

Hyainailourine and teratodontine cranial material from the late Eocene of Egypt and the application of parsimony and Bayesian methods to the phylogeny and biogeography of Hyaenodontida (Placentalia, Mammalia) (#10831)

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Hyainailourine and teratodontine cranial material from the late Eocene of Egypt and the application of parsimony and Bayesian methods to the phylogeny and biogeography of Hyaeodontida (Placentalia, Mammalia)

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Hyaenodontida is a diverse, extinct group of carnivorous mammals that included weasel- to rhinoceros-sized species. The oldest-known hyaenodontidan fossils are from the middle Paleocene of North Africa and the antiquity of the group in Afro-Arabia lead to the hypothesis that it originated there and dispersed to Asia, Europe, and North America. Here we describe two new hyaenodontidan species based on the oldest hyaenodontidan cranial specimens known from Afro-Arabia. The material was collected from the latest Eocene Locality 41 (L-41, ~34 Ma) in the Fayum Depression, Egypt. *Akhnatenavus nefertiticyon* sp. nov. has specialized, hypercarnivorous dentition and an elongate cranial vault. In *A. nefertiticyon* the tallest piercing cusp on M¹-M² is the paracone. *Brychotherium ephalmos* gen. et sp. nov. has more generalized dentition that retains a metaconid and complex talonid on M₁-M₃. In *B. ephalmos* the tallest piercing cusp on M¹-M² is the metacone. We incorporate this new material into a series of phylogenetic analyses using a character-taxon matrix that includes novel dental, cranial, and postcranial characters, and samples extensively from the global record of the group. The phylogenetic analysis includes the first application of Bayesian methods to hyaenodontidan relationships. *B. ephalmos* is consistently placed close to members of Teratodontinae, an Afro-Arabian clade with several generalist and hypercarnivorous forms. *Akhnatenavus* is consistently recovered in Hyainailourinae as part of an Afro-Arabian radiation. The phylogenetic results suggest that hypercarnivory evolved independently three times within Hyaenodontida: in Teratodontinae, in Hyainailourinae, and in Hyaenodontinae. Teratodontines are consistently placed in a close relationship with Hyainailouridae (Hyainailourinae + Apterodontinae) to the exclusion of “proviverrines,” hyaenodontines, and several basal North American clades, and we propose that the superfamily Hyainailouroidea be used to

describe this relationship. Using the topologies recovered from each phylogenetic method, we reconstructed the biogeographic history of Hyaenodontida using parsimony optimization, likelihood optimization, and Bayesian Binary MCMC to examine support for the Afro-Arabian origin of Hyaenodontida. Across all analyses, we found that Hyaenodontida originated on northern continents (Europe or North America), rather than Afro-Arabia. The clade is estimated by tip-dating analysis (given a ~K-Pg boundary prior on root age) to have undergone a rapid radiation in the Paleocene; a radiation currently not documented by fossil evidence. During the Paleocene lineages are reconstructed as dispersing to Asia, Afro-Arabia, and either Europe or North America. The place of origin of Hyainailouroidea is ambiguous but at least three of the constituent clades — Hyainailourinae, Apterodontinae, and Teratodontinae — are estimated by tip-dating to be established in Afro-Arabia by the middle Eocene.

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ABSTRACT

Hyaenodontida is a diverse, extinct group of carnivorous mammals that included weasel- to rhinoceros-sized species. The oldest-known hyaenodontidan fossils are from the middle Paleocene of North Africa and the antiquity of the group in Afro-Arabia lead to the hypothesis that it originated there and dispersed to Asia, Europe, and North America. Here we describe two new hyaenodontidan species based on the oldest hyaenodontidan cranial specimens known from Afro-Arabia. The material was collected from the latest Eocene Locality 41 (L-41, ~34 Ma) in the Fayum Depression, Egypt. *Akhnatenavus nefertiticyon* sp. nov. has specialized, hypercarnivorous dentition and an elongate cranial vault. In *A. nefertiticyon* the tallest, piercing cusp on M¹–M² is the paracone. *Brychotherium ephalmos* gen. et sp. nov. has more generalized dentition that retain the metacone and complex talonids on M₁–M₃. In *B. ephalmos* the tallest, piercing cusp on M¹–M² is the metacone. We incorporate this new material into a series of phylogenetic analyses using a character-taxon matrix that includes novel dental, cranial, and postcranial characters, and samples extensively from the global record of the group. The phylogenetic analysis includes the first application of Bayesian methods to hyaenodontidan relationships. *B. ephalmos* is consistently placed close to members of Teratodontinae, an Afro-Arabian clade with several generalist and hypercarnivorous forms, and *Akhnatenavus* is consistently recovered in Hyainailourinae as part of an Afro-Arabian radiation. The phylogenetic results suggest that hypercarnivory evolved independently three times within Hyaenodontida: in Teratodontinae, in Hyainailourinae, and in Hyaenodontinae. Teratodontines are consistently placed in a close relationship with Hyainailouridae (Hyainailourinae + Apterodontinae) to the exclusion of “proviverrines,” hyaenodontines, and several basal North American clades, and we propose that the superfamily Hyainailouroidea be used to describe this relationship. Using the

