and nimravids.

Hyaenids experienced vast ecological diversity optimized for body mass and dental toolkit. This ecospace trajectory may have been necessitated by the early postcranial modifications to cursoriality in the clade and correlated face-centric predation. With the loss of this ancestral postcranial morphology, both hyaenids and canids may have been excluded from soft-flesh specialization, even if the opportunity existed, such as the “cat-gap” in the early Miocene of North America. However, retention of more generalized dentition combined with cursorial adaptations may channel body size and dental tool kit optimization per dietary category. Finally, small feliforms experience apparent random evolution in both body size and dentition. These clades’ appearance and diversification can also be correlated with global tectonic and climatic events, but given the absolute size of their members, are free to drift across a range of ecological

options, being freed of the constraints of large size. However, once opportunities do present themselves the above ecospace trajectories come into play with growing body size and postcranial adaptations. For example, the fossa (*Cryptoprocta ferox*) acquired familiar felid ecomorphology in Madagascar after a sweepstakes dispersal of a herpestid-like ancestor from Africa. Further analysis within a paleoecological framework may find more similarities than differences in subzone occupation of additional Carnivoran clades. The caniform groups of Mustelidae, Mephitidae, Ailuridae and Procyonidae may occupy the small ecospace of sister group small feliforms, while certain subfamilies of ursids and amphicyonids may fall within that of canids and hyaenids. Regardless, contingent opportunity from global events seems to drive the evolution of feliform carnivorans, but the path they take is mediated by ecological pathways previously taken and consequent phylogenetic baggage.

Chapter IV

Evolution of feliform cranial shape

Introduction

The processes that govern the evolution of shape amongst the pageant of life, are central questions in biology (Dobzhansky, 1951; Hutchinson, 1959; Gould, 2002). Studies suggest that there is a variable degree of connection between morphology and ecology (Marroig and Cheverud, 2005; Hunt, 2007; Harmon et al., 2010; Santana and Cheung, 2016; Slater and Friscia, 2019). For example, mammals have a strong association between dental and gnathic morphology and their diet (Evans et al., 2007; Boyer, 2008; Christensen, 2014; Pineda-Munoz et al., 2016; Grossnickle, 2020; Wang et al., 2021). Taxa that consume large amounts of vertebrate material possess reduced dentary lengths and enhanced shearing surfaces to maximize power and efficiency in processing animal tissue, while folivorous mammals lengthen the dentary and increase tooth occlusal area and complexity to aid in grinding of tough floral material. However, how this form and function correlation extends to overall cranial shape has remained less clear (Figueirido et al., 2011; Tseng, 2013; Tseng and Flynn, 2018). While some authors have found a connection between diet and cranial shape (Sacco and Van Valkenburgh, 2004; Wroe and Milne, 2007), others recover only a predictive connection for bite force (Christiansen, 2008b; Maestri et al., 2016; Law et al., 2018b), which when tied to diet, only discriminates between hypercarnivores and generalists in terrestrial carnivorans (Radinsky, 1981b; Rovinsky et al., 2021).

For the latter studies, the lack of predictive power for a broad swath of diet (0-70% vertebrate material = hypo-mesocarnivores) may relate to constraint in phylogeny, which, by limiting

possible morphologies, creates stochastic variation that disrupts expected mapping of form to function (Raup and Gould, 1974). However, ecomorphological categories have been assessed in the fossil and living record (Martin, 1989; Werdelin, 1996; Van Valkenburgh, 2007; Turner et al., 2008; Coca-Ortega and Pérez-Claros, 2019; Barrett, 2021) by the iterative appearance of certain morphologies over geologic time, and presumably comparable ecologies to which they belong. This observation can be extended to the conclusion that a lineage that entered many dietary ecologies should be more morphologically disparate than one that did not, and by some metrics, more successful (Guillerme et al., 2020). Of the carnivoran clades, low amounts of cranial-dental variation have been historically presented in literature for “cat-like” carnivores such as felids and nimravids (Radinsky, 1981a, 1982; Van Valkenburgh, 1991). Foreshortened faces and reduced tooth counts optimize forces in slicing meat at the scissor-like carnassials and prey seizing with the canines. This reduced raw material for selection is argued to relate to increased specialization and narrow morphological disparity amongst hypercarnivores with concomitant increased extinction risk (Holliday and Stepan, 2004; Van Valkenburgh et al., 2004; Van Valkenburgh, 2007). Specifically, loss of posterior grinding molars in soft-flesh specialist hypercarnivores may have put them on an evolutionary road of no return (evolutionary ratchet), resulting in an ecomorphological constraint that did not allow them to evolve additional ecologies. However, recent 3D Geometric Morphometric (3DGM) analyses suggest that cranial disparity for hypercarnivores may be greater than that of generalists among living carnivorans, particularly amongst feliforms (Michaud et al., 2018, 2020). This disparity may in turn be an underestimate, for living carnivores do not occupy the entire range of morphologies, and presumably ecologies, of extinct lineages. Sabertooth and bone-cracking carnivores were once species-rich components of past ecosystems, and it has been suggested that their cranial

morphology may have operated under different rules than their extant relatives in terms of disparity and cranial modularity (Holliday and Stepan, 2004; Goswami et al., 2015).

Even with the seeming inability to recover molar crushing basins (Solé and Ladevèze, 2017), there may be another reason for aberrant disparity patterns in the crania of soft-flesh hypercarnivores (i.e. felids and nimravids). Recent literature has shown that morphology is often integrated from developmental genetic sequences (Gehring, 1996; Shubin et al., 1997; Tomarev et al., 1997) to gross anatomy (Goswami, 2006; Goswami and Polly, 2010a; Goswami et al., 2014, 2015) in such ways that structures can covary, generating morphology that changes in sync. Do felids and nimravids present limited evolutionary potential resulting from overly integrated cranial development compared to other clades, or does developmental integration provide a fruitful channel to more extreme morphologies (Goswami et al., 2015)? In this study, I use 3DGM analyses to assess feliform cranial allometry and morphology within and among 73 species spanning approximately 34 million years of evolution. Specifically, I ask the following questions:

- (1) Are there distinct cranial morphologies for each ecological category?
- (2) Does disparity differ among these categories?
- (3) What is the source of disparity in more morphologically diverse clades?
 - (3a) Does morphological disparity increase in clades that have had more time to evolve, or
 - (3b) Does greater variance in size allow a line of least evolutionary resistance for morphological variation via allometry?
 - (3c) If allometry is important, is there a common allometric trajectory amongst feliforms?
- (4) Does integration (an indicator of developmental constraints), enable or limit potential in the evolution of feliform cranial shape?

Methods

Materials

The morphological dataset is composed of 157 cranial specimens, representing 73 extinct and extant feliform species (Appendix I). When possible, I sampled one male and female individual of a species to approximate the range of sexual dimorphism for that species, while I chose species to sample the cranial disparity of a given clade, including an “average” shape and more outlying morphologies as well. I then sorted these species into ten monophyletic clades as recovered in Chapter II: Felinae/Pantherinae (FP), Machairodontinae, Felidae, Stenoplesictidae, Nimravidae, Viverridae, Hyaenidae, Herpestidae, Eupleridae, and Prionodontidae. I digitized 69 three-dimensional (3D) landmarks (Figure 6, Table 11) using a Microscribe G2LX digitizer (Immersion Corp., San Jose, CA). During data collection I stabilized individual crania with clay supports and digitized landmarks in two sets, one in dorsal view and the other in ventral view. I used a set of four reference landmarks in both views to facilitate alignment of the dorsal and ventral datasets. The two sets were then stitched together using the ‘unifyLandmarks’ function of the ‘StereoMorph’ package (Olsen and Westneat, 2015) in R v. 4.1.2 (R Core Team, 2020). I considered alignments sufficient when alignment error was less than or equal to the manufacturer stated accuracy of the Microscribe G2LX digitizer (0.3mm). I supplemented the Microscribe-generated data set with a few rare taxa/specimens landmarked from published CT scans or photogrammetry-generated 3D models. These latter specimens were digitized in Landmark Editor v. 3.0 (Institute for Data Analysis and Visualization, University of California, Davis).

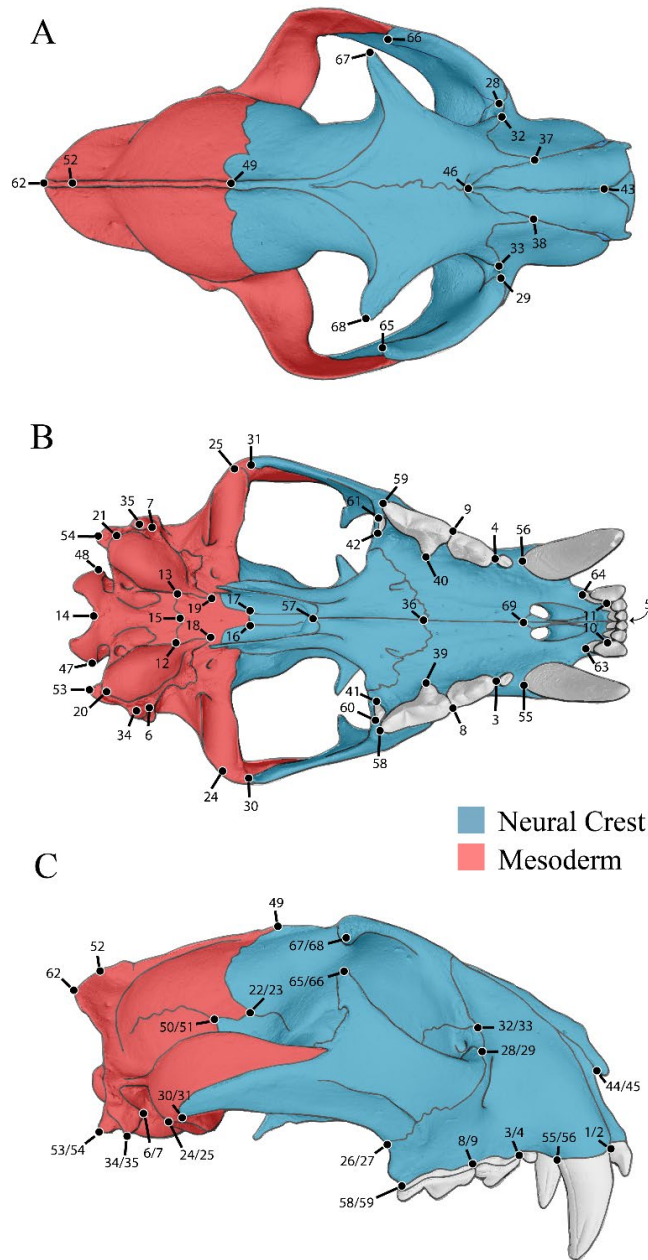


Figure 6. Position of the landmarks taken on the cranium for 3DGM analyses (69 landmarks) to quantify variation in shape of feliform crania. A, dorsal view. B, ventral view. C, right lateral view. Landmarks are subset into two modules, Neural Crest (NC, blue) and Mesoderm (MD, red), based on tissue origin of cranial elements. The skull used for this representation is a leopard (*Panthera pardus*, Felidae).

Table 11. Definition of anatomical landmarks used in the three-dimensional geometric morphometric analyses.

Landmark	Definition
1	Anterior border of canine at alveolus-left
2	Anterior border of canine at alveolus-right
3	Anterior border of P3 at alveolus-left
4	Anterior border of P3 at alveolus-right
5	Anterior midline suture of premaxilla
6	Anteromedial point of mastoid process-left
7	Anteromedial point of mastoid process-right
8	Anterolateral border of P4 alveolus-left
9	Anterolateral border of P4 alveolus-right
10	Anteromesial border of I3 at alveolus-left
11	Anteromesial border of I3 at alveolus-right
12	Basioccipital basisphenoid bulla suture-left
13	Basioccipital basisphenoid bulla suture-right
14	Basion
15	Basisphenoid basioccipital midline suture
16	Basisphenoid presphenoid suture-left
17	Basisphenoid presphenoid suture-right
18	Bulla anterior medial extreme-left
19	Bulla anterior medial extreme-right
20	Bulla posterior lateral extreme-left
21	Bulla posterior lateral extreme-right
22	Frontal parietal alisphenoid suture-left
23	Frontal parietal alisphenoid suture-right
24	Glenoid fossa lateral extreme-left
25	Glenoid fossa lateral extreme-right

Table 12 continued.

Landmark	Definition
26	Jugal maxilla ventral suture-left
27	Jugal maxilla ventral suture-right
28	Jugal maxilla lacrimal suture-left
29	Jugal maxilla lacrimal suture-right
30	Jugal squamosal ventral suture-left
31	Jugal squamosal ventral suture-right
32	Lacrimal frontal maxilla suture-left
33	Lacrimal frontal maxilla suture-right
34	Mastoid process ventral tip-left
35	Mastoid process ventral tip-right
36	Maxilla-palatine midline suture
37	Maxilla frontal nasal suture-left
38	Maxilla frontal nasal suture-right
39	Medial border of P4 at widest point of alveolus-left
40	Medial border of P4 at widest point of alveolus-right
41	Medial M1 alveolus-left
42	Medial M1 alveolus-right
43	Nasal-anterior midline suture
44	Nasal-premaxilla suture anterior-left
45	Nasal-premaxilla suture anterior-right
46	Nasals frontal midline suture
47	Occipital condyle lateral extreme-left
48	Occipital condyle lateral extreme-right
49	Parietal-Frontal midline suture
50	Parietal-squamosal-alisphenoid suture-left
51	Parietal-squamosal-alisphenoid suture-right
52	Parietals occipital midline suture
53	Paroccipital process tip-left

Table 13 continued.

Landmark	Definition
54	Paroccipital process tip-right
55	Posterior border of canine at alveolus-left
56	Posterior border of canine at alveolus-right
57	Posterior border of palatine at midline
58	Posterior of carnassial at alveolus-left
59	Posterior of carnassial at alveolus-right
60	Posterolateral border alveolus M1-left
61	Posterolateral border alveolus M1-right
62	Posterodorsal tip of occiput at midline
63	Posterolateral border of I3 at alveolus-left
64	Posterolateral border of I3 at alveolus-right
65	Postorbital process base (jugal)-right
66	Postorbital process base (jugal)-left
67	Postorbital process tip (frontal)-left
68	Postorbital process tip (frontal)-right
69	Premaxilla maxilla ventral midline suture

Because the crania of extinct taxa were often incompletely preserved, I imputed missing landmarks to maximize the size of the dataset. Two additional fossil specimens, TMM 933-3444 (*Homotherium serum*) and CB 07 (*Eusmilus sicarius*) were retrodeformed to correct for postdepositional shape changes using the ‘symmetrize’ function of the ‘Morpho’ R package (Schlager, 2017). I first performed imputation via reflection across the plane of symmetry using the ‘mirrorfill’ function in the ‘paleomorph’ package (Lucas and Goswami, 2017). These mirrored models I then used to impute absent landmarks by the ‘estimate.missing’ function in the ‘geomorph’ package (Adams et al., 2021) with the thin-plate spline method. Imputation

proceeded in three iterations to maximize accuracy, given the ‘estimate missing’ function interpolates landmarks using a reference specimen within the analyzed dataset. Thus, felids and nimravids were grouped for imputation, with a second group composed of durophagous hyaenids, and a final group containing the remaining taxa (i.e., viverroids). This final group included the hyaenid genera: *Ictitherium*, *Hyaenotherium* and *Tungurictis*. While paraphyletic, these hyaenids and other viverroid families exhibit similar dolichocephalic cranial shapes.

The digitized landmarks for all crania I then subjected to Generalized Procrustes Analysis (GPA) superimposition which translates the specimens to a common origin, scales each specimen to unit centroid size, and rotates each specimen to minimize landmark distances using a least-squares calculation. The resulting Procrustes coordinates I projected into tangent space with a principal components analysis (PCA) using the ‘gm.prcomp’ geomorph function to identify the major axes of cranial shape among all the crania in the analysis. I identified morphological changes associated with the major PC axes by calculating a series of indices of individual crania and then examined their Pearson’s correlation to said axes.

Disparity and Integration

I calculated disparity as the Procrustes variance (trace of the group covariance matrix, divided by group n) of each clade of interest using the ‘morphol.disparity’ function in geomorph v. 4.0.1 (Adams et al., 2021; Baken et al., 2021) with 1000 randomized residual permutations (Collyer et al., 2015). I performed this calculation while assessing the impact of allometry and clade age on disparity, because certain feliform clades span orders of magnitude in body mass while others do not. Thus, strong allometric trends may provide a line of least evolutionary resistance towards generating disparity in clades with large size variance. Similarly, morphological disparity for a clade may simply be the result of having more time to accrue within relatively ancient lineages

compared to recently diverging ones. I further calculated disparity per dietary category (Table 12) as determined in Chapter III, while adding extant invertebrate specialists as those with $\geq 70\%$ invertebrate material in their diet as determined by the Elton Trait dataset (Wilman et al., 2014), checked against the recent carnivoran ecological analysis of Hopkins et al. (2021). I compared ecological cranial disparity by using the ‘morphol.disparity’ function and model coords $\sim \log(Csize)$ with 1000 randomized residual permutations. Randomization of residuals allows assessment of model effects and summary statistics, especially important for the high dimensionality of trait data versus sample size of 3DGM analyses (Adams, 2014a; Adams and Collyer, 2015). The Bonferroni correction accounted for multiple comparisons (Bonferroni, 1936).

Table 14. Definitions of dietary categories for analysis of cranial shape.

Dietary Category	Definition
Invertivore	$\geq 70\%$ invertebrate material
Hypocarnivore	$\leq 40\%$ vertebrate material
Mesocarnivore	50-69% vertebrate material
Hypercarnivore	$\geq 70\%$ vertebrate material
Durophagous	Hypercarnivore with bone-cracking morphology
Sabertooth	Hypercarnivore with sabertooth morphology

I calculated cranial integration two ways. The first measure used was eigenvalue dispersion (equations 7&8, Goswami and Polly, 2010b), equal to the standard deviation of eigenvalues from the correlation matrix of the PCA. With high values of eigenvalue dispersion, variance will be concentrated in the first few eigenvectors resulting from high covariance between landmarks.

The second measure calculated the integration of the mesoderm (MD) and neural crest (NC) developmental modules. I determined module assignment for each landmark by the tissue origin of the bone on which a given landmark was located (Figure 6). The origins of cranial bones, as neural crest or mesoderm derived, were assigned following Ferguson and Atit (2019) for the face and vault elements, and McBratney-Owen et al. (2008) for the cranial base. The squamosal is derived from both Neural crest and Mesoderm tissues (Ferguson and Atit, 2019), thus landmarks 30-31 were treated as NC, while 24-25 were assigned to MD. Landmark 49 was located on the sutural boundary between the NC and MD modules and was assigned to the MD module, as the coronal suture is of mesoderm origin (Mishina and Snider, 2014). I assessed integration of these two developmental modules with the ‘integration.test’ function geomorph. This is a two-block partial least squares analysis (PLS, Rohlf and Corti, 2000), also referred to as a singular warps analysis (Bookstein et al., 2003). The z-scores were used for clade comparisons while significance was derived from 1000 random permutations of individuals in one partition to those in the other.

I tested the relationship between morphological disparity and integration by performing two sets of regressions using the base R function `lm()`. I regressed morphological disparity against both eigenvalue dispersion values and against between-module integration (z-scores) of the MD and NC regions.

Allometric Variation

I assessed the impact of allometry on clade evolution in two ways. The first looked at per-clade influence of allometry on shape variation by using the geomorph function ‘`procD.lm`’ and the equation (Procrustes coordinates) $\sim \log(\text{centroid size}) + \text{RCS}$. Relative canine size (RCS) was

included in particular to assess its role in predicting cranial shape in sabertooth carnivorans (Slater and Van Valkenburgh, 2008). Significance was evaluated with Goodall's (1991) F-test with 1,000 permutations for this and the subsequent analyses.

For the second set of analyses, variation in evolutionary (among-clades) allometries was tested using an ANCOVA model where Procrustes shape coordinates were regressed against log centroid size and clade membership with the model $\text{coords} \sim \log(\text{Csize}) * \text{clade}$. A post hoc test using the package RRPP (ver. 1.1.2; Collyer and Adams, 2018, 2019) function pairwise evaluated whether the evolutionary allometric slopes of clades ($n=10$) significantly differ from one another. Multiple comparisons were accounted for by reducing α to .01. The model was visualized by plotting the regression scores of shape on size versus log centroid size (Drake and Klingenberg, 2008). I also compared these results with a phylogenetic ANCOVA (pANCOVA) using geomorph's `procD.pgls` (Adams, 2014a), which executes the ANCOVA model in a phylogenetic framework. This pANCOVA used mean averaged crania from all 73 species and a pruned version of the phylogenetic tree of Chapter 2 (Figure 7) that only included taxa sampled for this analysis.

Phylogenetic Signal and Evolutionary Rates

I calculated the phylogenetic signal of the cranial landmark dataset with a multivariate K-value (K_{mult}) (Adams, 2014b) using the 'physignal' function in geomorph. K_{mult} uses 1000 random permutations to assess how well the morphometric data fit a phylogenetic tree. A K_{mult} value of zero corresponds to absence of phylogenetic signal, whereas a K_{mult} value greater than one indicates a strong phylogenetic signal, implying that morphological traits are conserved within the phylogeny.

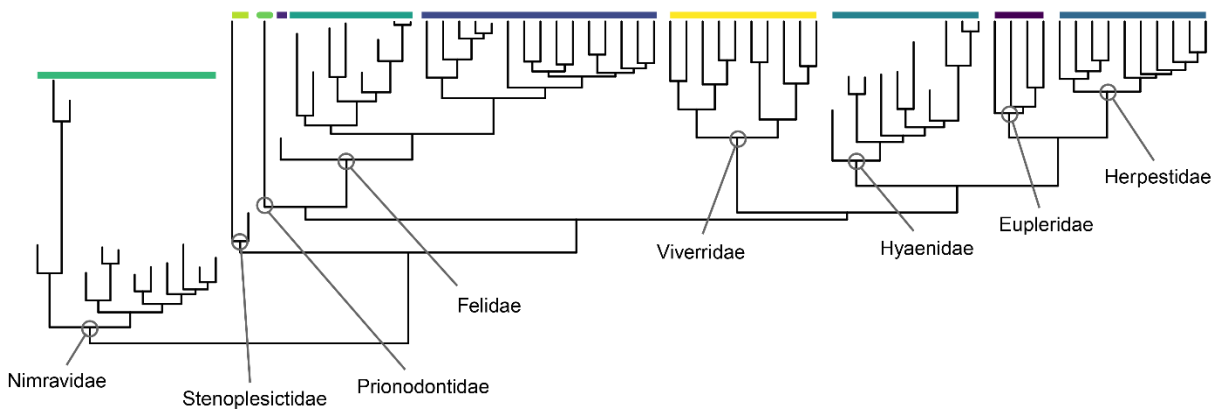


Figure 7. Pruned MCC phylogeny of Chapter II to include only those feliforms analyzed in the present cranial morphology chapter.

I calculated the morphological rates of evolution for each clade of interest by using the geomorph function ‘compare.evol.rates’ on the same pruned tree. I performed 1000 simulations of Brownian motion trait evolution which were summarized with the net evolutionary rate of each clade obtained from the sum of squared distances between taxa and the origin of their clade (O’Meara et al., 2006; Adams, 2014c). This procedure was also performed on mean natural log centroid sizes for species crania to estimate rates of cranial size evolution. I compared the clade-wise rates of size and shape evolution and morphological disparity with ordinary least squares regression analysis in the base R function `lm()`. I further compared rates of evolution per dietary category making pairwise comparisons (over 1000 iterations) of shape evolution rates between all dietary categories. The Bonferroni correction accounted for multiple comparisons (Bonferroni, 1936).

Dietary Impact

I tested the effect of diet on feliform cranial shape by first calculating the degree of carnivory (proportion of vertebrate material in the diet) for extant taxa, taken from the Elton Traits (Wilman et al., 2014) database and checked against Hopkins et al. (2021). I then regressed this value against relative blade length (RBL) of the lower first molar (taken from the dataset in Appendix H) and estimated the degree of carnivory for extinct taxa using the base `lm()` and `predict()` functions in R. Degree of carnivory for all taxa was then regressed against mean cranial shape for feliforms using the `geomorph` `procD.pgls` function within a phylogenetic framework.

Results

PC1 (Figure 8) accounts for 44.68% of feliform shape variation and describes morphological changes associated with sabertooth morphology, with progressively more derived sabertooth taxa towards the negative side of the axis. This is echoed by the correlation of relative canine size (distance from landmark 1 to 55 divided by centroid size) to the PC1 axis, ($r = -0.87$, $p = 2.2 \times 10^{-16}$). PC2 (14.57% of variation) describes changes from brachycephalic to dolichocephalic morphology, reflected in the correlation of relative palate length (distance from landmark 5 to 57 divided by centroid size) to the PC2 axis, ($r = 0.70$, $p = 2.2 \times 10^{-16}$). Every other PC axis describes less than 10% of remaining cranial shape variation. Within the PC 1 and 2 morphospace, all viverrids save hyaenids overlap each other with positive scores on the PC1 axis and positive to slightly negative scores on the PC2. Hyaenids occupy an area near the origin, but primarily extend into positive PC2 morphospace. Felines and pantherines extend the furthest into negative PC2, with the largest members also having the most negative PC1 scores. The aforementioned

taxa generally occupy an upper right to lower left orientation in the PC1 and 2 morphospace while extending perpendicular to them lie the entirety of the sabertooth machairodontine and nimravid taxa. This is a similar pattern to that recovered in the 2D GM analysis of Slater and Van Valkenburgh (2008).

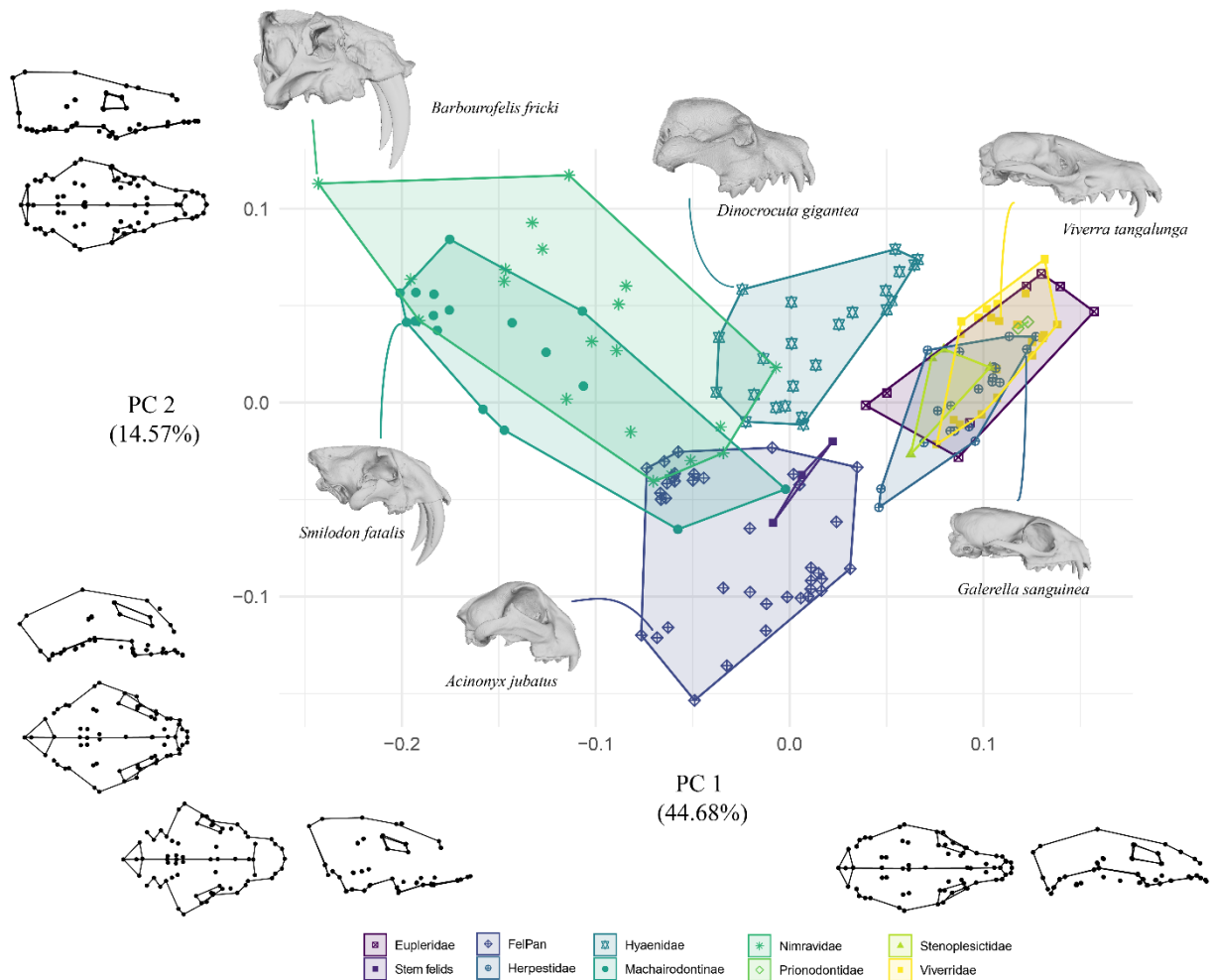


Figure 8. PCA of all cranial feliform specimens. Convex hulls surround clades of interest while individual taxa are indicated by a surface scan of their place in morphospace. Below and to the left side of PC1 and 2 are wire frame models of the change in landmarks at the extreme of each principal component from a right lateral and dorsal perspective.

Procrustes ANOVA Results

Clade membership, log centroid size, and relative canine size are significant predictors of cranial shape, though the influence on each clade of the latter two variables differs, Table 13 and Table 14. Felines and pantherines had by far the greatest allometric signal (49%) while nimravids had the least (9%) and almost all other clades (save herpestids) had an intermediate signal between 20 and 26%. Relative canine size was minimally explanatory for cranial variation in most clades (3-7%) except for the euplerids (47%) and sabertooth machairodontines (19%) and nimravids (24%).

Table 15. Allometry and effect of relative canine size (RCS) on cranial shape as determined by ANOVA of shape (Procrustes coordinates) ~ log(centroid size)+RCS for each clade. Disparity was calculated by Procrustes variance adjusted for allometry and clade age. Statistically significant ($p < 0.05$) values are in bold. Eigenvalue dispersion does not include a significance assessment.

	In Centroid Size	RCS	Disparity	Eigenvalue dispersion	Developmental module integration
Eupleridae	0.204	0.466	0.012	0.408	1.909
Felinae/Pantherinae	0.487	0.035	0.013	0.167	4.708
Herpestidae	0.119	0.070	0.008	0.236	3.522
Hyaenidae	0.246	0.043	0.016	0.218	3.013
Machairodontinae	0.259	0.185	0.020	0.250	3.763
Nimravidae	0.090	0.238	0.017	0.236	3.411
Viverridae	0.256	0.071	0.011	0.229	2.459

Table 16. Evolutionary allometry ANCOVA. Evolutionary allometry (among clades) uses the mean shapes and mean centroid sizes of the 73 species, which were then grouped into ten clades (including the one monospecific lineage). Df = degrees of freedom, SS = sum of squares, MS = mean square, R² = coefficient of determination, F = F statistic, Z = effect sizes, Pr(>F) = significance value.

	Df	SS	MS	R ²	F	Z	Pr(>F)
log(Csize)	1	0.871	0.871	0.271	120.64	5.158	<0.001
clade	9	1.159	0.129	0.361	17.842	12.253	<0.001
log(Csize):clade	9	0.193	0.021	0.06	2.968	5.48	<0.001
Residuals	137	0.989	0.007	0.308			
Total	156	3.21					

Levels of Morphological Disparity and Integration

Age of lineage had a significant correlation with allometrically adjusted disparity (Figure 9). Adjusting Procrustes variance for both allometry and lineage age found machairodontines with the highest level of morphological cranial disparity (Table 13), followed by nimravids and hyaenids. Felines/pantherines, euplerids and viverrids possessed moderate levels of disparity, while herpestids had the least overall. Disparity per dietary category (Table 15) recovered sabertooth taxa having the greatest amount of size-adjusted variance. This is followed by durophagous taxa in second; mesocarnivores, hypercarnivores and invertivores with comparable intermediate values, and hypocarnivores with the least. However, Bonferroni-corrected significance values only recover sabertooth and hypocarnivores as significantly different in disparity.

Table 17. Cranial disparity (Procrustes variance adjusted for size) per dietary category. Upper triangle is absolute difference between dietary categories while lower triangle contains p-values.

	Hypocarn.	Mesocarn.	Hypercarn.	Durophag.	Sabertooth	Invertivor.
Hypocarn.	-	0.0062	0.0058	0.0086	0.0136	0.0044
Mesocarn.	1	-	3.00E-04	0.0024	0.0074	0.0018
Hypercarn.	1	1	-	0.0028	0.0077	0.0014
Durophag.	1	1	1	-	0.0049	0.0042
Sabertooth	0.015	1	0.105	1	-	0.0091
Invertivor.	1	1	1	1	0.495	-

Integration, as determined by both eigenvalue dispersion and developmental module integration, has no significant correlation to allometric and lineage age adjusted disparity (Figure 10 and Figure 11). Eigenvalue dispersion was similar for all clades save euplerids, which possessed a value almost twice as great as other feliforms. However, felines/pantherines had the greatest between-module integration value. There was also a greater spread of this integration metric for other clades, with the sabertooth clades, hyaenids, and herpestids having moderate values, and viverrids and euplerids the least overall.

Phylogenetic Signal and Evolutionary Rates

The phylogenetic signal of feliform cranial shape is $K = 0.59$ ($p < 0.001$). This is substantially greater than that observed across extant Carnivora in Michaud et al. ($K = 0.38$: 2018), though less than that of extant feliforms in Michaud et al. ($K = 0.78$: 2020), implying that feliforms have a more conserved ancestral cranial morphology than carnivorans overall, and that fossil taxa may have a disproportionate impact on this calculation. Clade-wise rates of size evolution (Figure 12)

Feliformia Clade Age and Disparity (Allometry Adjusted)

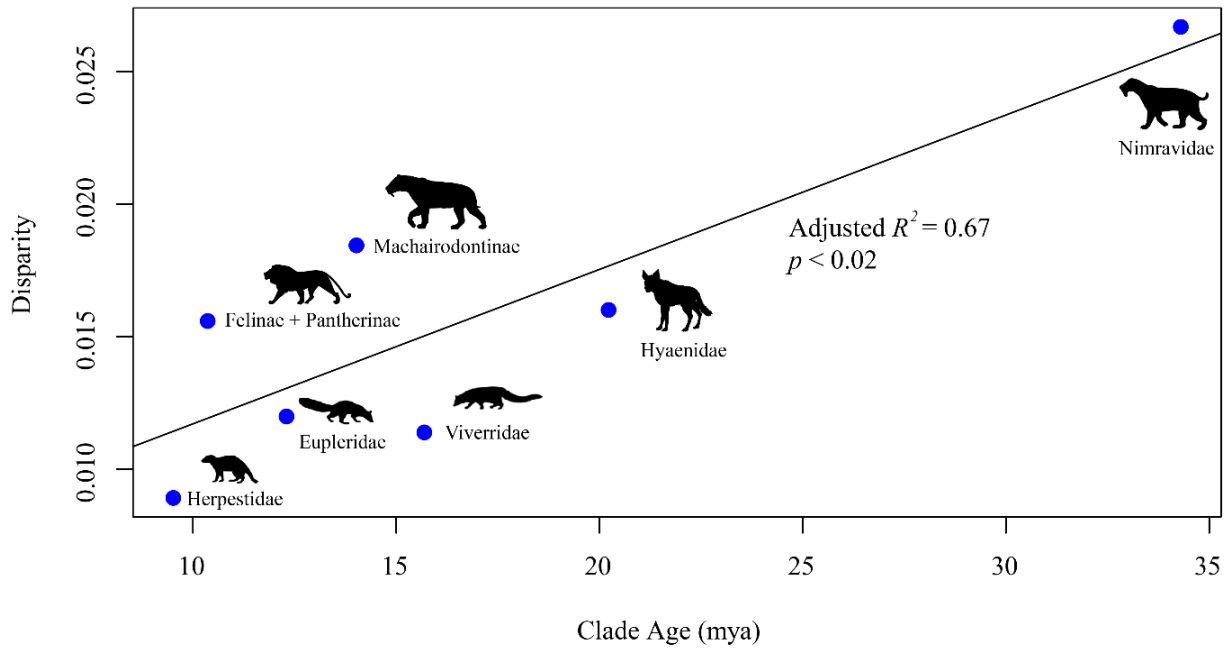


Figure 9. Relationship between feliform lineage age and disparity (Procrustes variance). Disparity has been adjusted for allometry.

Feliformia Integration and Disparity (Allometry & Age Adjusted)

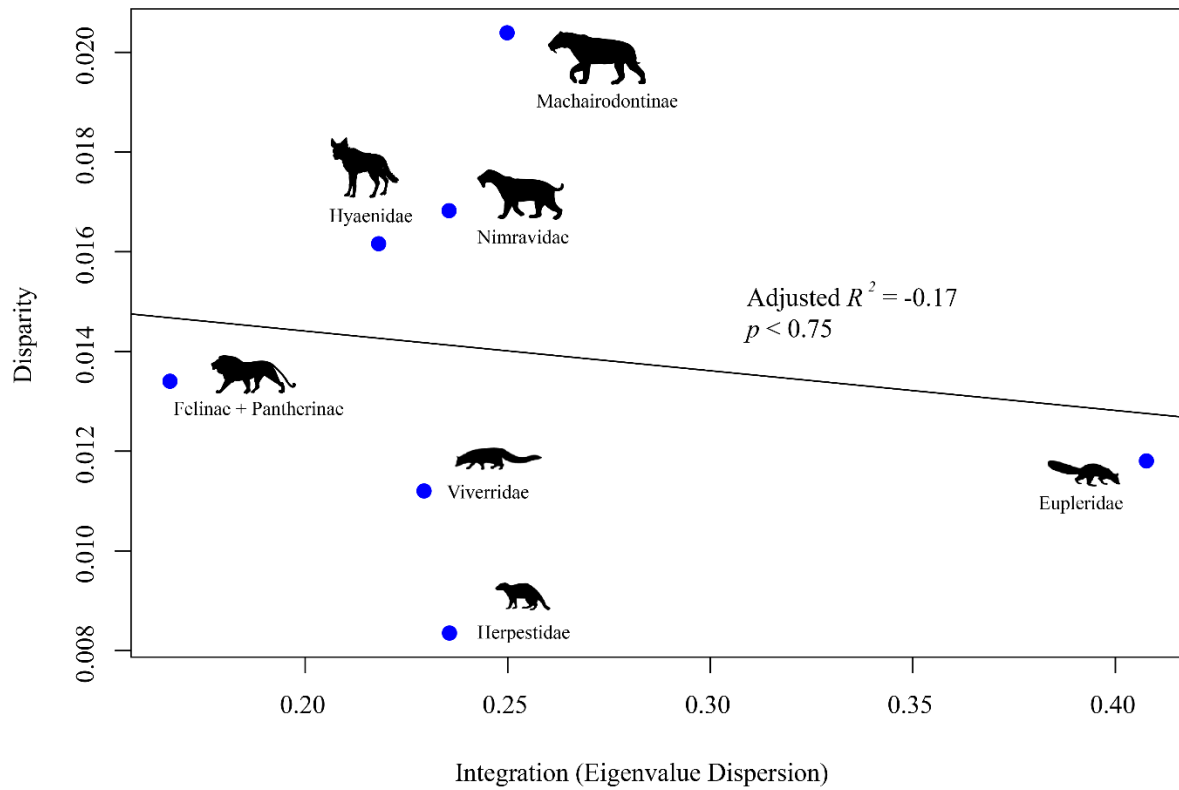


Figure 10. Relationship between feliform cranial integration (Eigenvalue dispersion) and disparity (Procrustes variance). Disparity has been adjusted for allometry and age of lineage.

Feliformia Integration and Disparity (Allometry & Age Adjusted)

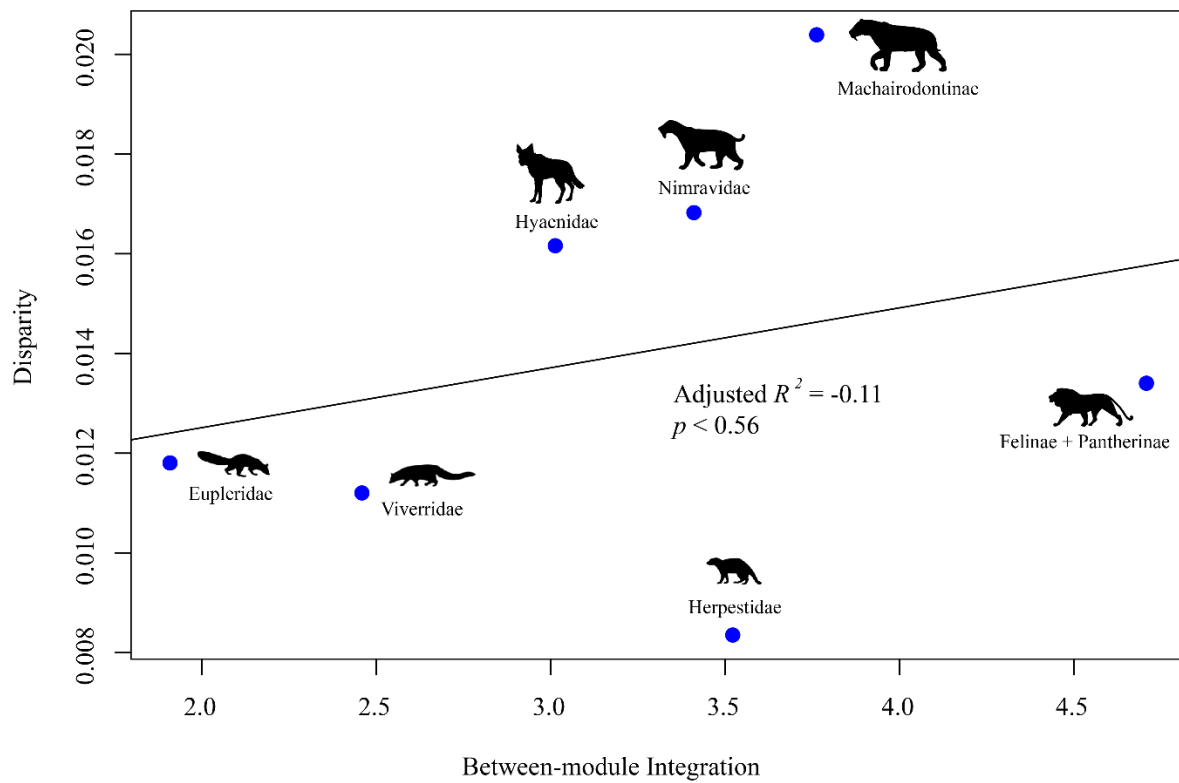


Figure 11. Relationship between feliform cranial integration (between developmental module) and disparity (Procrustes variance). Disparity has been adjusted for allometry and age of lineage.

poorly predicted rates of morphological shape evolution ($R^2 = -0.08$, $p < 0.52$). Of note, machairodontines and nimravids appear as outliers, having the greatest rates of shape evolution, but even with their removal the fit is non-significant ($R^2 = 0.46$, $p < 0.08$). For the rates of size and shape evolution, only that of shape evolution significantly predicted cranial disparity (Figure 12).

Pairwise analysis of shape evolution rates amongst dietary categories revealed that crania of sabertooth carnivores evolved 2.2-5.1 times faster than those of non-sabertooths (Table 16; $p <$

0.02). A similar result was found for durophagous and hypercarnivorous carnivores relative to hypocarnivorous ones, with a value 1.9 times ($p < 0.02$) faster for the former, and 1.74 times ($p < 0.02$) faster for the latter. All other pairwise comparisons were nonsignificant.

Allometric Variation

Feliform cranial morphology exhibits substantial evolutionary (among-clades) allometry ($R^2 = 0.27$, $p < 0.001$). This is less than that of clade membership ($R^2 = 0.36$, $p < 0.001$) indicating strength in phylogenetic signal over a common allometric trajectory (Table 14). The ANCOVA of the interaction between clade membership and log centroid size further shows very little support for distinct allometric trends per clade ($R^2 = 0.06$, $p < 0.001$). However, the pANCOVA (Table 17) of mean shapes against size returned contradictory results with size being the only significant variable accounting for 7% of variation. All other variables were insignificant within this phylogenetic framework. Figure 13B shows the similarity in evolutionary trajectories for each clade, which when taken with the post hoc test for homogeneity of slopes found that, out of 55 pairwise comparisons, only two had significant differences in slopes (Table 18). The significantly different comparisons are the felines/pantherines to the hyaenids ($p < 0.002$) and nimravids as compared to the machairodontines ($p < 0.004$).

Dietary Impact

The regression of RBL on degree of carnivory returned a significant correlation ($R^2 = 0.55$, $p < 2.2e^{-16}$). However, the phylogenetic ANOVA of cranial shape on diet was not significant ($R^2 = 0.02$, $p < 0.12$). Figure 14 shows the relationship between these variables, where from 0 to 70% vertebrate material in the diet, feliforms possess a narrow range of cranial shapes, while at $\geq 80\%$ feliforms occupy a very diverse range. This pattern is reflected in the cranial disparity

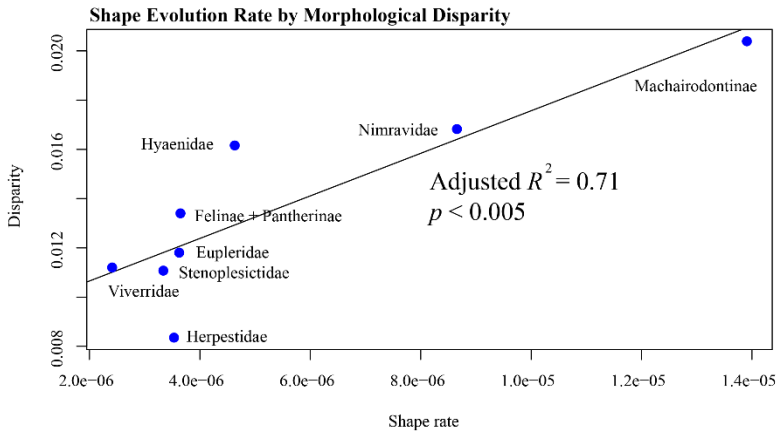
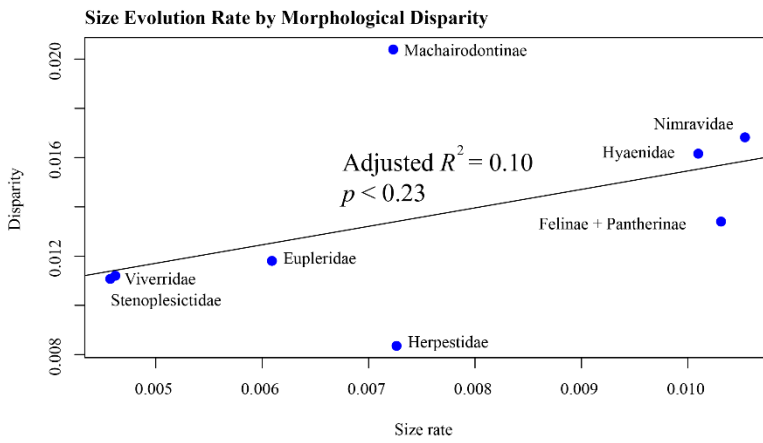
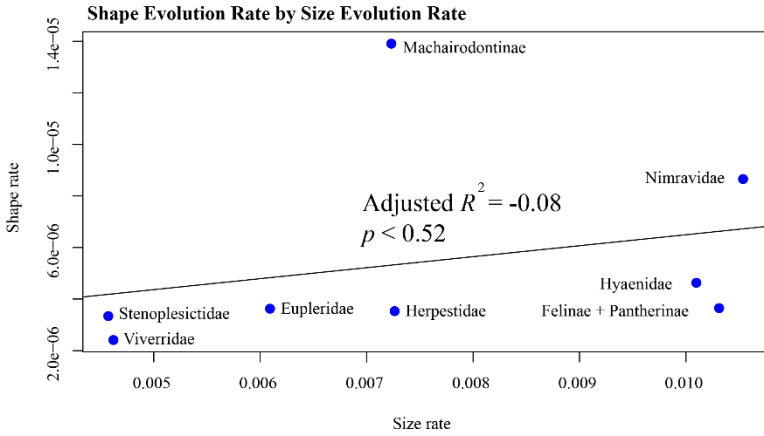


Figure 12. Relationship between feliform size and shape evolutionary rates, and morphological disparity (Procrustes variance). Disparity has been adjusted for allometry and age of lineage.

Table 18. Pairwise cranial shape evolution rates between dietary ecologies in upper triangle, with p-value significance in lower triangle.

	Hypocarn.	Mesocarn.	Hypercarn.	Durophag.	Sabertooth	Invertivor.
Hypocarn.	-	1.29	1.74	2.36	5.07	1.81
Mesocarn.	1	-	1.35	1.82	3.92	1.4
Hypercarn.	0.015	1	-	1.35	2.91	1.04
Durophag.	0.015	0.06	0.944	-	2.15	1.3
Sabertooth	0.015	0.015	0.015	0.015	-	2.8
Invertivor.	0.03	1	1	1	0.015	-

(Procrustes variance) of species with $\geq 80\%$ vertebrate material in their diet being greater than that of those $\leq 70\%$, 0.014 versus 0.009. Furthermore, phylogenetic signal was greater for those species with $\leq 70\%$ vertebrate material in their diet ($K = 0.6587$, $p < 0.001$), while less for those with $\geq 80\%$ ($K = 0.4003$, $p < 0.001$).

Discussion

Ecological cranial shape and disparity

The PCA of cranial morphospace (Figure 8) and phylogenetic regression of degree of carnivory on cranial shape (Figure 14) found broad connections to ecology, but not the degree reported in some past analyses (Wroe and Milne, 2007; Goswami et al., 2011). There is a distinct region of morphospace occupied by sabertooth feliforms, but almost the entirety of hypo-mesocarnivores, i.e., herpestids, viverrids, euplerids, stenoplesictids, prionodontids overlap each other. What remains are two other distinct regions, occupied by hyaenids and felids respectively (with some overlap from sabertooth clades) indicating that phylogeny might have substantial input on morphospace occupation compared to dietary category in most cases among feliforms.

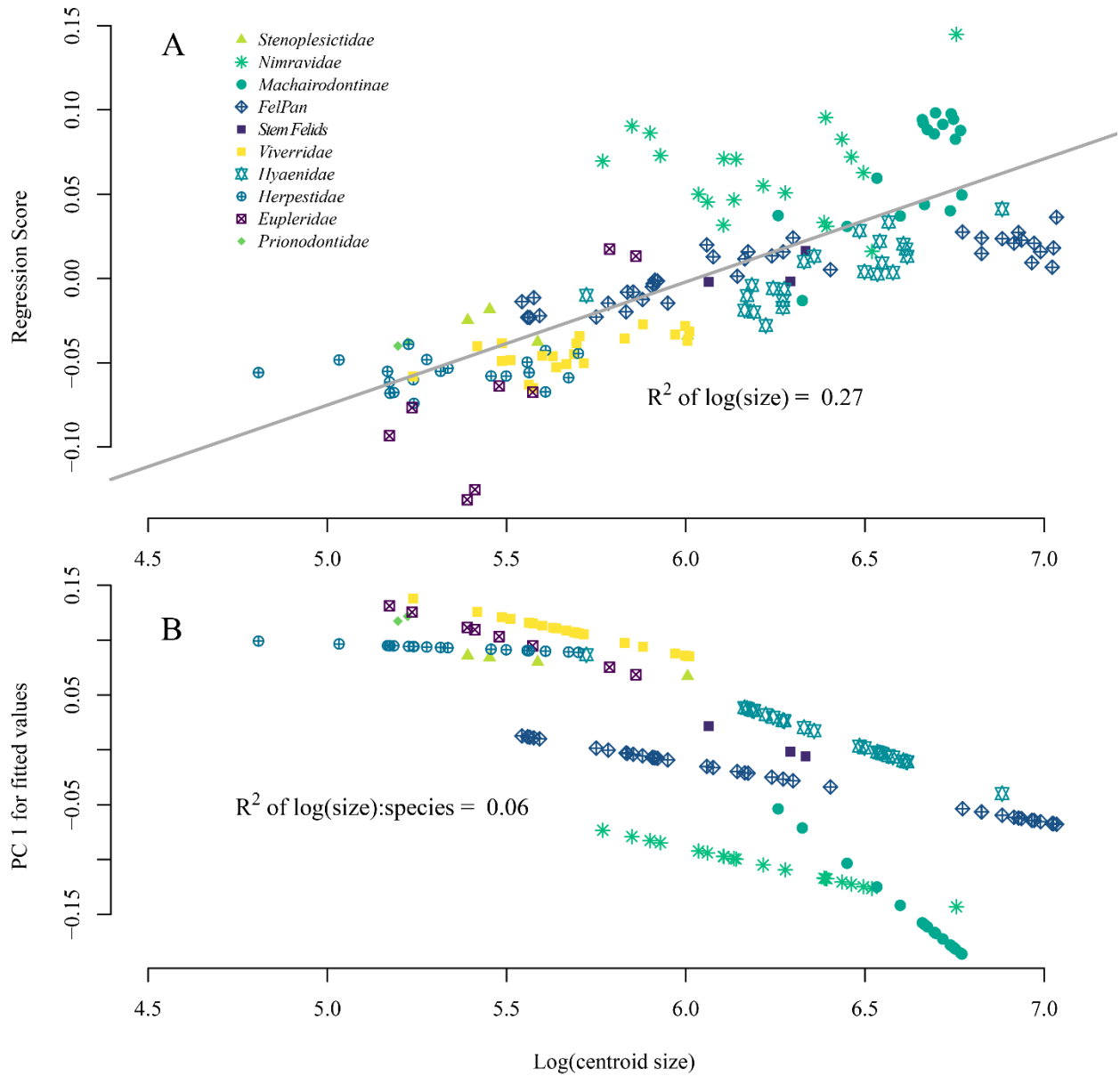


Figure 13. Log centroid size versus the regression scores of shape and size for each specimen (A). Idealized allometric trajectories predicted values for each clade, highlighting similarities in evolutionary allometric slopes (B).

Table 19. Evolutionary allometry pANCOVA. Csize = centroid size, Df = degrees of freedom, SS = sum of squares, MS = mean square, R2 = coefficient of determination, F= F statistic, Z= effect sizes, Pr(>F) = significance value.

	Df	SS	MS	Rsq	F	Z	Pr(>F)
log(Csize)	1	0.006	0.006	0.073	5.216	3.506	<0.001
clade	9	0.006	0.001	0.07	0.553	-2.666	<0.994
log(Csize):clade	8	0.009	0.001	0.102	0.91	-0.132	<0.55
Residuals	54	0.064	0.001	0.756			
Total	72	0.085					

This lack of convergence of skull shape on diet or ecology is reflected in the regression of degree of carnivory, where there exists a narrow range of cranial shapes for the vast majority of the dietary spectrum, and only within the realm of hypercarnivory do cranial shapes occupy new and more variable zones. This result is more aligned with recent studies that were unable to find significant correlation between cranial shape and diet among carnivorans (Law et al., 2018b; Rovinsky et al., 2021).

The present results support a decoupling of cranial shape and diet until hypercarnivory is reached. The vast majority of diets are served by a narrow cranial shape, or “one-to-many” ecological mapping. This dietary regime does coincide with changes in dental morphology, implying dentition is far more labile relative to a species’ environment than what its skull looks like. Crania within this range are thus little altered (or subject to stabilizing selection) from ancestral morphology as indicated by the stronger phylogenetic signal ($K=0.66$), with observed variation likely the outcome of phylogenetic stochastic processes (Raup and Gould, 1974).

Table 20. Pair-wise homogeneity of slope test summary of p values for distinct evolutionary allometric trajectories. Significantly different comparisons are in bold. Fel Pan = Felinae + Pantherinae, Machair. = Machairodontinae, Prionodont. = Prionodontidae, Stenoples = Stenoplesictidae

	Eupleridae	Stem Felid	FelPan	Herpestidae	Hyaenidae	Machair.	Nimravidae	Prionodont.	Stenoples.	Viverridae
Eupleridae	1	0.94	0.745	0.383	0.982	0.97	0.926	0.95	0.473	0.257
Stem Felid	0.94	1	0.353	0.681	0.347	0.986	0.669	0.942	0.936	0.605
FelPan	0.745	0.353	1	0.311	0.002	1	0.515	0.9	0.854	0.663
Herpestidae	0.383	0.681	0.311	1	0.976	0.944	0.138	0.936	0.703	0.964
Hyaenidae	0.982	0.347	0.002	0.976	1	0.822	0.09	0.928	0.411	0.659
Machair.	0.97	0.986	1	0.944	0.822	1	0.004	0.948	0.998	0.99
Nimravidae	0.926	0.669	0.515	0.138	0.09	0.004	1	0.91	0.341	0.499
Prionodont.	0.95	0.942	0.9	0.936	0.928	0.948	0.91	1	0.95	0.936
Stenoples.	0.473	0.936	0.854	0.703	0.411	0.998	0.341	0.95	1	0.313
Viverridae	0.257	0.605	0.663	0.964	0.659	0.99	0.499	0.936	0.313	1

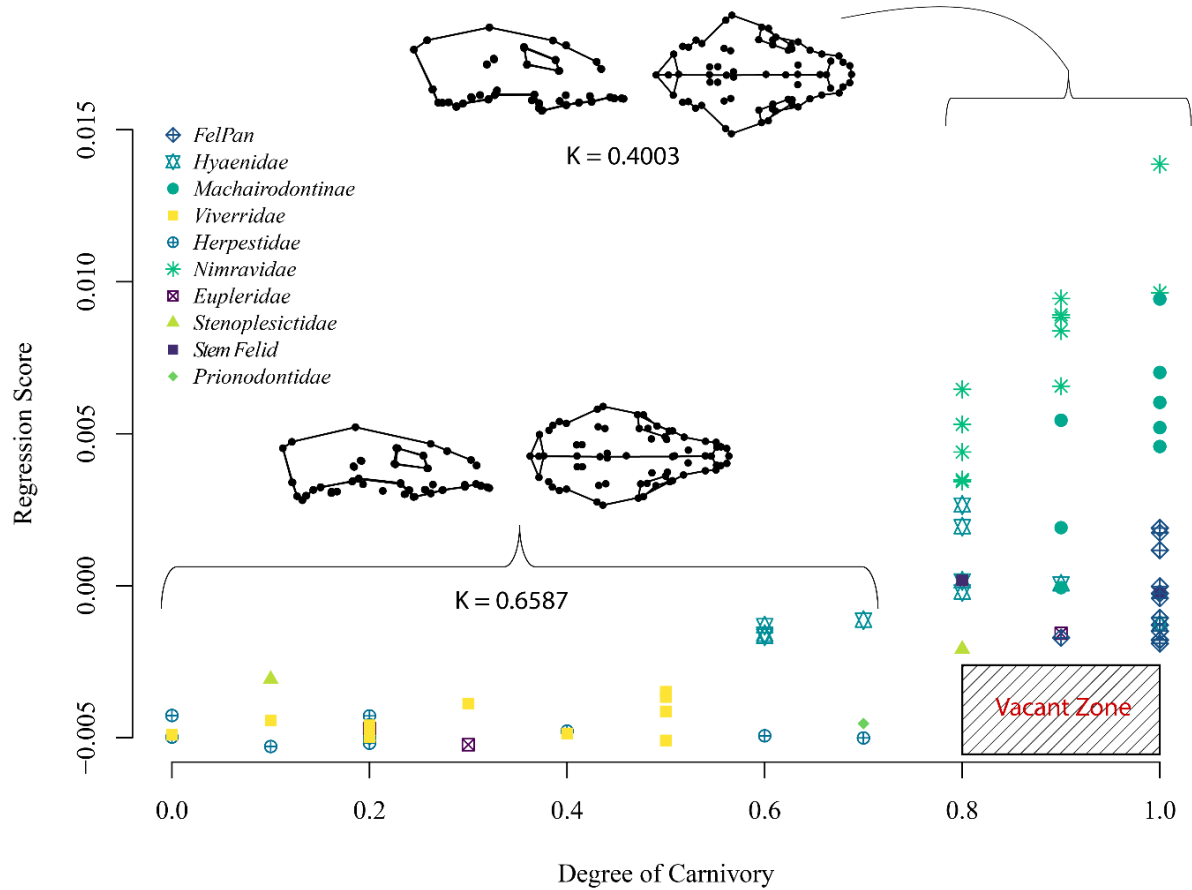


Figure 14. Relationship between degree of carnivory and feliform cranial shape (PGLS). Mean cranial shape (in right lateral and dorsal views) of species with $\leq 70\%$ vertebrate material in their diet below and $\geq 80\%$ above. Presented K values indicate associated phylogenetic signal for the cranial shapes of those species.

Hypercarnivores, on the other hand, occupy a diverse range of cranial shapes that likely are needed to subdue and consume a proportionally diverse set of prey or animal materials. This can be viewed as “many-to-one” mapping of morphology to ecology, with the “one” truly referring to the narrow band of almost exclusively vertebrate material in the diet. Within this zone there

are differential demands upon the feliform skull that are not met by the ancestral shape, and thus no hypercarnivore taxon analyzed occupied that zone. Other studies have shown the demands of bite force and its effect on cranial shape when it comes to hypercarnivory (Law et al., 2018b), durophagy (Tseng and Wang, 2011; Figueirido et al., 2013; Tseng, 2013), or sabertooth morphology (Figueirido et al., 2011; Christiansen, 2012). Taken together, these demands require different optimization leading to distinct cranial shapes, such as the dissipation of compressive force in durophagous hyaenids, the required increase in the gape of sabertooth feliforms, and overall cranial rigidity and strength in bite force for hypercarnivores in subduing/consuming their prey.

Surprisingly, only one of the analyzed pair-wise comparisons of ecological category and cranial disparity found significance: sabertooth forms versus hypocarnivores. While each ecological category has a distinct cranial morphology, the range of variance within each category is similar. This feature of sabertooths was also observed in the osteometric analysis of Holliday and Stepan (2004) where increasing specialization did not correlate with morphological diversity except in the most specialized sabertooth taxa. The uniqueness of sabertooth taxa may relate to niche partitioning of scimitar- and dirk-tooth forms occupying additional morphospace (Lautenschlager et al., 2020). This greater disparity is reflected in extremely high rates of morphological evolution (Table 16), greater than all other ecological categories (2.2-5.1 times faster), suggesting high selective pressures for these cranial shapes. High rates were also observed for durophagous and hypercarnivorous carnivores relative to hypocarnivorous ones, but the associated disparity of these categories was not significantly different. The disparity of non-sabertooth hypercarnivores compared to more generalized ecomorphs has been contradictory. Holliday and Stepan (2004) recovered hypercarnivores with less disparity than non-

hypercarnivorous sister groups, while Michaud et al. (2020), found greater cranial disparity among hypercarnivorous feliforms than generalists (all other taxa) in their analysis. However, both may be accurate in describing certain patterns through respective methodological approach. Holliday and Stepan (2004)'s data primarily looked at dentognathic measurements, such as specific tooth lengths and widths and dentary output lever lengths. As previously stated, hypercarnivory showed trends in tooth loss and tooth row length reduction to accommodate higher bite forces, while dentition was often simplified in overall topography to facilitate slicing or bone-crushing mechanics. With the loss of posterior molars, overall variance would necessarily go down (no variance for these structures), leading to less overall disparity than taxa with broader diets. Michaud et al. (2020) and the present study suggest that from a cranial shape point of view, hypercarnivores are just as capable of occupying a range of shapes as other dietary categories with many pathways/shapes lending themselves to a hypercarnivorous ecology (many-to-one mapping). Conversely, dentognathic restrictions on a diet high in vertebrate material are limiting, especially in regard to evolvability of non-hypercarnivorous ecologies and broader diets.

Clade disparity and impact of lineage age

As questioned at the start of this study, the age of a lineage may play a substantial role in explaining disparity among clades, as an ancient lineage may have simply accrued substantial disparity by random walk dynamics over geologic time, disparity that younger clades may also achieve if provided with enough time. Indeed, there is a correlation of cranial disparity and age of lineage, where nimravids, as the oldest lineage, (34.3 Ma), have the greatest disparity. Similarly, herpestids have the least and are the youngest lineage (9.52 Ma), while all others are intermediate. Thus, adjusting for both allometry and age of lineage, where do we find the

greatest variance in cranial shapes amongst feliforms? In other words, on a more level playing field of size and time to evolve numerous and varied shapes, do certain clades still possess exceptional cranial disparity? Yes, with this adjustment machairodontines become the most diverse clade of cranial shapes, followed by similar values for nimravids and hyaenids. Felines/pantherines, euplerids and viverrids form a clump of similar values in third, while herpestids still remain the least disparate clade. In short, felids possess the greatest cranial disparity amongst feliforms. Setting aside sabertooth morphs for a moment, this great level of disparity is still observed in felines/pantherines, having comparable values to ecologically and taxonomically diverse euplerids and vivverids. Though perhaps not apparent in the outward appearance of many felids, derived cranial shapes have been the subject of several analyses, such as the unique skull of the cheetah (*Acinonyx jubatus*) that possesses resistance to compressive forces more analogous to a durophage and unlike the expectation for a cursorial specialist (Chamoli and Wroe, 2011; Tseng, 2013). The incipient sabertooth morphology of the clouded leopard (Christiansen, 2006, 2008c) also adds to the diverse morphological range of this clade, as does the primarily piscivorous flat-headed cat (*Prionailurus planiceps*), with a cranial shape consistent with its name. These relatively high cranial disparity values for felids were also observed by Michaud et al. (2018) and Figueiridoe et al. (2011) in their analyses, in spite of a different method of assessment and range of taxa.

Perhaps unsurprisingly, relative canine size had substantial impact on cranial shape for machairodontines (~19%) and nimravids (~24%), the clades containing sabertooth feliforms. However, euplerids saw the greatest impact of this variable (~47%), a result which may be correlated with the taxa sampled. Only four species of euplerid were included in this study, representing extremes and apparent average of cranial shape for the family. Most euplerids

appear similar to their African herpestid relatives (e.g., *Salanoia*), while others are ecomorphologically divergent towards invertebrate diets, such as *Eupleres*, or hypercarnivory in *Cryptoprocta*. This high cranial variance was found to be the greatest among living feliforms by Michaud et al. (2018), but with the narrow sample of this study, the hypercarnivorous outlier of *Cryptoprocta* may be driving an overrepresented relative canine size signal. Greater taxonomic inclusion may reduce the RCS signal for the clade and/or inform on the extent of modification that occurs in the euplerid skull to accommodate hypercarnivorous canines.

For the sabertooth clades, hypertrophied canines no doubt contribute to the greater range of cranial shapes not seen in other hypercarnivores. The required reorganization of the cranium to wield such hardware has been argued as a possible escape of soft-flesh specialists into new realms of disparity, when retreating back into omnivory or a more general diet is no longer possible (Holliday and Stepan, 2004). Nimravids' high disparity may be summarized across several ecomorphs that would later appear in machairodontines and maybe even felines (Barrett, 2021). The “cat-like” cranial morphology may represent the only way to exist as a soft flesh specialist unless sabertooth modifications are undertaken. However, once that evolutionary path is opened, differential niches in scimitar- or dirk-tooth morphology may allow renewed variation to exist as large canines (and associated behavioral adaptations) are incorporated into the hypercarnivore mold. What follows are high rates of morphological evolution, with rapid selection for these features, generating a relationship between rates of morphological evolution and disparity (Figure 12), not seen in other clades (Slater, 2013; Jones et al., 2015; Michaud et al., 2018; Simons et al., 2020).

Allometry

The relatively large predictive influence of size on cranial shape (27%) suggests that allometry is indeed important within Feliformia (for some clades such as felines and pantherines extremely so) such that there may be a common allometric trajectory for this clade. Furthermore, if size variation represents a line of least evolutionary resistance for morphological evolution, it would be expected that (1) rates of size evolution would be correlated with rates of cranial shape evolution, and (2) rates of size evolution would be predictive of cranial disparity. Taken at face value these connections do not exist within the results of the present study (Figure 12). However, when comparing size and shape rates of evolution, machairodontines and nimravids exist as outliers from what appears to be an otherwise linear relationship. Removal of these clades still results in a non-significant relationship ($R^2 = 0.46$, $p < 0.08$), but the reduced power of fewer observations may obfuscate a real correlation. As discussed throughout, sabertooth taxa exhibit anomalously high rates of evolution, and nimravids are recovered with the lowest levels of allometry of any feliform clade assessed, a non-statistically significant 9%. Part of this may relate to the existence of highly derived (e.g. dirk-tooth) nimavid taxa at either end of the size spectrum (Barrett, 2021), demonstrating that size is not required to generate these extreme morphologies. These low allometric values are not seen in machairodontines, but the even higher rates of morphological evolution within this clade fits into a narrative of high selective pressure and rapid evolution for this ecology.

Even with these deviations in morphological rates of evolution for sabertooth clades, support for some level of common allometry amongst feliforms was found in this study (Table 14, Figure 13). Save sabertooth taxa and the vermivore specialist *Eupleres*, most taxa present a linear relationship in shape with increasing size. Comparisons of idealized allometric trajectories

further found only two significantly different results, that of machairodontines and nimravids; and hyaenids with felines/pantherines. Machairodontines and nimravids evolved similar cranial shapes but did so under apparently different allometric trajectories. Implying that size, once again, has a differential impact on cranial evolution for these clades. The other clades that differ significantly, hyaenids and non-sabertooth felids, perhaps demonstrate the uniqueness in size-correlated changes amongst soft-flesh specialists with reduced tooth counts and brachiocephalic crania compared to those of incipient to fully developed durophagy and comparatively dolichocephalic crania. Regardless, the deviants are all clades with large size ranges, and all contain hypercarnivores, with hyaenids the only of these clades containing taxa that are not solely hypercarnivorous. The lack of significance between other clades may thus relate to a lack of selective pressure to pull them off this common allometric trajectory of utility of mapping a narrow range of generalized cranial shapes onto a broad swath of dietary possibilities. The lack of significant differences in allometric trajectories between hypercarnivorous clades and more generalized ones may then simply be a result of lack of overlap in size ranges to robustly infer these differences, or small members of hypercarnivorous clades are not that different from large members of generalist clades, as in hyaenids.

A variable connection in macroevolutionary size to shape is observed in several clades. For example, Simons et al. (2020) found no correlation in catarrhine primate morphological evolutionary rates (size or shape) and disparity, but did find a correlation for size and shape evolutionary rates, unlike the present study. However, their additional finding that most of the variation in within-clade allometries is best explained by a shared allometry model indicates that allometry is still an important factor in catarrhine cranial evolution. This hypothesis is supported by numerous other primate studies (Collard and O'Higgins, 2001; Singleton, 2002; Mitteroecker

et al., 2004; Schaefer et al., 2004), which found that allometric trends are apparent in interspecific cranial shape differences, but that species do not merely share allometric scaling trajectories. Instead, details of primate evolution are likely constrained by the necessity of maintaining the numerous functional roles of the cranium throughout an organism's life span preventing size from being the sole force in the production of morphological disparity (Simons et al., 2020).

Comparatively, Marcy et al. (2020) found strong support for conserved allometric slopes across Australian murids, save for carnivore and folivore specialists. The static (within-species) allometric trajectories were self-similar to evolutionary (among-species) Australian murid allometry. This pattern is more similar to that seen in non-mammalian vertebrate clades. Bird cranial evolution seems to possess strong allometric patterns; for example, the shape of bird of prey beaks is controlled almost entirely by size (~80%, Bright et al., 2016). In another example of this strong allometry in birds, most nightbird (Strisores) cranial shapes display changes associated with heterochrony (Navalón et al., 2021). Similarly, encephalization, or growth of the brain causes changes in the topology of its bony base inside the cranium leading to predictable effects on the shape of the whole skull (Marugán-Lobón et al., 2022).

Overall, mammals are thought to have a high degree of evolvability in cranial allometry (Tsuboi et al., 2018), such that specific or generic allometric slopes can be far more variable than seen at higher taxonomic levels. Taken together with the present study, it appears that feliforms share relatively similar allometric trajectories until ecological selection on some aspect of hypercarnivory pulls them off into new realms of shape space. Certain clades, such as hyaenids, appear to deviate less from generalized small feliform taxa, while soft-flesh specialists like felids

and nimravids possess the greatest shift in allometric intercepts and possibly slopes to accommodate their derived ecology.

Cranial integration

The idea that variation, or the raw material for evolution, may not be isotropic in nature, but instead has limitations that facilitate or constrain subsequent evolution, has been a prominent hypothesis within evolutionary theory for well over a century (Galton, 1869; Gould, 2002).

Strong correlations between traits may limit or outright prevent certain traits from existing, while on the other hand, such correlations may funnel or fruitfully channel variation in extreme directions that increase the rate and/or magnitude of observed variation (Goswami et al., 2014).

This idea of constraint may then be a fertile hypothesis for why certain feliform clades never achieved a given level of disparity in their evolutionary history, representing a “smoking gun” of underlying processes worthy of investigation. For the present study, magnitude of cranial integration was employed as a proxy of developmental constraint, one that has the additional benefit of being collected from the fossil record.

Amongst carnivorans, there have been contradictory results and arguments for the effect of integration on the generation of cranial disparity. For example, increasing integration has been used to explain increased disparity across the latest Pleistocene in *Smilodon* and dire wolves (Goswami et al., 2015), while that same integration may also be responsible for differential morphospace occupation of machairodontines compared to nimravids (Goswami et al., 2011). Conversely, in assessment of cranial module integration and disparity for living terrestrial carnivorans and primates, over half of comparisons found no significant correlation between these variables, but when significant results were found the effect of integration on disparity is in limitation of morphological variability (Goswami and Polly, 2010a). A similarly complicated

result was found for pinnipeds, wherein ecology may be driving integration values (Randau et al., 2019), while no correlation was found in levels of integration and disparity generated when comparing domesticated mammals with their wild ancestors (Wilson et al., 2021).

Like these latter studies, the predictive power of integration on disparity of this analysis returned insignificant results (Figure 10 and Figure 11). This was still the case when values of raw clade disparity were used for eigenvalue dispersion ($R^2 = -0.16, p < 0.69$), while even poorer results for between-module integration ($R^2 = -0.20, p < 0.90$). These results suggest that no connection exists between how tightly integrated (developmentally or otherwise) a feliform's cranium is and the range of morphological variation it can achieve. Instead, crania remain generally similar to each other, fulfilling a wide variety of dietary and ecological roles until the constraint of hypercarnivory comes into play. At this time, necessary considerations for subduing or processing non-compliant vertebrate prey overrides the ancestral cranial shape in feliforms generating new morphologies. Some of these shapes appear to fall on a common allometric trajectory of smaller clades (i.e., hyaenids), suggesting that the path to generating diverse prey material hypercarnivory and durophagy has a solution different than that of soft-flesh specialized hypercarnivores. Felids and nimravids occupy their own allometric and morphospace realms reflecting a presumed similar ecology and path into their varied cranial shapes, perhaps ending in sabertooth morphology. Regardless, feliform cranial shape seems to remain the same until it isn't. There is no underlying restriction (as assessed via integration) that prevents them from achieving disparate cranial forms; instead, a high dietary/ecological bar must be cleared before selection pressure directs cranial evolution into new realms.

Chapter V

Conclusion

Feliforms of small size exist within a realm of opportunity. This ecospace allows the exploitation of diverse resources including invertebrate-dominated diets, folivory, frugivory, hypocarnivory and mesocarnivory. A narrow range of cranial shapes accomplishes these diverse diets, while the dental toolkit is unencumbered to optimize for the challenges in processing each food material (Figure 15). This pattern is seen in the random walk small feliform body size and dental toolkit take as they evolve, the labile nature of convergent evolution of living small feliform species (Gaubert et al., 2005), and the challenges in resolving phylogenetic relationships amongst fossil taxa of this ecospace. However, there is a tipping point where extreme diet, and to a lesser extent body mass, take over, to shape the morphology and ecology of feliform evolution.

Hypercarnivory, as observed at $\geq 80\%$ vertebrate material in the diet, forces selection for more robust cranial morphology to subdue and process prey items. This selection necessitates vacating the ancestral feliform cranial mold and occupying a distinct, broader area of shape space.

However, what path a feliform takes into this realm depends upon its style of hypercarnivory and distinct ecospace. Soft-flesh specialists such as felids, nimravids, *Cryptoprocta* and *Proailurus* rapidly acquire their familiar cranial and dentognathic condition, with loss of posterior molars, enhancement of the shearing surfaces of the carnassials, robust canines and brachiocephalic crania. With the loss of grinding dentition and the associated capacity to process plant material, there appears to be no return to former ecospace. This is not all bad, for soft-flesh hypercarnivory is tenable across multiple orders of magnitude in body size; one can be minute as in the black-footed cat (*Felis nigripes*), less than 2.5 kg (Renard et al., 2015), or enormous as in

the extinct North American Lion (*Panthera leo atrox*), up to possibly 457 kg (Wheeler and Jefferson, 2009). Furthermore, allometry may offer a line of least evolutionary resistance for these hypercarnivores, for access to new prey items may only require the cranial (and likely post-cranial) changes associated with allometric scaling (Meachen-Samuels and Van Valkenburgh, 2009; Slater and Van Valkenburgh, 2009), scaling that differs compared to non-soft-flesh-specialists. Though, a more extreme realm exists beyond these familiar cat-like shapes from this ecospace, one of sabertooth morphology. Becoming sabertooth opens new doors into cranial disparity, variance not seen within any other ecomorphology. An obvious source for this increased variance is the reorganization of the cranium to facilitate wielding such hardware, but two new ecologies appear to open up as well, that of scimitar- and dirk-tooth morphs. Scimitar-tooth carnivores fall closer to the common allometric line of other feliforms (Fig. 13A), requiring fewer modifications in terms of gape management than dirk-tooth morphs. Studies of machairodontines find differentiation in their respective diets via isotopic analysis, which is also reflected in their respective *baupläne* argued to favor pursuit or ambush predation (Feranec, 2004; DeSantis et al., 2021). Regardless, body mass doesn't appear to be that important as a sabertooth carnivore. Some of the smallest nimravids were also the most derived dirk-tooth morphs, such as *Eusmilus cerebralis*, but the inferred largest feliform of this entire study, *Barbourofelis fricki*, was possibly the most derived dirk-tooth placental mammal to have ever existed (Barrett, 2021). This range of extremes is not as complemented in equal extremes of body mass in machairodontines, but bobcat sized members are known to have also existed (de Bonis et al., 2018), though unable to be included in this study.

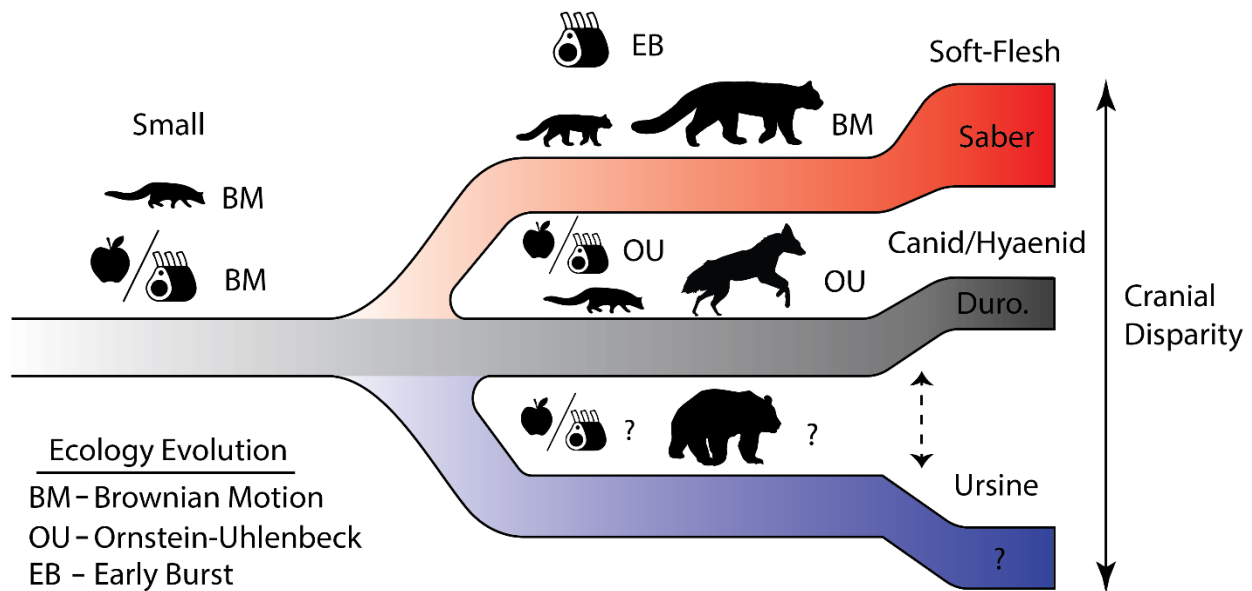


Figure 15. Hypothesis of terrestrial carnivoran evolution with regards to ecology and cranial morphology. Silhouettes reference relative body size possible within each ecospace (small to large), while food icons an approximation of dietary spectrum. Silhouettes taken from Phylopic.org.