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INTRODUCTION

Hyaenodontida is an extinct clade of carnivorous mammals whose members were broadly distributed across Europe, North America, Asia, and Afro-Arabia during the Paleogene (Rose, 2006). In Eurasia and Afro-Arabia, some hyaenodontidan lineages persisted into the Miocene (Lewis & Morlo, 2010). Hyaenodontidans ranged in body mass from small weasel-sized species like North American *Thinocyon* (Gunnell, 1998) and European *Eoproviverra* (Godinot, 1981) to gigantic, bear-sized species like North American *Hemipsalodon* (Mellet, 1969) and Afro-Arabian *Megistotherium* (Savage, 1973). In Europe, Asia, and North America, hyaenodontidans shared carnivorous niche space with species from Carnivoramorpha, Mesonychia, and Oxyaenida (Morlo, Gunnell & Nagel, 2010), but in Afro-Arabia, a continent that was largely isolated from all others from the Albian (Early Cretaceous, ~100 Ma, Gaina et al., 2013) to the Miocene (~16 Ma, Partridge, 2010), terrestrial carnivore niches were occupied almost exclusively by Hyaenodontida (Lewis & Morlo, 2010).

Historically, the first hyaenodontidans recovered from Afro-Arabia were found in the early Oligocene beds of the Fayum Depression, Egypt, and were placed in genera known from Europe (*Apterodon*, *Pterodon*, and *Hyaenodon*) and North America (*Sinopa*) thereby implicitly linking hyaenodontidans from the northern continents to the Fayum fauna (Andrews, 1904, 1906). The dominant phylogenetic hypothesis at the time (Matthew, 1901; Matthew, 1906; Matthew, 1915) placed *Pterodon* and *Hyaenodon* (genera with specialized hypercarnivorous dentitions [Van Valkenburgh, 2007]) in the subfamily Hyaenodontinae, and *Sinopa* in the more generalized Proviverrinae. In this taxonomic arrangement, proviverrines were distinguished from other hyaenodontidans by their retention of prominent metaconids on the lower molars and separated paracones and metacones on the upper molars; Proviverrinae was therefore seen as the

generalized “stock” that gave rise to the more specialized hyaenodontines, which were derived in having lost lower molar metaconids, and having fused the paracone and metacone on the upper molars. Schlosser (1911) built on this phylogenetic framework in his analysis of the Fayum hyaenodontidans, arguing for a North American origin of hyaenodontidans from a *Sinopa*-like ancestor, some of which then dispersed to Europe and gave rise to *Pterodon* and *Apterodon*, before members of *Pterodon*, *Apterodon*, and *Sinopa* dispersed to Afro-Arabia from Europe during the late Eocene. This biogeographic hypothesis framed Afro-Arabia as something of a cul-de-sac for hyaenodontidan lineages that evolved during the early and middle Eocene on northern continents.

This scenario had to be reevaluated when Crochet (1988) described *Koholia atlasense*, a hyaenodontidan from the late early Eocene of Algeria that they argued had no obvious links to North American, European, or Asian taxa. By providing evidence for the great antiquity of Hyaenodontida in Afro-Arabia, the presence of *Koholia* complicated the biogeographic history of the clade. The presence of Hyaenodontida in Afro-Arabia was pushed even deeper into time when Gheerbrant et al. (2006) described the early Eocene *Boualitomus marocanensis*, and Solé et al. (2009) described the middle Paleocene (Kocsis et al., 2014) *Lahimia selloumi*, both small-bodied species from Morocco that were hypothesized to be closely related to *Koholia* (Solé et al., 2009). *Lahimia* is the oldest-known hyaenodontidan from any continent, and multiple authors have recently advocated for the Afro-Arabian origin of Hyaenodontida in large part based on the great age of *Lahimia* (Solé, 2013; Morlo et al., 2013; Solé et al., 2014b).

In addition to the discovery of ancient Afro-Arabian hyaenodontidans, the reframing of the biogeographic history of Hyaenodontida has also been spurred by new phylogenetic hypotheses generated by parsimony-based cladistic analyses. Barry (1988) was the first to apply

cladistic methodology to hyaenodontidan systematics. Barry (1988) employed 40 dental characters in his study of the relationships within Proviverrinae, particularly among the Afro-Arabian proviverrines *Masrasector*, *Anasinopa*, *Metasinopa*, and *Dissopsalis*, which were found to be paraphyletic with respect to the proviverrines *Proviverra*, *Cynohyaenodon*, *Prodissopsalis*, *Paracynohyaenodon*, and *Allopterodon*. The results of his analysis implied multiple dispersal events between Europe and Afro-Arabia, and between Asia and Afro-Arabia.

Polly (1996) conducted the first cladistic study that included proviverrines as well as more specialized hyaenodontidans like *Pterodon* and *Hyaenodon* in the same character-taxon matrix. His study was also the first to incorporate cranial and postcranial characters. Polly found Proviverrinae to be paraphyletic, and to include at least two lineages that independently evolved specialized carnivory — Hyaenodontinae, which includes *Hyaenodon*, and Hyainailourinae, which includes *Pterodon*. Importantly, the cranial characters (particularly the construction of the nuchal crest) and postcranial characters (particularly the morphology of the astragalar-calcaneal joints) that he employed provided non-dental support for the hypothesis that hypercarnivory had evolved independently multiple times within Hyaenodontida.

More recent phylogenetic studies have focused on specific lineages within Hyaenodontida — Limnocyoninae (Morlo & Gunnell, 2003), Afro-Arabian and Asian proviverrines (Egi et al., 2005), early North American and European proviverrines (Zack, 2011; 2015), possible relatives of *Apterodon* (Grohé et al., 2012), European proviverrines (Solé, 2013; Solé, Falconnet & Yves, 2014a), and Hyainailourinae (Solé et al., 2015) — but each of these studies was limited in its biogeographic scope, and restricted its character sample to dental morphology. This restriction is understandable because much of the hyaenodontidan record is composed of isolated dentaries, rostral fragments, and isolated teeth, and the inclusion of cranial

and postcranial characters leaves a great deal of missing data, though simulation studies have shown that missing data is less problematic than might be expected (Wiens, 2003; Kearney & Clarke, 2003; Wiens & Moen, 2008; Prevosti & Chemisquy, 2010).

Rana et al. (2015) was the first study that used the cranial and postcranial characters described by Polly (1996) as part of an expanded cladistic analysis, an effort expanded by Zack & Rose (2015) in their study of North American hyaenodontidans. The study of Rana et al. (2015) was the first since that of Polly (1996) to include both *Hyaenodon* and *Pterodon* in the same analysis. Two clades recovered by Rana et al. (2015) are particularly relevant to the present study — Teratodontinae and Hyainailourinae. Teratodontinae is a subfamily that was first proposed by Savage (1965) to accommodate *Teratodon*, a strange early Miocene hyaenodontidan from East Africa with massive premolars. Solé et al. (2014b) found that many Afro-Arabian taxa formally considered to be proviverrines by Barry (1988) and Egi et al. (2005) — including *Masrasecor*, *Anasinopa*, and *Dissopsalis* — formed a clade with *Teratodon*. In the topology recovered by Solé, Falconnet & Yves (2014a), Teratodontinae was the sister clade to European Proviverrinae and North American *Arfia*, implying that dispersal had occurred between Afro-Arabia and Europe. Rana et al. (2015) also recovered a monophyletic Teratodontinae, but found that it was more closely related to *Apterodon* and Hyainailourinae, two predominantly Afro-Arabian clades. In Rana et al.’s study, Hyainailourinae (similar to Polly’s Pterodontinae [= Hyainailourinae; Lewis & Morlo, 2010]) groups *Pterodon* species with Miocene *Megistotherium*/*Hyainailouros* and Eocene-Oligocene *Akhnatenuvus* in an unresolved polytomy. Hyainailourinae is a cosmopolitan clade that was closely examined by Solé et al. (2015) that includes North American *Hemipsalodon*, several European forms (*Paroxyaena*, *Kerberos*, and *Pterodon dasyuroides*), Afro-Arabian “*Pterodon*” *africanus* and *Akhnatenuvus*, and possibly

Asian *Orienspterodon* (Egi, Tsubamoto & Takai, 2007). Rana et al. (2015) constructed the first character-taxon matrix since that of Polly (1996) that employed cranial characters, though Hyainailourinae was part of a polytomy with European *Oxyaenoides*, Afro-Arabian *Koholia*, and Afro-Arabian *Metapterodon*. Solé et al. (2015) proposed additional cranial features that distinguish Hyainailourinae from Hyaenodontinae, but these features were not incorporated into the Solé et al. (2015) phylogenetic analysis.

Here we describe several hyaenodontidan fossils from the latest Eocene of Egypt that bear on the content, interrelationships, and biogeography of Teratodontinae and Hyainailourinae, as well as Hyaenodontida generally. A new teratodontine genus and species is represented by two rostra and well-preserved mandibular remains, while a new hyainailourine species is represented by a largely complete, but crushed, crania. Both are known from sufficient dental material to facilitate estimations of body mass based on regression equations used by Van Valkenburgh (1990) and Morlo (1999). To place these species into phylogenetic context, we employed a character taxon matrix that includes 134 morphological characters and 76 taxa that builds upon previous analyses of hyaenodontidan systematic efforts. This matrix was analyzed using parsimony and Bayesian approaches.