The other feliform path into hypercarnivory is that occupied by hyaenids. Unlike soft-flesh specialists, hyaenids facilitate their cranial shape by use of the common allometric trajectory of most feliforms, those occupying the small-bodied ecospace. Hyaenids are notable in their ecological exploitation of nearly all dietary categories examined in this study, though with two exceptions, soft-flesh specialization as in living felids, and sabertooth morphology. Why didn't hyaenids evolve these ecomorphologies? As stated above, reduction or loss of posterior molars is associated with felid ecomorphology. This reduction is seen in *Hyaena*, and to a greater degree in *Crocota*, where M1s are typically not present. However, all hypercarnivorous hyaenids

maintain robust premolar dentition, something not seen in felids nor nimravids. Indeed, the upper P3 and lower p3-4 are used for durophagy in many hyaenids, but not all, such as *Chasmaporthetes* (Coca-Ortega and Pérez-Claros, 2019). So again, why the difference? It is informative that canids and hyaenids returned similar results in the mode of their ecological evolution. Both clades found the best fit for an optimal body mass and dental toolkit per dietary category, and canids also did not converge on soft-flesh specialization in the same way as felids and nimravids. Amongst canids, hypercarnivory is a delayed acquisition of ecospace evolution (Slater, 2015). It forms a terminus of ecomorphology across all three subfamilies. Compare this to the paleoecology analyses of felids and nimravids, which saw greatest support for early burst dynamics directly into hypercarnivory. A clearer picture of the evolutionary trajectory for hyaenids will require a more comprehensive phylogeny, that better samples the ‘ictitheres’ and the more hypo- to mesocarnivorous lineages. However, current literature suggests that the evolution of hypercarnivory in hyaenids is similar to that of canids with delayed acquisition (Werdelin and Solounias, 1991; Turner et al., 2008). Hyaenids may be unable to access soft-flesh specialization, as were canids, from insurmountable phylogenetic inertia. The fossil record suggests that both lineages developed cursorial morphology, early on losing the ability to supinate and pronate the forelimbs, and to retract the distal phalanges (Hunt Jr. and Solounias, 1991; Wang, 1993; Figueirido et al., 2015; Gracia, 2015). Generally speaking, the felid postcranial condition is plesiomorphic among Carnivoramorpha (Spaulding and Flynn, 2009, 2012; Solé et al., 2014, 2016) and likely associated with arboreal adaptations to the dense canopy forests of the Eocene (Tomiya et al., 2021). Cursoriality favors face-orientated predation in canid-like hypercarnivores, compared to ambush and grappling strategies found in felids, and presumably nimravids (Ewer, 1973; Andersson, 2005). The cranium of soft-flesh specialists

maximizes gape capability while balancing bite force (even in non-sabertooths) to allow quick dispatch of prey, a benefit in solitary predators (Figueirido et al., 2011; Meloro et al., 2015). Thus, the early trajectory of hyaenids and canids into cursoriality with increasing body size may not have allowed them to switch tracks to the ecospace shared by felids and nimravids. Instead, the hyaenid/canid postcranial situation may have predisposed these lineages to communal hypercarnivory, necessitating a different strategy in capturing large prey (Van Valkenburgh and Koepfli, 1993; Van Valkenburgh et al., 2003). This hyaenid/canid ecospace and associated evolutionary trajectory may also be shared by the amphicyonid lineages, Daphoeninae and Temnocyoninae, and the ursid hemicyonines (Hunt, 1996, 1998b, 2001b). All experienced similar patterns of cursorial adaptations and dolichocephalic cranial shapes with broad dental tool kits capable of omnivory. Furthermore, all of these lineages produced members with adaptations to durophagy via hypercarnivory, save perhaps hemicyonines. Future paleoecological and cranial morphology analyses could assess the validity of the comparison, but sufficient phylogenies are also in need.

Interestingly, a fourth ecospace category may exist, encompassing extant ursines. Turning to the fossil record it appears that the Amphicyoninae lineage once occupied this ecospace, featuring large size, relative plantigrade posture, but a range of hypo-hypercarnivorous diets. Much like the above comparisons to other caniforms, future study may find a unique hypercarnivorous end member for this ecospace, one possibly occupied by taxa such as *Ysengrinia* and *Magericyon* (Viranta, 1996; Peigné et al., 2008; Soledad Domingo et al., 2013). Furthermore, unlike the previous ecospace, both ursids and amphicyonids seemed capable of switching from canid/hyaenid ecospace to the ursine space during their evolutionary history and thus offer a

unique area of inquiry of why these clades were able to make the shift, while hyaenids and canids were not.

The above discussion offers potential pathways in carnivoran evolution, but not the process-based push that may get them moving or shifting to new zones. For that, contingency in natural history may be the best explanation. Small feliforms, and maybe even caniforms such as mustelids, procyonids, ailurids, mephitids, seem labile in their ability to shift rapidly in diet and associated dental toolkits. However, climatic and tectonic sourced opportunity may be required to facilitate rapid radiations into soft-flesh specialized hypercarnivory or the wide ecological occupation of canids and hyaenids. Nimravids gained purchase in North America, through circum-Pacific immigration from Asia, into an increasingly mosaic forested landscape after the Mid-Eocene climatic optimum. This was also shortly after the extinction of sabertooth machaeroidines (Zack et al., 2022), facilitating a potential contingent opportunity for nimravids. The Oligo-Miocene transition saw both global warming and the African-Eurasian interchange. This period correlates with the divergence of hyaenids from their common ancestors with herpestids and euplerids the origin of felids, the origin and diversification of lophocyonids, and initial diversification of the barbourfelids. In short, an immense diversification, in both taxonomic and ecological diversity of feliforms. The most recent example of such contingent global opportunities may be the Middle Miocene Climatic Optimum, which recovers this time as the appearance of the most recent common ancestor for the extant radiation of viverrids and herpestids + euplerids, and the divergence of machairodontine felids from felines + pantherines. The success of euplerids is itself a phenomenal example of contingent evolution with the sweepstakes dispersal of a herpestid-like ancestor rafting to Madagascar and diversifying into the

ecologically broad family known today. So, viewed in one light, feliforms have been capable of invading numerous ecologies around the globe; they just required the opportunity to do so.

Considering the original question: Is there evolutionary constraint in feliforms? Apparently yes, but not in the way typically framed. Herpestids, viverrids, euplerids, prionodontids, etc. are constrained in staying small to exploit the diverse range of ecologies they occupy, small size that frees them from metabolic and functional challenges of greater mass. Additionally, they can do all of this with relatively little change in cranial morphology. However, once a feliform enters one of the other ecospace pathways outlined above, new constraints come into play, such as retreating from soft-flesh specialist hypercarnivory into a broader dietary category or switching tracks from the canid/hyaenid ecospace into the aforementioned felid/nimravid space. These constraints fruitfully channel the extreme endmembers of cranial evolution and ecology that otherwise are inaccessible to other groups, i.e., sabertooth and durophagous morphology. An important distinction of this work is the lack of support for an inherent developmental or cranial disparity constraint on the variation observed for supposedly stymied specialists, such as felids. Quite the opposite in fact; felids possess the greatest range of cranial variety of any feliform. Though narrow in their vertebrate dominated diet, they seem to have explored a diverse set of options in cranial shape, options that do not exist for more generalist feliforms, or ones that maybe could not exist without the constraints that have affected their evolutionary trajectory.

In the end, it seems Galton was correct. Only certain channels or facets seem viable for the route of evolution. This is expressed in the irreversible loss of the cusps and teeth in hypercarnivores, or the “re-development” of grappling forelimbs with retractile claws in lineages with cursorial postcrania. These kinds of limitations shape the evolutionary landscape, generating channels down which variation can proceed. This in turn is seen as convergence in the fossil record, and

for this study, the smoking gun of channelized evolution among terrestrial mammalian carnivores. Indeed, the above discussion points out these patterns among carnivores, but broader taxonomic inclusion finds similar ecospace for Sparassodonts in South America (Prevosti et al., 2012; Forasiepi and Sánchez-Villagra, 2014), marsupials in Australia (Rovinsky et al., 2021) and hyaenodont and oxyaenid “creodonts” (Borths et al., 2016; Zack, 2019b), the latter of which also developed sabertooth morphology within the machaeroidines (Zack et al., 2022). These broad repeated patterns suggest that the interface of terrestrial mammalian carnivores with Cenozoic ecosystems has been consistent. That within this framework only certain trajectories are possible to be a successful carnivore. These channels do provide a limit on what ecology and morphology is feasible, but they also facilitate the fruitful possibilities of extreme carnivory, unique for each channel.

Appendix A

Genbank Accession numbers for molecular data in phylogenetic analysis

	Nuclear			Mitogenome												
	IRBP	CH RN A-1	TTR-intron 1	MT-ATP6	MT-ATP8	MT-COI	MT-CO2	MT-CO3	MT-CYB	MT-ND1	MT-ND2	MT-ND3	MT-ND4	MT-ND4L	MT-ND5	MT-ND6
<i>Acinonyx jubatus</i>	XM_027062497	DQ081826	DQ082517	AF344830.1	AF344830.1	AF344830.1	AF344830.1	AF344830.1	AF344830.1	AF344830.1	AF344830.1	AF344830.1	AF344830.1	AF344830.1	AF344830.1	AF344830.1
<i>Arctictis binturong</i>	DQ683125			KX449332.1	KX449332.1	KX449332.1	KX449332.1	KX449332.1	KX449332.1	KX449332.1	KX449332.1	KX449332.1	KX449332.1	KX449332.1	KX449332.1	KX449332.1
<i>Atilax paludinosus</i>			AY750604			JF444116.1			AF522324.1		AY750647.1					
<i>Bdeogale nigripes</i>			AY950643						AY950655.1		AY974022.1					
<i>Canis latrans</i>	KT447969			DQ480511	DQ480511	DQ480511	DQ480511	DQ480511	DQ480511	DQ480511	DQ480511	DQ480511	DQ480511	DQ480511	DQ480511	DQ480511
<i>Caracal caracal</i>		DQ081831	DQ082521	KP202272	KP202272	KP202272	KP202272	KP202272	KP202272	KP202272	KP202272	KP202272	KP202272	KP202272	KP202272	KP202272
<i>Catopuma temminckii</i>	AY525034	DQ081842	DQ082532	KP271500.1	KP271500.1	KP271500.1	KP271500.1	KP271500.1	KP271500.1	KP271500.1	KP271500.1	KP271500.1	KP271500.1	KP271500.1	KP271500.1	KP271500.1
<i>Civettictis civetta</i>	AY170078	GU931024	AY170023	NC_033378	NC_033378	NC_033378	NC_033378	NC_033378	NC_033378	NC_033378	NC_033378	NC_033378	NC_033378	NC_033378	NC_033378	NC_033378
<i>Crocuta crocuta</i>	AY170087	AY928700	DQ082540	JF894377.1	JF894377.1	JF894377.1	JF894377.1	JF894377.1	JF894377.1	JF894377.1	JF894377.1	JF894377.1	JF894377.1	JF894377.1	JF894377.1	JF894377.1
<i>Crocuta crocuta spelaea</i>				MN320462.1	MN320462.1	MN320462.1	MN320462.1	MN320462.1	MN320462.1	MN320462.1	MN320462.1	MN320462.1	MN320462.1	MN320462.1	MN320462.1	MN320462.1

<i>Crossarchus obscurus</i>	AY170 071		AF03 9726			JF444 131.1			AY17 0101. 1		AY17 0041. 1					
<i>Cryptoprocta ferox</i>	AY170 066	AY9 2870 5	AY1 7001 8						MG4 52178 .1		MG4 52299 .1					
<i>Cynogale bennettii</i>									DQ68 3992. 1		DQ68 3983					
<i>Eupleres goudotii</i>									KY30 5488. 1		MG4 52300 .1					
<i>Felis lybica ornata</i>		DQ0 8181 4	DQ0 8250 7	KP20 2275. 1	KP20 2275. 1	KP20 2275. 1	KP20 2275. 1	KP20 2275. 1	KP20 2275. 1	KP20 2275. 1	KP20 2275. 1	KP20 2275. 1	KP20 2275. 1	KP20 2275. 1	KP20 2275. 1	KP20 2275. 1
<i>Fossa fossana</i>	AY170 067	GU9 3102 2	AY1 7001 9						AF51 1062. 1		AY17 0037. 1					
<i>Galerella sanguinea</i>			AY9 5064 6						AF52 2331. 1		AY97 4027. 1					
<i>Genetta maculata</i>	DQ267 562		AY2 3262 7			KJ19 2810. 1			AF51 1055. 1		DQ68 3986. 1					
<i>Helogale parvula</i>		DQ0 8185 2	AY7 5060 5						AF52 2333. 1		AY75 0649. 1					
<i>Hemigalus derbyanus</i>	AY170 082		AY1 7002 7						AY17 0109. 1		AY17 0052. 1					
<i>Herpestes edwardsii</i>	AY170 080		AY1 7002 5						DQ51 9053		AY17 0050					
<i>Homotherium latidens</i>				MF87 1701	MF87 1701	MF87 1701	MF87 1701	MF87 1701	MF87 1701	MF87 1701	MF87 1701	MF87 1701	MF87 1701		MF87 1701	MF87 1701
<i>Homotherium serum</i>				MF87 1703	MF87 1703	MF87 1703	MF87 1703	MF87 1703	MF87 1703	MF87 1703	MF87 1703	MF87 1703	MF87 1703		MF87 1703	MF87 1703
<i>Hyaena hyaena</i>	DQ267 570	AY9 2870 2	DQ2 6755 2	NC_0 20669	NC_0 20669	NC_0 20669	NC_0 20669	NC_0 20669	NC_0 20669	NC_0 20669	NC_0 20669	NC_0 20669	NC_0 20669	NC_0 20669	NC_0 20669	NC_0 20669

<i>Ichneumia albicauda</i>		GU9 3102 0	AY9 5065 1			MN3 26093 .1			AF52 2341. 1		AY97 4034. 1					
<i>Leopardus pardalis</i>	AB109 335	DQ0 8183 4	DQ0 8252 4	KP20 2284. 1	KP20 2284. 1	KP20 2284. 1	KP20 2284. 1	KP20 2284. 1	KP20 2284. 1	KP20 2284. 1	KP20 2284. 1	KP20 2284. 1	KP20 2284. 1	KP20 2284. 1	KP20 2284. 1	KP20 2284. 1
<i>Lynx canadensis</i>	DQ205 910	AY9 2869 5	DQ0 8252 0	KP20 2281. 1	KP20 2281. 1	KP20 2281. 1	KP20 2281. 1	KP20 2281. 1	KP20 2281. 1	KP20 2281. 1	KP20 2281. 1	KP20 2281. 1	KP20 2281. 1	KP20 2281. 1	KP20 2281. 1	KP20 2281. 1
<i>Miracinonyx trumani</i>					DQ09 7168. 1					DQ09 7175. 1						DQ09 7170. 1
<i>Mungos mungo</i>	AY170 065	AY9 2869 8	AY1 7001 7						AF52 2347. 1		AY17 0035. 1					
<i>Nandinia binotata</i>	AY170 083	AY9 2870 4	AF03 9729	NC_0 24567	NC_0 24567	NC_0 24567	NC_0 24567	NC_0 24567	NC_0 24567	NC_0 24567	NC_0 24567	NC_0 24567	NC_0 24567	NC_0 24567	NC_0 24567	NC_0 24567
<i>Neofelis nebulosa</i>	AY525 032	DQ0 8184 9	DQ0 8253 9	DQ25 7669. 1	DQ25 7669. 1	DQ25 7669. 1	DQ25 7669. 1	DQ25 7669. 1	DQ25 7669. 1	DQ25 7669. 1	DQ25 7669. 1	DQ25 7669. 1	DQ25 7669. 1	DQ25 7669. 1	DQ25 7669. 1	DQ25 7669. 1
<i>Otocolobus manul</i>	AY525 039	DQ0 8181 9	DQ0 8251 1	MH9 78908 .1	MH9 78908 .1	MH9 78908 .1	MH9 78908 .1	MH9 78908 .1	MH9 78908 .1	MH9 78908 .1	MH9 78908 .1	MH9 78908 .1	MH9 78908 .1	MH9 78908 .1	MH9 78908 .1	MH9 78908 .1
<i>Paguma larvata intrudens</i>	AY525 040		AY5 2505 5	KT19 1130. 1	KT19 1130. 1	KT19 1130. 1	KT19 1130. 1	KT19 1130. 1	KT19 1130. 1	KT19 1130. 1	KT19 1130. 1	KT19 1130. 1	KT19 1130. 1	KT19 1130. 1	KT19 1130. 1	KT19 1130. 1
<i>Panthera atrox</i>					DQ89 9945. 1											
<i>Panthera leo</i>	AY525 036	AY9 2869 4	AF03 9725	NC_0 28302	NC_0 28302	NC_0 28302	NC_0 28302	NC_0 28302	NC_0 28302	NC_0 28302	NC_0 28302	NC_0 28302	NC_0 28302	NC_0 28302	NC_0 28302	NC_0 28302
<i>Panthera leo spelaea</i>				KX25 8452	KX25 8452	KX25 8452	KX25 8452	KX25 8452	KX25 8452	KX25 8452	KX25 8452	KX25 8452	KX25 8452	KX25 8452	KX25 8452	KX25 8452
<i>Panthera pardus</i>	AY525 041	DQ0 8184 5	DQ0 8253 5	KP00 1507. 1	KP00 1507. 1	KP00 1507. 1	KP00 1507. 1	KP00 1507. 1	KP00 1507. 1	KP00 1507. 1	KP00 1507. 1	KP00 1507. 1	KP00 1507. 1	KP00 1507. 1	KP00 1507. 1	KP00 1507. 1
<i>Paradoxurus hermaphroditus</i>	AY170 086	AY9 2869		MG2 00264	MG2 00264	MG2 00264	MG2 00264	MG2 00264	MG2 00264	MG2 00264	MG2 00264	MG2 00264	MG2 00264	MG2 00264	MG2 00264	MG2 00264

<i>laotum</i>		7		.1	.1	.1	.1	.1	.1	.1	.1	.1	.1	.1	.1	.1
<i>Poiana richardsonii</i>	DQ267 559		AY2 3262 0						AF51 1049. 1							
<i>Prionailurus planiceps</i>		DQ0 8182 3	DQ0 8251 5	KY68 2729. 1	KY68 2729. 1	KY68 2729. 1	KY68 2729. 1	KY68 2729. 1	KY68 2729. 1	KY68 2729. 1	KY68 2729. 1	KY68 2729. 1	KY68 2729. 1	KY68 2729. 1	KY68 2729. 1	KY68 2729. 1
<i>Prionodon linsang</i>	JN414 782	DQ0 8185 0	DQ2 6755 1	MT55 9410. 1	MT55 9410. 1	MT55 9410. 1	MT55 9410. 1		MT55 9410. 1	MT55 9410. 1	MT55 9410. 1			MT55 9410. 1	MT55 9410. 1	MT55 9410. 1
<i>Profelis aurata</i>		DQ0 8183 2	DQ0 8252 2	NC_0 28299 .1	NC_0 28299 .1	NC_0 28299 .1	NC_0 28299 .1	NC_0 28299 .1	NC_0 28299 .1	NC_0 28299 .1	NC_0 28299 .1	NC_0 28299 .1	NC_0 28299 .1	NC_0 28299 .1	NC_0 28299 .1	NC_0 28299 .1
<i>Proteles cristatus</i>		AY9 2870 3		MH6 62445 .1	MH6 62445 .1	MH6 62445 .1	MH6 62445 .1	MH6 62445 .1	MH6 62445 .1	MH6 62445 .1	MH6 62445 .1	MH6 62445 .1	MH6 62445 .1	MH6 62445 .1	MH6 62445 .1	MH6 62445 .1
<i>Puma concolor</i>	DQ205 911	DQ0 8182 4		NC_0 16470	NC_0 16470	NC_0 16470	NC_0 16470	NC_0 16470	NC_0 16470	NC_0 16470	NC_0 16470	NC_0 16470	NC_0 16470	NC_0 16470	NC_0 16470	NC_0 16470
<i>Rhynchogale melleri</i>		GU9 3102 1	AY9 5065 3						AF52 2344. 1		AY97 4036. 1					
<i>Salanoia concolor</i>			AY7 5060 7						AY18 7007. 1		MG4 52301 .1					
<i>Smilodon populator</i>				MF87 1700	MF87 1700	MF87 1700	MF87 1700	MF87 1700	MF87 1700	MF87 1700	MF87 1700	MF87 1700	MF87 1700	MF87 1700	MF87 1700	MF87 1700
<i>Suricata suricata</i>	AY170 084	DQ0 8185 3	DQ0 8254 2	NC_0 45900 .1	NC_0 45900 .1	NC_0 45900 .1	NC_0 45900 .1	NC_0 45900 .1	NC_0 45900 .1	NC_0 45900 .1	NC_0 45900 .1	NC_0 45900 .1	NC_0 45900 .1	NC_0 45900 .1	NC_0 45900 .1	NC_0 45900 .1
<i>Taxidea taxus jacksoni</i>	AB285 379	AF4 9814 8	AY7 5059 8	HM1 06330 .1	HM1 06330 .1	HM1 06330 .1	HM1 06330 .1	HM1 06330 .1	HM1 06330 .1	HM1 06330 .1	HM1 06330 .1	HM1 06330 .1	HM1 06330 .1	HM1 06330 .1	HM1 06330 .1	HM1 06330 .1
<i>Viverra tangalunga tangalunga</i>	AY170 085		AF03 9731						AF51 1045. 1		AY17 0055. 1					
<i>Viverricula indica schlegelii</i>	DQ267 568		AY2 3261 8	KX89 1745. 1	KX89 1745. 1	KX89 1745. 1	KX89 1745. 1	KX89 1745. 1	KX89 1745. 1	KX89 1745. 1	KX89 1745. 1	KX89 1745. 1	KX89 1745. 1	KX89 1745. 1	KX89 1745. 1	KX89 1745. 1

<i>Vulpes vulpes fulva</i>	GQ214 077	AY9 2869 3	AF03 9733	KP34 2452. 1	KP34 2452. 1	KP34 2452. 1	KP34 2452. 1	KP34 2452. 1	KP34 2452. 1	KP34 2452. 1	KP34 2452. 1	KP34 2452. 1	KP34 2452. 1	KP34 2452. 1	KP34 2452. 1	KP34 2452. 1
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Appendix B

Highest supported partition and evolutionary model scheme of molecular data as determined via PartitionFinder 2

Settings

alignment : ./infile.phy

branchlengths : linked

models : JC, K80, TRNEF, SYM, HKY, TRN, GTR, HKY+X, TRN+X, GTR+X, JC+G, K80+G, TRNEF+G, SYM+G, HKY+G, TRN+G, GTR+G, HKY+G+X, TRN+G+X, GTR+G+X, JC+I, K80+I, TRNEF+I, SYM+I, HKY+I, TRN+I, GTR+I, HKY+I+X, TRN+I+X, GTR+I+X, JC+I+G, K80+I+G, TRNEF+I+G, SYM+I+G, HKY+I+G, TRN+I+G, GTR+I+G, HKY+I+G+X, TRN+I+G+X, GTR+I+G+X

model_selection : bic

search : greedy

Best partitioning scheme

Scheme Name : step_10

Scheme lnL : -85150.29748535156

Scheme BIC : 171846.019025

Number of params : 169

Number of sites : 9363

Number of subsets : 10

Subset	Best Model	# sites	subset id	Partition names
1	HKY+I+G+X	1678	1810c769b8f916a03fd2a6c2d9373381	ND4L_1stpos, COX3, ATP6, COX2, COX1

2	GTR+I+G+X	3990	08696fe9fcedeb6bee35f068c3f81ae3	ND4, CYB, ND1, ATP8, ND5, ND3
3	SYM+G	1521	c9715b8586452f904d516ab02113b915	TTR, CHRNA_1
4	TRN+G+X	421	87e5cb9ee47837231e1b3b3e8777f356	IRBP_1stpos
5	TRNEF+I	421	8201d351e9239325f36dd35b4c61c9af	IRBP_2ndpos
6	HKY+G+X	421	785a339441a44dfd0e936358a6abde9b	IRBP_3rdpos
7	HKY+I+G+X	396	c61fec9e72928c8aa7170ad04a8e6142	ND2
8	HKY+I+G+X	98	eeb82570db336fc244e80a4f45ebdce5	ND4L_2ndpos
9	HKY+I+G+X	98	321271c4f6bceb00245ec5d843fdc285	ND4L_3rdpos
10	HKY+G+X	319	eae00a798be6d486926234462330d84	ND6

Scheme Description in PartitionFinder format

Scheme_step_10 = (ND4L_1stpos, COX3, ATP6, COX2, COX1) (ND4, CYB, ND1, ATP8, ND5, ND3) (TTR, CHRNA_1) (IRBP_1stpos) (IRBP_2ndpos) (IRBP_3rdpos) (ND2) (ND4L_2ndpos) (ND4L_3rdpos) (ND6);

Nexus formatted character sets

begin sets;

charset Subset1 = 5160-5453\3 1827-2164 1-125 1388-1826 710-1387;

charset Subset2 = 5454-6268 2165-2846 4110-4644 126-321 6269-7911 5041-5159;

charset Subset3 = 8231-9363 322-709;

charset Subset4 = 2847-4109\3;

charset Subset5 = 2848-4109\3;

charset Subset6 = 2849-4109\3;

charset Subset7 = 4645-5040;

charset Subset8 = 5161-5453\3;

charset Subset9 = 5162-5453\3;

charset Subset10 = 7912-8230;

```
charpartition PartitionFinder = Group1:Subset1, Group2:Subset2, Group3:Subset3,  
Group4:Subset4, Group5:Subset5, Group6:Subset6, Group7:Subset7, Group8:Subset8,  
Group9:Subset9, Group10:Subset10;
```

```
end;
```

Appendix C

Source Material for Morphological Character Scoring and Continuous Variables

American Museum of Natural History, New York City, New York, USA (**AMNH**)

American Museum of Natural History – Frick Collection, New York City, New York, USA
(**F:AM**)

American Museum of Natural History, Comparative Anatomy Collection, New York City, New York, USA (**AMNH C.A.**)

Field Museum of Natural History, Chicago, Illinois, USA (**FMNH**)

Smithsonian National Museum of Natural History, Washington D.C., USA (**USNM**)

John Day Fossil Beds National Monument, Kimberly, Oregon, USA (**JODA**)

Grand Canyon National Park, Grand Canyon, Arizona, USA (**GRCA**)

University of Nebraska Lincoln State Museum, Lincoln, Nebraska, USA (**UNSM**)

Florida Museum of Natural History, University of Florida, Gainesville, Florida, USA (**UF**)

Texas Memorial Museum, University of Texas at Austin, Austin, Texas, USA (**TMM**)

Museum of Evolution of Uppsala University, Uppsala, Sweden (**M**)

University of California Museum of Paleontology, Berkeley, California, USA (**UCMP**)

Yale Peabody Museum, New Haven, Connecticut, USA (**YPM**)

Yale Peabody Museum, Princeton University Collection, New Haven, Connecticut, USA (**YPM
PU**)

University of Kansas, Natural History Museum, Lawrence, Kansas, USA (**KUVP**)

Raymond M. Alf Museum of Paleontology, Claremont, California, USA (**RAM**)

Museum of Geology, South Dakota School of Mines and Technology, Rapid City, South Dakota,
USA (**SDSM**)

University of Oregon, Museum of Natural and Cultural History-Modern Collection, Eugene,
Oregon, USA (**B**)

Los Angeles County Museum, George C. Page Museum (Hancock Collection), Los Angeles,
California, USA (**LACMHC**)

Museo Nacional de Ciencias Naturales-CSIC, Madrid, Spain (**MNCN**)

Museum National d'Histoire Naturelle, Paris, France (**MNHN**)

Museum für Naturkunde, Berlin, Germany (**MFN MB. Ma.**)

Beijing Natural History Museum, Beijing, China (**BNHM**)

Institute of Vertebrate Paleontology and Paleoanthropology, Chinese Academy of Sciences
Beijing, China (**IVPP**)

Collection du Quercy, Faculté des Sciences de Marseille, France (**FSM PQ**)

University of Florence, Florence, Italy (**IGF**)

University of Washington Burke Museum, Seattle, Washington, USA (**UWBM**)

Kenya National Museum, Nairobi, Kenya (**KNM**)

Uganda Museum, Kampala, Uganda (**UM**)

Taxa	Specimens	Literature
<i>Tungurictis spocki</i>	AMNH 26600, 26610, 99146	(Hunt Jr. and Solounias, 1991; Wang, 2004)
<i>Ictitherium viverrinum</i>	AMNH 20696, China 51-L437; F:AM 144906, 144905	(Coca-Ortega and Pérez-Claros, 2019)
<i>Hyaenotherium wongii</i>	AMNH 20555, 22878, 99082, 99088, 99084, 99091, 99081, 99093, 99080, 99095, 20554, 20586	(Coca-Ortega and Pérez-Claros, 2019)
<i>Hyaenictitherium hyaenoides</i>	AMNH 144883; F:AM 144892, 144889	(Coca-Ortega and Pérez-Claros, 2019)
<i>Lycyaena chaeretis</i>	F:AM 145002, 144899, 144902	-
<i>Chasmaporthetes lunensis</i>	AMNH 99789, 99786, 99781, 26955, 101261, 113847; F:AM 99787, 99783; MNCN 67100	(Baryshnikov and Averianov, 1993a; Antón et al., 2006; Coca-Ortega and Pérez-Claros, 2019)
<i>Chasmaporthetes ossifragus</i>	UF 18088, 18089, 27366	(Berta, 1981)
<i>Palinhyena reperta</i>	F:AM 144897	-
<i>Adcrocuta exima</i>	China -41L-339; AMNH 22880, 140301, 140298, 140299, 140300; F:AM 144903	(Baryshnikov and Averianov, 1993a; Kovachev, 2012; Coca-Ortega and Pérez-Claros, 2019)
<i>Pachycrocuta brevirostris</i>	AMNH 27757, 27756	(Werdelin and Solounias, 1991; Baryshnikov and Averianov, 1993a; Mutter et al., 2001; Palmqvist et al., 2011; Liu et al., 2021)
<i>Tongxinictis primordialis</i>	-	(Qiu et al., 1988b)
<i>Allohyaena kidici</i>	-	(Howell and Petter, 1985; Werdelin and Kurten, 1999; Coca-Ortega and Pérez-Claros, 2019)
<i>Dinocrocuta gigantea</i>	-	(Qiu et al., 1988a; Koufos, 1995; Zhang, 2005; Tseng and Binder,

		2010; Xiong, 2019)
<i>Percrocuta carnifex</i>	-	(Howell and Petter, 1985; Morales and Pickford, 2006; Ghaffar et al., 2019)
<i>Percrocuta algeriensis</i>	-	(Howell and Petter, 1985)
<i>Percrocuta tobieni</i>	-	(Howell and Petter, 1985; Werdelin, 2019)
<i>Proteles cristatus</i>	FMNH 211365; AMNH 24219	(Baryshnikov and Averianov, 1993a)
<i>Crocuta crocuta</i>	FMNH 34582, 18855	(Baryshnikov and Averianov, 1993a)
<i>Hyaena hyaena</i>	FMNH 101982, 47416	(Baryshnikov and Averianov, 1993a)
<i>Plioviverrops orbignyi</i>	MFN MB. Ma. 29580	(de Beaumont, 1969; Koufos, 2006, 2009, 2012)
<i>Crocuta crocuta spelaea</i>	MFN MB. Ma. 43, 44381, 29593, 29940, 30359, 30360, 29945, 30357, 29730, 29744, 29735, 29733, 29745, 51190.9, 92	(Anyonge, 1993; Baryshnikov and Averianov, 1993a; Coca-Ortega and Pérez-Claros, 2019)
<i>Protictitherium crassum</i>	-	(Chen and Schmidt-Kittler, 1983; Gracia, 2015)
<i>Belbus beaumonti</i>	-	(de Beaumont, 1968; Werdelin and Solounias, 1991; Koufos, 2011)
<i>Proailurus lemanensis</i>	AMNH 101931 (cast of holotype MNHN S.G. 3509)	(Schmidt-Kittler, 1976)
<i>Pseudaelurus validus</i>	AMNH 62128, 62167; F:AM 61847	(Hunt, 1998; Rothwell, 2001, 2003)
<i>Promegantereon ogygia</i>	-	(Salesa, 2002; Salesa et al., 2005, 2010a, 2010b; Christiansen, 2013; Siliceo et al., 2014)
<i>Metailurus major</i>	AMNH 131854 (cast of IVPP 5679), AMNH 26379, China-57-L548, Bx45L399; M 3841	(Kovatchev, 2001)
<i>Nimravides pedionomus</i>	F:AM 61855, 61852, 25205, 25206, 62156-B, 62156-C, 62154, 62153-A, 62155, 62174, 62158, 62157-B	-

<i>Machairodus catocopsis</i>	F:AM 104044; Hig. 315-2306, KAN-30-18, KAN-85 125	(Antón et al., 2013)
<i>Megantereon cultridens</i>	AMNH 105446, 113842 (cast of IGF 831), 113848 (cast of IGF 827), 101471, 105087	(Vekua, 1995; Antón and Werdelin, 1998; Qiu et al., 2004; Christiansen and Adolfssen, 2007; Palmqvist et al., 2007; Christiansen, 2013)
<i>Amphimachairodus giganteus</i>	F:AM 50478, 50476	(Koufos, 2016)
<i>Amphimachairodus coloradoensis</i>	F:AM 104726/104727, 104725, 69263; #1745 Bx 50 DKLA, GY-147-4995-H, #4142 Bx 117, #1066 Bx 34, #901 Bx 29, #3711 Bx 101, #368 Bx 16, #3492 Bx 99, RED 175-3262	(Antón et al., 2013)
<i>Dinofelis diastemata</i>	F:AM 50445, 50446	(Werdelin and Lewis, 2001)
<i>Homotherium serum</i>	F:AM 142497, 128069, 116841; TMM 933-3444	(Meade, 1961; Collins, 1981; Christiansen, 2013; Antón et al., 2014)
<i>Homotherium latidens</i>	AMNH 104641; F:AM 50461, 50462, 50469	(Anyonge, 1993; Sardella and Iurino, 2012; Antón et al., 2014)
<i>Homotherium ischyryus</i>	AMNH 95297, F:AM 131893, Chan.35-856, Chan-42-929	(Hearst et al., 2011)
<i>Smilodon fatalis</i>	AMNH 14349; LACMHC 2002-R-289, R10864, R10688, A-3708, K-65, K-876, K-1541, K-2281, Q-1609, Q-2965, 36960, 37415, 37873, 38504, 38731, 39221, U-3585, R-423, R-6739, 40416, K-3309, K-4507, K-4671, J-6083, T-5113, T-3068, Q-5192, Q-3903, 46699, K-2768, N-1219, N-1737, 133528, 60175	(Matthew, 1910; Merriam and Stock, 1932; Christiansen and Harris, 2005)
<i>Smilodon populator</i>	MFN MB. Ma. 48108 (cast of MNHN F.BRD21)	(Kurtén and Werdelin, 1990; Christiansen and Harris, 2005; Rincón, 2006; de Castro and Langer, 2008; Christiansen, 2013; Wallace and Hulbert, 2013; McDonald and Werdelin, 2018)
<i>Xenosmilus hodsonae</i>	UF 60000, 19400, 22907, 45340, 45428, 223829, 223830, 223831, 223832, 244471, 274280, 312700	(Martin et al., 2011; Christiansen, 2013)
<i>Caracal caracal</i>	FMNH 135042, 57220	-
<i>Lynx canadensis</i>	FMNH 129341	(Leche, 1915)

<i>Felis silvestris</i>	FMNH 97861	(Leche, 1915)
<i>Octolobus manul</i>	MNHN 2010-646, 2009-251	-
<i>Prionailurus planiceps</i>	MNHN CG 1873-228	-
<i>Catopuma temminckii</i>	MNHN 1941-293	-
<i>Profelis aurata</i>	MNHN 1932-5233	-
<i>Leopardus pardalis</i>	FMNH 88887, 68895, 93174	(Schmidt-Kittler, 1976; Christiansen, 2008)
<i>Acinonyx jubatus</i>	AMNH C.A. 145071; FMNH 34589, 29635	(Leche, 1915; Van Valkenburgh et al., 1990)
<i>Miracinonyx trumani</i>	GRCA 21734	(Orr, 1969; Adams, 1979; Van Valkenburgh et al., 1990; Wang and Martin, 1993)
<i>Puma concolor</i>	FMNH 15532	(Van Valkenburgh et al., 1990; Christiansen, 2008)
<i>Neofelis nebulosa</i>	FMNH 75831	-
<i>Panthera pardus</i>	MNHN C.G. 1962-2884, MNHN A7927, MNHN 1996-521	(Leche, 1915; Christiansen, 2008)
<i>Panthera leo</i>	FMNH 31121; B 8707	(Leche, 1915; Hunt, 1987; Salles, 1992; Hsieh and Takemura, 1994; Mattern and McLennan, 2000; Christiansen, 2008; Lueders et al., 2012; De Schepper, 2016)
<i>Panthera leo spelaea</i>	MFN MB. Ma. 0948, 1956, 2246, 1953, 1906, 30090, 30118, 30112a, 30114a, b; MFN MB. Ma. 14322, 14321, 14317, 14320, 30124, 3642, 3643, 1964	(Anyonge, 1993)
<i>Panthera atrox</i>	AMNH 14397; LACMHC 572, 575, 597, 1564, 2903-R-6, 14621, X-6716, 14661, 14844, 14926, 14696, 14905, X-5036, R6740, 16311, 2911-R-1, 2907-R-4, 14722, 2908-R-7, 15297, 15460, 15379, 15536, 15582, X-7067, X-5552, 2937-2, X-5642, X-6274, X-6405, X-7279, 16043, X-9759	(Merriam and Stock, 1932; Wheeler and Jefferson, 2009)
<i>Barbourofelis morrиси</i>	AMNH 79999; F:AM 61876, 61900, 80000, 61895, 25204, 69359, 61893,	-

	61976, 61898, 61970, 125665, 61882, Bx-5-Bx-69 #25138-B	
<i>Oriensmilus liupanensis</i>	AMNH 144755 (cast of an uncatalogued BNHM specimen)	(Wang et al., 2020)
<i>Sansanosmilus palmidens</i>	-	(Filhol, 1890; Ginsburg, 1961; Morlo et al., 2004; Peigné, 2012)
<i>Barbourofelis fricki</i>	AMNH 108193 (cast of UNSM 76000); F:AM 61986, 61994, 61997, 99258, 68234, 2672, 61984, 61983, 125670, 116854, 61991; UWBM 72291	(Schultz et al., 1970; Joeckel and Stavas, 1996)
<i>Barbourofelis loveorum</i>	UF 24447, 36855, 36871, 37000, 36867, 23796, 24432, 36867, 25081, 25103, 25156, 25191, 25228, 25249, 25267, 25283, 25294, 25302, 27258, 37939, 25054, 25034, 36800, 25013, 24429; AMNH 125125	(Baskin, 1981; Neff, 1983; Hunt, 1987; Bryant, 1988a, 1988b, 1991)
<i>Albanosmilus whitfordi</i>	AMNH 14308; F:AM 61856, 61858, 61861, 61864, 61849, 61680, 61885	-
<i>Eusmilus cerebralis</i>	AMNH 6941; F:AM 98189, 69377; UCMP 123180, 123181; JODA 7047	-
<i>Hoplophoneus oharrai</i>	SDSM 2417	-
<i>Hoplophoneus primaevus</i>	F:AM 62007, AMNH 5338, 82440, 38980; USNM 18184; YPM PU 10741	(Bryant, 1988a; Barrett, 2016)
<i>Hoplophoneus occidentalis</i>	F:AM 102387, 62025, 62022; AMNH 1407, 655; KUVV 2874, 2561; RAM 10356	-
<i>Nimravus brachyops</i>	UCMP 1681, 2556, 76111; AMNH 6930, 6993, 6940, 6933; F:AM 62020, 62151; JODA 1312	(Welsh et al., 2015; Barrett, 2016)
<i>Nimravus intermedius</i>	AMNH 137130 (cast of FSM PQ 327), 105390 (cast of CM 2587); MFN MB. Ma. 29987, 29988, 29986, 29991, 29993, 29994, 29995; YPM PU 11569	(Schmidt-Kittler, 1976; Peigné and De Bonis, 1999; Peigné, 2003; Egi et al., 2016)
<i>Pogonodon platycopis</i>	AMNH 6938, 6953	(Barrett, 2016)
<i>Pogonodon davisi</i>	UCMP 789; AMNH 102156; F:AM 62026, 62042, 62024, 62018; JODA 5841; YPM 10520; YPM PU 11430	(Barrett, 2016)

<i>Dinictis felina</i>	AMNH 6937, 8777, 38805; YPM PU 12551, 13625, 12577, 11431	(Barrett, 2016)
<i>Nanosmilus kurteni</i>	UNSM 25505	-
<i>Ginsburgsmilus napakensis</i>	KNM-SO-5670; UM-P67-13	(Morales et al., 2001, 2008; Morlo et al., 2004; Morales and Pickford, 2018)
<i>Prosansanosmilus eggeri</i>	-	(Morlo et al., 2004)
<i>Prosansanosmilus peregrinus</i>	-	(Heizmann et al., 1980; Morlo et al., 2004; Morlo, 2006)
<i>Afrosmilus hispanicus</i>	-	(Belinchón and Morales, 1989; Azanza et al., 1993; Morales et al., 2001)
<i>Afrosmilus turkanae</i>	KNM-MO-15929, KNM-RU-15984, KNM-RU-15986, KNM-SO15973	(Morales et al., 2001; Werdelin and Peigné, 2010; Morales and Pickford, 2018)
<i>Afrosmilus africanus</i>	-	(Andrews, 1914; Savage, 1965; Morales et al., 2001)
<i>Albanosmilus jourdani</i>	-	(Robles et al., 2013)
<i>Maofelis cantonensis</i>	-	(Averianov et al., 2016)
<i>Quercylurus major</i>	-	(Ginsburg, 1979; Peigné, 2003)
<i>Dinailurictis bonali</i>	MFN MB. Ma. 29985	(Ginsburg, 1979; Peigné, 2003)
<i>Eofelis edwardsii</i>	-	(Ginsburg, 1979; Peigné, 2000; de Bonis et al., 2019)
<i>Dinaelurus crassus</i>	-	(Eaton, 1922)
MA-PHQ 348	-	(Peigné, 2001)
<i>Eusmilus dakotensis</i>	YPM PU 11079; UNSM 1068	(Hatcher, 1895; Morea, 1975; Bryant, 1996)
<i>Eusmilus sicarius</i>	YPM PU 12953 A (cast of YPM PU 12953)	-
<i>Eusmilus adelos</i>	USNM 12820, 18214	-
<i>Eusmilus bidentatus</i>	MFN MB. Ma. 30154, 30151	(Piveteau, 1931; Ringead and Michel, 1994; Peigné and Brunet, 2001; Joeckel et al., 2002)
<i>Eusmilus villebramarensis</i>	-	(Peigné and Brunet, 2001; Peigné,

		2003)
<i>Prionodon linsang</i>	FMNH 88606	(Leche, 1915)
<i>Nandinia binotata</i>	AMNH 2409 C.A.; FMNH 149361, 55758	(Wesley-Hunt and Flynn, 2005; Spaulding and Flynn, 2012; Wible and Spaulding, 2013)
<i>Hemigalus derbyanus</i>	AMNH C.A. 9; FMNH 68717	(Leche, 1915)
<i>Arctictis binturong</i>	AMNH C.A. 1182; FMNH 53747	(Leche, 1915)
<i>Civettictis civetta</i>	FMNH 108174	(Leche, 1915)
<i>Viverra zangalunga</i>	FMNH 85116	(Leche, 1915)
<i>Genetta maculata</i>	FMNH 73044, 85987	-
<i>Paradoxurus hermaphroditus</i>	FMNH 338000, 140476	(Leche, 1915)
<i>Paguma larvata</i>	MNHN CG 1988-163, 1962-2062, 1913-577	-
<i>Cynogale bennettii</i>	MNHN CG 1962-170; MNHN A-2094	(Leche, 1915)
<i>Poiana richardsonii</i>	MNHN CG 1976-389	-
<i>Viverricula indica</i>	MNHN CG 1962-2113	(Leche, 1915)
<i>Atilax paludinosus</i>	MNHN CG 1995-426, 1877-153; MNHN 1871-121	-
<i>Herpestes edwardsii</i>	FMNH 83097	(Spaulding and Flynn, 2012)
<i>Ichneumia albicauda</i>	FMNH 73024, 157991	(Leche, 1915)
<i>Bdeogale nigripes</i>	FMNH 167685	-
<i>Mungos mungo</i>	FMNH 149365	-
<i>Suricata suricata</i>	FMNH 38348, 180674	-
<i>Crossarchus obscurus</i>	FMNH 54410	-
<i>Rhynchogale melleri</i>	MNHN CG 1962-992	-
<i>Galerella sanguinea</i>	MNHN CG 2000-1054, 2001-2188	-
<i>Helogale parvula</i>	MNHN CG 1962-1056, 1987-176	-
<i>Fossa fossana</i>	FMNH 85196	-
<i>Cryptoprocta ferox</i>	FMNH 33950, 5655	(Carlsson, 1911)

<i>Eupleres goudotii</i>	FMNH 30492, MNHN CG 1962-2105	-
<i>Salanoia concolor</i>	MNHN CG 1962-2111	-
<i>Kanuites lewisae</i>	-	(Dehghani and Werdelin, 2008; Werdelin, 2019)
<i>Kichechia zamanae</i>	-	(Savage, 1965; Schmidt-Kittler, 1987; Morales and Pickford, 2011; Adrian et al., 2018)
<i>Herpestides antiquus</i>	-	(Chen and Schmidt-Kittler, 1983; Hunt, 1991; Morlo, 1996; Wolsan and Morlo, 1997; Wesley-Hunt and Flynn, 2005; Spaulding and Flynn, 2012)
<i>Euboictis aliverensis</i>	-	(Schmidt-Kittler, 1983; Fejfar and Schmidt-Kittler, 1984)
<i>Sivanasua viverroides</i>	-	(Fejfar and Schmidt-Kittler, 1984; Fejfar et al., 1997; Ginsburg and Morales, 1999)
<i>Izmirictis cani</i>	-	(Morales et al., 2019)
<i>Palaeoprionodon lamandini</i>	-	(Hunt, 1998, 2001; Wesley-Hunt and Flynn, 2005; Hans-Volker et al., 2007; Spaulding and Flynn, 2012)
<i>Stenogale julieni</i>	-	(Hunt, 1998; Wesley-Hunt and Flynn, 2005; Spaulding and Flynn, 2012; Wang et al., 2019)
<i>Tapocyon robustus</i>	-	(Wesley and Flynn, 2003; Wesley-Hunt and Flynn, 2005; Spaulding and Flynn, 2012)
<i>Procynodictis vulpiceps</i>	AMNH 2514	(Wesley-Hunt and Flynn, 2005; Spaulding and Flynn, 2012)
<i>Hesperocyon gregarius</i>	AMNH 50276	(Bryant, 1992; Wang, 1993, 1994; Wesley-Hunt and Flynn, 2005; Spaulding and Flynn, 2012)
<i>Canis latrans</i>	FMNH 135222	(Baryshnikov and Averianov, 1993b)
<i>Vulpes vulpes</i>	FMNH 64610	(Baryshnikov and Averianov, 1993b)

<i>Taxidea taxus</i>	FMNH 47747	(Leche, 1915)
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Appendix D

Morphological Character List

1. Lacrimal facial process: (0), broad rostral flange; (1), small, present on face; (2), not present on face; (3), orbital flange reduced to area around lacrimal foramen (Wesley-Hunt and Flynn, 2005: character 1).