As part of the Bayesian analysis, we employ a recently developed expansion of Bayesian phylogenetic inference that has been called “tip-dating” (Pyron, 2011; Ronquist et al., 2012b; Beck & Lee, 2014). In standard Bayesian phylogenetic inference, a posterior distribution of unique topologies with different branch lengths is generated using Markov chain Monte Carlo (MCMC) sampling, taking into account the data (character-taxon matrix), a model of evolution (for morphology typically the M_k model [Lewis, 2001]), and a parameter for evolutionary rate (Huelsenbeck et al., 2002, Archibald, Mort & Crawford, 2003). Clades are sampled by the

MCMC process in proportion to their posterior probabilities. Tip-dating is a logical extension of standard Bayesian inference that more realistically constrains rates of evolution across the tree by taking into account the actual ages of fossil taxa (Beck & Lee, 2014; Arcila et al., 2015); therefore, tip-dating provides additional information that contributes to the comparative likelihood of the branch-length-scaled topologies, and it can also be used to estimate divergence times among living and extinct taxa. This method has recently been applied to phylogenetic analysis of several clades (Schrager, Mello & Soares, 2013; Wood et al., 2013; Beck & Lee, 2014; Lee et al., 2014; Dembo et al., 2015; Arcila et al., 2015; Close et al., 2015; Sallam & Seiffert, 2016; Gorscak & O'Connor, 2016) and is applied here for the first time to hyaenodontidan systematics.

A Note on the taxonomic terms “Creodonta” and Hyaenodontida

Hyaenodontida is discussed in this study as an elevation of the clade Hyaenodontidae, which has traditionally been nested within Creodonta along with another extinct family, Oxyaenidae (e.g., Matthew, 1915; Gunnell, 1998; Rose, 2006). Creodonta is then traditionally considered sister clade to Carnivoramorpha in the larger clade Ferae (McKenna & Bell, 1997; Wesley-Hunt & Flynn, 2005; Spaulding & Flynn, 2012; Halliday, Upchurch & Goswami, 2015). Cope (1875) originally defined Creodonta and modified its definition through time, eventually determining that the Creodonta was part of Insectivora and that Insectivora also included Miacidae, Mesonychidae, Chrysochloridae, Centetidae, Talpidae, Mythomyidae, Oxyaenidae, and Hyaenodontidae (Cope, 1884). With additional fossil, osteological, and eventually genetic information, each of these families was moved to other orders and clades (Miacidae to Carnivoramorpha [Spaulding & Flynn, 2012]; Mesonychidae as a sister group of artiodactyls and

perissodactyls [Spaulding, O’Leary & Gatesy, 2009]; “Centetidae” and “Mythomyidae” [tenrecs] and Chrysochloridae to Afrosoricida, and Talpidae to Eulipotyphla or Lipotyphla [Stanhope et al., 1998]) except Oxyaenidae and Hyaenodontidae, which have been retained as members of Creodonta by Gunnell & Gingerich (1991) and Gunnell, (1998).

Multiple authors, first Van Valen (1966) then later Polly (1996), raised the possibility that Oxyaenidae and Hyaenodontidae are not sister taxa and that Creodonta is not a clade. This suggestion has been adopted in many recent studies (Grohé et al., 2012; Morlo et al., 2013; Solé et al., 2014b), but there has been little discussion of what the sister taxon of Hyaenodontidae is if not Oxyaenida as a whole or if these groups of mammalian carnivores are each indeed clades. Spaulding, O’Leary & Gatesy (2009), O’Leary et al. (2013), and Halliday, Upchurch & Goswami (2015) each applied cladistic methodology to an examination of large-scale relationships within Placentalia which included representatives of Ferae (Carnivora + Pholidota and possibly Creodonta). Ferae and Creodonta were monophyletic in Spaulding, O’Leary & Gatesy (2009), but their study was focused on the relationships within Cetartiodactyla, rather than Ferae, and only included four species from Creodonta (and did not include Pholidota). O’Leary et al. (2013) also resolved a monophyletic Ferae, but only included one representative from Creodonta, the hyaenodontidan *Sinopa rapax*, thus this large-scale examination of Placentalia did not test for the monophyly of Creodonta. Halliday, Upchurch, & Goswami (2015) focused on Paleocene mammal groups and found a monophyletic Ferae and a monophyletic Creodonta when all topological constraints were applied to the analysis, though their analysis was limited to four North American creodonts: the hyaenodonts *Prolimnocyon* and *Pyrocyon* and the oxyaenidans *Dipsalidictis* and *Tytthaena*.

Recent phylogenetic studies that have examined relationships among non-oxyaenid creodonts have employed the order Hyaenodontida, and named clades (families and subfamilies) that reflect their inclusion in that order (Grohé et al., 2012; Solé, 2013; Solé et al., 2014b; Solé et al., 2015). These studies cite Van Valen (1967) as the source of Hyaenodontida, but Van Valen (1967) actually used the suborder Hyaenodonta, a taxon that he employed to encompass Oxyaenidae, Hyaenodontidae, and Palaeoryctoidea. The name Hyaenodontida in the sense used in the present study was first used by Solé (2013) to encompasses placental mammals with a carnassial complex between P^4 and M_1 , M^1 and M_2 , and M^2 and M_3 that were previously placed in Hyaenodontidae. Future analyses that sample broadly from Oxyaenida, Hyaenodontida, and other placental orders are required to rigorously test the monophyly or polyphyly of Creodonta and the phylogenetic definition of Hyaenodontida; such an analysis is, however, beyond the scope of the current study.

Institutional Abbreviations

AMNH, American Museum of Natural History, New York; **BSPG**, Bayerische Staatssammlung für Paläontologie und Historische Geologie, Munich; **CGM**, Cairo Geological Museum, Cairo; **DPC**, Duke Lemur Center, Division of Fossil Primates, Durham; **KNM**, National Museums of Kenya, Nairobi; **SMNS**, Staatliches Museum für Naturkunde, Stuttgart.

MATERIALS AND METHODS

Geological Context

The material described here was collected from Locality 41 (L-41) in the Fayum Depression, Egypt (Fig. 1). The Fayum area preserves a near-continuous terrestrial record from the early late Eocene through the early Oligocene (Bown & Kraus, 1988). Quarry L-41 is at the top of the lower variegated sequence in the Jebel Qatrani Formation, and is interpreted to have been deposited during a period of reversed magnetic polarity (Kappelman, Simons & Swisher, 1992) that has been correlated with the Eocene-Oligocene spanning Chron C13r (Seiffert, 2006). The latest Priabonian (latest Eocene, ~37 Ma) age of L-41 is supported by the identification of a major erosional unconformity just above L-41 that Seiffert (2006) hypothesized was caused by the major drawdown in global sea level that occurred during the earliest Oligocene (e.g., Miller et al., 2008). The age is also supported by biostratigraphic correlation with well-dated mammal sites in Oman (Seiffert, 2006), and extinctions of multiple strepsirrhine primate lineages upsection from L-41 that might have been due to earliest Oligocene cooling (Seiffert, 2007).

Many of the productive quarries in the Fayum are composed of a poorly consolidated fine- to medium-grained sandstone and gravel that are quarried through aeolian weathering, sweeping, and dry sieving (Bown & Krause, 1988). In contrast, L-41 is a well-consolidated deposit that is dominated by green to yellow clay and postdepositional salt that is quarried in sheets, with fossils exposed by carefully prying apart silt and claystone bedding planes (Simons, Cornero & Bown, 1996). Vertebrate fossils are abundant at L-41 and the fine-grained matrix is capable of preserving small fossils that are delicately prepared from the clay matrix. The larger mammals known from the Fayum fauna, such as anthracotheres and hyraxes (Rasmussen & Simons, 1991) are preserved at L-41, but the quarry is particularly important for preserving the smaller components of the mammalian fauna, such as bats (Gunnell, Seiffert & Simons, 2008), rodents (Sallam, Seiffert & Simons, 2011; Sallam, Seiffert & Simons, 2012; Sallam & Seiffert,

2016), tenrecoids (Seiffert & Simons, 2000; Seiffert et al., 2007) and small primates (Simons, 1990, 1997; Simons & Rasmussen, 1996; Simons et al., 2001). Complete crania, jaws, and isolated skeletal elements are preserved in abundance, though most are crushed through post-depositional taphonomic processes (Simons, Cornero & Bown, 1996). The quarry was likely formed in the distal portion of a large freshwater lake, as suggested by the abundant preservation of freshwater fish fossils. The vertebrate remains are hypothesized to have floated into the lake during periodic flooding events and been buried with little disturbance from flowing water or predation (Simons, Cornero & Bown, 1996).

Taxonomy

The electronic version of this article in Portable Document Format (PDF) will represent a published work according to the International Commission on Zoological Nomenclature (ICZN), and hence the new names contained in the electronic version are effectively published under that Code from the electronic edition alone. This published work and the nomenclatural acts it contains have been registered in ZooBank, the online registration system for the ICZN. The ZooBank LSIDs (Life Sciences Identifiers) can be resolved and the associated information viewed through any standard web browser by appending the LSID to the prefix <http://zoobank.org/>. The LSID for this publication is urn:lsid:zoobank.org:pub:4EB91175-33FF-4A6C-B5B2-2F9933C0DED9. The online version of this work is archived and available from the following digital repositories: PeerJ, PubMed Central and CLOCKSS. The physical specimens described here with a CGM specimen code are deposited at the Cairo Geological Museum, Cairo, Egypt and specimens described here with a DPC specimen code are deposited at the Duke Lemur Center, Division of Fossil Primates, Duke University, Durham, NC.

Morphological Measurements and Nomenclature

Dental measurements of the specimens were collected from digital photographs using ImageJ (Schneider, Rasband & Eliceiri, 2012) or with digital calipers, following the methods of Holroyd (1999). Dental nomenclature and measurements used in this description are illustrated in Fig. 2.