2. Ventral exposure of premaxilla; posterior extent of premaxilla, lateral to palatal foramen: (0), lateral to canine; (1), anterior to canine (Wesley-Hunt and Flynn, 2005: character 2).

3. Shape of infraorbital foramen: (0), elongate; (1), round (Wesley-Hunt and Flynn, 2005: character 3).

4. Length of palate – position of the posterior edge of palatine midline relative to tooth row: (0) posterior to upper tooth row; (1) anterior or equal to upper tooth row (Wesley-Hunt and Flynn, 2005: character 5).

5. Palatine canal primary anterior opening: (0), opening through palatine; (1), at maxilla–palatine suture; (2) opening through maxilla (Wesley-Hunt and Flynn, 2005: character 6).

6. Relative length of frontal and parietal at midline: (0) parietal greater than frontal; (1) parietal equal or subequal to frontal; (2) frontal midline much longer than parietal (Wesley-Hunt and Flynn, 2005: character 7).

7. Postorbital process: (0) prominent; (1) small, reduced (Wesley-Hunt and Flynn, 2005: character 8).
8. Paroccipital process size: (0) well-developed; (1) reduced (Wesley-Hunt and Flynn, 2005: character 9).
9. Paroccipital process shape: (0) simple process; (1) laterally flattened, thin, but is distinct process; (2) cupped around bulla, process not distinct; (3) absent (Wesley-Hunt and Flynn, 2005: character 10).
10. Placement of postglenoid foramen: (0) medially placed; (1) more lateral, external, very near edge of skull (Wesley-Hunt and Flynn, 2005: character 11).
11. Postglenoid foramen: (0) present; (1) greatly reduced, or missing (Wesley-Hunt and Flynn, 2005: character 12).
12. Shape of mastoid process: (0) forming a distinct process, extending out farther than paroccipital process, or subequal; (1) blunt, rounded, does not protrude significantly, more a swelling of the mastoid; (2) thin plate, no distinct process; (3) large tabular process, anteriorly sloping, obscuring much, if not all, of the auditory bulla; (4) large tabular process, extremely anteriorly inclined, closing or nearly enclosing the external auditory meatus by its junction with the glenoid pedicle, medially encroaching and affixed to the ventral floor of the bulla in the

vicinity of the ectotympanic (modified from Wesley-Hunt and Flynn, 2005: character 13 to incorporate states of Christiansen (2013): character 35).

13. Direction of mastoid process extension: (0) lateral – ventral; (1) ventral; (2) lateral; (3) none, or only swelling (Wesley-Hunt and Flynn, 2005: character 14).

14. Condylod (hypoglossal) foramen position relative to postlacerate foramen: (0) distant; (1) close (less than the diameter of the hypoglossal foramen away); (2) conjoined with posterior lacerate foramen (Wesley-Hunt and Flynn, 2005: character 15).

15. Condylod (hypoglossal) foramen position relative to groove between the occipital condyle and the paroccipital process: (0) inline or within groove; (1) anterior to groove (Wesley-Hunt and Flynn, 2005: character 16).

16. Posterior lacerate foramen: (0), present as a vacuity between the promontorium and the basioccipital; (1), present as an individual foramen (Wesley-Hunt and Flynn, 2005: character 17).

17. Fenestra cochleae (rotunda) position relative to mastoid tubercle: (0) posterior to mastoid tubercle; (1) anterior, subequal to mastoid tubercle (Wesley-Hunt and Flynn, 2005: character 18).

18. Relative distance between the foramen ovale and the alisphenoid canal: (0) separated by at least the diameter of the alisphenoid canal; (1) separated only by a thin wall; (2) no alisphenoid canal present (Wesley-Hunt and Flynn, 2005: character 19).

19. Ossification of tegmen tympani: (0) facial nerve exposed ventrally; (1) facial nerve partially embedded within tegmen tympani and floored in anteromedial segment; (2) facial nerve beneath a bony sheath that defines the fossa for tensor tympani muscle (Wesley-Hunt and Flynn, 2005: character 20).

20. Composition of mastoid tubercle: (0) mastoid tubercle formed by petrosal; (1) mastoid tubercle formed by squamosal (Wesley-Hunt and Flynn, 2005: character 22).

21. Anterior loop of internal carotid artery: (0) lack of an anterior loop of the internal carotid artery; (1) presence of the loop – excavation in basisphenoid; (2) presence of loop – but extrabullar (Wesley-Hunt and Flynn, 2005: character 23).

22. Suprameatal fossa (fossa on squamosal anterior to mastoid: (0) absent; (1) small; (2) large, well developed (Wesley-Hunt and Flynn, 2005: character 24).

23. Position of internal carotid artery: (0) internal carotid artery laterally positioned, transpromontorial, runs close to margin of fenestra cochlea, presence of a promontory artery, groove for stapedia artery may or may not be present; (1) internal carotid artery transpromontorial but medially positioned, course far from fenestra cochlea; (2) internal carotid

artery medial, extrabullar, inside a bony canal formed by the caudal entotympanic (Wesley-Hunt and Flynn, 2005: character 25).

24. Apron shelf on promontorium posterior to fenestra cochleae for entotympanic attachment: (0) absent; (1) blunt – surface present posterior to fenestra cochleae, but no extensive attachment possible; (2) extended, large area for attachment, may roof posterior bullar chamber (Wesley-Hunt and Flynn, 2005: character 26).

25. Ventral process of promontorium: (0) absent; (1) present, medially positioned on promontorium (Wesley-Hunt and Flynn, 2005: character 27).

26. Shape of the promontorium, anterior extension: (0) elongate, apron extension tapers to a point anteriorly, almond like in appearance; (1) elongate, rounded anteriorly; (2) blunt, quickly truncating; (3) elongate, apron is broad, flat extension, not almond-shaped and not blunt (Wesley-Hunt and Flynn, 2005: character 28).

27. Facet on promontorium indicative of ectotympanic contact: 0, absent; 1, present (Wesley-Hunt and Flynn, 2005: character 29).

28. Inferior petrosal sinus: (0) inferior petrosal sinus small; (1) inferior petrosal sinus greatly enlarged (Wesley-Hunt and Flynn, 2005: character 31).

29. A deep, well developed fossa or pit on the squamosal/alisphenoid recording the contact with the anterior crus or anterior face of the ectotympanic: (0) absent, may have slight/shallow indentation; (1) present, well developed, or bulla present and fully ossified (Wesley-Hunt and Flynn, 2005: character 32).

30. Shelf between mastoid process and paroccipital process: (0) laterally wide, curved trough with smooth surface; (1) laterally wide, could have flat surface, rugose or bulbous, no smoothed out trough; (2) very thin, outside edge could be raised; (3) no shelf present (Wesley-Hunt and Flynn, 2005: character 33).

31. Extent of flange on basioccipital lateral edge bordering auditory region: (0) absent; (1) small, nascent; (2) well developed when compared to basal 'miacids' (Wesley-Hunt and Flynn, 2005: character 34).

32. Evidence on basisphenoid and basioccipital for marked medial inflation of the entotympanic: (0) absent; (1) present – inflation of entotympanic pushing medially onto and over the basioccipital (Wesley-Hunt and Flynn, 2005: character 35).

33. Evidence of marked posterior inflation of the entotympanic; entotympanic attached during life to paroccipital process or to extensive area posterior to the petrosal: (0) absent; (1) present (Wesley-Hunt and Flynn, 2005: character 36).

34. Epitympanic wing of the petrosal forms ventral floor to the anterior medial corner of the fossa for the tensor tympani muscle: (0) absent; (1) present, but relatively flat and horizontal; (2) ventral floor present, but not horizontal, instead it forms a delicate ‘tube’, the bony floor is not an extension of the petrosal (Wesley-Hunt and Flynn, 2005: character 38).

35. Placement of middle lacerate foramen: (0) foramen a vacuity – not defined anteriorly nor posteriorly, positioned directly anterior to petrosal; (1) foramen anteriorly defined, posteriorly bordered by petrosal – positioned equal or posterior to basisphenoid/basioccipital suture; (2) foramen defined anteriorly, petrosal may be undefined posterior border, foramen positioned in basisphenoid (or edge of alisphenoid) just anterior to basisphenoid/basioccipital suture; (3) foramen defined anteriorly and posteriorly completely bordered by basisphenoid, foramen positioned far anterior to basisphenoid/basioccipital suture; (4) lack of a foramen (Wesley-Hunt and Flynn, 2005: character 40).

36. M1, a defined cingulum continuous around the lingual face of the protocone: (0) absent; (1) complete cingulum present; (2) anterior segment of cingulae absent or smaller than posterior cingulae (Wesley-Hunt and Flynn, 2005: character 41).

37. M1, protocone height relative to paracone: (0) protocone shorter than paracone; (1) protocone equal or subequal to height of paracone; (2) protocone absent or lacks a cusp associated with the root (modified from Wesley-Hunt and Flynn, 2005: character 42).

38. M1, parastyle projects farther labially than metastyle: (0) absent; (1) present (Wesley-Hunt and Flynn, 2005: character 44)

39. M1, parastyle direction: (0) buccally with anterior direction; (1) buccally (Wesley-Hunt and Flynn, 2005: character 45).

40. M1, size of posterior lingual cingular shelf at base of protocone: (0) posterior lingual cingular shelf equal or subequal to anterior cingulum; (1) posterior lingual cingular shelf more pronounced, larger than anterior cingulum (Wesley-Hunt and Flynn, 2005: character 47).

41. M1, relative height of paracone and metacone: (0) paracone equals metacone in height; (1) paracone greater than metacone; (2) metacone absent (modified from Wesley-Hunt and Flynn, 2005: character 48).

42. M1, relative height of paraconule and metaconule: (0) paraconule greater than metaconule; (1) paraconule equal or subequal to metaconule; (2) both absent (Wesley-Hunt and Flynn, 2005: character 49).

43. M1, presence of hypocone: (0) absent; (1) present (distinct cusp); (2) present, formed by swelling of entire cingulum ridge (Wesley-Hunt and Flynn, 2005: character 50).

44. M1, width of parastylar shelf: (0) lack of a shelf; (1) broad; (2) narrow, consisting mainly of ridge (Wesley-Hunt and Flynn, 2005: character 51).

45. Presence of M3: (0) present; (1) absent (Wesley-Hunt and Flynn, 2005: character 53).

46. P4 protocone: (0) large, well-developed; (1) reduced or absent (Wesley-Hunt and Flynn, 2005: character 56).

47. Posterior accessory cusps on P3: (0) one cusp present; (1) two cusps present; (2) absent (Wesley-Hunt and Flynn, 2005: character 58).

48. Palatine, relative size: (0) midline length of palatine less than midline length of maxilla; (1) midline length greater than midline length of maxilla (Wesley-Hunt and Flynn, 2005: character 60).

49. Turbinal bones: (0) simple development of maxilloturbinals in nasal cavity; (1) maxilloturbinals large and branching, excluding nasoturbinals from narial opening (Wesley-Hunt and Flynn, 2005: character 62).

50. Jugal: (0) jugal reaches lacrimal, or is separated from it by only thin sliver of maxilla; (1) jugal widely separated from lacrimal, maxilla broadly laps posteriorly over anterior orbital rim (Wesley-Hunt and Flynn, 2005: character 64).

51. Anterior extent of palatine in orbit: (0) broadly contacts lacrimal; (1) fails to contact lacrimal (Wesley-Hunt and Flynn, 2005: character 65).

52. Postorbital constriction: (0) just anterior of frontoparietal suture, near posterior margin of frontal; (1) braincase expanded, with frontals making much greater contribution; fronto–parietal suture located more anteriorly in frontal (Wesley-Hunt and Flynn, 2005: character 66).

53. Posterior entrance of carotid artery into auditory capsule: (0) posterior entry, artery not enclosed in osseous tube; (1) posterior entry, artery enclosed in tube; (2) anterior entry, artery not enclosed in tube; (3) anterior entry, artery not enclosed in tube (Wesley-Hunt and Flynn, 2005: character 67).

54. Entotympanic: (0) fails to ossify, or is only weakly attached to auditory capsule; (1) ossified at least partially, and firmly fused to the skull (Wesley-Hunt and Flynn, 2005: character 68).

55. Ectotympanic contributes to external auditory meatal tube: (0) no; (1) yes (Wesley-Hunt and Flynn, 2005: character 69).

56. Ectotympanic septum: (0) absent; (1) present (Wesley-Hunt and Flynn, 2005: character 70).

57. Entotympanic septum: (0) absent; (1) present (Wesley-Hunt and Flynn, 2005: character 71).

58. Fenestra cochleae: (0) approximately equal in size to fenestra ovalis, cochlear fossula not developed; (1) at least three times the area of oval window, cochlear fossula well developed (Wesley-Hunt and Flynn, 2005: character 72).

59. Major a2 arterial shunt: (0) small; (1) large, intracranial rete (Wesley-Hunt and Flynn, 2005: character 75).

60. Major a4 arterial shunt: (0) present; (1) present, intracranial rete (Wesley-Hunt and Flynn, 2005: character 76).

61. Major anastomosis x: (0) absent; (1) present (Wesley-Hunt and Flynn, 2005: character 77).

62. P1: (0) present; (1) absent (Wesley-Hunt and Flynn, 2005: character 79).

63. P3 lingual cusp: (0) absent; (1) present (Wesley-Hunt and Flynn, 2005: character 80).

64. P4 hypocone: (0) absent; (1) present (Wesley-Hunt and Flynn, 2005: character 83).

65. p1: (0) present; (1) absent (Wesley-Hunt and Flynn, 2005: character 84).

66. Lower molars: (0); subequal in size; (1); m1 much larger than m2–3 and progressive decrease in size from m1–3 (Wesley-Hunt and Flynn, 2005: character 86).

67. M2 hypocone: (0) absent; (1) present (Wesley-Hunt and Flynn, 2005: character 87).

68. m3: (0) present; (1) absent (Wesley-Hunt and Flynn, 2005: character 88).

69. Baculum: (0) small and simple or absent; (1) long, stylized (Wesley-Hunt and Flynn, 2005: character 89).
70. Scapula, postscapular fossa: (0) absent; (1) present (Wesley-Hunt and Flynn, 2005: character 90).
71. Tail: (0) long; (1) reduced (Wesley-Hunt and Flynn, 2005: character 91).
72. Femur, third trochanter: (0) present; (1) absent (Wesley-Hunt and Flynn, 2005: character 94).
73. Cowper's (bulbourethral) gland: (0) present; (1) absent (Wesley-Hunt and Flynn, 2005: character 95).
74. Prostate gland: (0) small/vestigial; (1) large, ampulla bilobed (Wesley-Hunt and Flynn, 2005: character 96).
75. Anal glands: (0) simple; (1) enlarged and having enlarged anal sac (Wesley-Hunt and Flynn, 2005: character 98).
76. Scapula – supraglenoid tubercle morphology: (0) expands out over the glenoid fossa (*Didymictis*); (1) blunt, does not extend over the glenoid fossa (*Vulpavus*) (Spaulding and Flynn, 2012: character 100).

77. Scapula – acromion process angle: Either a short or a long process can be dorsally directed at the acromion process apex, or remain in the same plane as the scapular spine: (0) process angles dorsally (*Vulpavus*); (1) process remains in same plane as the scapular spine (*Canis*) (Spaulding and Flynn, 2012: character 101).

78. Scapula – acromion process length: The acromion process can terminate far distally to the glenoid fossa or terminate at or before the border. A long acromion can be used as a proxy for the presence of clavicles in extinct taxa. (0) process extends past glenoid fossa (*Vulpavus*); 1– process terminates before or at glenoid fossa (*Gulo*) (Spaulding and Flynn, 2012: character 102).

79. Scapula – coracoid process: (0) present, as a large clearly projecting process (*Felis*); (1) extremely small or absent (*Canis*) (Spaulding and Flynn, 2012: character 103).

80. Scapula – scapular spine morphology: Coded while viewing the spine from a ventral view of the scapula. (0) spine forms one continuous, smooth, downward curve (*Öodectes*); (1) spine has a dip or embayment in the curve (*Herpestes*) (Spaulding and Flynn, 2012: character 104).

81. Scapula – metacromion process: (0) present and well developed (*Herpestes*); (1) weak or absent (Otariidae) (Spaulding and Flynn, 2012: character 105).

82. Humerus – indentation on the anterior surface of the capitulum: (0) present (*Hyeaenodon*); (1) absent (*Vulpavus*) (Spaulding and Flynn, 2012: character 106).

83. Humerus – olecranon fossa shape: (0) shallow and round (*Vulpavus*); (1) deep and slot-like (*Miacis uintensis*); (2) perforated (*Didymictis*) (Spaulding and Flynn, 2012: character 107).
84. Humerus – medial edge of posterior trochlea: (0) vertical (*Vulpavus*); (1) slanted (*Öodectes*) (Spaulding and Flynn, 2012: character 108).
85. Humerus – delto-pectoral crest: (0) present (*Vulpavus*); (1) absent (*Didymictis*) (Spaulding and Flynn, 2012: character 109).
86. Humerus – medial epicondyle: (0) ends with a well rounded head (*Vulpavus*); (1) poorly defined, appearing more like a blunt tubercle (*Didymictis*) (Spaulding and Flynn, 2012: character 110).
87. Humerus – medial epicondyle orientation (new): (0) lacks curvature (is straight) (*Öodectes*); (1) curves posteriorly (*Didymictis*) (Spaulding and Flynn, 2012: character 111).
88. Humerus – greater tuberosity height: (0) extends past head (*Didymictis*); (1) flush with head in height (*Vulpavus*) (Spaulding and Flynn, 2012: character 112).
89. Humerus – posterior trochlea: (0) not bound by high ridges (*Öodectes*); (1) bound by high ridges (*Canis*) (Spaulding and Flynn, 2012: character 113).

90. Humerus – brachial flange: (0) present and large, extending out from the body of the bone as a flat surface (*Vulpavus*); (1) small, nothing but a small raised line of bone (*Didymictis*) (Spaulding and Flynn, 2012: character 114).

91. Humerus – lesser tuberosity with a crest or ridge of bone leading from this feature down the shaft: (0) present (*Didymictis*); (1) absent (*Canis*) (Spaulding and Flynn, 2012: character 115).

92. Humerus – trochlea extent: (0) extends distally past capitulum when viewed anteriorly (*Didymictis*); (1) two articular surfaces are more inline (*Vulpavus*) (Spaulding and Flynn, 2012: character 116).

93. Humerus – epicondylar foramen: (0) present and round (*Hyaenodon*); (1) present and elongated (*Vulpavus*) (Spaulding and Flynn, 2012: character 117).

94. Humerus – distal L-shaped ridge of bone on capitulum in distal view: (0) present (*Vulpavus*) (1) absent (*Felis*) (Spaulding and Flynn, 2012: character 118).

95. Humerus – orientation of bone on the lateral distal margin: (0) faces laterally (*Hyaenodon*); (1) faces posteriorly (*Vulpavus*) (Spaulding and Flynn, 2012: character 119).

96. Humerus – ulnar collateral ligament insertion site size: (0) very large, forming a distinct circular pit (*Didymictis*); (1) small, forming only a shallow depression (*Vulpavus*) (Spaulding and Flynn, 2012: character 120).

97. Humerus – greater tuberosity angle: (0) greater tuberosity angled away from head; smooth arch is not formed with lesser tuberosity (*Didymictis*); (1) greater tuberosity more flush with head (*Vulpavus*) (Spaulding and Flynn, 2012: character 121).

98. Humerus – prominence of bicipital groove: (0) groove is very noticeable and deep (*Nandinia*); (1) groove is very subtle if noticeable at all (*Civetticits*) (Spaulding and Flynn, 2012: character 122).

99. Humerus – capitulum shape: (0) flat for the whole length with a uniform distal margin (*Thinocyon*); (1) rounded (*Vulpavus*) (Spaulding and Flynn, 2012: character 123).

100. Humerus - tricipital line: (0) large and distinctive (*Didymictis*); (1) reduced (*Nandinia*) (Spaulding and Flynn, 2012: character 124).

101. Ulna – semi-lunar notch distal border morphology: (0) W-shaped distal border; an indentation occurs between the articular surface with the radius and the rest of the facet (*Öodectes*); (1) indentation lacking (*Canis*) (Spaulding and Flynn, 2012: character 125).

102. Ulna – semi-lunar notch proximal border extent: (0) proximal ridge extends far from shaft surface (*Hyeanonodon*); (1) proximal ridge flush with shaft surface (*Öodectes*) (Spaulding and Flynn, 2012: character 126).

103. Ulna – *m. brachialis* insertion site: (0) present (*Vulpavus*); (1) absent (*Ailurus*) (Spaulding and Flynn, 2012: character 127).
104. Ulna – *m. brachialis* insertion site position: (0) on anterior surface of ulna (*Vulpavus*); (1) on the medial margin of the shaft (*Öodectes*) (Spaulding and Flynn, 2012: character 128).
105. Ulna – radial notch curvature: (0) absent (*Vulpavus*); (1) present (*Ailurus*) (Spaulding and Flynn, 2012: character 129).
106. Ulna – deep tendon groove on proximal end of ulna: (0) present (*Hyaenodon*); (1) absent (*Vulpavus*) (Spaulding and Flynn, 2012: character 130).
107. Ulna – deep tendon groove on proximal end of ulna (Heinrich and Rose, 1997): (0) present (*Hyaenodon*); (1) absent (*Vulpavus*) (Spaulding and Flynn, 2012: character 131).
108. Ulna – olecranon process shape: (0) mediolaterally robust, square in shape (*Vulpavus*); (1) mediolaterally compressed (*Felis*) (Spaulding and Flynn, 2012: character 132).
109. Ulna – anconeal process extent: (0) projecting from the shaft, shelf like (*Didymictis*); (1) flush with shaft (*Vulpavus*) (Spaulding and Flynn, 2012: character 133).
110. Ulna – proximal border of semi-lunar notch, position: (0) lateral to the shaft (*Hyaenodon*); (1) centered with respect to the shaft (*Öodectes*) (Spaulding and Flynn, 2012: character 134).

111. Ulna – anteriomedial protuberance development (Taylor, 1974): (0) well developed (*Nandinia*); (1) small (*Canis*) (Spaulding and Flynn, 2012: character 135).

112. Ulna – groove on lateral side of shaft: (0) present (*Hyaenodon*); (1) absent (*Vulpavus*) (Spaulding and Flynn, 2012: character 136).

113. Ulna shape – sigmoidal; the ulna is used as a proxy for the curved nature of all forelimb bones noted by Matthew (1909): (0) sigmoidal (*Vulpavus*); (1) straight (*Canis*) (Spaulding and Flynn, 2012: character 137).

114. Ulna – radial notch orientation (Heinrich and Rose, 1997): (0) faces anteriorly (*Didymictis*); (1) faces more laterally (*Vulpavus*) (Spaulding and Flynn, 2012: character 138).

115. Radius – radial head shape: (0) round (*Vulpavus*); (1) oval (*Didymictis*) (Spaulding and Flynn, 2012: character 139).

116. Radius – large scaphoid articulation surface: (0) present (*Didymictis*); (1) surface small (*Vulpavus*) (Spaulding and Flynn, 2012: character 141).

117. Radius – capitular eminence of radial head development; (0) small (*Vulpavus*); (1) large, disrupts radial rim (*Canis*) (Spaulding and Flynn, 2012: character 142).

118. Radius – distal articulation surface shape: (0) with a deep sulcus (*Erinaceus*); (1) smooth, lacks a deep sulcus (*Vulpavus*) (Spaulding and Flynn, 2012: character 143).

119. Carpus – cuneiform shape in proximal view: (0) triangular (*Nandinia*); (1) rectangular (*Vulpavus*) (Spaulding and Flynn, 2012: character 144).

120. Carpus – proximal surface of scapholunar, curvature: (0) fully convex (*Nandinia*); (1) convex and concave (*Herpestes*) (Spaulding and Flynn, 2012: character 145).

121. Carpus – unificiform width (new): (0) as wide as trapezoid and magnum combined (*Canis*); (1) small, only as wide as magnum alone (*Nandinia*) (Spaulding and Flynn, 2012: character 146).

122. Carpus – trapezium position (Yalden, 1970): (0) on the posterior surface of the trapezoid (*Canis*); (1) on the radial surface of the trapezoid (*Felis*) (Spaulding and Flynn, 2012: character 147).

123. Carpus – metacarpal III overlaps IV proximally (Bryant, 1991): (0) absent (*Canis*); (1) present (*Vulpavus*) (Spaulding and Flynn, 2012: character 148).

124. Carpus – distal surface of scapholunar shape (Yalden, 1970): (0) relatively smooth/even (*Canis*); (1) a sharp projection exists between the magnum and trapezoid (*Ursus*) (Spaulding and Flynn, 2012: character 149).

125. Carpus – cuneiform articulation with ulna, position: (0) on medial (radial) margin (*Felis*); (1) on distal surface of ulna (*Ursus*) (Spaulding and Flynn, 2012: character 150).
126. Carpus –metacarpal II strongly overlaps III proximally: (0) overlap small or absent (*Canis*); (1) overlap present and substantial (*Felis*) (Spaulding and Flynn, 2012: character 151).
127. Carpus – metacarpal length: (0) metacarpal lengths are equivalent to sum of phalanges (*Vulpavus*); 1– phalanges are longer than metacarpals (Otariidae) (Spaulding and Flynn, 2012: character 152).
128. Carpus – medial phalanx distal articular surface symmetry: (0) symmetrical (*Vulpavus*); (1) asymmetrical (*Felis*) (Spaulding and Flynn, 2012: character 153).
129. Carpus – proximal phalanges compressed dorsoventrally: (0) absent (*Vulpavus*); (1) present (*Hoplophoneus*) (Spaulding and Flynn, 2012: character 154).
130. Carpus – lateral excavation of the medial phalanx; (0) absent (*Vulpavus*); (1) present (*Felis*) (Spaulding and Flynn, 2012: character 155).
131. Femur – lesser trochanter orientation: (0) projects posteriorly (*Didymictis*); (1) projects medially (*Vulpavus*) (Spaulding and Flynn, 2012: character 156).

132. Femur – intertrochanteric crest extent: (0) extends to lesser trochanter (*Didymictis*); (1) becomes flush with shaft before reaching the lesser trochanter (*Vulpavus*) (Spaulding and Flynn, 2012: character 157).

133. Femur – position of lesser trochanter relative to the third trochanter: (0) third trochanter is lower (*Vulpavus*); (1) third trochanter is roughly at the same level (*Didymictis*) (Spaulding and Flynn, 2012: character 158).

134. Femur – supracondylar tuberosities: (0) absent (*Vulpavus*); (1) presence of two or more raised tuberosities just proximal to the condyles of the femur on the posterior shaft (*Canis*) (Spaulding and Flynn, 2012: character 160).

135. Femur – height of greater trochanter relative to head of femur: (0) greater trochanter is higher or sub-equal (*Vulpavus*); (1) greater trochanter is lower than head of femur (*Ursus*) (Spaulding and Flynn, 2012: character 161).

136. Femur – medial condyle morphology: (0) proximal edge of the articular surface of condyles are flush with the shaft, due to the lack of development of a condylar neck (*Vulpavus*); (1) proximal edge of the articular surface of condyles are not flush with the shaft, due to the development of a condylar neck (*Canis*) (Spaulding and Flynn, 2012: character 162).

137. Femur – lesser trochanter development: (0) strong, prominently projecting feature (*Vulpavus*); (1) small, barely more than a small bump or ridge on the shaft (*Ursus*) (Spaulding and Flynn, 2012: character 163).
138. Femur – greater trochanter broadest surface, orientation: (0) faces laterally (*Vulpavus*); (1) faces posteriorly (*Canis*) (Spaulding and Flynn, 2012: character 164).
139. Femur – patellar groove shape: (0) deep and narrow (*Didymictis*); (1) wide and flat (*Vulpavus*) (Spaulding and Flynn, 2012: character 166).
140. Femur – position of greater trochanter relative to shaft: (0) greater trochanter over distal midline (*Erinaceus*); (1) greater trochanter lateral to midline (*Didymictis*) (Spaulding and Flynn, 2012: character 167).
141. Tibia – deep groove on the posterior surface of the tibia (Matthew, 1909): (0) present (*Vulpavus*); (1) absent (*Canis*) (Spaulding and Flynn, 2012: character 169).
142. Tibia – posterior bone spur on distal tibia: (0) presence of a prominent bone spur on the posterior margin (*Vulpavus*); (1) spur absent (*Nandinia*) (Spaulding and Flynn, 2012: character 170).
143. Tibia – contact of inner borders of condyles: (0) in contact (*Vulpavus*); (1) separate (*Canis*) (Spaulding and Flynn, 2012: character 171).

144. Tibia – internal (medial) malleolus morphology: (0) forms a clear and distinct well-defined point (*Vulpavus*); (1) indistinct, forming a general extension of the medial surface of the tibia (*Civettictis*) (Spaulding and Flynn, 2012: character 172).

145. Pes – dorsal surface of astragalus, shape (Matthew, 1909): (0) smooth (*Vulpavus*); (1) grooved (*Canis*) (Spaulding and Flynn, 2012: character 174).

146. Pes – astragalus – height of fibular facet: (0) height subequal to length, resulting in a roughly square shaped facet (*Vulpavus*); (1) height much less than length, resulting in a more crescent shaped feature (*Canis*) (Spaulding and Flynn, 2012: character 175).

147. Pes – astragalar head shape when viewed dorsally: (0) rounded (*Vulpavus*); (1) flattened (*Canis*) (Spaulding and Flynn, 2012: character 176).

148. Pes – astragalus fossa, on the lateral edge, posterior ventral quadrant: (0) present (*Didymictis*); (1) absent (*Vulpavus*) (Spaulding and Flynn, 2012: character 178).

149. Pes – astragalus lateral margin, anterior ventral edge expansion: (0) lateral expansion present (*Vulpavus*); (1) expansion absent, creating a much smoother margin (*Procyon*) (Spaulding and Flynn, 2012: character 179).

150. Pes – astragalar head medial articulation surface extent: (0) extends backwards a great distance, past the border of the sustentacular facet (*Hyaenodon*); (1) short, does not extend past the start of the neck (*Vulpavus*) (Spaulding and Flynn, 2012: character 180).

151. Pes – astragalus sustentacular facet shape: (0) has clear edges, is somewhat convex, and does not extend into gully (*Vulpavus*); (1) is more flat than convex and extends into gully (*Canis*) (Spaulding and Flynn, 2012: character 181).

152. Pes – astragalar foramen; (0) present and dorsally positioned (*Vulpavus*); (1) present and posteriorly positioned (*Hyaenodon*); (2) absent (*Canis*) (Spaulding and Flynn, 2012: character 182).

153. Pes – astragalus, posterior ridge for ligament attachments, presence: (0) present, high (*Vulpavus*); (1) low or absent (*Felis*) (Spaulding and Flynn, 2012: character 183).

154. Pes – astragalus, orientation of posterior ridge for ligament attachments: (0) orientated at an oblique angle relative to the long axis of the astragalar trochlea (*Vulpavus*); (1) orientated in line with the trochlea (*Canis*) (Spaulding and Flynn, 2012: character 184).

155. Pes – astragalus-tibia articulation surface, extent: (0) covers entire posterior dorsal surface (*Canis*); (1) restricted, fails to cover entire posterior dorsal surface, leaving a gap in the lateral posterior quadrant (*Vulpavus*) (Spaulding and Flynn, 2012: character 185).

156. Pes – astragalus, cotylar fossa presence: (0) present (*Didymictis*); (1) absent (*Vulpavus*) (Spaulding and Flynn, 2012: character 187).

157. Pes – Calcaneus, sustentaculum position (Heinrich and Rose, 1997): (0) far from anterior border, roughly in the middle of the calcaneus (*Didymictis*); (1) close to anterior border (*Vulpavus*) (Spaulding and Flynn, 2012: character 188).

158. Pes – Calcaneus, peroneal tubercle development: (0) weakly developed, little more than a ridge (*Didymictis*); (1) well developed (*Vulpavus*) (Spaulding and Flynn, 2012: character 189).

159. Pes – astragalus neck development: (0) absent (lacks a clearly defined neck of astragalus) (*Erinaceus*); (1) present (*Vulpavus*) (Spaulding and Flynn, 2012: character 190).

160. Pes – calcaneus, cuboid facet shape: (0) irregularly shaped (*Didymictis*); (1) round (*Vulpavus*) (Spaulding and Flynn, 2012: character 191).

161. Pes – calcaneus, cuboid facet orientation: (0) angled dorsally (*Vulpavus*); (1) in planes other than dorsal (*Didymictis*) (Spaulding and Flynn, 2012: character 192).

162. Pes – calcaneus, fibular facet (Flynn and Galiano, 1982): (0) present (*Didymictis*); (1) absent (*Vulpavus*) (Spaulding and Flynn, 2012: character 193).

163. Pes – calcaneus –dorsal facet morphology: (0) smooth (*Vulpavus*); (1) clearly defined, sharp corner (rather than a smooth curve) (*Canis*) (Spaulding and Flynn, 2012: character 194).

164. Pes – cuboid, contact with metatarsal V (Bryant, 1991): (0) small (less than 40%) articular surface for metatarsal V (*Dinictis*); (1) large, articular surface for metatarsal V at least 40% of distal surface (*Canis*) (Spaulding and Flynn, 2012: character 195).

165. Pes – cuboid shape: (0) relatively rectangular (*Didymictis*); (1) wider proximally than distally (*Vulpavus*) (Spaulding and Flynn, 2012: character 196).

166. Pes – cuboid, tubercle for the long plantar ligament, position (Heinrich and Rose, 1997): (0) distal to the ectocuneiform articulation facet (*Didymictis*); (1) even with the ectocuneiform articulation facet (*Vulpavus*) (Spaulding and Flynn, 2012: character 197).

167. Pes – cuboid/astragalus contact (Matthew, 1909): (0) present (*Thinocyon*); (1) absent (*Vulpavus*) (Spaulding and Flynn, 2012: character 198).

168. Pes – navicular height: (0) height less than width (*Vulpavus*); (1) height roughly equal to or greater than width (*Canis*) (Spaulding and Flynn, 2012: character 199).

169. Pelvis – ilium, anterior expansion: (0) not expanded (*Felis*); (1) expanded dorsoventrally (*Canis*) Primitively for Carnivoramorpha the anterior ilium is not dorsoventrally expanded;

however in *Canis*, *Ursus*, *Hyaena*, and *Civettictis* a clear expansion is seen (Spaulding and Flynn, 2012: character 200).

170. Pelvis – ischial spine position: (0) located just posterior of the border of the acetabulum (*Didymictis*); (1) far posterior from acetabulum (*Vulpavus*); (2) spine absent (*Erinaceus*) (Spaulding and Flynn, 2012: character 201).

171. Pelvis – dorsal margin of acetabulum, position: (0) even with or above dorsal surface of pelvis (*Vulpavus*); (1) ventral to dorsal surface of pelvis (*Canis*) (Spaulding and Flynn, 2012: character 202).

172. Pelvis – angle at pubic symphysis: (0) ‘U-like’ (*Canis*); (1) ‘V-like’ (*Felis*) (Spaulding and Flynn, 2012: character 203).

173. Pelvis – ilium, anterior region morphology: (0) broad and flat (*Canis*); (1) divided by a distinct ridge running antero-posteriorly (*Vulpavus*) (Spaulding and Flynn, 2012: character 204).

175. Pelvis – ilium, ventral surface morphology: (0) broad and flat (*Thinocyon*); (1) narrow (*Vulpavus*) (Spaulding and Flynn, 2012: character 205).

176. Atlas – alar foramen: (0) absent, only a notch is present (*Canis*); (1) present, confluent with lateral vertebral foramen (*Herpestes*); (2) present, separate from lateral vertebral foramen (*Procyon*) (Spaulding and Flynn, 2012: character 207).

177. Atlas – transverse processes, orientation: (0) projects at right angle from the body (*Canis*); (1) extends posteriorly at an acute angle to the body (*Nandinia*) (Spaulding and Flynn, 2012: character 208).

178. Atlas – ventral arch length (Gaubert et al., 2005): (0) equal to or shorter than dens of axis (*Canis*); (1) longer than dens of axis (*Civettictis*) (Spaulding and Flynn, 2012: character 209).

179. Axis – body length: (0) roughly as long as it is wide (*Vulpavus*); (1) elongated relative to its width (*Felis*) (Spaulding and Flynn, 2012: character 210).

180. Cervical vertebrae – keel: (0) large ventral keel present (*Nandinia*); (1) ventral keel absent (*Dinictis*) (Spaulding and Flynn, 2012: character 211).

181. Cervical vertebrae – spinous processes, size: (0) large (*Canis*); (1) small (*Felis*) (Spaulding and Flynn, 2012: character 212).

182. Cervical vertebrae – dorsal lateral margin shape: (0) concave (*Öodectes*); (1) convex (*Felis*) (Spaulding and Flynn, 2012: character 213).

183. Sacrum – size compared to pelvis: (0) small, does not reach border of acetabulum (*Canis*); (1) large, reaches border of acetabulum (*Felis*) (Spaulding and Flynn, 2012: character 215).

184. Sacrum – neural spines: (0) clear and distinct from one another (*Nandinia*); (1) fused to one another, appearing as one long keel (*Canis*) (Spaulding and Flynn, 2012: character 216).

185. Alisphenoid, foramen ovale (position): (0) anterior to glenoid fossa; (1) medial to glenoid fossa. Comparisons made to the posterior-most edge of the glenoid fossa, not the process. Serves for the passage of the trigeminal nerve (V), internal maxillary artery and the medial meningeal artery (modified from Gaubert et al., 2005: character 71).

186. Basisphenoid, medial lacerate foramen: (0) covered by bullae; (1) anteriomedial to bullae (e.g., *Herpestes*). [Serves for the passage of the ascending pharyngeal artery.] (Gaubert et al., 2005: character 79).

187. Ectotympanic/entotympanic division: (0) not externally visible; (1) externally visible with infolding at junction, without clear suture; (2) externally visible, with clear suture. [In the viverrids, the point of contact between the two elements is marked by an inbending of the plates of bone. In the other feliforms, although one can detect the point of contact, it is because of structural differences.] (Modified from Gaubert et al., 2005: character 85).

188. Entotympanic, ventral floor ossification: (0) ossified; (1) unossified (i.e. *Nandinia*) (modified from Gaubert et al., 2005: character 102).

189. Vagina processus hyoideus: (0) confluent with stylomastoid foramen (giving the appearance of one foramen); (1) slightly separate from stylomastoid foramen (Gaubert et al., 2005: character 129).

190. i1- i3 projection: (0) extends upward; (1) procumbent (less than 45 degrees) (Gaubert et al., 2005: character 151).

191. C1, flanges: (0) posterior flange present; (1) absent; (2) anterior and posterior flanges present (Gaubert et al., 2005: character 156).

192. P3 number or roots: (0) two roots; (1) one root; (2) three roots (Gaubert et al., 2005: character 164).

193. P3, posterolingual cingulum: (0) present, reduced; (1) present, broad; (2) vestigial/absent (Gaubert et al., 2005: character 165).

194. p3, talonid: (0) absent; (1) present (Gaubert et al., 2005: character 169).

195. P4, parastyle: (0) absent/vestigial; (1) present, small (less than size of protocone); (2) present, large (near equal to protocone); (3) present, larger than protocone (Gaubert et al., 2005: character 172).

196. P4 posterolingual cingulum: (0) present; (1) vestigial; (2) absent (Gaubert et al., 2005: character 177).
197. p4 talonid: (0) absent/vestigial; (1) present (Gaubert et al., 2005: character 178).
198. p4 posterior accessory cusps: (0) 2 cusps, linear; (1) 1 cusp; (2) no cusps; (3) 2 or more cusps, nonlinear (Gaubert et al., 2005: character 179).
199. P4-M1 carnassial embrasure pit: (0) present; (1) absent (Gaubert et al., 2005: character 181).
200. M1 roots: (0) three roots; (1) two roots; (2) one root (Gaubert et al., 2005: character 183).
201. m1, trigonid: (0) present, considerably higher than talonid; (1) present, near equal in height to talonid; (2) absent (modified from Gaubert et al., 2005: character 187).
202. m1, trigonid proportion: (0) length less than talonid; (1) length near equal length of talonid; (2) trigonid length is 60% to 73% of total length; (3) 77-87%; (4) 88% and higher; (5) no talonid (modified from Gaubert et al., 2005: character 188; Barrett, 2016: character 30).
203. m1 metaconid: (0) large; (1) considerably smaller than paraconid; (2) absent (Gaubert et al., 2005: character 189).

204. m1, protoconid : (0) present; (1) absent (Gaubert et al., 2005: character 190).

205. m1 entoconid: (0) present; (1) absent (Gaubert et al., 2005: character 191).

206. m1 hypoconid: (0) present; (1) absent (Gaubert et al., 2005: character 192).

207. m1, hypoconulid: (0) absent; (1) present (Gaubert et al., 2005: character 193).

208. m1, small cusp between hypoconid and protoconid: (0) absent; (1) present (Gaubert et al., 2005: character 194).

209. M2, paracone and metacone: (0) metacone and paracone present, paracone larger; (1) metacone absent; (2) tooth without distinguishable cusps; ? = tooth absent (Gaubert et al., 2005: character 195).

210. M2, roots: (0) three roots; (1) two roots; (2) one root; (3) tooth absent (modified from Gaubert et al., 2005: character 198).

211. m2, cusps: (0) high trigonid with extremely elongate talonid due to large hypoconulid, tooth elongate oval outline; (1) talonid not elongate, tooth oval outline, no enlarged hypoconulid; (2) low trigonid, extremely elongate with low, well developed talonid cusps; (3) low trigonid, well developed talonid cusps; (4) tooth with cusps but no clear trigonid or talonid; (5) tooth without clearly defined cusps; (6) absent (modified from Gaubert et al., 2005: character 202).

212. Buccal cingulum, upper molars: (0) small/not developed; (1) enlarged (Gaubert et al., 2005: character 206).

213. Mandible, mandibular symphysis: (0) strong (well fused); (1) weak (not well fused) (Gaubert et al., 2005: character 212).

214. Mandible, medial shelf of angular process: (0) present, small ridge; (1) present, wide shelf; (2) absent (Gaubert et al., 2005: character 214).

215. p4 anterior accessory cusp: (0) absent; (1) smaller than posterior; (2) about equal to posterior; (3) larger than posterior (Gaubert et al., 2005: character 221).

216. Volume contribution of the feloid auditory bulla: (0) caudal entotympanic envelopes ectotympanic chamber (e.g. Felidae); (1) both chambers meet over the petrosal and display an external 'infolding' at their juncture with a septum oblique to the long axis of the skull, such that the caudal entotympanic penetrates the anterointernal (rostromedial) corner of the auditory region (e.g. viverrids); (2) both chambers meet over the petrosal and display an external 'infolding' at their juncture with a septum orthogonal to the long axis of the skull (e.g. herpestids); (3) ectotympanic chamber dominates with caudal entotympanic chamber restricted to posterior third of bulla with the division separating anterior and posterior chambers rostral of the mastoid and paroccipital processes (e.g. Ictitheriines); (4) ectotympanic chamber dominates bulla, partially or totally overlaying caudal entotympanic chamber via ventral overgrowth,

recumbent septum concealing posterior chamber within mastoid and paroccipital process (e.g. *Crocota*, *Hyaena*): (5) anterior chamber formed by rostral entotympanic or pseudoseptum.

217. Mastoid invasion by bulla: (0) absent; (1) present.

218. P4 nimravid “parastyle”: (0) absent; (1) present (Barrett et al., 2021: character 222).

219. P2: (0) double-rooted; (1) single-rooted; (2) absent (Barrett et al., 2021: character 224).

220. p3 posterior cusps: (0) no cusps; (1) one cusp (posterior cingular cusp); (2) two cusps (posterior cingular cusp and posterior accessory cusp) (Barrett et al., 2021: character 229).

221. Basicranial foramina: (0) petrobasilar venous sinus and sigmoid sinus merge intracranially and exit the posterior lacerate (jugular) foramen; (1) veins merge extracranially, passing through the petrobasilar and posterior lacerate foramina respectively (Barrett et al., 2021: character 231).

222. P4 protocone: (0) medial or posterior to paracone; (1) anterior to paracone or paracone-parastyle juncture; (2) anterior face of protocone approximately level with anterior face of parastyle; (3) protocone extending anteriorly of parastyle (modified from Werdelin and Solounias, 1991: character 9).

223. Shape of dentary tooth row: (0), tooth row straight; (1), tooth row curved, or convex (Werdelin and Solounias, 1991: character 10).

224. P4 metacone/metastyle blade length to paracone length ratio: (0): 0.54 or less; (1): 0.6-0.99; (2): 1-1.3; (3): 1.4 and greater (modified from Werdelin and Solounias, 1991: character 11).

225. Placement of carnassials in tooth row: (0) carnassials in line with tooth row, i.e. at an angle relative to the sagittal plane); (1) carnassials parallel to sagittal plane (Werdelin and Solounias, 1991: character 14).

226. Placement of anterior accessory cusp of p4: (0) free of main cusp; (1) appressed to main cusp (Werdelin and Solounias, 1991: character 14).

227. Shape of anterior face of p3: (0) concave/straight; (1) convex (Werdelin and Solounias, 1991: character 15).

228. Position of infraorbital foramen: (0) positioned anterior to middle of P3; (1) positioned above middle to posterior of P3; (2) positioned above anterior edge of P4; (3) positioned above mid-posterior portion of P4 (modified from Werdelin and Solounias, 1991: character 22).

229. Position of anterior margin of orbit: (0) above or behind metastylar blade of P4; (1) above the anterior end of P4; (2) above P3 (modified from Werdelin and Solounias, 1991: character 23).

230. Suture between premaxillary and frontal on snout: (0) absent; (1) present (Werdelin and Solounias, 1991: character 24).

231. Size of inferior oblique muscle fossa at maxillary-lacrimal suture postero-dorsal to infra-orbital foramen: (0) small; (1) large; (2) absent (modified from Werdelin and Solounias, 1991: character 25).

232. Inferior oblique muscle Fossa II at juncture between maxillary, lacrimal, and Frontal: (0) absent; (1) present (Werdelin and Solounias, 1991: character 26).

233. Sphenoid foramen and postpalatine foramen position: (0) well separated, distinct foramina; (1) foramina located close together in a single depression (Werdelin and Solounias, 1991: character 27).

234. The contribution of the maxilla to the antero-internal rim of the zygomatic arch: (0) small to none; (1) maxillary makes up a substantial portion of the antero-dorsal margin of the zygomatic arch (Werdelin and Solounias, 1991: character 28).

235. Shape of basioccipital in ventral view: (0) flat; (1) lateral ridges and central groove (Werdelin and Solounias, 1991: character 32).

236. Position of premaxillary-maxillary suture on palate: (0) near the middle of the incisive fossa; (1) at the postero-lateral margin of the incisive fossa (Werdelin and Solounias, 1991: character 33).

237. Shape of jugal-maxillary suture in external view: (0) strongly sinusoid; (1) angled downwards posteriorly in a straight or weakly sinusoid manner; (2) horizontally straight; (3) vertical (modified from Werdelin and Solounias, 1991: character 36).

238. Position of external auditory meatus: (0) far forwards of nuchal crest; (1) level with nuchal crest (Werdelin and Solounias, 1991: character 43).

239. Shape of nuchal crest: (0) antero-posteriorly inclined; (1) nearly vertical or vertical (Werdelin and Solounias, 1991: character 44).

240. Size of metacarpal 1: (0) metacarpal 1 has a long, slender diaphysis resembling the other four metacarpals; (1) metacarpal 1 has a blunt and rectangular shape (e.g. felids); (2) vestigial (modified from Werdelin and Solounias, 1991: character 45).

241. Angle of scapular spine in posterior view: (0) angled; (1) straight (Werdelin and Solounias, 1991: character 47).

242. Relative width of p3 (ranked in order by ratio of Wp3 to Lp3): (0) 0.2-0.39; (1) 0.4-0.6; (2) 0.61-0.66; (3) 0.69 and greater (Tseng and Wang, 2007: character 12).

243. Relative width of p4 (ranked in order by ratio of Wp4 to Lp4): (0) 0.38 and less; (1) 0.40-0.54; (2) 0.55-0.68; (3) 0.72 and greater (Tseng and Wang, 2007: character 13).

244. Relative width of P3 (ranked in order by ratio of WP3 to LP3): (0) 0.38 and less; (1) 0.4-0.65; (2) 0.66-0.79; (3) 0.81 and above (Tseng and Wang, 2007: character 14).

245. Labiolingual compression of the C1: (0) very slightly compressed (length/breadth index smaller than 1.5); (1) markedly compressed (index between 1.5 and 1.8); (2) very compressed (index 1.81-3.0); (3) extremely compressed 4.0 and greater (Robles et al., 2013: character 3).

245. C1 vertical grooves: (0) absent; (1) present (Robles et al., 2013: character 4).

247. P3 anterior cingulum cusp: (0) absent; (1) present (Robles et al., 2013: character 7).

248. P4 preparastyle: (0) absent; (1) present (Robles et al., 2013: character 10).

249. p2: (0) present; (1) absent (Robles et al., 2013: character 16).

250. Orbit: (0) open; (1) closed (Robles et al., 2013: character 23).

251. Position of M1. Polarity: (0) distal to P4; (1) medial to P4 (Robles et al., 2013: character 27).

252. c1: (0) larger than i3; (1) same size (Robles et al., 2013: character 31).

253. Ratio P4 length /p4 length: (0) 0.93 and less; (1) 1.0-1.87; (2) 1.95-2.1; (3) 2.2 and higher (modified from Robles et al., 2013: character 32).

254. Masseteric fossa on the lateral surface of the maxilla and jugal: (0) shallow or absent; (1) deep with distinct dorsal margin (Barrett, 2016: character 3).

255. Fossa on the medial face of the zygomatic arch, below the postorbital process: (0) no fossa; (1) presence of a marked fossa (Peigné, 2003: character 12).

256. Zygomata shape in dorsal view: (0) broadly circular; (1) triangular (Barrett, 2016: character 5).

257. Shape of the glenoid socket of the craniomandibular joint: (0) anterior lip is missing; (1) posterior lip of the glenoid socket projects more ventrally than anterior lip; (2) anterior lip and posterior lip project equally ventrally (Barrett, 2016: character 10).

258. Anterior mandible position: (0) in line with the tooth row, mandibular border of cheek tooth row is in the same plane as the mandibular border of the incisors and canines; (1) elevated above tooth row; (2) cheek teeth and anterior teeth brought again into same plane by elevation of cheek teeth on pedestal (Barrett, 2016: character 13).

259. Development and orientation of the coronoid process of the dentary: (0) posteriorly

orientated posterior border without surpassing the level of the mandibular condyle; (1) surpassing the level of the mandibular condyle; (2) vertically orientated posterior border; (3) anteriorly orientated posterior border (Barrett, 2016: character 20).

260. Size of the genial flange of the dentary in adult taxa. Measured as the height of the genial flange from the anterior portion of the postcanine diastema to the ventral apex of the genial flange/length of dentary from the posterior articular surface to the most anterior aspect: (0) no flange, the ventral rim of the chin is regularly curved; (1) no flange, but the ventral rim of the chin is distinctly angulate; (2) short flange, between 22 and 31% of the total length of mandible; (3) deep flange, 32-50% of the total length of the mandible; (4) extremely deep flange, 54% or more of the total mandibular length (Barrett, 2016: character 15).

261. Mental fossa. Fossa on the ventral-internal face of the chin: (0) no fossa; (1) fossa present and marked (Barrett, 2016: character 16).

262. Incisors: (0) spatulate; (1) mostly spatulate, I3 caniform; (2) all caniform (Barrett, 2016: character 17).

263. C1 length. Mesial-distal length of C1 measured at the dentine/enamel boundary: (0) less than that of P4; (1) greater than that of P4 (Barrett, 2016: character 18).

264. Serration density of permanent upper canines per millimeter. Measured over an average of 5 mm: (0) none; (1) 0.7-2.7; (2) 2.8-5.0; (3) ≥ 5.5 (modified from Barrett, 2016: character 19).

265. Size of P3 vs. size of P4. Measured as a ratio of crown height (base of cingulum to apex of tooth) on adult minimally worn teeth: (0) 0.69-1.1; (1) 1.2 and greater; (2) 0.48-0.69; (3) 0.45 and lower (modified from Barrett, 2016: character 20).

266. p3 crown height compared to p4: (0) 0.6-0.98; (1) 1.0 and greater; (2) less than 0.58; (3) p3 absent (modified from Barrett, 2016: character 26).

267. Cheek tooth serrations. Serrations on adult minimally worn cheek teeth: (0) absent; (1) present (Barrett, 2016: character 31).

268. Articulation between the calcaneum and navicular : (0) absent; (1) present (Barrett, 2016: character 33).

269. Anterior palatine canal opening location: (0) level with P3; (1) between P2 and P3; (2) P4; (3) M1; (4) P2 or anterior (modified from Bryant, 1996: character 4).

270. Position of nasals relative to maxilla-frontal suture: (0) nasals extend beyond the maxillofrontal suture; (1) nasals shortened, the posterior border lies across or anterior to the maxillofrontal suture (Peigné, 2003: character 9).

271. P4, orientation of the protocone: (0) anterolingually projected; (1) lingually projected (modified from Peigné, 2003: character 23).

272: Processus muscularis on malleus: (0) short, cone-shaped and with tapering apex; (1) distinctly enlarged and cylindrical; (2) absent (modified from Christiansen, 2008: character 2).

273: Lambdoidal-squamous sutures: (0) converging along lamboid crest; (1) separate (modified from Christiansen, 2008: character 12).

274. Dorsal part of frontoparietal (coronal) suture: (0) smooth, lacking a parietal process; (1) suture irregular with a distinct, often very large, medio-dorsally directed parietal process (Christiansen, 2008: character 13).

275. Dorsal Jugal-squamosal suture in zygomatic arch: (0) abuts the postorbital process; (1) does not abut the postorbital process (modified from Christiansen, 2008: character 19).

276. Paroccipital process: (0) ventrally directed; (1) posteriorly directed (modified from Christiansen, 2008: character 22).

277. Angle of long axis of bulla to long axis of skull: (0) Less than or equal to 19° ; (1) 20° - 27° ; (2) 28° - 37° (modified from Christiansen, 2008: character 29).

278: Entotympanic process: (0) narrow and raised; (1) wide and flattened; (2) absent (modified from Christiansen, 2008: character 30).

279. Upper incisor arcade: (0) strongly parabolic; (1) slightly parabolic such that the anterior edge of I3 does not contact a straight edge held across the anterior of the arcade; (2) straight (modified from Christiansen, 2013: character 1).

280. P4 anterior cingulum: (0) indistinct; (1) distinct and often forming a ridge; (2) forming a distinct ectoparastyle (Christiansen, 2013: character 11).

281. Mediolateral width of P3 across the metacone relative to width across the paracone: (0) 56 and less; (1) 58- 68; (2) narrow (~70–93%); (3) wide (~95–130%) (modified from Christiansen, 2013: character 17).

282. Relative height of the m1 major cusps, measured from tip of cusp to base of cingulum: (0) 61% and lower; (1) height of paraconid low compared with height of protoconid (65–93%); (2) height of paraconid tall compared with height of protoconid (95–130%). (modified from Christiansen, 2013: character 24).

283. Relative length of p4: (0) 7% and lower; (1) small relative to mandible length (~7.5–9%); (2) large relative to mandible length (~10–15%) (modified from Christiansen, 2013: character 26).

284. Snout area elevation compared with braincase: (0) snout area low, line from dorsal narial aperture to juncture of occipital/sagittal crest lies below frontal postorbital process; (1) snout area elevated, line passes above frontal postorbital process (modified from Christiansen, 2013: character 34).

285. Size of the jugal postorbital process: (0) small, rounded, often almost absent; (1) tall, triangular and tapering (Christiansen, 2013: character 39).

286. Relative width across the upper incisor arcade compared to cranial basilar length (CBL): (0) 11% and less; (1) narrow (12–15% of CBL); (2) wide (16–19% of CBL); (3) extremely wide (21–25% of CBL) (modified from Christiansen, 2013: character 42).

287. Palatal region relative width compared to CBL: (0) 14% and lower; (1) 16–22%; (2) ~23–25%; (3) palatal region across center of P3 relatively wide (~27–34% of CBL); (4) palatal region across center of P3 extremely wide (~36–43% of CBL) (modified from Christiansen, 2013: character 43).

288. Mandibular fossa termination: (0) posterior to the carnassial; (1) terminating below talonid or before carnassial notch; (2) well anterior of the posterior edge of the carnassial, frequently terminating around carnassial saddle or even at the M1/P4 junction (modified from Christiansen, 2013: character 49).

289. Height of horizontal dentary ramus (below m1) relative to ramus length (articular to symphysis between i1s): (0) 14 and less; (1) slender (~15–17%); (2) robust (~18–25%) (modified from Christiansen, 2013: character 50).

290. Lower canines, buccal vertical groove/ridge: (0) present; (1) absent (modified from Salesa et al., 2012: character 22).

291. C1 lingual ridge: (0) absent; (1) present (Salles, 1992: character 11).

292. Relative position of p3 and p4: (0) aligned; (1) not aligned (Salesa et al., 2010: character 24).

293. Palatal ridge/groove: (0) no visibly obvious groove or ridge (but may be felt by touch); (1) visibly obvious but shallow groove with ridges; (2) deep groove with distinctive ridges; (3) extreme medial ridges displacing medial palate ventrally from the main plane of the palate (Sakamoto and Ruta, 2012: character 39).

294. Stylomastoid groove: (0) groove originating from the stylomastoid foramen; (1) groove originating from the tympanohyal pit (Sakamoto and Ruta, 2012: character 41).

295. Metatarsal 1: (0) functional metatarsal, articulating with a phalanx; (1) vestigial metatarsal 1 (Rothwell, 2003: character 20).

296. Orientation of premaxillary-maxillary suture relative to upper tooth row: (0) 50 and less; (1) 52-70°; (2) moderately steep, 70-80°; (3) very steep, greater than 80° (modified from Van Valkenburgh et al., 1990: character 3).

297. Shape of sphenopalatine foramen: (0) oval with long axis oriented anteroposteriorly; (1) round/oval with long axis oriented dorsoventrally (Van Valkenburgh et al., 1990: character 12).

298. Teres major fossa: (0) absent; (1) small, triangular; (2) long (modified from Van Valkenburgh et al., 1990: character 20).

299. Radius, orientation of distal ulnar facet: (0) horizontal; (1) vertical (Van Valkenburgh et al., 1990: character 23).

300. Tibia, cnemial crest in lateral view: (0) straight; (1) concave (Van Valkenburgh et al., 1990: character 27).

301. Fibula, shape of proximal end: (0) without anterior projection; (1) expanded anteriorly with bony process (Van Valkenburgh et al., 1990: character 29).

302. Patella, ridge separating articular facets: (0) absent; (1) present (Van Valkenburgh et al., 1990: character 30).

303. Scapholunar, articular surface for trapezoid: (0) convex and concave; (1) concave only (Van Valkenburgh et al., 1990: character 37).

304. Pisiform, shape of cuneiform facet: (0) oval; (1) triangular (Van Valkenburgh et al., 1990: character 41).

305. Astragalus and calcaneum articulation: (0) astragalus reaches distal end of calcaneum; (1) astragalus does not reach distal end of calcaneum (Van Valkenburgh et al., 1990: character 42).

306. Seventh lumbar vertebra, shape of transverse processes: (0) similar to preceding vertebrae; (1) shorter and angled anteriorly (Van Valkenburgh et al., 1990: character 43).

307. m1 anterolingual cingulum: (0) absent; (1) present.

308. Buccal cingulum, lower molars: (0) absent; (1) present.

309. P2 parastyle: (0) absent or vestigial; (1) present-cuspidate (Morales et al., 2019: character 2).

310. P2 metastyle (posterior cusp): (0) absent or vestigial; (1) strong (Morales et al., 2019: character 3).

311. P3 metastyle (blade on P3): (0) absent or vestigial; (1) strong (Morales et al., 2019: character 8).

312. P3 mesostyle: (0) absent or weak; (1) strong (Morales et al., 2019: character 12).

313. P3 Paracone-Metastyle disposition: (0) aligned with the antero-posterior axis; (1) inclined as in the P4 (Morales et al., 2019: character 14).

314. P4 mesostyle: (0) absent or weak; (1) strong (Morales et al., 2019: character 23).
315. P4 alignment of protocone with paracone and metastylar blade: (0) absent; (1) present (modified from Morales et al., 2019: character 16).
316. M1 paracone-metacone shape: (0) coniform; (1) crestiform (Morales et al., 2019: character 26).
317. M1 protocone shape: (0) coniform with cristas; (1) crestiform with undifferentiated cristas (Morales et al., 2019: character 27).
318. p2 molarization: (0) metaconid absent; (1) metaconid present (Morales et al., 2019: character 38).
319. p3 molarization: (0) no metaconid; (1) with metaconid (Morales et al., 2019: character 40).
320. Masseteric fossa on maxilla below orbit: (0) absent; (1) present.
321. Auriform process of basioccipital: (0) absent; (1) present, large wing-like projection.
322. Frontal sinus, caudal extension: (0) terminates antero-dorsally to the brain cavity; (1) terminates dorsally above brain cavity, >50% of its length; (2) expands caudally over the complete length of the brain cavity.

323. dp4 metaconid alignment: (0) non-linear, triangular alignment with paraconid and protoconid, separated from talonid by transverse deep valley; (1) linear alignment with paraconid and protoconid; (2) no metaconid.

324. Petrobasilar foramen: (0) open vacuity; (1) closed foramen in basioccipital (Barrett, 2021: character 223).

325. Crenulations on the anterior face of the paracone of P4 and occlusal face of the protocone: (0) absent; (1) present (Barrett, 2021: character 225).

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Appendix E

Nexus formatted morphological character matrix

#NEXUS

[written Fri Oct 01 13:40:37 PDT 2021 by Mesquite version 3.61 (build 927) at LAPTOP-CRLI5NPQ/128.223.221.117]

BEGIN TAXA;

TITLE Taxa;

DIMENSIONS NTAX=129;

TAXLABELS

Tungurictis_spocki Ictitherium_viverrinum Hyaenotherium_wongii
Hyaenictitherium_hyaenoides Lycyaena_chaeretis Chasmaporthetes_lunensis
Chasmaporthetes_ossifragus Palinhyaena_reperta Adcrocuta_eximia Pachycrocuta_brevirostris
Crocuta_crocuta Crocuta_crocuta_spelaea Hyaena_hyaena Proteles_cristata
Plioviverrops_orbigny Protictitherium_crassum Belbus_beaumonti Tongxinictis_primordialis
Allohyaena_kadici Dinocrocuta_gigantea Percrocuta_carnifex Percrocuta_algeriensis
Percrocuta_tobieni Proailurus_lemanensis Pseudaelurus_validus Metailurus_major
Nimravides_pedionomus Machairodus_catocopis Megantereon_cultridens
Amphimachairodus_giganteus Amphimachairodus_coloradoensis Dinofelis_diastemata
Homotherium_ischyryrus Homotherium_serum Homotherium_latidens Promegantereon_ogygia
Smilodon_fatalis Smilodon_populator Xenosmilus_hodsonae Neofelis_nebulosa
Panthera_pardus Panthera_leo Panthera_leo_spelaea Panthera_atrox Caracal_caracal
Lynx_canadensis Felis_lybica Leopardus_pardalis Acinonyx_jubatus Miracinonyx_trumani
Puma_concolor Otocolobus_manul Prionailurus_planiceps Catopuma_temminckii
Profelis_aurata Prionodon_linsang Arctictis_binturong Civettictis_civetta
Paradoxurus_hermaphroditus Hemigalus_derbyanus Viverra_tangalunga Genetta_maculata
Paguma_larvata Cynogale_bennettii Poiana_richardsonii Viverricula_indica Bdeogale_nigripes
Mungos_mungo Suricata_suricata Herpestes_edwardsii Ichneumia_albicauda
Crossarchus_obscurus Atilax_paludinosus Rhynchogale_melleri Galerella_sanguinea
Helogale_parvula Fossa_fossana Cryptoprocta_ferox Eupleres_goudotii Salanoia_concolor
Kichechia_zamanae Kanuites_lewisae Izmirictis_cani Euboictis_aliverensis
Sivasua_viverroides Nandinia_binotata Palaeoprionodon_lamandini Stenogale_julieni
Herpestides_antiquus Ginsburgsmilus_napakensis Prosansanosmilus_eggeri
Prosansanosmilus_peregrinus Afrosmilus_hispanicus Afrosmilus_turkanae Afrosmilus_africanus
Albanosmilus_jourdani Maofelis_cantonensis Eofelis_edwardsii Dinailurictis_bonali

Quercylurus_major Dinaelurus_crassus Hoplophoneus_oharrai 'MA-PHQ 348'
Hoplophoneus_dakotensis Hoplophoneus_sicarius Hoplophoneus_adelos
Hoplophoneus_bidentatus Hoplophoneus_villebramarensis Barbourofelis_morrisi
Oriensmilus_liupanensis Sansanosmilus_palmidens Barbourofelis_fricki
Barbourofelis_loveorum Albanosmilus_whitfordi Hoplophoneus_cerebralis
Hoplophoneus_primaevus Hoplophoneus_occidentalis Nimravus_brachyops
Pogonodon_platycopis Pogonodon_davisi Dinictis_felina Nanosmilus_kurteni
Nimravus_intermedius Tapocyon_robustus Procynodictis_vulpiceps Hesperocyon_gregarius
Canis_latrans_frustror Vulpes_vulpes Taxidea_taxus

;

END;

BEGIN CHARACTERS;

TITLE Character_Matrix;

DIMENSIONS NCHAR=325;

FORMAT DATATYPE = STANDARD RESPECTCASE GAP = - MISSING = ?
SYMBOLS = " 0 1 2 3 4 5 6";

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Metailurus major

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Nimravides pedionomus

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Megantereon cultridens

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Amphimachairodus giganteus

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Amphimachairodus_coloradoensis

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Homotherium_ischyryus

101111011?121210112??012??0110211???211?22011101?0?0310110??10011?1??11??01000
0110100001102101011010??11011101111001?1??11?1??101?0?10?1?1111110010021101000
{0
1}11000?10000?0?111?10101?100010201032000205201100?3601230102001?3001200??01?2
001121120001010100101??02013011011?1001200022?1033??0??111??100000?001??00000?
??0000?-0

Homotherium_serum

100011001?121210?2???0?2000010211????????????1101?0?0310110??10011?1??11??001?00
1101110011021010010100111??111111100??1{0
1}?11?111?010?00?0011?1011?0?????110??00??10?101?1?0111111010?010001021?032010
205201100?360122000210112001300000?1?2001?31220?01010200101{0 2}2{0
1}20??011201??001000032{1 2}1033121002110000?0??0000????00??0000?-0

Homotherium_latidens 2{0 1}10{1 2}{1

2}001?121210?2???0?????10211??0211?22011101?00131011????10011?1?????????????????
??
????????????100010201032000205201100?360123010210112101300200010100??31120101010
{1 3}00111{0 2}2{0 1}201321?011?1001{1 2}000{2 3}?{1 2}10{0 3}31{1 2}10021?{0
1}0?????????01??00000???0000?-0

Promegantereon_ogygia

200011101?101210?2???0?0?00122110?0011?22011011?0?03?011????1001101??01??01000
001011?001?02??1?01?110111010101101011?11?11?121?100?00?001101101100{0 1}{0
1}0{0
2}1101001111001110011?0110001?1010100000202032000104101100?3601020002201020011
10??0?01100111111000{0 1}0101101110101002000201?000010{1
2}13220011111010111?00000001?00??000000?00000?-0

Smilodon_fatalis 2000{0 1}0{0
1}10?131210122?021?020010211030211?220111{0 1}100{0
1}0310110???10011?10111???0010011111101011020010110100111001101111001111111010
11101?001000110101100001{0
1}01011010110101100011011010110010100010202032000105{1
2}01100?3601220102?011200?2101{0 1}001110111?11200010101001212212012{2 3}{0
1}1211000010222322002{3 4}1{1 2}10?3112{0 1}0000000000??0000000?00001-0

Smilodon_populator
2?0??1?10?31210????0????11211??021??2201111??00031011????10011?1??11?????????
10?1???1??2??1??1?100111001101111011??????1?1?11?00?1000??1011??01011011010110
????021?01????01????00010202032000105201100?36010201020011210?210??00??101??31
12010101001213212112{2
3}01?11?011??1222201241210131?20????????00??0000000?0000?-0

Xenosmilus_hodsonae 2000{1 2}0111?12121012???0?20???1{2
3}211???2??2?0?11?1?0?031011????10011?1?111??001001110110001102101011011011110
1101110000?1??11?11?1?10?0010010011011000012110110011100??10??????????00?0??1000
1020??31010?05201100?36?1210002?000200?300????1?11011?1320?010?1100111220201?31
1211??000300012210331210?2??1?000000?0?00??0000000?0000?-0

Neofelis_nebulosa
201010101?101210122?00120?0011211030211?220111110101310110???10011?10101???0110
001111111010021010110111?1100010110100110111101211101?011000111101100110011010
110110011100111011000111110100000202032000204101100?36012300012010200102000000
111011111000010101100110000000000201000012120322011211011001210000?00000000000
00??00000?-0

Panthera_pardus
201011002?101210122?00120?00122110?0211?220110110001310110???10011?10101???0110
001{1 2}011100100210100111101110111011{0
1}1001?1??11?1110100?001100111101101101211011011110101100011011000111010100000
20203201010{4
5}201100?360123000010101000210000001000111110010101010001100010000002011100021
2022201121101010111100000000000000000000?00001-0

Panthera_leo
200010102?101210122?00120?0011211030211?22011111000031011011?10011?10001?1?011
000110111101102101001110011101110010100111101101111101?00100011110110001111101
0110110001100011011000011110100010202032000205201100?3601230001201010012002000
010001111100101010100011100000020020111100212131201121{1
2}000101110000?000000000000000000000001-0

Panthera_leospelaea
201012102?101210122?00120?001121103????2???11110000310110???10011?1??1?????????
1111110010021010110100111011101111011?1??11?1?1?101?00100011111110010111101011

Miracinonyx_trumani {2 3}01012{0
1}120001210?2?????0???12211?0211?220111110{0
1}?0?1011????10011?1?01??0?10??1??1111?1?02??011??0??11??1?1?100??1?1110111?0
????01?001??01000?10211010011110?????0??101?????1?101000102020{2
3}2000105201100?360123000{0 2}20101000020??00011001?111001010{0 1}0100000{0
1}0?1000001200?1?003220312013301?000012?00010000100000000000?0000?-0

Puma_concolor
2010100120101210122?0012020012211030211?220111110{0
1}0131011011010011?10001110011000111111011021010110101?1101010110100110111101
111100?00100011110110010?211010010111011100{0
1}11011000111110100010202032000205201100?3601230001202010011101000011001111100
1010101011100000000020100{0
1}00202032201231111100120000100000000000000??00000?-0

Otocolobus_manul
201011012?102210122?001202001221101?21??2?0111110000310110???10011?10101???0110
001001101011020010011110111011101111001?1??11?1110100?001000111101100110011010
11011000110001101100011011010000020203200010{4
5}201100?36?123000210101001020000001110111110000101010110000000000201?100010
20222011311010001310000?010000??0000000?0000?-0

Prionailurus_planiceps
201011012?10121012???0?0?00121110?0211?220111110001310110???10011?1??????????
??
????????????????????100000200032000105201100?360122000020102000020001001210??111000
01110100011000000010?201?1010202021201111101000?20?????????00000000000?0000?-0

Catopuma_temminckii
201011012?101110122??0120?0012211010211?220111110001310110???10011?10101???0110
00100110101102001001011011101110111100111011?01010101?00100011110110010?001010
11011?001100010011000111010100010202032000105201100?36010300022020100012020000
110011111000010101010112001000000201?000020203120102120000?12100010?0000000000
0000?0000?-0

Profelis_aurata
201011012?10121012???0120?0012?110?0011?220111110001310110???10011?10??1???????
?10011100100210100111101110111011{0
1}10011111101110100?00110010110110010??1101111011?00110?????????????????1000?020
2032000105201100?3601230001201010001202000011001?11100001010101011100000000020
0?000032203120113210000?130?000?01?00000000000?0000?-0

Prionodon_linsang
201020112?113110002?00122200122110310110020110110001210110???00001?1??????????
??

????????????????201010000010000003101000?340101100020101001020201001110??001001
00000100010000000000?400?0000102031200010010000020?????????000000000000000000-0

Arctictis binturong

1110221020113210102??22?2??012211?320?21020010210001310110??00011010101??0001
001011111011120001010110001101000111001100111012?1?11?001001000101100100211011
011110010100101001101001110112011000000131012101000224012210000000000120100100
0100012221000000000001100001001000012100021?0011001101100010112000000000000000
0001000000-0

Civettictis civetta

211022102?113210002?0012221012201021011011011001000131011000000001010001110011
100120111010102001011000011101010010100111101100110000?00110011111110001121100
011111101110111001111110101020100100101011100200001000301011000201010011100010
0121001121000000001000010000000000100?000010112110011001000?020000000000000000
00001000000-0

Paradoxurus hermaphroditus

211022102?113210002?0012220012201020011?112110210001310110??00001110101??0101
00101111101012001100011010110010110101110111100211010?000001111001100000211001
111110011100111001110101010101001021000121000000010004110210000020101121{0
1}00100021001222000000001000100000000100401?100012110110001000101?010000000000
00000000000000000-0

Hemigalus derbyanus 2110221020113{1 2}10{0

1}02100122200122010210110021210110001310110??01101110101??010000121111101111
001001010011110110110100100111100011010?0110001110011000012110111111001100011
10111110101020100102101013100000001000311011000201010002110010011000101210100
000000000{0 1}00000010040120000020110200110010000000000?00000100000001000000-
0

Viverra tangalunga

2010211020113210002?00122200122010210110011110010001310110??00001110101??011
0000211110111000010110001?11010111101001111110111110?00100011111110001111101
01111100111001110111111011111100100101013000200001100311011000201010101100010
0010001111100000001000000000000100400?100022110120011001000?0100000?0?00110000
00001000000-0

Genetta maculata

201021002?113210002?00122200122010210110010110110001310110??01001010101??011
00010111110010200101011001010101011010111111100????10?00100000100110011121101
011111101110011101111010011021100000201010000210100001301021000201020001212010
01210011110010000010001020000001004000100002201110001000000?0100000?0000110000
0000100000?-0

Paguma_larvata

2100221020013210102?00122??012211020010?020110210001311110???00001010?01??????
??1011101001020010?111000011111?0101011101??10?011110?001001110101100111111011
1101100111?????????????????0110100221011310120000102240101100010200010211001001
1000?3320000000010001000100001004002101012101110011011000?021?0000000?00000000
00100000?-0

Cynogale_bennettii

2010221??00????11??0?1?22??1??1?0210020110010110011311110???000011?0?0?????????
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?????????????????1110?1201010031011000011003110110002?00101130020?0?11???0110000
0000000000000000110?4012?01???2122200??001000??0?????????11000000001000000-0

Poiana_richardsonii

2010211120013210102?0012220012211020011?12011001000131011????01001010?0????????
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?????????????????11100?022000000003101000?350121100020302000020200000210??00100
000000100010200?00000?400?100002100120000001100?020?????????0100000010100000?-0

Viverricula_indica

2010211120013210122?00122200122110210110010110110001310110???00001010101??101
00012111000110200100010001110111011010111?111101???01?0010001011011001??01101
011?11?111110111111111101010111000021010130002100010004110210002020000212100
002000111100000000100000200000010?4002001002101120001001000?02000000??00010000
00101000000-0

Bdeogale_nigripes

210021012?113210002?0012220012201230011?010210010001211110???01101010001??0111
00120111011102001001000011111011010101111010100100000?001000100101100000211010
11111?011100111011110101110211011221110131011000000002111120002021101010000100
1?102112300100000100011200000000040101000121000{1
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Mungos_mungo

200022012?113110002?0012220012201230010?020110010001211110???11011010001??0111
101211110001120000000001?11010111101011111001001?1?00?001000111101100000211011
111110111100111010110101110211010221012131001000010003010120001010000002010100
121001122000000000000000000011004010101022100021111011000?0200000?00100000000
000100100?-0

Suricata_suricata

101022012?113210?02?001222?012211230010?02011001000121111????11011010101??0111
1011011101110200100100001111111010100111000000101001?001000001001100010211011
1101000111001010101100?1111111010222012131001001000003010120001000100111100100
1100211221000010010011000000001014010101032100220111011101?13101000?0110000000
000100000?-0

Herpestes_edwardsii

200022012?113210002?0012220012201230010?020110010{0
1}01211110??010010100011110111101201010001021010010001?110101011010111111?11?
000000?00100011110110001121100011010001110011101111010001021101022001213100200
10000030101200020101001020201001210??11210100000100000200000000?400?1010122001
21101011000??21????????0000000000100000?-0

Ichneumia_albicauda 211022012{0

1}113210002?001222?0122012310110020110010{0
1}01211111????01001010001???0110101201100011020010110001?11010110101001???0?01
?1?00?001000101111100010{0
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0201001210?111200100000100000200100010?400?100022100120111001001??100000????00
000000001000000-0

Crossarchus_obscurus

210022012?113210002?001222?012201230010?02011001000121111????1101101?????????????
??
????????????????????21101122201213100100101000301012000101020011001010012?0??122101
00000100010000000000?400?1010121011201{0
1}1001000??30????????0000000000100000?-0

Atilax_paludinosus 200022012?113210?0??00122??01221123{0

1}010002011001000121111????10011010101???01111002011000010210?1011010111111101
101001?10011?1000001?0?1?01111?1100000??1101011011?0111001100102001011102110102
210101310020000100130101200020201001120201001110011231000000010000020000000014
00?111022100120111011010?020000?0?1?0100000000100000?-0

Rhynchogale_melleri

201022012?11311010??00122?0012211230011?010210010001211110??0110101??0?????????
??
????????????????????2110111220101310010000?00030001200020211000110200001200??233001
00100100000200000100?400?101012100?10111001000??20????????0000000000100100?-0

Galerella_sanguinea

200021012?11321010??00122?0012211230011?1201100100?1211110??01011010001??0110
10120110001102100011000010111111010101111011?01000000?001000101101100110211010
11011000?100110010110101110211010222012130002001010013010120001020100102020000
121001112101001001000102000000100400?101012201020101001000?02000000?0000100000
000100100?-0

Helogale_parvula

210021012?113210?0??00122??012211230011?02011001000121111????11011010001??0111
10121110101102101001000011111100101011????????????01?00100011110????????????????
????????????????????????????????2110102220121300000010100030101200010211001021000001200?