Body mass was calculated using two sets of regression equations. The first is that of Morlo (1999), which predicts body mass based on an average of the mesiodistal lengths of M_1 - M_3 . The second regression equation was proposed by Van Valkenburgh (1990), which is based on the mesiodistal lengths of M_1 in carnivorans. Although carnivorans show clear functional parallels with hyaenodontidans due to their similar diets (Morlo, 1999; Van Valkenburgh, 2007; Friscia & Van Valkenburgh, 2010), their capacity for dental shearing was achieved in a different way, with carnivorans only having one pair of functional carnassials, and hyaenodontidans having three (Rose, 2006). Many hyaenodontidan specimens have heavily worn M_1 s and shearing facets on M_2 and M_3 , which suggests that the distal molars were used in adult hyaenodontidans in the same way that the M_1 carnassial is used by carnivorans; therefore, any results derived from Van Valkenburgh's (1990) equation must be viewed with caution. The Van Valkenburgh (1990) equation was used in three ways, using 1) average mesiodistal molar length, 2) length of M_2 , and 3) length of M_3 . Because the L-41 hyainailourine is only known from upper teeth, M_2 length is inferred from the distance between the postprotocrista of M^2 and the distal aspect of the M^3 protocone.

Specimen scanning

All specimens presented in this analysis were micro-CT scanned on a Nikon XTH 225 ST scanner housed in the Duke MicroCT lab in the Shared Materials Instrumentation Facility in the Pratt School of Engineering at Duke University. All specimens described here are available for viewing and download on MorphoSource, an NSF-supported repository for 3D scan data <www.morphosource.org> in Project P200. Reviewers and editors can access this project before publication by logging on to MorphoSource with the username “morphsourcereviewer@gmail.com” and the password “reviewer.” The voxel size, voltage, and amperage used for each scan are also accessioned in MorphoSource with with PLY files. Three-dimensional surface models were constructed using Avizo 8.0 and are were visualized using volume rendering or isosurface rendering for two-dimensional illustration.

Phylogenetic Analysis

Multiple phylogenetic analyses were conducted to place the two new L-41 hyaenodontidans into a broad phylogenetic framework. These analyses were also intended to test existing hypotheses about relationships among multiple recently proposed hyaenodontidan clades (e.g., Polly, 1996; Egi et al., 2005; Solé, 2013; Solé, Falconnet & Yves, 2014a; Solé et al., 2014b; Solé et al., 2015; Rana et al., 2015) with new character data. Of particular interest for this study are the structure of, and relationships within, Teratodontinae, Hyainailourinae, and Hyaeodontinae, the latter clade having only been incorporated into two other cladistic analyses (Polly, 1996; Rana et al., 2015) with an in-group expanded beyond *Hyaenodon* (note that Bastl, Nagel & Peigné, [2014] limited their analysis to evaluation of the genus *Hyaenodon*). The character taxon matrix used in this study includes 134 discrete dental, cranial, and postcranial characters and 76 operational taxonomic units (OTUs — 4 outgroup taxa and 72

hyaenodontidans). For this study three basal eutherian taxa — Early Cretaceous *Eomaia scansoria* from China (Ji et al., 2002), Late Cretaceous *Maelestes gobiensis* from Mongolia (Wible et al., 2007, 2009), and Late Cretaceous *Cimolestes magnus* from North America (Lillegraven, 1969; Kielan-Jaworowska, Cifelli & Luo, 2004) — were included as outgroups for each analysis. This follows the outgroup selection used in previous phylogenetic analyses of Hyainodontida (Polly, 1996; Zack, 2011; Zack, 2015; Solé et al., 2014b; Rana et al., 2015; Zack & Rose, 2015). Species level OTUs were used for all taxa except *Teratodon* and *Lesmesodon* which were a composite of specimens referred to these genera.

Some of the characters used in this analysis were sampled from previous studies including those of Polly (1996), Egi et al. (2005), Zack (2011), and Solé et al. (2014b). Some of these characters were modified by concatenating similar characters and anatomical terminology was modified to make the character descriptions consistent. Characters were expanded with additional character states and 65 new characters are described, some initially proposed as “features” in Solé et al. (2015). Inapplicable characters were reductively coded (Strong & Lipscomb, 1999). Eighteen multistate characters were treated as ordered following the recommendations of Slowinski (1993) in designating these characters and all characters were equally weighted. All characters are listed in Table S1 with relevant citations, and ordered characters are noted. All OTUs were rescored for each character in the analysis. Codings for each taxon are provided in Data S1 and references, including age, formation, and locality, are listed in Table S2. Character descriptions, nexus files, and photographs of the specimens described in this study are also available on Morphobank (Project 2336) <www.morphobank.org> and are accessible to editors and reviewers with the reviewer login password “fayumreviewer.”

Parsimony Analysis—Maximum parsimony analysis was performed in Tree Analysis using New Technology software package (TNT) version 1.1 (Goloboff, Farris & Nixon, 2008). The traditional search heuristic search algorithm was used across 10,000 replicates with random addition sequence and TBR (tree bisection and reconnection) branch swapping, holding 10 trees per TBR replicate. Consistency index (CI) and retention index (RI) values were calculated using STATS.RUN in TNT. Support for each node in the maximum parsimony analysis was calculated by running 10,000 bootstrap pseudoreplicates (Felsenstein, 1985) and Bremer support was calculated for each node (Bremer, 1994) in TNT. Parsimony character optimization across all MPTs was conducted in PAUP 4.0 (Swofford, 2003).

Standard Bayesian Inference—Bayesian phylogenetic inference analysis was performed in MrBayes 3.2.3 (Ronquist et al., 2012a), using the CIPRES Scientific Gateway (Miller, Pfeiffer & Schwartz, 2010). The M_k model (Lewis, 2001) for morphological data was selected and the data type was set to “standard” with coding set to “variable” (Clarke & Middleton, 2008). The analysis was run for 10×10^6 generations. Two runs were performed simultaneously with four Markov chains, three of which were heated ($\text{temp} = 0.02$). A total of 2,000 generations were sampled (every 5000th generation of the 10×10^6 generations, to avoid autocorrelation), the first 500 (25%) of which were discarded as burn-in. After the analysis was run, convergence was examined using the effective sample sizes and average standard deviation of split frequencies for the final generation. The resulting posterior probabilities (PP) for the standard Bayesian analysis are listed to the right of the relevant node in the “allcompat” (majority rule plus compatible groups) tree. Parsimony character optimization for the “allcompat” tree was conducted in PAUP 4.0 (Swofford, 2003). PP values between 0 and 0.25

will be discussed as “very weakly supported,” between 0.26 and 0.50 “weakly supported,” between 0.51 and 0.75 “moderately supported,” and between 0.76 and 1.00 “strongly supported.”

Bayesian “Tip-Dating”—Bayesian “tip-dating” takes into account the relationships between morphological character evolution and the temporal succession of fossil taxa to simultaneously infer rates of morphological evolution and phylogenetic relationships. The reconstructed evolutionary rates are taken into account in estimates of phylogenetic relationships, and divergence dates between all included taxa are estimated (Ronquist et al., 2012b; Lee et al., 2014). Note that this method does not operate directly upon a continuous temporal character as is utilized in stratocladistic methods. Instead, the inferred branch length from the Bayesian phylogenetic inference is divided by the tip-age to generate an implied rate along the branch and estimate divergence dates for branches. Beck & Lee (2014) showed that when a temporal constraint is imposed on an in-group, deeply nested but ancient taxa can be recovered at nodes where rapid evolutionary change is taking place and evolutionary rates are consistent across sister nodes. Tip-dating is an interesting alternative to parsimony analysis or standard Bayesian inference for inferring phylogenetic relationships among members of “explosive” adaptive radiations, such as those which are thought to have taken place in the placental mammalian lineage near the K-Pg extinction event (O’Leary et al., 2013). Rapid radiations might be expected to pose problems for parsimony analysis in particular, because rapid evolutionary change near the base of a radiation might be overwritten by subsequent evolution along long branches (Felsenstein, 1978) as lineages invade open niche space. Tip-dating seems especially appropriate for Hyaenodontida, given the variable phylogenetic positions occupied by the oldest Afro-Arabian hyaenodontidans *Lahimia*, *Boualitomus*, and *Tinerhodon* in the analysis by Rana et al. (2015). These taxa were recovered deeply nested within Hyainailourinae in some MPTs and

in very basal positions in other MPTs, a result consistent with early phylogenetic experiments performed with this data set using only dental characters.

The tip-dating analysis presented here was run in MrBayes 3.2.3 (Ronquist et al., 2012a) following methods employed by Beck & Lee (2014). The M_k model was used to model morphological character change and the independent gamma rates (IGR) relaxed clock model (Lepage et al., 2007; Ronquist et al., 2012b), which assumes no autocorrelation of rates in the phylogeny, was used to infer divergence ages from terminal taxa and reconstruct rates of morphological evolution. Tip-dating requires specific dates for each terminal taxon. Each OTU, with citations justifying its assigned date range, are listed in Table S2, from the oldest taxon in the analysis (*Eomaia*, 129.7–122.1 Ma) to the youngest (*Dissopsalis*, 15–9 Ma). The root of the tree was set with a prior of 120–130 Ma (Wible et al., 2009; O’Leary et al., 2013). Beck & Lee (2014) demonstrated that, in the case of placental mammalian supraordinal phylogeny, node ages tend to be reconstructed as particularly ancient and in extreme conflict with the fossil record if an in-group constraint is not applied. The prior for the divergence date of Hyaenodontida was set conservatively to be between 62 and 70 Ma, bracketing before and after the K/Pg boundary by four million. This prior is also consistent with the estimated divergence date for Ferae, 63.8 Ma, a divergence proposed by O’Leary et al. (2013). The analysis was run for 50×10^6 generations. Shorter runs with 10×10^6 generations, the number of generations used in the standard Bayesian analysis, had very low or inconsistent convergence parameters. Even with the greater number of generations, convergence diagnostics remain low in this analysis (ESS 0.014). The priors that produced the strongest convergence across all parameters was $\text{clockratepr} = \text{normal}(0.01, 0.007)$, and $\text{igrvarpr} = \text{exp}(3)$. Two runs were performed simultaneously with four Markov chains, three of which were heated ($\text{temp} = 0.02$). A total of 10,000 generations were sampled, the first 25%