112310000000100000000100010?400?101002100120111011000??100100?????0100000010100
000?-0

Fossa_fossana

100022112?113210002?0012?200132112310100020110010001210110??00001010101???0111
0012111100110210001101001110101101010011111101111000?001000111111100101011010
110111011100111111100101010211011000010130002000000002010120002010100111020100
11100111100100000100000000000000040000000120020210000010000010010000000000000
000100100?-0

Cryptoprocta_ferox

2010220120113210102?0012?20013211230011?120110010001210110??00011?10101???0101
00101111101112000011110011111010011100110110?01011111?001000101101100000211011
11011001110010101111010101011201022202010003201100?36010110001010100012001100
010001221000000001000000001000000100?000000211120011011000112000000??000000000
0001000001-0

Eupleres_goudotii

0100211120113210002?0012220012201230110?020110000001210111??00000010{0 1}0{0
1}??011{0 1}001201100011021010111{0 1}001111111110100111111{0 1}0{0 1}10{0
1}0{0 1}{0 1}?001000{0 1}01101{0 1}00{0 1}100{0 1}101011111001110011101{0 1}1{0
1}010111021101100201210100200100000001132000200010013?010100111001000101000011
0000000000000004000000012002200000001000?0000{0 1}000100000000000001000000-0

Salanoia_concolor

201021012?113210?2??00122??012211230010?02011001000121111??00011010101???0101
101201101010001000111010111111001110011111101???01?001000100111000101211011
110110011100111010100011110211010200012130002001000002010120001021200021020100
011001121001000001000100000000100400?101012101120011011000?02000000?0000000000
010100000?-0

Kichechia_zamanae

?1?02????????????????????????????????1110002011001???1????????0010101????????????
??
????????????????????20101013100210001000311?1?001?20100002??????1?????123100000?
1????????000010?0?0??????1021????????000????????????01000000001000?0?-0

Kanuites_lewisae

210022012?113210?0??0?????12211?21011012011001?00121011??0000?0????????????
??
?????????????????1120??201010??10021000100??110?1000?03010??120?01?01?00????10000
000??000000?000?0?400?00?1021031?0?01??0?0??10????????01000000001??0000-0

Izmirictis_cani

????????????????????????????????111001202100????????????????10?1????????????????
??

??????????????????0212013?01200001000?1??1??0??3?200??????????????11??100?0?0??
?????????0?0??0?0??????031?????????????????????01??10001110????-0

Euboictis_aliverensis

?????????????????????????????????111100201?01?????????????0100????????????????????
??
?????????????????????????111013?0?????????????1?2?002?3?2000?????????????333??100?001??
?????0??00??0?0??????11?????????1?0?????????????????1110111111????-0

Sivanasua_viverroides

?????????????????????????????????111000201?00?????????????0100001?????????????10??
??00?12?????1???0?000?00?111010110??????
?????????????????????20111013?0020000100001?3?002?312001??????????????12210100?00
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Nandinia_binotata

20102{1 2}001011301000200011120011200020{0 1}110{0
1}2011{0 1}{0 1}{0 1}00013000000000001010{0 1}01110111{0 1}001{0
1}01001000120110001011?00{0
1}101010100010011110001111?00010110110110101121100111101101110010101111010011
010210{0 1}20{0 2}002121002101{0 1}00224{0 1}12310000010{1 2}0{0 1}1{1 2}{1 2}{0
1}{1 2}0100{0 1}{1 2}1001{1 2}21000000001000{0 1}00000000100{1 4}00010{0 1}{0
1}021{0 1}{0 1}110001010100002000000000000000000001000000-0

Palaeoprionodon_lamandini

2011211?101131100011001212101210002?????????1??000?300??0??0000101??0?????????
??
?????????????????1021??0?00?000003101100?34?1?1100020200010020?????0?000?????110000
0001??01000000000?000??0?00210?121??1011?001?1?????????100000000?000000?-0

Stenogale_julieni

2?1020101??131100021001222101221003011101201112??00?300??0??0000101??0?????????
??
??????????????????10210??2?01?000103101100?35?1?110001020100002?????0?100??113?00
000?1?0?0?00?0?000?0?0?11?002?011?1???0?1?00??1?????????0000000000100000?-0

Herpestides_antiquus

201020002011311000200112121012211022111012011?0??001210110???0100101??0?????????
??
??????????????????111000?0001000100210000001311?1100020311001121????00200??11100
00000010001000??00000?000??0?102103110??011?01??1??????????11000000001000000-0

Ginsburgsmilus_napakensis ?-?????????-

?????????????????????????0011?1202101?????????????????1001101?????????????-????-????????-
????????????-?????????????????????1?????1????????????-?????????????????-
?????????????????????????????????????20-0010000?????????36-

??3??102?2010000????????????11111000?0?1????1?11?02000??0?????????0-??-??0-?0--??-
?????0????-0000000?00?????-0

Prosansanosmilus_eggeri ?--?????????-
????????????????????????0011?1202101????????????????1001101????????????????-????-????????-
????????????-??-????????????????-
???0?2-002000104101100?36-
122??101?1120001?????????????????010??011?001?????0?1????001?????????????0-1?-??0-1?-??-
????????????0-0000000?0?0?????-0

Prosansanosmilus_peregrinus ?--?????????-
??011?1????????????????-????-????????-
????????????-??-????????????????-
?????????0?????????????????????????????????????02?-?0200?04101100?6-
122??1?2?111?00?????????????????10?2??11?01????1231??2?2?????0?????????0-12-??1-10--??-
????????????0-??00000?????0??1-0

Afrosmilus_hispanicus ?--?????????-
??01?????????????????100????????????????????-????-????????-
????????????-??-????????????????-
???0-002??0?04101100??-
?????12??1?10?????????????????????2??1?????????????????0?2?????0?????????0-1?-??-??-??-
????????????0-??00000?????????-0

Afrosmilus_turkanae ?--?????????-
?????????????????????????????????????0?0????????????????????0011?1????????????????-????-????????-
????????????-??-????????????????-
???0-?02??0004101100?36-
1????1?2?2110?00?????????????????1?????00?00?1?????11?????0?????0?????????0-12-??1-??-??-
????????????0-??00000?????0??-0

Afrosmilus_africanus ?--1??0?????-
?????????????????????????????????????101?????????????????1001????????????????????-????-????????-
????????????-??-????????????????-
???0?0-0020001????????????3?-
1?3??122?112000120?????11?????1112?10000011?????1?1?0?20?????0?????????10-??-??-??-??-
??-????????????-??00000?????0??-0

Albanosmilus_jourdani ?--12?013??2-
200?0?????0?????10211?0211?22021111?????0110??????10011?1????????????????-????-????????-
????????????-??-????????????????-
?????????????????????????????????????1000?020-002000105201100?36-
12251121001210010?????11?01??211211111{0 1}121?11233120?221???1??0011200-22-1341-
10--??1-????????????-??00000????0000?-0

Maofelis_cantonensis 1--12??01??0-
010?0?????10??01????0011?12021001?0?0????????000????????????-????-??????-
?????????-????????????????????????????????????-????????????????-
?????????????????????????????1??10?22-002??01?????????3?-
????000?11?10??020????0?100????20000?00?0?00????1010??0?0?1?010?10-??-001?-?0--
??2-?????????-??0000000??000?00

Eofelis_edwardsii ?--????????-
????????????????????011??202100?????????????{0 1}00{0 1}1?1????????????-????-
??????-?????????-????????????????????????????????-????????????????-
????????????????????????????22-00?010103201100?3 {5 6}-
121??001?1010001????????????11110000?001????101010200????0??????10-12-??1-10--
??-?????????0-0000000?000?????1

Dinailurictis_bonali ?--12???????-
????????????????????0011?22021001????????????00?1?1????????????-01??-??????-
0??1?????-?????????????????????????????1????????-????????????????-
????????????????????????????22-001010103201100?36-
121??0?1?1010001??2?0????????11110000?0?1????1?10?02?0?0?0????????0-1?-??0-?0--
??-?????????0-??00000?0?00?0??1

Quercylurus_major ?--?2???????-
????????????????????2?0?100????????????100????????????????-????-??????-
?????????-????????????????????????????????-????????????????-
????????????????????????????2-001??01?????????3?-
?????00??1?10??20????????????????1??0?0?0????????????0?0?0?0????????0-??-????-??--??-
?????????-0000000?????????1

Dinaelurus_crassus ?--122101000-
010?0??????????10211??0211?22021001????01000????100????????????????-????-??????-
?????????-????????????????????????????????????-????????????????-
????????????????????????????10?1??20-002??11?????????3?-
??5002?11?10??020????00?00????10000?00??1111????0000?0?000??012210-??-013?-?0--
??2-?????????-??00000????000?10

Hoplophoneus_oharrai 1--120000002-
01010??0010?0110211????11?22021101?00001000????10011?1??00???0?1?00-0100-
0001020-0101110000-11010011?0?1?0??1????1?1100100011-110????????????-
????????????010?10111???????10?100?0-0??010004101100?36-
12050?01110?00?110?00?00100?1?1?20?0100010011123021??2??100?0?11200-?1-?231-10--
??1-??0??1??0-0000000?0?0000?00

'MA-PHQ 348' ?--1??01?000-
010?00??0201011021110?????????10?????01?00????00????????????????-????-??????-
?????????-????????????????????????????????????-????????????????-
????????????????????????????10?1??22-?????1????????????-?

????0?0?11??0??0??????0??00??200??00??0??0????0?????00????2?1?-??-?12?-?0--??-
?????????-????????????0?0?

Hoplophoneus_dakotensis 2--1?0010?12-
????????0?????10211??0211?2202110??0?0?1000????10011?1????????????-????-??????-
?????????-????????????????????????????????????-????????????????-
?????????????????????????????????0?1?020-002010104201100?36-
12150?2?110?00?200??0??200??11200?100110012223021?231?101?1001??00-11-0??1-?0--
??1-?????????0-??00000??0?0?00

Hoplophoneus_sicarius 2--122010?12-
11011??00?0?110211??0211?2202110??00001000????10011?1????????????-????-??????-
?????????-????????????????????????????????????-????????????????-
?????????????????????????????????10?10020-002010104201100?36-
1215012?110100?110200011111??103000100110012234021?231?101?10011?00-11-0131-10-
-??1-?????????0-??00000??000?00

Hoplophoneus_adelos 2--122010012-
10010??00?0?01?0211??0210?22021100?00001000????100?1?1?????????????0?0?0?-?00?02?-
??0?1?010-??0?0011?1????????????????????????-????????????????-
?????????????????????10?01100??10?1??20-002??01?????????36-?2?501 {1
2} ?11?10??110??0011201?1?01?000?00?10012????2132?1?111?10110?00-??-0231-?0--??1-
?????????-00000000??000?00

Hoplophoneus_bidentatus 2--122010?12-
210112?100202011021101?21??1?0?1100?001010000??10011?1??0??000000-0?01-
000??2?-??1?0??-0??000?00?????????21?11??0?0011-????????????-
0?????????0?0?????0?????1010?10020-00?010004 {1 2} 01100?36-1215012?10 {0
1} 200?110200?10?0111? {0 1} {1 2} 00010011??22340203331?101?10?12210-12-?230-10--
?02-?????????0-??00000??000?00

Hoplophoneus_villebramarensis 2--12?010?12-
000?0??1001020110211?10211?22021101?0??01000????10011?1????????????-????-??????-
?????????-????????????????????????????????????-????????????????-
?????????????????????????????????10?1??20-002010004 {1 2} 01100?36-
1225012?100200?110????10201??102000100?1??213?0?1?33??1?1??11200-?2-?230-?0--
??-?????????0-??00000??000?00

Barbourofelis_morrisi 3--120010?12- {0
2} 00002??1020?0010211??0211?220?1111?1?0110?0?0??10011?1??0????????-0111-
0011021-1011010011-101101111001??1??1?1??11000?0001-10????????????-
1?0110?????00?1??????????10001020-002000105201100?36-1225112?001 {2
3} 10?21000001?101??31121111111310122331202321?001?10012200-22-1241-?0--1?1-
?00?????0-??00000??00?0?-0

Oriensmilus_liupanensis 3--120000?12-00010???0020001102110?0211?2202111{0
1}?0?111000????10011?1?????????????-????-????????-??????????-
????????????????????????????????????-????????????????-????????????????????10?0?020-
002000105201100?36-123501210{0 1}12101210??00?100??111211110{0
1}0100101221202?21?00{0 1}?10012200-22-0??0-10--??-?????????0-??00000???000?-0

Sansanosmilus_palmidens 2--120010012-
210102?00020001102110?0211?22021111?1?0110??????10011?1???0???0????-0111-
001102?-1011?11011-1111001110?1????1??1?11110100?00?1-1101?0000011101-
11?110???10?00?1????0????010001020-002000105201100?36-
??3511210112101210??001011?11121111000110121?3120222?0000?10012200-2?-0240-?0--
1?2-?0?????0?0-??00000???0000?-0

Barbourofelis_fricki 3--122013012-
210012??0020001102110??2???2???1101????110??0???10011?1???0?????????-0111-0011011-
1011010010-1011?1111001?1??11?????1100110000-100????????????-
0?0110?????100?11111???????10001021-002000205?0110??36-
12351121001?101200??011101??3133111111310122341202?2??011?10011200-?2-1240-10-
-1?1-?00??0??0-??00000???0001?-0

Barbourofelis_loveorum 3--122013?12-
200102??0020001102110??2???1?0?1100?1?0110?????10011?1?0?0???001000-0111-0011{0
1}11-10110100{0 1}1-10110111001?111110121111000000?1-1101100?0011101-
11011000?100??1??1????????1000?021-002000205201100?36-
12351120001310120?????1?011?111?11111131?11233120232100?1??0?12200-22-1241-10--
?1?-000??0?0?0-??00000???0000?-0

Albanosmilus_whitfordi 3--12?013?12-
200?12??002??0?102110?0211?220?1111?0??110?????10011?1???0?????????-0111-0011011-
10110?????-????????1?0?????????????1100?00000-????????????????-
1?0110????????????????????10000020-002000105201100?36-
123511220012101210??011100??2112111{0 1}?1121012{1 2}231202321?0?1?1?012200-22-
1241-10--?1-?????????0-??00000???0000?-0

Hoplophoneus_cerebralis 2--1220100{0 1}2-
210112?0001020110211030211?22021100?0?1010000???10011?1???0???0???0?-0101-
0001011-1101111?0-1?????11001????????????110000000?-?1010?00?00110?-
1?1110?????00?1?100011101000?10020-00201010{4 5}201100?36-
1215012?100110?110200{0 1}10201???11201010012001223402033310111?10111210-11-
?1?1-10--?2-??0??????0-??000000???0000?00

Hoplophoneus_primaevus 2--121010002-
010102??0010201102110?0211?22021101?0?0010000???10011?1?100???000000-0100-
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111110001100101111{0 1}1?11101000?1?020-00201010{3 4}101100?36-121501{0

1}111020002102000111001111110{0 1}010011001112{2 3}02022210100?10011200-12-0231-10--?01-100000?000-00000000??0000?00

Hoplophoneus_occidentalis 2--120010012-010112?1001020110211000211?220211?1?000010000???10011?1??00???0??0??-0100-0001020-1101111000-11010111100110011?1121111100000011-110100000021101-1111100011001011111101010??10?1?020-??01010{3 4}101100?36-122501211102000200000?1110011111200?10011001112302022210100?1?01020?-11-0230-10--??1-?00?0?000{0 1}-??000000??0000?00

Nimravus_brachyops 2--122101000-{0 1}0010210{0 1}02000110211000211?22021001?000010000???{0 1}0011?1??00?????????-0101-0011021-1101011010-111100111001?11?110121111100010001-110110000011101-01011000110010111100011101?10?11020-00201010{3 4}201100?35-12350{0 1}0111020001102?00001001?111100000001110110110010101000011012210-12-0120-10--?12-?00??0?0?0-00000000?00000110

Pogonodon_platycopis 2--12?101000-000102??002010110211?0011?12021001???101000????10011?1???0?????????-????-????????-??????????-????????????????????????????????1100010001-????????????????-????????????????????????????00?11020-002010003201100?36-121500011101001200??0000100??12110000000100101120211001?000?1??10?10-11-?220-10-??1-?????????0-00000000000000?10

Pogonodon_davisi 2--122101000-00000??002010110211?00011?12021000?0?1010000???10011?1??0?0??0??0??-0101-?001020-0101111??0-1100?0111?0?0????????????111??00??-??110000010100-110110?01?0010?11??0?1?????10?1?020-002010003201100?36-121500{0 1}2}11101000200??001100??121200000001001011{2 3}01020011100?1?010?10-1{1 2}-0220-10--??1-??0?0?0?0-00000000000000?10

Diniectis_felina 2--122101000-0{0 1}0102?0002010110211000011?12021001?001010000???10011?1?100??000000-0101-0001020-0101111000-110100111011?10?110121111100010001-100100000010101-110110001?0?10?111{0 1}0011101000?1102{0 2}-002010003101100?3{4 5}-12{1 2}50001110100011020000110011{0 1}1{0 1}10000000100{0 1}100201020010000?10012210-12-0{1 2}21-10--10{2 3}-100?00?000-00000000000000?10

Nanosmilus_kurteni 2--122?00002-000102?1001020110211000211?22021101?0?0010000???10011?1????????????????-????-????????-??????????-??-????????????????????-????????????????????00?1?020-002010104201100?36-121501111102000210????01?00??111?00010011???1123020?221?101?0?112?0-12-?121-1?--??1-?????????0-00000000??0000?00

Nimravus_intermedius 2--1?{1 2}?01000-0001?2??0020001102110?0211?{1
2}2021001?0??010000??00001?1????????????- {0 1}101-?01102{0 1}-1??10?????-
????????1?1?????1??1??1??????????-??????????????-
0?0110?????????????????????10?11?20-002010104201100?35-
??3500011101000110????00100??1111000000011101101100101010?0?11012210-12-?1?0-10--
??1-?????????0-00000000?00000110

Tapocyon_robustus
10101?0000010010112010010100000010?201101102000??0000??0??0000100??0??0100?
?1100010000020010100010111100101?11111??0?1??1?1?11?0001001100000?0??1?100111?1
??1?0??10?????????????????1??1?0?2?0000000021010000131103?000201010001100?000?00?
?11110000000111001000000000?200??1??201110100010000??1?????????01000000101000
00?-0

Procynodictis_vulpiceps 1?1??0000001111011??11000100101000010111110100{0
1}??00?000?0??00001?0??????0110?0111111010020010?001101110101?111111??????
?0010101010001000011010112101110111?001110?1??110010??????????0200003?0020000
00??10?20?002?1010?10????????????111000000?1??0?0?00000??0??????021??????
?00?????????????0000000000100?0??-0

Hesperocyon_gregarius
10111?11000121100020112103001120011201111201010?001010010??0000100??00??1?1?
?012011?0000020000000110100010101111011??????000000?101010101101111101101011
1111??111?0101111??0000000000?00020000000021000000030121?00020101011110????011
00??1111000000010?000000000200?200????112112120011011001??1?????????00000000001
000000-0

Canis_latrans_frustror 1001111000010111012?2{0
1}2103001120111101111120110010010100100010000110100100001110102011?01110010101
10{0
1}0011101111110101111000000100000?10111011110111101120101001011110?11101001000
01000011000102000000000021000000030120?000201010?11001010000100111010000000101
0000000002000200?1001200021100110010001110010000?0000000000000000000-0

Vulpes_vulpes
2001110000010111012?2021030011201111011110201000100101001000100001101001000011
10102011?01110010101100001110111110101111100000100001?10111011110111101121101
001011110?1110100100001001011000102020000000021000100030120?000201010?11002010
0001001010{0 1}000000111000000000000200?{0
1}0012010311000100100011200110000000000000000000000-0

Taxidea_taxus
2000111000000001022?0221030011201111111110211001100121100000110111?11001001001
110001110100102000011010000110001011101111010000200001?00110011110100001120001
111111111?10010100?????10110200010200010001002000011?340020?100001010?121020100

100001112000000001000102001000000301??0102210021012102000000101?000??000000000
?000000000-0

;

END;

Appendix F

Custom Evolutionary Models (Rate Matrices)

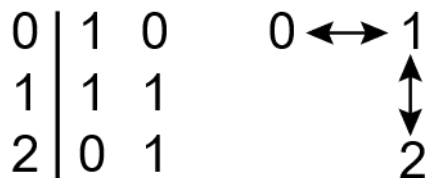
Beast 2.6.3 does not include a method to order characters from the BEAUti graphic user interface, thus only non-ordered characters are available for an analysis that does not manually edit the xml file. Below are schematic depictions of the rate matrices used in this analysis, with diagonal elements removed. The xml versions of these models are visible in the provided xml code.

3-state Characters

Ordered

Feliformia_trim_2_3_ordc_ratematrix

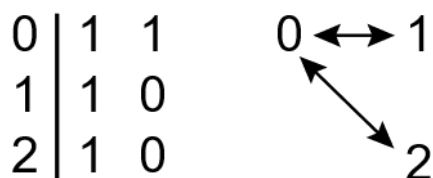
Characters: 5, 6, 14, 18, 19, 22, 24, 31, 37, 41, 42, 83, 185, 196, 200, 203, 219, 220, 229, 257, 258, 262, 279, 280, 282, 283, 288, 289, 322, 323



Ordered, multipath

Feliformia_trim_2_3m_ordc_ratematrix

Characters: 47, 127, 192, 193, 231

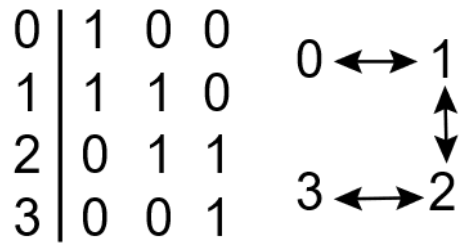


4-state Characters

Ordered

Feliformia_trim_2_4c_ord_ratematrix

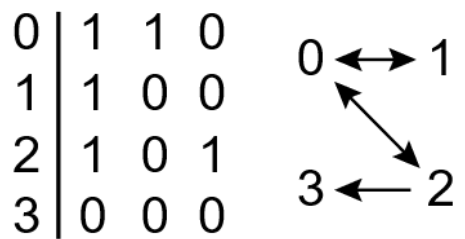
Characters: 1, 195, 210, 215, 222, 224, 228, 242, 243, 244, 245, 253, 264, 277, 281, 286, 293, 296



Ordered, multipath 1, irreversible

Feliformia_trim_2_4mi_1ord_ratematrix

Characters: 266



Ordered, multipath 2

Feliformia_trim_2_4m_2ord_ratematrix

Characters: 198

$$\begin{array}{c|cccc}
 0 & 1 & 0 & 1 & 0 & \longleftrightarrow & 1 \\
 1 & 1 & 1 & 0 & \updownarrow & & \updownarrow \\
 2 & 0 & 1 & 0 & 3 & & 2 \\
 3 & 1 & 0 & 0 & & &
 \end{array}$$

Ordered, multipath 3

Feliformia_trim_2_4m_3ord_ratematrix

Characters: 12, 259, 265

$$\begin{array}{c|cccc}
 0 & 1 & 1 & 0 & 0 & \longleftrightarrow & 1 \\
 1 & 1 & 0 & 0 & & \nearrow & \\
 2 & 1 & 0 & 1 & & \searrow & \\
 3 & 0 & 0 & 1 & 3 & \longleftrightarrow & 2
 \end{array}$$

Ordered, multipath 4

Feliformia_trim_2_4m_4ordered_ratematrix

Characters: 53

$$\begin{array}{c|cccc}
 0 & 1 & 0 & 1 & 0 & \longleftrightarrow & 1 \\
 1 & 1 & 1 & 0 & \updownarrow & & \updownarrow \\
 2 & 0 & 1 & 1 & & & \\
 3 & 1 & 0 & 1 & 3 & \longleftrightarrow & 2
 \end{array}$$

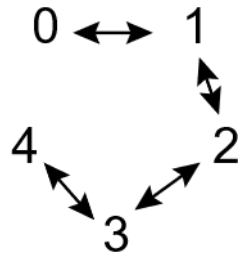
5-state Characters

Ordered

Feliformia_trim_2_5c_ord_ratematrix

Characters: 260, 287

0		1	0	0	0
1		1	1	0	0
2		0	1	1	0
3		0	0	1	1
4		0	0	0	1

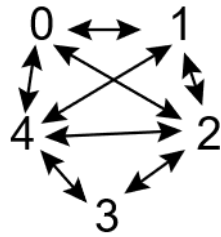


Ordered, multipath

Feliformia_trim_2_5m_ordered_ratematrix

Characters: 35

0		1	1	0	1
1		1	1	0	1
2		1	1	1	1
3		0	0	1	1
4		1	1	1	1

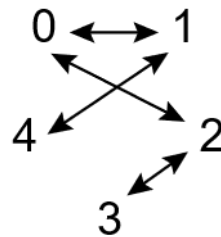


Ordered, multipath 2

Feliformia_trim_2_5m_2ordered_ratematrix

Characters: 269

0		1	1	0	0
1		1	0	0	1
2		1	0	1	0
3		0	0	1	0
4		0	1	0	0



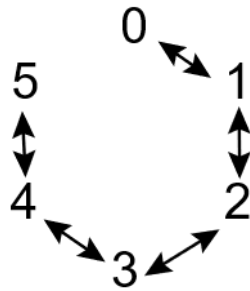
6-state Characters

Ordered

Feliformia_trim_2_6_ordered_ratematrix

Characters: 202

0		1	0	0	0	0
1		1	1	0	0	0
2		0	1	1	0	0
3		0	0	1	1	0
4		0	0	0	1	1
5		0	0	0	0	1

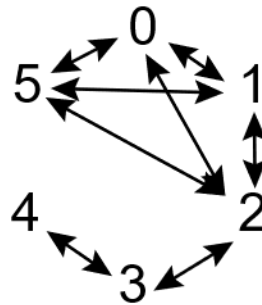


Ordered, multipath

Feliformia_trim_2_6m_ordered_ratematrix

Characters: 216

0		1	1	0	0	1
1		1	1	0	0	1
2		1	1	1	0	1
3		0	0	1	1	0
4		0	0	0	1	0
5		1	1	1	0	0



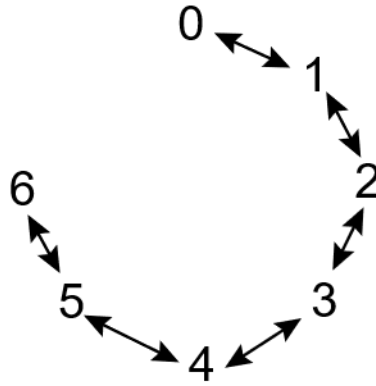
7-state Characters

Ordered

Feliformia_trim_2_7_ordered_ratematrix

Characters: 211

0		1	0	0	0	0	0
1		1	1	0	0	0	0
2		0	1	1	0	0	0
3		0	0	1	1	0	0
4		0	0	0	1	1	0
5		0	0	0	0	1	1
6		0	0	0	0	0	1



Appendix G

Stratigraphic Ranges and Tip Date Priors

Extant Taxa

Due to the preponderance of molecular data, compared to morphological data, for extant taxa in this analysis, tip dates were fixed to zero for these taxa (n=45). All remaining taxa were given uniform distributions of equal probability between their FAD and LAD, unless otherwise stated.

Caniformia

Hesperocyon gregarious. **Locality:** Numerous across North America, see Wang (1994).

Absolute age estimate: 41.4-29.75 Ma. A relatively ubiquitous taxon of the Chadronian through Whitneyan, the earliest records extend into possibly the earliest Duchesnean (Wang, 1994).

These earliest specimens come from the Lac Pelletier Lower Fauna of Saskatchewan, but precise age constraints for this fauna is still debated (Bryant, 1992). Thus, the age range chosen for this taxon was the entirety of the Duchesnean through Whitneyan (as defined by Kelly et al., 2012; Ogg et al., 2016) pending more precise dating.

Procynodictis vulpiceps. **Locality:** Wyoming, USA. **Absolute age estimate:** 45.15-41.4 Ma. The stratigraphic range of this taxon appears to encompass the entire Uintan (Robinson et al., 2004), though the latest occurrence is in some doubt (Spaulding et al., 2010; Solé et al., 2016). For this study the entire Uintan NALMA was used (as defined by Kelly et al., 2012; Ogg et al., 2016).

Feliformia

Tapocyon robustus. **Locality:** California, Montana, Wyoming, Utah, USA. Stratigraphy: All Uintan. **Absolute age estimate:** 46.5 - 39.7 Ma (Robinson et al., 2004). *Tapocyon* has typically been placed as the immediate sister taxon to crown Carnivora based on parsimony analysis of morphological data (Wesley-Hunt and Flynn, 2005). However, Barrett et al (2021) recovered it as a stem feliform, as did Tomiya and Tseng (2016).

Feloidea

Stem Feloids

Proailurus lemanensis. **Localities:** Quercy Fissures, Laugnac, Paulhiac, Bassin de St-Gérard, France. **Absolute age estimate:** 27.82-20.44 Ma (Slater and Friscia, 2019).

Stenogale julieni **Locality:** Quercy Fissures, France. **Absolute age estimate:** 27.82 - 23.03 Ma (Slater and Friscia, 2019).

Palaeoprionodon lamandini **Locality:** Quercy Fissures, France. **Absolute age estimate:** 27.82-23.03 Ma (Slater and Friscia, 2019).

Herpestides antiquus **Locality:** France, Germany. **Absolute age estimate:** 23.03-20.44 Ma. Following the revision of Wolsan and Morlo (1997), this taxon is known from the Aquitanian/Agenian (Hunt, 1991). The absolute dates of the former were taken from Ogg et al. (2016).

Felidae

Pseudaelurus validus **Localities:** Various in New Mexico, Nebraska, USA (see Rothwell, 2001, 2003) **Absolute age estimate:** 17.0-14.5 Ma (Slater and Friscia, 2019).

Promegantereon ogygia **Localities:** Eppelsheim, Germany; Batallones-1 and Crevillente-2, Spain. **Absolute age estimate:** 11.1-7.75 Ma (Slater and Friscia, 2019).

Metailurus major **Locality:** Bulgaria, Greece, China. **Absolute age estimate:** 7.6-5.7 Ma. The referred AMNH material is from the Mahui Formation, 6.7-5.8 Ma (Qiu et al., 2013). The oldest dated specimen of this taxon is from the MN11/12 boundary of Bulgaria (Kovatchev, 2001). Roussiakis (2001) lists further European occurrences from MN12-13. However, the taxonomic revision of *Metailurus* by Spassov and Geraads (2015) casts doubt on the diagnosis of many of these specimens. Confidently referred material comes from Pikermi, Greece (7.37-7.11 Ma; Roussiakis, 2001; Böhme et al., 2017), the type skull from Loc. 30, Tay-Chia-Kou (5.7 Ma; Kaakinen et al., 2013), and intermediate aged dates from Greece and China (Spassov and Geraads, 2015). Thus, the absolute date of this taxon follows the material that was examined for this study and referable to *Metailurus major* by Spassov and Geraads (2015). Absolute age dates given for MN zones follow Hilgen et al. (2012).

Dinofelis diastemata **Locality:** France, China. **Absolute age estimate:** 5.3-1.0 Ma. Referred specimens F:AM 50445, 50446 differ in osteometrics from published values of *Dinofelis diastemata*, namely in smaller values of absolute C1 and P3 size (length, width) (Werdelin and Lewis, 2001). Furthermore, they are substantially smaller than that of Asian *D. cristata*, though a

geographically more-likely taxon, than the French *D. diastemata* (Werdelin and Lewis, 2001). Another possibility is the same species to which the Georgian Melaani skull belongs (Gabunia and Vekua, 1998; Werdelin and Lewis, 2001). The Melaani skull also differs from the above named species by having smaller osteometrics, but more compressed canines, and is stated by Werdelin and Lewis (2001) to be most-similar in dimensions to South African *D. barlowi*. However, barring a more in-depth taxonomic review of additional Eurasian *Dinofelis* specimens, I chose to diagnose F:AM 50445, 50446 to *D. diastemata* based upon similar length of the P4, unreduced P3 and shape of the sagittal crest. *Dinofelis diastemata* is attributed to MN 14 in Europe (Werdelin and Lewis, 2001). The referred Chinese material has an attributed date of Ruscinian-Villafranchian, thus overlapping absolute age dates are given above based on Rook and Martínez-Navarro (2010) and Hilgen et al. (2012).

Nimravides pedionomus **Locality:** Nebraska, USA. **Absolute age estimate:** 13.55-9.95 Ma.

Referred material to this taxon has been collected from the Nenzel quarry, Valentine Formation, Crookston Bridge Member; Xmas quarry, channel fills within the Ash Hollow Formation, Cap Rock Member and UCMP locality V-3327 (Antón et al., 2013). The Crookston Bridge Member lies above the Hurlbut Ash, dated at 13.55 ± 0.09 Ma (Tedford et al., 2004), while the Xmas quarry was viewed as stratigraphically correlative with the *Machairodus* quarry by Skinner and Johnson (1984), which is capped by a dated ash at 9.95 ± 0.8 Ma. UCMP locality V-3327 is where the holotype of *Nimravides pedionomus* comes, also Cap Rock Member of the Ash Hollow Formation, and is thought to be intermediate in age of the previously listed sites (Tedford et al., 2004).

Machairodus catocopis **Locality:** Kansas, USA. **Absolute age estimate:** 7.5-6.6 Ma. This taxon is well known from the Jack Swayze Quarry and Sebastian Ranch fossil localities (Antón et al., 2013). Both of these localities are viewed to be Hh2 in age (Martin, 1998). Absolute dates for this Hemphillian subunit follows Hilgen et al. (2012).

Amphimachairodus coloradoensis **Locality:** USA. **Absolute age estimate:** 6.6-4.9 Ma. This taxon is known from various late Hemphillian sites in the American west (Antón et al., 2013), while material assigned to this taxon from Arroyo Tepalcates, Mexico has since been removed to a new species (Ruiz-Ramoni et al., 2020). Hh3-Hh4 were chosen as the time range for this taxon given imprecise dates for many of these localities. Absolute dates for the Hemphillian subunits follow Hilgen et al. (2012).

Amphimachairodus giganteus **Locality:** Various, Europe, Asia. **Absolute age estimate:** 8.7-5.3 Ma (Slater and Friscia, 2019).

Xenosmilus hodsonae **Locality:** Florida, USA. **Absolute age estimate:** 2.5-1.0 Ma. Specimens from University of Florida localities span the latest Blancan to early Irvingtonian. The Santa Fe River locality is likely the oldest at approximately 2.5 Ma, while the youngest locality is likely Haile 21A, site of the holotype, inferred to be slightly younger than the dated Leisy Shell Pit at 1.1-1.55 Ma (Bell et al., 2004).

Homotherium ischyryus **Locality:** North America. **Absolute age estimate:** 4.9-2.0 Ma. Following the findings of Antón et al. (2014), I limited the biostratigraphic age of this species to the

Blancan, compared to the later, morphologically diverse *Homotherium latidens* (Paijmans et al., 2017). Dates follow Hilgen et al. (2012).

Homotherium latidens **Locality:** Europe. **Absolute age estimate:** 0.033049-0.031674 Ma. The date for this species is tied to the radiocarbon date of the specimen sampled for DNA, Natuurmuseum Rotterdam catalogue number 02-011, GenBank: MF871701. Six total radiocarbon dates have been collected on this specimen (Reumer et al., 2003). The last two of these dates were considered most reliable, with inferred contamination in the first four. Of these two dates I chose the date obtained from the tooth ($28,100 \pm 220$ ^{14}C age yr. BP), as it is the one primarily reported by Reumer et al. (2003) for the age of this specimen. This date in two sigma calibrated years (using CalPal Rev 8.1.0) is the range reported above. A normal distribution spanning this range (2 sigma confidence interval, mean=0.03236, sigma = 0.0004) was used as the tip prior in the phylogenetic analysis.

Homotherium serum **Locality:** North America. **Absolute age estimate:** > 0.0565 Ma. The date for this species is tied to the radiocarbon date of the specimen sampled for DNA, Canadian Museum of Nature, Ottawa, CMN46442; GenBank: MF871703. The provided radiocarbon date (>56,500 ^{14}C age yr. BP; Paijmans et al., 2017) is beyond the 45–50 ka resolution limit of radiocarbon dating and thus provides a minimum age of the specimen. I chose an exponential distribution (mean 0.0511, 95% quantile 0.2 Ma, offset 0.0565) such that the 95% quantile extended to the start of the Rancholabrean, the first occurrence of this species in North America (Slater and Friscia, 2019).

Megantereon cultridens **Locality:** Various, Africa, Eurasia, ?North America. **Absolute age estimate:** 3.5-0.4 Ma (Slater and Friscia, 2019).

Smilodon fatalis **Localities:** North America (USA, Mexico) and possibly western South America. **Absolute age estimate:** 0.6-0.0095 Ma (Slater and Friscia, 2019).

Smilodon populator **Localities:** Various, Venezuela, Ecuador, Bolivia, Argentina, Brazil. **Absolute age estimate:** 0.013372-0.013235 Ma. The date for this species is tied to the radiocarbon date of the specimen sampled for DNA, an uncatalogued left tibia from the Kruiemel collection, Naturalis, Leiden, GenBank: MF871700 ($11,335 \pm 30$ ^{14}C age yr. BP; Paijmans et al., 2017). This date in two sigma calibrated years (using CalPal Rev 8.1.0) is the range reported above. A normal distribution spanning this range (2 sigma confidence interval, mean=0.0133035, sigma = 0.00004) was used as the tip prior in the phylogenetic analysis.

Panthera leo spelaea **Localities:** Various, Europe, Asia, North America (Barnett et al., 2009). **Absolute age estimate:** > 0.061Ma. The date for this species is tied to the radiocarbon date of the specimen sampled for DNA, hair bolus, sample F-2678/70, GenBank: KX258452 (Barnett et al., 2016). However, there is a discrepancy in the radiocarbon dates for the hair sample and that of associated skeletal material (Kirillova et al., 2015). This discrepancy the authors attributed to contamination of the hair sample, while not of the skeletal material. Thus, I chose to use the radiocarbon date for the skeletal material, but given its extent beyond the resolution limit of radiocarbon dates I applied an exponential distribution (mean 0.61, 95% quantile 1.89 Ma, offset

0.061) such that the 95% quantile extended to inferred split between *Panthera leo* and *Panthera leo spelaea* (Barnett et al., 2016).

Panthera atrox **Localites:** Various, North America. **Absolute age estimate:** 0.013401-0.013226 Ma. The date for this species is tied to the radiocarbon date of the specimen sampled for DNA, Metatarsal II, Royal Alberta Museum EDM P89, GenBank: DQ899945.1 (11,355 ± 55 ¹⁴C age yr. BP; Barnett et al., 2009). This date in two sigma calibrated years (using CalPal Rev 8.1.0) is the range reported above. A normal distribution spanning this range (2 sigma confidence interval, mean = 0.0133135, sigma = 0.00004) was used as the tip prior in the phylogenetic analysis.

Miracinonyx trumani **Localites:** Various, North America. **Absolute age estimate:** 0.024037-0.023781 Ma. The date for this species is tied to the radiocarbon date of the specimen sampled for DNA, University of Kansas, KS28 NTC43093, GenBank: DQ097168.1, DQ097175.1, DQ097170.1 (19,765 ± 80 ¹⁴C age yr. BP; Barnett et al., 2005). This date in two sigma calibrated years (using CalPal Rev 8.1.0) is the range reported above. A normal distribution spanning this range (2 sigma confidence interval, mean=0.023909, sigma = 0.0001) was used as the tip prior in the phylogenetic analysis.

Lophocyonidae

Izmirictis cani **Localites:** Sabuncubeli, Turkey. **Absolute age estimate:** 19.5-17.2 Ma. This taxon comes from the lower part of the Soma Formation of western Turkey (Morales et al., 2019). No absolute dates are available for this locality, but biostratigraphy suggests an early MN

3 fauna (Morales et al., 2019). However, barring more-detailed temporal placement, I chose to use the entire MN 3 zone for this phylogeny, following Hilgen et al. (2012).

Euboictis aliverensis **Localites:** Aliveri, Greece. **Absolute age estimate:** 18.01-17.5 Ma. Hoek Ostende et al. (2015) place the only known fossil locality of this taxon at the above absolute age.

Sivanasua viverroides **Localites:** France, Germany. **Absolute age estimate:** 17.2-11.2 Ma. This taxon is known from MN4-MN7/8 (Morales et al., 2019), with absolute ages following Hilgen et al. (2012).

Herpestidae

Kichechia zamanae **Localites:** Rusinga, Kenya. **Absolute age estimate:** 20.0-17.0 Ma. A recent revision has split this taxon between at least two species, with *Kichechia zamanae* now only explicitly known from Rusinga and Songhor (Adrian et al., 2018). Additional eastern African localities report this taxon (e.g. *Kichechia sp.* from Napak; Werdelin and Peigné, 2010), but barring additional taxonomic study at these sites I chose to only use the temporal age associated with Rusinga and Songhor (Werdelin and Peigné, 2010; Adrian et al., 2018).

Kanuites lewisae **Localites:** Fort Ternan, Kenya. **Absolute age estimate:** 14.0-13.4 Ma. All material attributable to this taxon is known from Fort Ternan (Werdelin, 2019). The age of this locality is well known from whole-rock K/Ar and single-crystal $^{40}\text{Ar}/^{39}\text{Ar}$ at 13.7 ± 0.3 Ma (Pickford et al., 2006). This date in two sigma years is the range reported above. A normal

distribution spanning this range (2 sigma confidence interval, mean=13.7, sigma = 0.2) was used as the tip prior in the phylogenetic analysis.

Hyaenidae

Tongxinictis primordialis **Locality:** Tongxin, China. **Absolute age estimate:** 13.8-12.5 Ma. As described by Qiu et al. (1988), this taxon is known from the earliest Tungurian, roughly equivalent to MN6. The absolute dates follow Agustí et al. (2001).

Allohyaena kadici **Locality:** Hungary, Germany. **Absolute age estimate:** 8.7-7.5 Ma. The described temporal age (MN 11) and geographic range of this taxon follow Turner et al. (2008), while the absolute dates follow Agustí et al. (2001).

Plioviverrops orbigny **Locality** Greece, Spain: **Absolute age estimate:** 9.7-6.8 Ma. The described temporal age (MN 10-12) and geographic range of this taxon follow Turner et al. (2008), while the absolute dates follow Agustí et al. (2001).

Protictitherium crassum **Locality:** France, Germany, Greece, Spain, Turkey. **Absolute age estimate:** 17.1-5.1 Ma. Following the in-depth study of this species (particularly at Cerro de los Batallones, Spain) by Gracia (2015), the temporal range now extends from the end of MN 4 to MN 13.

Tungurictis spocki **Locality:** Tung Gur, China. **Absolute age estimate:** 12.75-11.1 Ma (Slater and Friscia, 2019).

Ictitherium viverrinum **Locality:** Various Europe, Asia. **Absolute age estimate:** 11.5-4.9 Ma. The described temporal age and geographic range of this taxon follow Turner et al. (2008), while the absolute dates follow Agustí et al. (2001).

Hyaenictitherium wongii **Locality:** Germany, Greece, Ukraine, Turkey, Iran, Kazakhstan, China. **Absolute age estimate:** 11.5-4.2 Ma. This cosmopolitan species ranges from MN 9-14 (Tseng and Wang, 2007). However, there is debate as to the generic assignment of this and other *Hyaenictitherium* taxa (see Semenov, 2008). Here, I followed the taxonomy of Tseng and Wang (2007) and Turner et al. (2008).

Hyaenictitherium hyaenoides **Locality:** China, Ukraine, Iran, Turkey, Kazakhstan, Mongolia. **Absolute age estimate:** 7.5-4.2 Ma. Temporal (MN 11-14) and geographic ranges follow Tseng and Wang (2007).

Lycyaena chaeretis **Locality:** Greece, Spain, Ukraine. **Absolute age estimate:** 8.7-6.8 Ma. The described temporal age (MN 11-12) and geographic range of this taxon follow Turner et al. (2008), while the absolute dates follow Agustí et al. (2001).

Palinhyena reperta **Locality:** China. **Absolute age estimate:** 7.5-6.8 Ma. The described temporal age (MN 12) and geographic range of this taxon follow Werdelin and Solounias (1991), while the absolute dates follow Agustí et al. (2001).

Belbus beaumonti **Locality:** Greece, Turkey. **Absolute age estimate:** 8.7-6.8 Ma. The described temporal age (MN 11-12) and geographic range of this taxon follow Turner et al. (2008), while the absolute dates follow Agustí et al. (2001).

Adcrocuta eximia **Locality:** Various China, Kyrgyzstan, Europe. **Absolute age estimate:** 8.7-4.9 Ma (Slater and Friscia, 2019; Miller et al., 2020).

Pachyrocute brevirostris **Locality:** Various South and East Africa, China, Europe and South Asia. **Absolute age estimate:** 3.0 (Asia, Africa) - 0.5 (Europe) Ma (Slater and Friscia, 2019).

Chasmaporthetes lunensis **Locality:** Various China, Europe, Asia. **Absolute age estimate:** 5.332-2.0 Ma (Slater and Friscia, 2019).

Chasmaporthetes ossifragus **Locality:** Various; USA, Mexico, China? **Absolute age estimate:** 5.332-0.85 Ma. Werdelin and Solounias (1991) recognized most North American hyaenid material as *C. ossifragus*, except for the Florida specimens, which were distinguished by a longer m1 relative to the p4. However, Tseng et al. (2013) found this value to be on a continuum of other *Chasmaporthetes* specimens, and thus cast doubt on the validity of this specific character.

Thus, until more clear specific diagnostic criteria for a purported Florida species of *Chasmaporthete* is determined, I chose to include this material into *C. ossifragus*.

Chasmaporthetes is a Blancan index taxon and thus was used as the first appearance datum (Bell et al., 2004; Tseng et al., 2013). The latest described specimens appear to come from the Mexican El Golfo Fauna, thought to be Irvingtonian in age, but with no associated radiometric or paleomagnetic dates (Bell et al., 2004). For this study an Irvingtonian 1 latest occurrence was used, given the preponderance of Blancan dates for this taxon, and lack of other known Irvingtonian occurrences.

Crocota crocuta spelaea **Localites:** Various, Europe, Asia. **Absolute age estimate:** 0.021889-0.126 Ma. The date for this species is tied to the age of the specimen sampled for DNA, petrous bone, GenBank: MN320462.1 (Westbury et al., 2020). Unfortunately, there is no connection between GenBank accession numbers and the radiocarbon dates of the three German cave hyena specimens in Westbury et al. (2020). Thus, I chose to use a uniform prior to encompass the dates of all three German cave hyena specimens to be assured of sampling the most likely date. The youngest specimen, Ccsp043, has a reported date of $18,030 \pm 50$ ^{14}C age yr. BP, while the oldest specimen, Ccsp040, as “Late Pleistocene” (Westbury et al., 2020). The Late Pleistocene is an informal unit, but has been defined by the Subcommittee on Quaternary Stratigraphy (<http://quaternary.stratigraphy.org/definitions/pleistocene-subdivision/> accessed on 12/22/2020) at the base of the Eemian, or 0.126 Ma. The youngest date in two sigma calibrated years (using CalPal Rev 8.1.0) returns 0.021889-0.022191 Ma. A uniform distribution spanning the minimum 2 sigma confidence interval to the base of the Late Pleistocene was used as the tip prior in the phylogenetic analysis.

Dinocrocuta gigantea **Localites:** Bulgaria, Mongolia, China. **Absolute age estimate:** 11.5-8.0 Ma. The precise geologic age of this taxon has long been unclear (Zhang, 2005). However, European remains attributed to this taxon are thought to be Vallesian in age (Spasov and Koufos, 2002), with a slightly later appearance at approximately Chron 5n.2n in China (Zhang, 2005). The youngest dated record is at approximately 8.0 Ma from the Red Clays of Fugu, China (Zhang, 2005).

Percrocuta carnifex **Localites:** Pakistan. **Absolute age estimate:** 14.2-9.5 Ma. Recent work has reviewed the occurrence of this taxon in the Middle Siwalik (Ghaffar et al., 2019). *Percrocuta carnifex* is known from the Chinji and Nagaro Formations, with referrals to the younger Dhok Pathan Formation as unlikely (Ghaffar et al., 2019).

Percrocuta algeriensis **Localites:** Algeria. **Absolute age estimate:** 12.18-7.0 Ma. Howell and Petter (1985) give localities at Bou Hanifia (12.18-9.7 Ma.; Bernor et al., 1980) and Menacer. The latter locality is viewed as Middle Turolian by Howell and Petter (1985), and approximately 7 Ma by Benefit et al. (2008).

Percrocuta tobieni **Localites:** Kenya, Tunisia. **Absolute age estimate:** 13.8-11.0 Ma. Recent finds of this taxon at Fort Ternan extend the temporal range of this taxon to 13.8 Ma (Werdelin, 2019), while the youngest occurrences span the Ngorora Formation (12.5-11.0 Ma; Morales and Pickford, 2005; Werdelin, 2019).

Nimravidae

Oriensmilus liupanensis. **Locality:** Tongxin area of Ningxia Hui Autonomous Region, northern China (Wang et al., 2020). **Absolute age estimate:** 16.0-15.0 Ma (Qiu et al., 2013). The holotype and additionally referred material is from an informal middle member of the Zhang'enbao Formation, from which emanates the Ma'erzhuizi Gou Fauna (Wang et al., 2016), that the authors included within the Dingjia'ergou Fauna. The latter fauna is the date to which I applied the age estimate of this taxon, as did Wang et al. (2020).

Sansanosmilus palmidens. **Locality:** France. **Absolute age estimate:** 16.0-13.0 Ma. The majority of *S. palmidens* material comes from southern France at the locality of Sansan, MN 6 (Peigné, 2012). However, additional fragmentary material has been described from Savigné-sur-Lathan (MN5) of western France (Ginsburg, 2001).

Barbourofelis fricki **Locality:** Kansas, Nebraska, Texas, Nevada, USA. **Absolute age estimate:** 9.0–7.0 Ma (Tseng et al., 2010).

Barbourofelis loveorum **Locality:** Florida, USA. **Absolute age estimate:** 9.5–8.0 Ma (Tseng et al., 2010).

Barbourofelis morrissi **Locality:** Nevada, South Dakota, Texas, USA. **Absolute age estimate:** 12.0–9.5 Ma (Tseng et al., 2010).

Albanosmilus whitfordi **Locality:** California, Colorado, Nebraska, Texas, Florida, USA.

Absolute age estimate: 12.0–7.0 Ma (Tseng et al., 2010).

Albanosmilus jourdani **Locality:** Spain, France, Turkey. **Absolute age estimate:** 11.9–9.7 Ma (Robles et al., 2013).

Hoplophoneus cerebralis. **Locality:** South Dakota, California, Oregon, Wyoming, USA.

Absolute age estimate: 34.7–29.586 Ma. The earliest specimen referable to this taxon is an edentulous dentary from the Crazy Johnson Member of the Chadron Formation (Barrett, 2016). The latest well-documented occurrence is from below the “Blue Basin Tuff” of the Turtle Cove Member of the John Day Formation (29.586 Ma; Famoso et al., 2015).

Hoplophoneus primaevus. **Locality:** Nebraska, South Dakota, Wyoming, Colorado, Oregon, USA. **Absolute age estimate:** 35.7–30.58 Ma. Following the taxonomy of Barrett (2016), the oldest occurrence of this taxon is from Flagstaff Rim Wyoming (Bryant, 1996; Prothero and Emry, 2004). The youngest specimens attributed to this taxon are found just below the “Upper Whitney Ash” in Nebraska and the basal *Leptauchenia* beds of the Poleslide Member of the Brule in South Dakota (Bryant, 1996; Prothero and Emry, 2004).

Hoplophoneus occidentalis. **Locality:** Nebraska, North Dakota, South Dakota, Wyoming, USA.

Absolute age estimate: 33.4–31.4 Ma. The earliest stratigraphically constrained specimens of this taxon come from the “lower nodules” of the Scenic Member of the Brule Formation, correlated to 33.4–33.1 Ma (Bryant, 1996; Prothero and Emry, 2004). The latest occurring

specimens emanate from the *Protoceros* channel sandstones of the Poleslide Member of the Brule Formation (Bryant, 1996; Barrett, 2016).

Nimravus brachyops. **Locality:** Nebraska, South Dakota, California, Oregon, Wyoming (USA); Saskatchewan (Canada). **Absolute age estimate:** 31.4- 27.14 Ma. This is a geographically wide-ranging taxon in North America with its first occurrence in the *Protoceros* channel sandstones of the Poleslide Member of the Brule Formation, South Dakota (Bryant, 1996; Prothero and Emry, 2004). The last reported occurrence of this taxon is from the K1 unit of the Turtle Cove Member of the John Day Formation (Famoso et al., 2015). The K1 unit is capped by the “Biotite Tuff” and forms the LAD for this study.

Pogonodon platycopis. **Locality:** South Dakota, Nebraska, Oregon, USA. **Absolute age estimate:** 32.0-29.586 Ma. Numerous specimens of Whitneyan age are referred to this taxon, with none being clearly older (Bryant, 1996; Barrett, 2016). The youngest age comes from Unit E of the Turtle Cove Member of the John Day Formation, below the “Blue Basin Tuff” (Famoso et al., 2015).

Pogonodon davisi. **Locality:** Wyoming, Nebraska, South Dakota, Oregon, USA. **Absolute age estimate:** 32.0-25.9 Ma. Like *P. platycopis*, the earliest record of this taxon is Whitneyan in age (Bryant, 1996; Barrett, 2016). The youngest specimen (JODA 5841) attributable to this taxon comes from the K2 unit of the Turtle Cove Member of the John Day Formation. This specimen was referred to as a possible new species of *Pogonodon* by Bryant and Fremd (1998) and Albright et al. (2008), but is included in this taxon following the diagnosis of Barrett (2016).

Dinictis felina. **Locality:** South Dakota, North Dakota, Nebraska, Oregon, Montana, Wyoming (USA); Saskatchewan (Canada). **Absolute age estimate:** 35.7- 29.586 Ma. The oldest record known is at Flagstaff Rim, at just over 35.5 Ma, though several slightly older occurrences are possible from fragmentary remains and provisional dates (Bryant, 1996). For example, *Dinictis* sp. has been collected from the Medicine Poles local fauna of southwestern North Dakota, thought to be Ch2 in age (Boyd and Webster, 2018). This latter occurrence is used as the FAD of this taxon. The LAD includes the occurrence of *Dinictis cyclops* (= *D. felina*; Barrett, 2016) below the Blue Basin Tuff (29.586 Ma; Famoso et al., 2015).

Nanosmilus kurteni. **Locality:** Nebraska, USA. **Absolute age estimate:** 33.89-32.0 Ma. The holotype and only known specimen is from the Orella Member of the Brule Formation (Martin, 1992). Absolute radiometrically dated boundaries for the Orella Member are not known, but bracketed to 34.6-31.5 Ma (Zanazzi et al., 2009) based on stratigraphically and geographically, nearest dated ash layers. However, dates for the Orellan NALMA are better known and what is used for the range applied to this taxon (Prothero and Emry, 2004; Zanazzi et al., 2009).

Nimravus intermedius. **Locality:** France, Germany, Mongolia. **Absolute age estimate:** 35.37-27.24 Ma. Numerous fragmentary remains are known from the old Quercy collections, as well as the new stratigraphically documented ones (MP 22 to 25; Peigné, 2003; Peigné et al., 2014). Additional French material comes from Villebramar, MP 22 (Peigné, 2003). Of similar age in Southern Germany are attributed dentition at Möhren 13 (MP 22) and Liptingen (MP 22 or MP 23; Peigné, 2003). Mongolian *Nimravus* material, of Ergilian age, was separated into its own

species, *Nimravus mongoliensis*, for much of the 20th century (Gromova, 1959; Dashzeveg, 1996), but was synonymized to *N. intermedius* by Peigné (2003). Most recently this material was re-established as a valid species by Egi et al. (2016) based upon depth of the horizontal ramus and relative size of p1 and p2. However, the variability in anterior premolars for *Nimravus* has been well documented in the literature (Toohey, 1959; Peigné, 2003; Barrett, 2016). Thus, until more complete material of this purported species is described I chose to follow the assessment of Peigné (2003) in its synonymy. The Thai, '*Nimravus*' material described by Peigné et al. (2000) lacks the apomorphy of p4 morphology for this genus, and may be more closely related to *Maofelis* for which no lower dentognathic remains are known.

Ginsburgsmilus napakensis. **Locality:** Langental, Fiskus, Grillental-6, Sperrgebiet, Namibia; Songhor, Kenya; Napak, Uganda. **Absolute age estimate:** 20.0-19.0 Ma. An updated occurrence list can be found in Morales and Pickford (2018), while Werdelin (2010) describes all of the above sites to be correlative to 20-19 Ma.

Prosansanosmilus eggeri. **Locality:** Bavaria, Germany. **Absolute age estimate:** 16.7-15.97 Ma. Thus far, the only known specimens of this taxon come from Sandelzhausen (MN 5) of Bavaria (Morlo et al., 2004). Sandelzhausen is constrained in age to about 16 Ma based on magnetochronological events and biostratigraphy; see Moser et al. (2009) for a detailed overview.

Prosansanosmilus peregrinus. **Locality:** Germany, France. **Absolute age estimate:** 18.0-16.0 Ma. In their original description, Heizmann et al. (1980) named three localities for the

occurrence of this taxon: Langenau 1 of Germany; and Bézian and Artenay of France. To this list, Petersbuch 2 of Germany was added by Morlo (2006). Petersbuch 2 and Artenay are MN 4a in age while Langenau 1 and Bézian are MN 4b. The age of MN 4 is skewed slightly older in the depositional basins of Switzerland and Southern Germany (see Reichenbacher et al., 2013) than the European “standard” (compare to Agustí et al., 2001). Furthermore, the exact age of the above fossil localities within their respective subzones is unequally known, save with Langenau 1 at slightly less than 17.2 Ma (Reichenbacher et al., 2013). Thus conservatively, the base of the South German MN 4a was used as the FAD of this taxon, while the LAD the “standard” top of MN 4.

Afrosmilus africanus. **Locality:** Locherangan, Rusinga, and Karungu (Kenya); Buñol, Spain. **Absolute age estimate:** 17.8-16.0 Ma. *A. africanus* is known from the African sites of Locherangan, Rusinga, and Karungu (Kenya), as well as the Spanish locality of Buñol. The Kenyan locality Locherangan (c. 17.5 Ma; Anyonge, 1991) is located west of Lake Turkana, while Rusinga (c. 17.8 Ma; Werdelin, 2010) and Karungu (c. 17.7-17.5 Ma; Drake et al., 1988), though likely contemporaneous with Rusinga (Werdelin, 2010) or slightly older (Morales and Pickford, 2018) based on biostratigraphy, are localities along the northwestern shore of Lake Victoria. The Spanish locality of Buñol (MN4, 16.6-16.0 Ma; Agustí et al., 2001) is located in the east of Spain in the province of Valencia.

Afrosmilus turkanae. **Locality:** Moruorot Hill and Rusinga, Kenya. **Absolute age estimate:** 17.8-16.8 Ma. *A. turkanae* is known from the African localities of Moruorot Hill and Rusinga (Kenya). Moruorot Hill (c. 17.5-16.8 Ma; Boschetto et al., 1992) is located west of Lake

Turkana, while Rusinga is the same locality (and chronology) as mentioned above for *A. africanus*.

Afrosmilus hispanicus. **Locality:** Artesilla, Spain. **Absolute age estimate:** 16.7-16.0 Ma. *A. hispanicus* is the only non-African originating species of *Afrosmilus*, known only from the Spanish locality of Artesilla (c. 16.7 Ma; Azanza et al., 1993; Morales et al., 2001), in the northeast of the country in the province of Saragossa. *A. hispanicus* is typically correlated to the MN 4 zone (Morlo, 2006; Morales and Pickford, 2018), thus the younger date of 16.0 Ma is applied to its range, being the boundary between MN 4 and 5 (Agustí et al., 2001).

Maofelis cantonensis. **Locality:** Maoming Basin, Guangdong Province, China. **Absolute age estimate:** 41.03-33.9 Ma. The holotype, and only known specimen, is from the Youganwo Formation, middle-upper Eocene (Averianov et al., 2016). The vertebrate fauna is only known from the upper portion of the formation containing dark oil shales and alternating mudstones (Averianov et al., 2016). The precise stratigraphic horizon of the holotype is unknown, but based on magnetostratigraphy and biostratigraphy it has been correlated to the Bartonian through Priabonian (Li et al., 2016; Averianov et al., 2019).

Eofelis edwardsii. **Locality:** France, Mongolia. **Absolute age estimate:** 35.37-30.83 Ma. The vast majority of material referred to *Eofelis edwardsii* comes from the old collections of the phosphorites of Quercy with no precise age (Peigné, 2000). However, material questionably referred to this taxon has been described from Villebramar, France, MP 22 (Peigné, 2000). Egi et al. (2016) described *Eofelis sp.* from the Ergilin Dzo Formation, Mongolia, which based on their

measurements most closely resembles *Eofelis edwardsii* compared to the larger *E. giganteus* (Peigné, 2000). The Mongolian specimens are dated to the Ergilian ALMA (Egi et al., 2016) and thus forms the oldest occurrence of this taxon while MP 22 the youngest for this study.

Dinailurictis bonali. **Locality:** France, Spain. **Absolute age estimate:** 32.63-27.24 Ma

Most material attributed to this taxon comes from the Quercy fissures, dated MP 22 to 25, and Villebramar, MP 22 (Peigné, 2003; Peigné et al., 2014). The Spanish material, canine fragments, comes from Carrascosa del Campo, approximately MP 25 (Peigné, 2003). Thus, the range of this taxon was chosen as MP 22-25, with absolute dates for these zones following Ogg et al. (2016).

Quercylurus major. **Locality:** France, Spain. **Absolute age estimate:** 28.82-27.24 Ma

The French material, including the holotype, come from the old collections of Quercy which have no precise age (Peigné, 2003). The Spanish material from Carrascosa del Campo has an estimated age of MP 25 and thus the only reliably dated material (Peigné, 2003). Absolute dates follow Ogg et al. (2016).

Dinaelurus crassus. **Locality:** Oregon, USA. **Absolute age estimate:** 29.5-28.5 Ma. The precise stratigraphic context for the holotype, and only known specimen of this taxon, were unknown when Eaton (1922) initially described it. However, a provisional Early Arikareean (Upper John Day Formation) was attributed to the specimen based on preservation and associated matrix (Eaton, 1922; Bryant, 1996). Albright et al. (2008) suggest the origin to be the E unit of the Turtle Cove Member of the John Day Formation. This assessment is given without evidence, but is one of most fossiliferous units of the Turtle Cove Member. The associated absolute dates for

the E unit were used for this study pending additional justification for the provenience of this taxon.

Hoplophoneus oharrai. **Locality:** South Dakota, USA. **Absolute age estimate:** 35.7-34.7 Ma.

The type and only specimen comes from the Crazy Johnson Member of the Chadron Formation in southwest South Dakota (Barrett, 2016). Absolute dates are not available for the Crazy Johnson member, though it contains a middle Chadronian fauna (Ch3: 34.7-35.7 Ma: Janis et al., 2008) which is used for its range here.

MA-PHQ 348. **Locality:** Phosphorites of Quercy, south-western France. **Absolute age estimate:** 47.4-23.03 Ma. This plesiomorphic nimravid specimen comes from the old collections of Quercy and thus has little to no stratigraphic context. The Phosphorites have a total extent from the base of MP 11 to the early Miocene (Sigé et al., 1991; Legendre et al., 1992). Given the poor understanding of this specimen's stratigraphic context a broad prior from the base of MP 11 to the end of the Oligocene was chosen.

Eusmilus dakotensis. **Locality:** South Dakota, USA. **Absolute age estimate:** 30.5-29.75 Ma.

Three referable specimens come from the Brule Fm., Poleslide Member of South Dakota (Barrett, 2016). Bryant (1996) limits the first appearance to the latter Whitneyan, during Chron C12n or C11r. This leads to the FAD as stated with the LAD being the end of the Whitneyan.

Eusmilus sicarius. **Locality:** South Dakota, USA. **Absolute age estimate:** 33.4-33.1 Ma.

Following the results of this study, the only known specimen belonging to this species is the

holotype, which comes from the lower nodule zone of the Scenic Member of the Brule Formation. This stratum is roughly correlative to Chron C13n (Prothero and Emry, 2004).

Eusmilus adelos. **Locality:** Niobrara County, Wyoming, USA. **Absolute age estimate:** 33.7-32.0 Ma. The holotype specimen (Barrett, 2021) comes from the Northwest corner of Seaman Hills, Niobrara County, Wyoming. The additional referred specimen was collected about one mile North of Whitman, Wyoming. Both of these specimens come from the Seaman Hills which spans the entirety of the Orellan in typical outcrops (Prothero and Whittlesey, 1998; Prothero and Emry, 2004). Unfortunately, with no greater stratigraphic or geographic resolution, the entirety of the Orellan was used as the occurrence for this taxon.

Eusmilus bidentatus. **Locality:** France, Germany. **Absolute age estimate:** 33.77-32.63 Ma. This taxon is well known in the Phosphorites of Quercy, but also Soumailles (Ringade and Michel, 1994; Peigné and Brunet, 2001). Additional material is known from southern Germany, but all of it (along with the French material) has been correlated to MP 21 (Peigné and Brunet, 2001).

Eusmilus villebramarensis. **Locality:** France, Switzerland, Germany. **Absolute age estimate:** 32.63-30.83 Ma. Most material for this taxon comes from France in the old collections of Quercy, but also Villebramar (Peigné and Brunet, 2001). However, occurrences in Switzerland and Germany are also known, which with the Villebramar material also has a MP 22 date (Peigné and Brunet, 2001).

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Appendix H

Dietary Classification and Ecological Data Tables

Table 1. Extant taxa and associated data used for CVA training set. Dentognathic metrics are averages per species taken from Slater and Friscia (2019). C1 = compression of the upper C1, P4S = ratio of width to length of fourth lower premolar, RBL = relative blade length of the trigonid of m1, M1BS = blade length of the m1 relative to total dentary length. Degree of carnivory is calculated by percent of diet belonging to the Diet-Vend (vertebrate endotherm), Diet-Vect (vertebrate ectotherm), Diet-Vfish (vertebrate fish), Diet-Vunk (vertebrate unknown), Diet-Scav (scavenge) categories of the Elton Traits dataset (Wilman et al., 2014). Diet reflects the following categories: 1 = hypocarnivore, 2 = mesocarnivore, 3 = hypercarnivore.

	C1	P4S	RBL	M1BS	degree of carnivor y	diet	clade
<i>Acinonyx jubatus</i>	0.77205 4	0.40163 2	1	0.15139 4	100	3	Felidae
<i>Ailurus fulgens</i>	0.66926 3	0.63478 6	0.62610 6	0.09532 5	10	1	Ailuridae
<i>Arctictis binturong</i>	0.61020 8	0.72164 4	0.5939	0.05107 7	50	2	Viverridae
<i>Arctogalidia trivirgata</i>	0.72781 8	0.64677 4	0.59326 7	0.05687 9	60	2	Viverridae

<i>Atelocynus microtis</i>	0.66531 4	0.47592 5	0.64459 2	0.08397	80	3	Canidae
<i>Atilax paludinosus</i>	0.72967 1	0.68234 5	0.72531 2	0.09809 1	60	2	Herpestidae
<i>Bassaricyon alleni</i>	0.80870 7	0.79115 7	0.45601 1	0.04745 2	10	1	Procyonidae
<i>Bassaricyon gabbii</i>	0.78306 9	0.85210 2	0.49278 8	0.05059 6	10	1	Procyonidae
<i>Bassariscus astutus</i>	0.70332 3	0.50174 7	0.61185 3	0.08803 3	10	1	Procyonidae
<i>Bassariscus sumichrasti</i>	0.69778 4	0.60897 8	0.61452 7	0.07765 1	10	1	Procyonidae
<i>Bdeogale crassicauda</i>	0.72887 5	0.58803 4	0.56413 3	0.05421 3	20	1	Herpestidae
<i>Bdeogale nigripes</i>	0.68366	0.62357 8	0.47748 4	0.04761 9	40	1	Herpestidae
<i>Canis adustus</i>	0.63840 5	0.45317 8	0.62803 6	0.08493 9	50	2	Canidae
<i>Canis aureus</i>	0.61618 1	0.45807 9	0.68265 7	0.10987 4	80	3	Canidae
<i>Canis latrans</i>	0.57667 6	0.44749 6	0.69641 1	0.10958 3	100	3	Canidae
<i>Canis lupus</i>	0.62145	0.52157	0.70792	0.11052	100	3	Canidae

	5	4	7	8			
<i>Canis mesomelas</i>	0.61704	0.44972	0.65814	0.10824	60	2	Canidae
	5	4	2	2			
<i>Canis simensis</i>	0.63720	0.45429	0.68465	0.08964	100	3	Canidae
	7	3	2	7			
<i>Caracal caracal</i>	0.75985	0.46037	1	0.14873	100	3	Felidae
	6	9		7			
<i>Caracal serval</i>	0.74340	0.42630	1	0.14057	100	3	Felidae
	4	7		1			
<i>Cerdocyon thous</i>	0.65387	0.46994	0.62643	0.08952	50	2	Canidae
		5	1	6			
<i>Chrotogale owstoni</i>	0.59932	0.39607	0.42447	0.03764	10	1	Viverridae
	3	5	3	1			
<i>Chrysocyon brachyurus</i>	0.62425	0.50251	0.64114	0.08739	70	3	Canidae
	8	5	3				
<i>Civettictis civetta</i>	0.80786	0.59631	0.61508	0.08220	50	2	Viverridae
	7		7	7			
<i>Crocuta crocuta</i>	0.72886	0.55983	0.91677	0.14806	100	3	Hyaenidae
	4	2	7	3			
<i>Crossarchus alexandri</i>	0.64787	0.59487	0.54375	0.05782	20	1	Herpestidae
		1	1	8			
<i>Crossarchus obscurus</i>	1.11303	0.56667	0.48447	0.05396	20	1	Herpestidae
	6	2	2	4			

<i>Crossarchus platycephalus</i>	0.59279 8	0.54115 2	0.51644 1	0.05680 9	50	2	Herpestidae
<i>Cryptoprocta ferox</i>	0.75258 3	0.56267 3	0.80478 9	0.11767 8	90	3	Eupleridae
<i>Cuon alpinus</i>	0.60538 1	0.49566 1	0.72617 9	0.12377 6	100	3	Canidae
<i>Cynictis penicillata</i>	0.68673 3	0.51814 7	0.70852 2	0.08666 5	10	1	Herpestidae
<i>Cynogale bennettii</i>	0.70279 7	0.45827	0.48085 8	0.05338 6	50	2	Viverridae
<i>Diplogale hosei</i>	0.68627 5	0.52584 7	0.47788 6	0.04921 8	40	1	Viverridae
<i>Dusicyon australis</i>	0.63463 6	0.48011 4	0.71256 6	0.10422 1	100	3	Canidae
<i>Eupleres goudotii</i>	0.69980 4	0.35062 7	0.58566 6	0.05052 4	10	1	Eupleridae
<i>Felis chaus</i>	0.78590 9	0.38494 4	1	0.14050 8	100	3	Felidae
<i>Felis margarita</i>	0.78431 4	0.43255 1	1	0.14258 5	100	3	Felidae
<i>Felis nigripes</i>	0.72576 8	0.46701 4	1	0.14099 1	100	3	Felidae
<i>Felis silvestris</i>	0.77786	0.43040	1	0.14629	90	3	Felidae

		3		4			
<i>Fossa fossana</i>	0.65510	0.45010	0.59251	0.07058	20	1	Eupleridae
	7	7	7	4			
<i>Galerella pulverulenta</i>	0.68484	0.48016	0.63871	0.08980	20	1	Herpestidae
	5	1		9			
<i>Galerella sanguinea</i>	0.66263	0.48112	0.74556	0.10447	20	1	Herpestidae
	6	6	7	8			
<i>Galidia elegans</i>	0.69114	0.50299	0.65632	0.10911	80	3	Eupleridae
	9	2		6			
<i>Galidictis fasciata</i>	0.67052	0.57047	0.62718	0.08372	70	3	Eupleridae
	5	9	2	9			
<i>Genetta angolensis</i>	0.74320	0.44367	0.73872	0.09010	90	3	Viverridae
	9	1	3	5			
<i>Genetta genetta</i>	0.71593	0.41667	0.74356	0.0892	90	3	Viverridae
	9		1				
<i>Genetta maculata</i>	0.73610	0.41833	0.72120	0.08754	90	3	Viverridae
	3	4	6	7			
<i>Genetta pardina</i>	0.68675	0.36535	0.67536	0.08288	70	3	Viverridae
		3	1	4			
<i>Genetta servalina</i>	0.70336	0.39411	0.73857	0.08590	90	3	Viverridae
	7	9		9			
<i>Genetta thierryi</i>	0.74921	0.37385	0.65037	0.07870	90	3	Viverridae
	8	9	8	6			

<i>Genetta tigrina</i>	0.77994 5	0.40295 2	0.69505 7	0.08791	90	3	Viverridae
<i>Helogale hirtula</i>	0.62981 8	0.64546 4	0.82431 6	0.09499 6	20	1	Herpestidae
<i>Helogale parvula</i>	0.60952 8	0.61413 8	0.78429 8	0.08741 5	20	1	Herpestidae
<i>Hemigalus derbyanus</i>	0.65491 8	0.48340 4	0.43740 7	0.04683 9	0	1	Viverridae
<i>Herpestes brachyurus</i>	0.71376 3	0.56041 9	0.61636 2	0.08512 2	60	2	Herpestidae
<i>Herpestes edwardsii</i>	0.72307 2	0.50759 8	0.63488 9	0.09126 6	70	3	Herpestidae
<i>Herpestes fuscus</i>	0.69979 1	0.49810 8	0.61004 7	0.07851 8	60	2	Herpestidae
<i>Herpestes ichneumon</i>	0.69149 5	0.49819 5	0.72273 8	0.09655 7	60	2	Herpestidae
<i>Herpestes javanicus</i>	0.70009 6	0.49491 1	0.62057 9	0.08465 2	60	2	Herpestidae
<i>Herpestes naso</i>	0.71421	0.52738 4	0.62267 2	0.08236 2	60	2	Herpestidae
<i>Herpestes urva</i>	0.70438 2	0.56240 7	0.64142 8	0.09024 1	60	2	Herpestidae
<i>Herpestes</i>	0.65284	0.54782	0.58815	0.06880	60	2	Herpestidae

<i>vitticollis</i>	9	7	1	3			
<i>Hyaena hyaena</i>	0.68306	0.55372	0.78850	0.10393	80	3	Hyaenidae
	4	1	2	4			
<i>Ichneumia</i>	0.72193	0.50991	0.64076	0.07146	20	1	Herpestidae
<i>albicauda</i>	7	9	4	3			
<i>Leopardus</i>	0.69735	0.50534	1	0.15216	100	3	Felidae
<i>colocolo</i>	7			3			
<i>Leopardus</i>	0.71350	0.44556	1	0.15004	100	3	Felidae
<i>geoffroyi</i>	2	1		6			
<i>Leopardus guigna</i>	0.79109	0.45977	1	0.12585	100	3	Felidae
	7	3					
<i>Leopardus</i>	0.75554	0.44825	1	0.13775	100	3	Felidae
<i>pardalis</i>	9	4					
<i>Leopardus tigrinus</i>	0.74622	0.40528	1	0.13745	100	3	Felidae
	8			3			
<i>Leopardus wiedii</i>	0.71439	0.43518	1	0.14158	80	3	Felidae
	6	2		6			
<i>Liberiictis kuhni</i>	0.62619	0.47969	0.52670	0.04932	20	1	Herpestidae
	1	1	4	7			
<i>Lycaon pictus</i>	0.64928	0.49252	0.71066	0.11969	100	3	Canidae
	8	3	1	8			
<i>Lynx canadensis</i>	0.78898	0.44634	1	0.15941	100	3	Felidae
	1	2		2			

<i>Lynx lynx</i>	0.79083 4	0.50001 2	1	0.14758 3	100	3	Felidae
<i>Lynx pardinus</i>	0.81483	0.48392 8	1	0.15210 3	100	3	Felidae
<i>Lynx rufus</i>	0.80711 5	0.49118 2	1	0.14546 9	100	3	Felidae
<i>Mungos mungo</i>	0.65398 3	0.65529	0.75450 9	0.07647 2	20	1	Herpestidae
<i>Mungotictis decemlineata</i>	0.73336 1	0.54262 6	0.60088 4	0.08917 3	20	1	Eupleridae
<i>Nandinia binotata</i>	0.69825 2	0.65049 6	0.66409 7	0.06867 4	10	1	Nandiniidae
<i>Nasua narica</i>	0.56090 6	0.64758 3	0.54355 9	0.05286 4	20	1	Procyonidae
<i>Nasua nasua</i>	0.52934	0.57890 1	0.50048 2	0.04732 8	20	1	Procyonidae
<i>Nasuella olivacea</i>	0.43911 6	0.56308 4	0.45791	0.03555 4	20	1	Procyonidae
<i>Neofelis nebulosa</i>	0.73510 8	0.46239 9	1	0.13438 2	100	3	Felidae
<i>Nyctereutes procyonoides</i>	0.67459	0.44269 7	0.62048 3	0.09377 2	40	1	Canidae
<i>Otocolobus manul</i>	0.76252	0.46755	1	0.16595	100	3	Felidae

	7	8		1			
<i>Paguma larvata</i>	0.67564	0.75779	0.56497	0.06633	60	2	Viverridae
	3	4	7	1			
<i>Panthera uncia</i>	0.82155	0.48066	1	0.14734	100	3	Felidae
	9	1		1			
<i>Panthera leo</i>	0.69909	0.47720	1	0.12219	100	3	Felidae
	2	8		2			
<i>Panthera onca</i>	0.80370	0.45631	1	0.12654	100	3	Felidae
	3			4			
<i>Panthera pardus</i>	0.77458	0.49165	1	0.13171	100	3	Felidae
	6			5			
<i>Panthera tigris</i>	0.74551	0.47559	1	0.12687	100	3	Felidae
	9	3		5			
<i>Paracynictis selousi</i>	0.65567	0.50331	0.68850	0.07914	40	1	Herpestidae
	9	2	1	7			
<i>Paradoxurus hermaphroditus</i>	0.71923	0.6925	0.59609	0.07465	40	1	Viverridae
	6		2	3			
<i>Paradoxurus zeylonensis</i>	0.69575	0.65321	0.60528	0.07331	40	1	Viverridae
	4	2					
<i>Parahyaena brunnea</i>	0.76328	0.60451	0.82032	0.11484	80	3	Hyaenidae
	7	8	5	1			
<i>Pardofelis badia</i>	0.76913	0.45521	1	0.15492	100	3	Felidae
	5	2		1			

<i>Pardofelis marmorata</i>	0.67560 7	0.47841 1	1	0.16031 3	100	3	Felidae
<i>Pardofelis temminckii</i>	0.77640 4	0.41433	1	0.14784 2	100	3	Felidae
<i>Potos flavus</i>	0.70417 8	0.72558 6	0.44098 2	0.04392	10	1	Procyonidae
<i>Prionailurus bengalensis</i>	0.75377	0.43890 2	1	0.13446 9	100	3	Felidae
<i>Prionailurus planiceps</i>	0.75193 2	0.34981 5	1	0.12842 5	100	3	Felidae
<i>Prionailurus rubiginosus</i>	0.77443 3	0.44923 6	1	0.14432 9	100	3	Felidae
<i>Prionailurus viverrinus</i>	0.76886 3	0.46159 8	1	0.13566 1	80	3	Felidae
<i>Prionodon linsang</i>	0.6281	0.35400 2	0.73947 1	0.10292 5	70	3	Prionodontidae
<i>Prionodon pardicolor</i>	0.70536 5	0.39311 9	0.77266 1	0.10606 3	70	3	Prionodontidae
<i>Procyon cancrivorus</i>	0.81627 9	0.75597 4	0.56880 5	0.07588 5	30	1	Procyonidae
<i>Procyon lotor</i>	0.73123 4	0.67924 3	0.57708 5	0.07438 4	20	1	Procyonidae
<i>Pseudalopex</i>	0.66431	0.40767	0.67306	0.09345	80	3	Canidae

<i>culpaeus</i>	6	5	5				
<i>Pseudalopex fulvipes</i>	0.60407 2	0.44854 8	0.62969 3	0.09501 1	60	2	Canidae
<i>Pseudalopex griseus</i>	0.66291 3	0.39103 9	0.64165 3	0.10007 1	60	2	Canidae
<i>Pseudalopex gymnocercus</i>	0.63880 5	0.40692 2	0.63459 9	0.09649 1	50	2	Canidae
<i>Pseudalopex sechurae</i>	0.65726 2	0.47037 3	0.62018 2	0.08393 3	60	2	Canidae
<i>Pseudalopex vetulus</i>	0.71278 8	0.50764 5	0.63281 3	0.08457 3	60	2	Canidae
<i>Puma concolor</i>	0.82354 3	0.48746 8	1	0.13520 3	100	3	Felidae
<i>Puma yaguarondi</i>	0.77382 5	0.47649 4	1	0.14714 5	80	3	Felidae
<i>Rhynchogale melleri</i>	0.87628	0.58857 4	0.53478 5	0.05118 4	30	1	Herpestidae
<i>Salanoia concolor</i>	0.66319 6	0.51300 6	0.57352	0.08124 5	30	1	Eupleridae
<i>Speothos venaticus</i>	0.70441 9	0.52094 3	0.74695	0.10685 1	100	3	Canidae
<i>Suricata suricatta</i>	0.70286 3	0.63987 9	0.70184 2	0.08038 5	20	1	Herpestidae

<i>Urocyon cinereoargenteus</i>	0.65778 2	0.47745 9	0.63150 9	0.08830 7	30	1	Canidae
<i>Urocyon littoralis</i>	0.65270 1	0.46811 1	0.62808 6	0.09530 4	30	1	Canidae
<i>Viverra megaspila</i>	0.66866 3	0.42413 8	0.60889 2	0.08615 4	70	3	Viverridae
<i>Viverra tangalunga</i>	0.67364 8	0.45058 1	0.59888 6	0.08093 3	70	3	Viverridae
<i>Viverra zibetha</i>	0.70795 7	0.49263	0.56774 6	0.08149 2	80	3	Viverridae
<i>Viverricula indica</i>	0.78034 9	0.41796 1	0.57179 7	0.07149 8	60	2	Viverridae
<i>Vulpes chama</i>	0.68879 9	0.45126 8	0.62393 1	0.08838 2	70	3	Canidae
<i>Vulpes ferrilata</i>	0.69365 1	0.45923 6	0.69462 2	0.10508 5	100	3	Canidae
<i>Vulpes lagopus</i>	0.63524 4	0.44493	0.70144 9	0.10541 8	90	3	Canidae
<i>Vulpes rueppelli</i>	0.63766 9	0.42088 3	0.65720 5	0.09894 2	60	2	Canidae
<i>Vulpes velox</i>	0.66293 4	0.37019	0.67880 7	0.09655 1	90	3	Canidae
<i>Vulpes vulpes</i>	0.64426	0.40331	0.67798	0.09955	70	3	Canidae

	5	8	3	3			
<i>Vulpes zerda</i>	0.67714	0.39484	0.60908	0.09014	50	2	Canidae
	8	7	8				

Table 2. Extinct taxa with associated averages of ecomorphological metrics.

Species	C1	P4S	RBL	M1BS
<i>Adcrocuta eximia</i>	0.747188	0.588566	0.835985	0.112602
<i>Afrosmilus africanus</i>	0.406736	0.489209	NA	NA
<i>Afrosmilus hispanicus</i>	0.513333	NA	0.983271	NA
<i>Afrosmilus turkanae</i>	NA	NA	0.969421	NA
<i>Albanosmilus jourdani</i>	0.373684	0.433526	1	0.167953
<i>Albanosmilus whitfordi</i>	0.386364	0.444976	1	0.171829
<i>Allohyaena kadici</i>	NA	0.571292	0.830248	NA
<i>Amphimachairodus giganteus</i>	0.396489	0.461898	0.935223	0.113028
<i>Barbourofelis fricki</i>	0.157042	0.497861	1	0.133913
<i>Barbourofelis loveorum</i>	NA	0.427078	1	0.176374
<i>Barbourofelis morrisoni</i>	0.355795	0.447192	1	0.167111
<i>Belbus beaumonti</i>	NA	0.525	0.75261	0.118533
<i>Chasmaporthetes lunensis</i>	0.750759	0.492451	0.83533	0.10658
<i>Chasmaporthetes ossifragus</i>	0.897561	0.399386	0.899157	0.126683

<i>Crocuta crocuta spelaea</i>	0.724907	0.618027	0.910248	0.134365
<i>Dinaelurus crassus</i>	0.709677	NA	NA	NA
<i>Dinailurictis bonali</i>	0.563907	0.428571	0.812039	NA
<i>Dinictis felina</i>	0.551178	0.455047	0.826374	0.120949
<i>Dinocrocuta gigantea</i>	0.842105	0.56474	0.860564	0.120973
<i>Dinofelis diastemata</i>	0.650263	0.470874	0.955863	0.14701
<i>Eofelis edwardsii</i>	0.666667	0.443872	0.820345	0.143968
<i>Euboictis aliverensis</i>	NA	0.772059	NA	NA
<i>Ginsburgmilus napakensis</i>	0.583333	0.59434	1	NA
<i>Herpestides antiquus</i>	0.767521	0.458333	0.678161	0.073861
<i>Homotherium ischyryus</i>	0.366998	0.44666	0.966745	NA
<i>Homotherium latidens</i>	0.416956	0.458315	1	0.1394
<i>Homotherium serum</i>	0.460004	0.432468	1	0.14193
<i>Hoplophoneus adelos</i>	NA	0.33574	NA	NA
<i>Hoplophoneus bidentatus</i>	0.487805	0.424895	0.914269	0.145238
<i>Hoplophoneus cerebralis</i>	0.477814	0.500697	0.926823	0.151966
<i>Hoplophoneus dakotensis</i>	0.443933	0.53125	0.929063	0.123486
<i>Hoplophoneus occidentalis</i>	0.440957	0.491782	0.950486	0.125868
<i>Hoplophoneus oharrai</i>	0.465559	0.44174	0.907312	0.122276
<i>Hoplophoneus primaevus</i>	0.537219	0.49914	0.906273	0.147058
<i>Hoplophoneus sicarius</i>	0.240255	0.420154	0.955703	0.11689
<i>Hoplophoneus</i>	0.327681	0.436975	0.921053	0.146346

<i>villebramarensis</i>				
<i>Ictitherium viverrinum</i>	0.636882	0.510467	0.673976	0.089825
<i>Izmirictis cani</i>	NA	0.514256	0.617248	NA
<i>Kanuites lewisae</i>	0.729167	NA	0.606173	NA
<i>Kichechia zamanae</i>	0.682927	0.619048	0.63871	NA
<i>Lycyaena chaeretis</i>	0.756263	0.523179	0.769853	0.107619
<i>Machairodus catocopis</i>	0.415963	0.431696	0.904503	0.126069
<i>Machairodus coloradoensis</i>	0.363719	0.401679	0.958988	0.131272
<i>Maofelis cantonensis</i>	0.76506	NA	NA	NA
MA-PHQ 348	0.725038	NA	NA	NA
<i>Megantereon cultridens</i>	0.497118	0.462991	0.974003	0.134235
<i>Metailurus major</i>	0.57248	0.434636	0.904655	0.098354
<i>Miracinonyx trumani</i>	0.816667	0.48125	0.95892	0.125692
<i>Nanosmilus kurteni</i>	0.404018	0.474055	0.881467	0.155248
<i>Nimravides pedionomus</i>	0.572538	0.457513	0.938835	0.141835
<i>Nimravus brachyops</i>	0.56505	0.445368	0.830725	0.143222
<i>Nimravus intermedius</i>	0.610619	0.416926	0.848941	NA
<i>Oriensmilus liupanensis</i>	0.445055	0.405316	1	0.191014
<i>Pachycrocuta brevirostris</i>	0.704545	0.651515	0.840678	NA
<i>Palaeoprionodon lamandini</i>	0.658436	NA	0.783824	0.085664
<i>Palhyaena reperta</i>	0.74669	0.633072	0.778208	0.114786

<i>Panthera atrox</i>	0.733222	0.491752	1	0.115471
<i>Panthera leo spelaea</i>	0.719254	0.477838	1	0.116486
<i>Percrocuta algeriensis</i>	NA	0.57193	0.831716	NA
<i>Percrocuta carnifex</i>	NA	0.573709	0.89735	NA
<i>Percrocuta tobieni</i>	NA	0.574713	0.838384	0.119752
<i>Plioviverrops orbigny</i>	0.669246	0.472991	0.674444	0.076506
<i>Pogonodon davisi</i>	0.569334	0.599482	0.840437	0.119177
<i>Pogonodon platycopis</i>	0.556972	0.617188	0.838545	0.114899
<i>Proailurus lemanensis</i>	0.671711	0.458333	0.887452	0.122739
<i>Promegantereon ogygia</i>	0.59299	0.447216	0.930521	0.128398
<i>Prosansanosmilus eggeri</i>	NA	0.522124	0.96875	NA
<i>Prosansanosmilus peregrinus</i>	0.467199	0.375	0.95241	0.114234
<i>Protictitherium crassum</i>	0.591837	0.468531	0.419863	0.059764
<i>Pseudaelurus validus</i>	0.704031	0.491611	0.858555	0.119611
<i>Quercylurus major</i>	NA	NA	NA	NA
<i>Sansanosmilus palmidens</i>	0.460606	0.412776	1	0.180789
<i>Sivanasua viverroides</i>	0.655518	0.680128	0.693564	NA
<i>Smilodon fatalis</i>	0.4905	0.483591	1	0.136957
<i>Smilodon populator</i>	0.463153	0.451665	1	0.136113
<i>Stenogale julieni</i>	NA	0.471074	0.831325	NA
<i>Tapocyon robustus</i>	0.598083	0.47106	0.695688	0.065691
<i>Thalassictis hyaenoides</i>	0.741935	0.502005	0.737882	0.101481

<i>Thalassictis wongii</i>	0.601575	0.484962	0.727808	0.102206
<i>Tongxinictis primordialis</i>	0.683761	0.552486	NA	NA
<i>Tungurictis spocki</i>	0.454198	0.463883	0.707547	NA
<i>Xenosmilus hodsonae</i>	0.525	0.510823	1	0.160784

Table 3. Dietary classification of *Percrocuta* species using the canonical variates analysis of Coca-Ortega and Pérez-Claros (2019). Diet category 3 = Fully developed bone cracker.

	Die t	Civet- like	cursorial_ meat	Full_b one	Jackal/wolf -like	Mongoose- like	Trans_b one
<i>Percrocuta carnifex</i>	3	3.62E- 07	3.34E-09	0.9244 57	1.23E-05	2.82E-06	0.07552 8
<i>Percrocuta algeriensis</i>	3	7.68E- 24	0.045511	0.9544 89	1.96E-14	1.79E-30	1.08E- 08
<i>Percrocuta tobieni</i>	3	0.0007 97	1.88E-10	0.9933 24	0.001611	8.33E-11	0.00426 8

Table 4. Dietary classification of extinct non-durophagous and questionable sabertooth taxa based on dentognathic variables in canonical variates analysis. Diet: 1 = hypocarnivorous; 2 = mesocarnivorous; 3 = hypercarnivorous.

	diet	P.hypo	P.meso	P.hyper	P.saber
<i>Belbus beaumonti</i>	3	0.070803	0.244877	0.531351	0.152969
<i>Chasmaporthetes lunensis</i>	3	0.058428	0.065953	0.87559	2.93E-05
<i>Chasmaporthetes ossifragus</i>	3	0.001783	0.008813	0.989404	3.78E-08
<i>Dinaelurus crassus</i>	3	0.312037	0.187957	0.497663	0.002343
<i>Dinofelis diastemata</i>	3	0.001254	0.012282	0.915439	0.071025
<i>Euboictis aliverensis</i>	1	0.922125	0.059729	0.010637	0.007509
<i>Herpestides antiquus</i>	1	0.426162	0.221477	0.352361	2.29E-07
<i>Ictitherium viverrinum</i>	2	0.340978	0.404937	0.253603	0.000481
<i>Izmirictis cani</i>	1	0.477878	0.406266	0.105721	0.010136
<i>Kanuites lewisae</i>	1	0.580569	0.326893	0.092534	4.08E-06
<i>Kichechia zamanae</i>	1	0.72625	0.238773	0.03492	5.75E-05
<i>Lycyaena chaeretis</i>	3	0.132535	0.193906	0.673541	1.86E-05
<i>Maofelis cantonensis</i>	3	0.276446	0.155494	0.567772	0.000289
MA-PHQ 348	3	0.302467	0.178764	0.517454	0.001314
<i>Metailurus major</i>	3	0.022531	0.01939	0.869325	0.088753
<i>Miracinonyx trumani</i>	3	0.004811	0.007994	0.987188	6.45E-06
<i>Palaeoprionodon lamandini</i>	3	0.122438	0.145578	0.72617	0.005814
<i>Panthera atrox</i>	3	0.008033	0.005211	0.986459	0.000297
<i>Panthera leo spelaea</i>	3	0.006048	0.00484	0.988571	0.000542
<i>Plioviverrops orbigny</i>	1	0.434927	0.281416	0.283625	3.23E-05
<i>Proailurus lemanensis</i>	3	0.008773	0.030235	0.957263	0.003729
<i>Promeganteron ogygia</i>	3	0.002953	0.013493	0.760499	0.223055
<i>Protictitherium crassum</i>	2	0.392143	0.599815	0.008037	4.23E-06
<i>Pseudaelurus validus</i>	3	0.022985	0.056354	0.919908	0.000754
<i>Sivanasua viverroides</i>	1	0.795004	0.171522	0.032811	0.000662

<i>Stenogale julieni</i>	3	0.02149	0.050873	0.675502	0.252136
<i>Tapocyon robustus</i>	1	0.588692	0.180363	0.230443	0.000503
<i>Thalassictis hyaenoides</i>	3	0.162663	0.244622	0.5927	1.56E-05
<i>Thalassictis wongii</i>	3	0.133929	0.324479	0.529699	0.011893
<i>Tungurictis spocki</i>	3	0.155341	0.280326	0.513479	0.050853

Table 5. Ecological data used in Chapter III analyses. Diet refers to dietary category, 1 = hypocarnivorous; 2 = mesocarnivorous; 3 = hypercarnivorous; 4 = durophagous; 5 = sabertooth; RBL = relative blade length of the lower m1; g = body mass in grams.

	diet	RBL	log_cuberoot_mass	g
<i>Acinonyx jubatus</i>	3	1	3.610417	50577
<i>Adcrocuta eximia</i>	4	0.835985	3.616675	51535.48
<i>Afrosmilus africanus</i>	5	NA	NA	NA
<i>Afrosmilus hispanicus</i>	5	0.983271	3.480055	34206.27
<i>Afrosmilus turkanae</i>	5	0.969421	3.187158	14206.77
<i>Albanosmilus jourdani</i>	5	1	3.85289	104680.8
<i>Albanosmilus whitfordi</i>	5	1	3.8472	102908.8
<i>Allohyaena kadici</i>	4	0.830248	3.588347	47336.72
<i>Amphimachairodus coloradoensis</i>	5	0.935223	4.121573	234384.7
<i>Amphimachairodus giganteus</i>	5	0.958988	4.150483	255620.7
<i>Arctictis binturong</i>	2	0.5939	3.157543	12999
<i>Atilax paludinosus</i>	2	0.725312	2.729563	3600
<i>Barbourofelis fricki</i>	5	1	4.233938	328342.7
<i>Barbourofelis loveorum</i>	5	1	4.179069	278509.7
<i>Barbourofelis morrиси</i>	5	1	3.977234	152009.9
<i>Bdeogale nigripes</i>	1	0.477484	2.624025	2623
<i>Belbus beaumonti</i>	3	0.75261	3.461368	32341.43
<i>Caracal caracal</i>	3	1	3.129886	11964

<i>Catopuma temminckii</i>	3	1	2.984116	7726
<i>Chasmaporthetes lunensis</i>	3	0.83533	3.454764	31706.94
<i>Chasmaporthetes ossifragus</i>	3	0.899157	3.540839	41048.8
<i>Civettictis civetta</i>	2	0.615087	3.132964	12075
<i>Crocuta crocuta</i>	4	0.916777	3.685577	63369
<i>Crocuta crocuta spelaea</i>	4	0.910248	3.686889	63618.99
<i>Crossarchus obscurus</i>	1	0.484472	2.41355	1395
<i>Cryptoprocta ferox</i>	3	0.804789	3.053016	9500
<i>Cynogale bennettii</i>	2	0.480858	2.784578	4246
<i>Dinaelurus crassus</i>	3	NA	3.521503	38735.41
<i>Dinailurictis bonali</i>	5	0.812039	3.954974	142190.5
<i>Dinictis felina</i>	5	0.826374	3.589415	47488.67
<i>Dinocrocuta gigantea</i>	4	0.860564	4.067907	199530
<i>Dinofelis diastemata</i>	3	0.955863	3.814638	93331.72
<i>Eofelis edwardsii</i>	5	0.820345	3.194692	14531.53
<i>Euboictis aliverensis</i>	1	NA	NA	NA
<i>Eupleres goudotii</i>	1	0.585666	2.641357	2763
<i>Felis lybica</i>	3	1	2.809308	4573
<i>Fossa fossana</i>	1	0.592517	2.508187	1853
<i>Galerella sanguinea</i>	1	0.745567	2.099036	543
<i>Genetta maculata</i>	2	0.721206	2.525195	1950
<i>Ginsburgmilus napakensis</i>	5	1	3.260098	17681.83
<i>Helogale parvula</i>	1	0.442353	1.879452	281
<i>Hemigalus derbyanus</i>	1	0.437407	2.380151	1262
<i>Herpestes edwardsii</i>	3	0.634889	2.391064	1304
<i>Herpestides antiquus</i>	1	0.678161	2.836014	4954.46
<i>Homotherium ischyryus</i>	5	1	4.102459	221322.4
<i>Homotherium latidens</i>	5	1	4.141736	249000
<i>Homotherium serum</i>	5	1	4.050205	189210.5
<i>Hoplophoneus adelos</i>	5	NA	3.87149	110687.8

<i>Hoplophoneus_bidentatus</i>	5	0.914269	3.513513	37817.95
<i>Hoplophoneus_cerebralis</i>	5	0.926823	3.286854	19159.63
<i>Hoplophoneus_dakotensis</i>	5	0.929063	3.85158	104270.1
<i>Hoplophoneus_occidentalis</i>	5	0.950486	3.800259	89391.28
<i>Hoplophoneus_oharraii</i>	5	0.907312	3.668141	60139.55
<i>Hoplophoneus_primaevus</i>	5	0.906273	3.59462	48235.91
<i>Hoplophoneus_sicarius</i>	5	0.955703	3.634071	54296.46
<i>Hoplophoneus_villebramarensis</i>	5	0.921053	3.645912	56259.84
<i>Hyaena_hyaena</i>	4	0.788502	3.488367	35070
<i>Hyaenictitherium_hyaenoides</i>	3	0.737882	3.39525	26522.56
<i>Hyaenotherium_wongii</i>	3	0.727808	3.317363	20996.01
<i>Ichneumia_albicauda</i>	1	0.491228	2.732146	3628
<i>Ictitherium_viverrinum</i>	2	0.673976	3.245832	16941.06
<i>Izmirictis_cani</i>	1	0.617248	2.937566	6719.02
<i>Kanuites_lewisae</i>	1	0.606173	2.793518	4361.422
<i>Kichechia_zamanae</i>	1	0.63871	2.634546	2707.111
<i>Leopardus_pardalis</i>	3	1	3.127537	11880
<i>Lycyaena_chaeretis</i>	3	0.769853	3.426575	29135.83
<i>Lynx_canadensis</i>	3	1	3.059341	9682
MA_PHQ_348	3	NA	2.894135	5898.212
<i>Machairodus_catocopis</i>	5	0.904503	4.120902	233913.7
<i>Maofelis_cantonensis</i>	3	NA	3.576047	45621.75
<i>Megantereon_cultridens</i>	5	0.974003	3.688356	63899.53
<i>Metailurus_major</i>	3	0.904655	3.581296	46345.93
<i>Miracinonyx_trumani</i>	3	0.95892	3.535222	40362.89
<i>Mungos_mungo</i>	1	0.516129	2.379622	1260
<i>Nandinia_binotata</i>	1	0.664097	2.560366	2167
<i>Nanosmilus_kurteni</i>	5	0.881467	3.410991	27805.08
<i>Neofelis_nebulosa</i>	3	1	3.204044	14945
<i>Nimravides_pedionomus</i>	5	0.938835	3.877899	112836.6

<i>Nimravus_brachyops</i>	5	0.830725	3.896134	119181.3
<i>Nimravus_intermedius</i>	5	0.848941	3.759695	79148.88
<i>Oriensmilus_liupanensis</i>	5	0.936422	3.616048	51438.58
<i>Otocolobus_manul</i>	3	1	2.06081	6324.129
<i>Pachycrocuta_brevirostris</i>	4	0.840678	3.869412	110000
<i>Paguma_larvata</i>	1	0.564977	2.78879	4300
<i>Palaeoprionodon_lamandini</i>	3	0.783824	2.68948	3192.12
<i>Palinhyena_reperta</i>	4	0.778208	3.203014	14898.91
<i>Panthera_atrox</i>	3	1	4.088114	212000
<i>Panthera_leo</i>	3	1	3.991429	158623
<i>Panthera_leospelaea</i>	3	1	4.141736	249000
<i>Panthera_pardus</i>	3	1	3.622214	52399
<i>Paradoxurus_hermaphroditus</i>	1	0.596092	2.690302	3200
<i>Percrocuta_algeriensis</i>	4	0.831716	3.627596	53251.82
<i>Percrocuta_carnifex</i>	4	0.89735	3.492805	35540.07
<i>Percrocuta_tobieni</i>	4	0.838384	3.407761	27536.88
<i>Plioviverrops_orbigny</i>	1	0.674444	2.699183	3286.407
<i>Pogonodon_davisi</i>	5	0.840437	3.84183	101264.3
<i>Pogonodon_platycopis</i>	5	0.838545	3.905489	122573.8
<i>Poiana_richardsonii</i>	1	0.779359	2.115212	570
<i>Prionailurus_planiceps</i>	3	1	2.723301	3533
<i>Prionodon_linsang</i>	3	0.739471	2.175986	684
<i>Proailurus_lemanensis</i>	3	0.887452	3.271761	18311.48
<i>Profelis_aurata</i>	3	1	3.110174	11277
<i>Promegantereon_ogygia</i>	3	0.930521	3.585968	47000
<i>Prosansanosmilus_eggeri</i>	5	0.96875	3.198023	14677.45
<i>Prosansanosmilus_peregrinus</i>	5	0.95241	3.508625	37267.45
<i>Proteles_cristata</i>	1	NA	3.001474	8139
<i>Protictitherium_crassum</i>	2	0.419863	2.93761	6719.9
<i>Pseudaelurus_validus</i>	3	0.858555	3.483199	34530.5

<i>Puma concolor</i>	3	1	3.631962	53954
<i>Quercylurus major</i>	5	NA	NA	NA
<i>Rhynchogale melleri</i>	1	0.534785	2.57141	2240
<i>Salanoia concolor</i>	1	0.730315	2.188891	711
<i>Sansanosmilus palmidens</i>	5	1	3.593764	48112.23
<i>Sivanasua viverroides</i>	1	0.693564	2.94273	6823.919
<i>Smilodon fatalis</i>	5	1	4.098942	219000
<i>Smilodon populator</i>	5	1	4.197112	294000
<i>Stenogale julieni</i>	3	0.831325	2.67532	3059.356
<i>Suricata suricata</i>	1	0.701842	2.197225	729
<i>Tapocyon robustus</i>	1	0.695688	3.030226	8872.208
<i>Tongxinictis primordialis</i>	4	NA	3.125784	11817.68
<i>Tungurictis spocki</i>	3	0.707547	2.798452	4426.461
<i>Viverra tangalunga</i>	1	0.598886	2.96744	7349
<i>Viverricula indica</i>	1	0.571797	2.659551	2918
<i>Xenosmilus hodsonae</i>	5	1	4.201001	297450.9

Table 6. Standard error of the mean in continuous variables listed in Table 3.

	RBL	log_cuberoot_mass
<i>Acinonyx jubatus</i>	0	0.0345
<i>Adcrocuta eximia</i>	0.0345	0.0345
<i>Afrosmilus africanus</i>	NA	NA
<i>Afrosmilus hispanicus</i>	0.0345	0.0345
<i>Afrosmilus turkanae</i>	0.0345	0.0345
<i>Albanosmilus jourdani</i>	0	0.0345
<i>Albanosmilus whitfordi</i>	0	0.0345
<i>Allohyaena kadici</i>	0.0345	0.0345
<i>Amphimachairodus coloradoensis</i>	0.0345	0.0345
<i>Amphimachairodus giganteus</i>	0.0345	0.0345

<i>Arctictis binturong</i>	0.013861	0.0345
<i>Atilax paludinosus</i>	0.009469	0.0345
<i>Barbourofelis fricki</i>	0	0.0345
<i>Barbourofelis loveorum</i>	0	0.0345
<i>Barbourofelis morrиси</i>	0	0.0345
<i>Bdeogale nigripes</i>	0.025931	0.0345
<i>Belbus beaumonti</i>	0.0345	0.0345
<i>Caracal caracal</i>	0	0.0345
<i>Catopuma temminckii</i>	0	0.0345
<i>Chasmaporthetes lunensis</i>	0.0345	0.0345
<i>Chasmaporthetes ossifragus</i>	0.0345	0.0345
<i>Civettictis civetta</i>	0.010171	0.0345
<i>Crocuta crocuta</i>	0.011597	0.0345
<i>Crocuta crocuta spelaea</i>	0.0345	0.0345
<i>Crossarchus obscurus</i>	0.012224	0.0345
<i>Cryptoprocta ferox</i>	0.011597	0.0345
<i>Cynogale bennettii</i>	0.012966	0.0345
<i>Dinaelurus crassus</i>	NA	0.0345
<i>Dinailurictis bonali</i>	0.0345	0.0345
<i>Dinictis felina</i>	0.004529	0.0345
<i>Dinocrocuta gigantea</i>	0.005321	0.0345
<i>Dinofelis diastemata</i>	0.0345	0.0345
<i>Eofelis edwardsii</i>	0.0345	0.0345
<i>Euboictis aliverensis</i>	NA	NA
<i>Eupleres goudotii</i>	0.013861	0.0345
<i>Felis lybica</i>	0	0.0345
<i>Fossa fossana</i>	0.010586	0.0345
<i>Galerella sanguinea</i>	0.009469	0.0345
<i>Genetta maculata</i>	0.007486	0.0345
<i>Ginsburgsmilus napakensis</i>	0	0.0345

<i>Helogale_parvula</i>	0.014971	0.0345
<i>Hemigalus_derbyanus</i>	0.010171	0.0345
<i>Herpestes_edwardsii</i>	0.025931	0.0345
<i>Herpestides_antiquus</i>	0.0345	0.0345
<i>Homotherium_ischyryus</i>	0	0.0345
<i>Homotherium_latidens</i>	0	0.0345
<i>Homotherium_serum</i>	0	0.0345
<i>Hoplophoneus_adelos</i>	NA	0.0345
<i>Hoplophoneus_bidentatus</i>	0.0345	0.0345
<i>Hoplophoneus_cerebralis</i>	0.013624	0.0345
<i>Hoplophoneus_dakotensis</i>	0.0345	0.0345
<i>Hoplophoneus_occidentalis</i>	0.028924	0.0345
<i>Hoplophoneus_oharraii</i>	0.0345	0.0345
<i>Hoplophoneus_primaevus</i>	0.00555	0.0345
<i>Hoplophoneus_sicarius</i>	0.0345	0.0345
<i>Hoplophoneus_villebramarensis</i>	0.0345	0.0345
<i>Hyaena_hyaena</i>	0.011597	0.0345
<i>Hyaenictitherium_hyaenoides</i>	0.0345	0.0345
<i>Hyaenotherium_wongii</i>	0.0345	0.0345
<i>Ichneumia_albicauda</i>	0.009469	0.0345
<i>Ictitherium_viverrinum</i>	0.0345	0.0345
<i>Izmirictis_cani</i>	0.0345	0.0345
<i>Kanuites_lewisae</i>	0.0345	0.0345
<i>Kichechia_zamanae</i>	0.0345	0.0345
<i>Leopardus_pardalis</i>	0	0.0345
<i>Lycyaena_chaereticus</i>	0.0345	0.0345
<i>Lynx_canadensis</i>	0	0.0345
MA_PHQ_348	NA	0.0345
<i>Machairodus_catocopis</i>	0.0345	0.0345
<i>Maofelis_cantonensis</i>	NA	0.0345

<i>Megantereon_cultridens</i>	0.0345	0.0345
<i>Metailurus_major</i>	0.0345	0.0345
<i>Miracinonyx_trumani</i>	0.0345	0.0345
<i>Mungos_mungo</i>	0.009469	0.0345
<i>Nandinia_binotata</i>	0.010586	0.0345
<i>Nanosmilus_kurteni</i>	0.0345	0.0345
<i>Neofelis_nebulosa</i>	0	0.0345
<i>Nimravides_pedionomus</i>	0.0345	0.0345
<i>Nimravus_brachyops</i>	0.008036	0.0345
<i>Nimravus_intermedius</i>	0.0345	0.0345
<i>Oriensmilus_liupanensis</i>	0.0345	0.0345
<i>Otocolobus_manul</i>	0	0.0345
<i>Pachycrocuta_brevirostris</i>	0.0345	0.0345
<i>Paguma_larvata</i>	0.010171	0.0345
<i>Palaeoprionodon_lamandini</i>	0.0345	0.0345
<i>Palinhyena_reperta</i>	0.0345	0.0345
<i>Panthera_atrox</i>	0	0.0345
<i>Panthera_leo</i>	0	0.0345
<i>Panthera_leospelaea</i>	0	0.0345
<i>Panthera_pardus</i>	0	0.0345
<i>Paradoxurus_hermaphroditus</i>	0.014971	0.0345
<i>Percrocuta_algeriensis</i>	0.0345	0.0345
<i>Percrocuta_carnifex</i>	0.008929	0.0345
<i>Percrocuta_tobieni</i>	0.0345	0.0345
<i>Plioviverrops_orbignyi</i>	0.0345	0.0345
<i>Pogonodon_davisi</i>	0.011505	0.0345
<i>Pogonodon_platycopis</i>	0.0345	0.0345
<i>Poiana_richardsonii</i>	0.0345	0.0345
<i>Prionailurus_planiceps</i>	0	0.0345
<i>Prionodon_linsang</i>	0.014971	0.0345

<i>Proailurus_lemanensis</i>	0.0345	0.0345
<i>Profelis_aurata</i>	0	0.0345
<i>Promeganteron_ogygia</i>	0.0345	0.0345
<i>Prosansanosmilus_eggeri</i>	0.0345	0.0345
<i>Prosansanosmilus_peregrinus</i>	0.0345	0.0345
<i>Proteles_cristata</i>	NA	0.0345
<i>Protictitherium_crassum</i>	0.0345	0.0345
<i>Pseudaelurus_validus</i>	0.0345	0.0345
<i>Puma_concolor</i>	0	0.0345
<i>Quercylurus_major</i>	NA	NA
<i>Rhynchogale_melleri</i>	0.018336	0.0345
<i>Salanoia_concolor</i>	0.012224	0.0345
<i>Sansanosmilus_palmidens</i>	0	0.0345
<i>Sivasua_viverroides</i>	0.0345	0.0345
<i>Smilodon_fatalis</i>	0	0.0345
<i>Smilodon_populator</i>	0	0.0345
<i>Stenogale_julieni</i>	0.0345	0.0345
<i>Suricata_suricata</i>	0.012966	0.0345
<i>Tapocyon_robustus</i>	0.0345	0.0345
<i>Tongxinictis_primordialis</i>	NA	0.0345
<i>Tungurictis_spocki</i>	0.0345	0.0345
<i>Viverra_tangalunga</i>	0.0164	0.0345
<i>Viverricula_indica</i>	0.0164	0.0345
<i>Xenosmilus_hodsonae</i>	0	0.0345

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Appendix I

Digitized Specimen List - Subsample

Sample of crania used in the three-dimensional geometric morphometric analyses of Chapter IV. Unless otherwise specified, specimens were digitized via Microscribe with the methodology described in Chapter IV. Specimen number institutional codes are the same as in Appendix C, save CB = Bone Clones, Inc. 9200 Eton Ave. Chatsworth, CA 91311 USA.

Clade	Genus	Species	Specimen #	Male (n)	Female (n)	Unknown sex (n)	Source
Eupleridae	<i>Cryptoprocta</i>	<i>ferox</i>	FMNH 161793, 33950			2	
Eupleridae	<i>Eupleres</i>	<i>goudotii</i>	FMNH 30492; MNHN CG 1962-2105	2			
Eupleridae	<i>Fossa</i>	<i>fossana</i>	FMNH 156648, 85196	1	1		
Eupleridae	<i>Salanoia</i>	<i>concolor</i>	MNHN CG 1866-233, 1962- 2111	1	1		
Felidae	<i>Pseudaelurus</i>	<i>validus</i>	FAM 61834, 61847; FM			3	

			61835				
Felinae	<i>Acinonyx</i>	<i>jubatus</i>	FM 45071; FMNH 29635, 34589	1		2	
Felinae	<i>Caracal</i>	<i>caracal</i>	FMNH 135042, 32945	1		1	
Felinae	<i>Catopuma</i>	<i>temminckii</i>	MNHN 1939- 2152, 1941-293	1	1		
Felinae	<i>Felis</i>	<i>lybica</i>	FMNH 104579, 97861	1	1		
Felinae	<i>Leopardus</i>	<i>pardalis</i>	FMNH 85503, 88887, 93174	2	1		
Felinae	<i>Lynx</i>	<i>canadensis</i>	FMNH 138821, 145822	1	1		
Felinae	<i>Otocolobus</i>	<i>manul</i>	MNHN CG 2009-251, 2010- 646	1	1		
Felinae	<i>Prionailurus</i>	<i>planiceps</i>	MNHN CG 1873-228			1	
Felinae	<i>Profelis</i>	<i>aurata</i>	MNHN CG 1917-8, 1939- 687	1	1		

Felinae	<i>Puma</i>	<i>concolor</i>	FMNH 28334, 51875	1	1		
Herpestidae	<i>Atilax</i>	<i>paludinosus</i>	MNHN CG 1950-266, 1995- 426	1	1		
Herpestidae	<i>Bdeogale</i>	<i>nigripes</i>	FMNH 8383, 85974	1	1		
Herpestidae	<i>Crossarchus</i>	<i>obscurus</i>	FMNH 4374, 54410	1	1		
Herpestidae	<i>Galerella</i>	<i>sanguinea</i>	MNHN CG 2000-1054, 2000-1072			2	
Herpestidae	<i>Helogale</i>	<i>parvula</i>	MNHN CG 1969-72, 1987- 176	1	1		
Herpestidae	<i>Herpestes</i>	<i>edwardsii</i>	FMNH 83094, 97856	1	1		
Herpestidae	<i>Ichneumia</i>	<i>albicauda</i>	FMNH 73024, 85970	1	1		
Herpestidae	<i>Mungos</i>	<i>mungo</i>	FMNH 149365, 177229	1	1		
Herpestidae	<i>Rhynchogale</i>	<i>melleri</i>	MNHN CG	2			

			1962-1577, 1962-992				
Herpestidae	<i>Suricata</i>	<i>suricata</i>	FMNH 38348, 38349	2			
Hyaenidae	<i>Adcrocuta</i>	<i>eximia</i>	AMNH 22880; China 32-L-255, 41L-339, C-L-6, 80-L613			5	
Hyaenidae	<i>Chasmaporthetes</i>	<i>lunensis</i>	MNCN 67100			1	CT scan (Tseng et al., 2011)
Hyaenidae	<i>Crocuta</i>	<i>crocuta</i>	FMNH 34582, 98952	1	1		
Hyaenidae	<i>Crocuta</i>	<i>crocuta spelaea</i>	MFN MB. Ma 44381, 49139			2	
Hyaenidae	<i>Dinocrocuta</i>	<i>gigantea</i>	IVPP V15649			1	CT scan (Tseng, 2009)
Hyaenidae	<i>Hyaena</i>	<i>hyaena</i>	FMNH 101982, 27008	1	1		
Hyaenidae	<i>Hyaenotherium</i>	<i>wongii</i>	Bx. 71-L665; China (G) L-49, 42-1331, 89-L 746, 95-L789			5	

Hyaenidae	<i>Ictitherium</i>	<i>viverrinum</i>	China 51-L437; FAM 19665			2	
Hyaenidae	<i>Palinhyaena</i>	<i>reperta</i>	FAM 129667, 144897			2	
Hyaenidae	<i>Tungurictis</i>	<i>spocki</i>	AMNH 26600			1	
Machairodontinae	<i>Amphimachairodus</i>	<i>giganteus</i>	FAM 50476			1	
Machairodontinae	<i>Dinofelis</i>	<i>diastemata</i>	FAM 50446			1	
Machairodontinae	<i>Homotherium</i>	<i>ischyrus</i>	AMNH 95297			1	
Machairodontinae	<i>Homotherium</i>	<i>latidens</i>	AMNH 104641 (cast); FAM 50462			2	
Machairodontinae	<i>Homotherium</i>	<i>serum</i>	TMM 933-3444			1	CT scan, DigiMorph
Machairodontinae	<i>Megantereon</i>	<i>cultridens</i>	AMNH 105446 (cast)			1	
Machairodontinae	<i>Metailurus</i>	<i>major</i>	AMNH 131854 (cast)			1	
Machairodontinae	<i>Smilodon</i>	<i>fatalis</i>	LACMHC 2001- 42, 2001-44, 2001-50, 2001- 58, 2001-59, 2001-63, 2001- 82, 2001-83;			10	

			LACMHC R-10688, R-10864				
Nimravidae	<i>Barbourofelis</i>	<i>fricki</i>	AMNH 108193 (cast)			1	
Nimravidae	<i>Barbourofelis</i>	<i>morrisoni</i>	AMNH 61870, 79999			2	
Nimravidae	<i>Dinictis</i>	<i>felina</i>	AMNH 38805, 6937, 8777			3	
Nimravidae	<i>Eusmilus</i>	<i>cerebralis</i>	AMNH 6941; JODA 7047			2	Microscribe and photogrammetry
Nimravidae	<i>Eusmilus</i>	<i>dakotensis</i>	CB 15			1	Photogrammetry, courtesy of D. Tamagnini
Nimravidae	<i>Eusmilus</i>	<i>sicarius</i>	CB 07			1	Photogrammetry, courtesy of D. Tamagnini
Nimravidae	<i>Hoplophoneus</i>	<i>occidentalis</i>	RAM 10356			1	CT scan, courtesy of A. Farke
Nimravidae	<i>Hoplophoneus</i>	<i>primaevus</i>	AMNH 38981, 38982, 9764; FAM 125662			4	

Nimravidae	<i>Nanosmilus</i>	<i>kurteni</i>	AMNH 140559.001 (cast)			1	
Nimravidae	<i>Nimravus</i>	<i>brachyops</i>	AMNH 6930, 6933			2	
Nimravidae	<i>Pogonodon</i>	<i>davisi</i>	AMNH 102156 (cast)			1	
Nimravidae	<i>Pogonodon</i>	<i>platycopis</i>	AMNH 6938			1	
Pantherinae	<i>Neofelis</i>	<i>nebulosa</i>	FMNH 75830, 75831	1		1	
Pantherinae	<i>Panthera</i>	<i>atrox</i>	AMNH 14397; LACMHC 2900- 10, 2900-7, 2900-8, 2900-9; UCMP 14001, 20049			7	
Pantherinae	<i>Panthera</i>	<i>leo</i>	FMNH 20757, 23970 (cast), 35739	3			
Pantherinae	<i>Panthera</i>	<i>leo spelaea</i>	MFN MB. Ma. 48115.1, 50947, 50948			3	

Pantherinae	<i>Panthera</i>	<i>pardus</i>	MNHN 1962-2884; MNHN CG 1996-521	1	1		
Prionodontidae	<i>Prionodon</i>	<i>linsang</i>	FMNH 8371, 88606	1	1		
Stenoplesictidae	<i>Proailurus</i>	<i>lemanensis</i>	AMNH 101931 (cast)			1	
Stenoplesictidae	<i>Nandinia</i>	<i>binotata</i>	AMNH 2409 C.A; FMNH 55758, 73804	1	1	1	
Viverridae	<i>Arctictis</i>	<i>binturong</i>	AMNH C.A. 1182; FMNH 53744, 53747	1	1	1	
Viverridae	<i>Civettictis</i>	<i>Civetta</i>	FMNH 108174, 27278	1	1		
Viverridae	<i>Cynogale</i>	<i>bennettii</i>	MNHN A-2094; MNHN CG 1962-170			2	
Viverridae	<i>Genetta</i>	<i>maculata</i>	FMNH 17525, 85984	1	1		
Viverridae	<i>Hemigalus</i>	<i>derbyanus</i>	AMNH 9 C.A; FMNH 33465,	1	1	1	

			68717				
Viverridae	<i>Paguma</i>	<i>larvata</i>	MNHN CG 1962-1588, 1988-163	1	1		
Viverridae	<i>Paradoxurus</i>	<i>hermaphroditus</i>	FMNH 338000, 39345	1	1		
Viverridae	<i>Poiana</i>	<i>richardsonii</i>	MNHN CG 1976-389			1	
Viverridae	<i>Viverra</i>	<i>tangalunga</i>	FMNH 68704, 85116	1	1		
Viverridae	<i>Viverricula</i>	<i>indica</i>	MNHN CG 1932-3552	1			

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