of which were discarded as burn-in. The “allcompat” tree that results from the analysis includes evolutionary rate estimates for each branch. Beck & Lee (2014:3) noted that rate estimates tend to have “strongly positively skewed distributions” and they advocated for the use of the median evolutionary rate rather than the mean evolutionary rate in discussions of branch evolution. Relative rates for each node are calculated by comparing the % change/Ma for a given node to the % change/Ma across the entire tree. The same definitions of the relative strength of posterior probability support (PP) that were used in the standard Bayesian analysis, will be used to discuss the results of the Bayesian tip-dating analysis.

Biogeographic Methods

Three separate biogeographic methods were applied to the phylogenetic topologies recovered through parsimony analysis (strict consensus trees), standard Bayesian analysis (allcompat tree), and tip-dating Bayesian analysis (allcompat tree). The three biogeographic methods were ancestral state reconstruction using parsimony optimization (PO) (Brooks, 1990), likelihood optimization (LO) (Maddison & Madison, 2015), and Bayesian Binary MCMC (BBM) (Yu et al., 2015). Four continental areas were designated (Afro-Arabia, Asia, Europe, and North America) for each analysis and each OTU was assigned to the continent where it was found (Table S2).

Parsimony optimization of a continental biogeographic character not used in the phylogenetic analysis was implemented in Mesquite (Maddison & Maddison, 2015) using Mesquite’s Parsimony Ancestral States reconstruction. Ambiguous reconstructions are interpreted as equally parsimonious continental reconstructions for the origin of a clade. Likelihood optimization of the continental biogeographic character was also implemented in

Mesquite using the Likelihood Ancestral States reconstruction with the model Mk1 (equally probable state change). Likelihood analysis incorporated branch length information from the standard Bayesian and tip-dating allcompat trees. Branch lengths for the maximum parsimony tree were all equal.

BBM, a statistical method for inferring ancestral states such as biogeographic distributions using Bayesian inference, was performed in RASP version 3.1 (Yu et al., 2015). The number of areas from which a lineage could originate was limited to one to model dispersal rather than vicariance events. Dispersal is a more likely explanation for the distribution of Hyaenodontida during the Late Cretaceous and early Paleogene than vicariance given global paleogeography during this interval. Vicariance would imply an origin for Hyaenodontida that proceeds the break-up of Pangea, which the fossil record does not currently support. The results of the analysis are the probability of a given clade originating from one of four continental areas. The MCMC analysis was performed over 10×10^6 generations with 10 Markov chains, sampling every 100 generations, with the temperature set to 0.1. The first 100 trees were discarded as part of the burn-in period, and the Jukes-Cantor model was used, with equal among-site rate variation.

SYSTEMATIC PALEONTOLOGY

HYAENODONTIDA Solé, 2013

TERATODONTINAE Savage, 1965

BRYCHOTHERIUM Borths, Holroyd, and Seiffert, gen. nov.

urn:lsid:zoobank.org:act:A39C1414-CF72-4FDC-A087-9912FCEDB0C8

Type Species—*Brychotherium ephalmos*, sp. nov.

Etymology—Meaning “greedily eating beast” in Greek from *brycho* (βρύχω) meaning to eat greedily or noisily and *thērion* (θηρίον) meaning beast. The name was first used by Holroyd (1994) in her doctoral dissertation, and was subsequently used as a *nomen nudum* by Egi et al. (2005) and Solé et al. (2014b).

Generic Diagnosis—As for type species.

A Note on the Genus—*Brychotherium* was originally coined and recognized as a distinct genus in a dissertation (Holroyd, 1994), and was therefore not yet validly published under ICZN rules. Subsequent studies (e.g., Egi et al., 2005; Solé et al., 2014b) have used the genus or lumped it into “African *Sinopa* spp.” (e.g., Rana et al., 2015), based solely on the lower dentition. We formally name the taxon here, with a diagnosis that includes the more complete sample now available including rostra and upper dentition. Notably, this formal diagnosis does not include all specimens initially assigned to the genus in Holroyd (1994), as an expansion of the L-41 sample in the last 22 years has further refined the understanding of the similarly-sized hyaenodont fauna at the locality.

BRYCHOTHERIUM EPHALMOS Borths, Holroyd, and Seiffert, sp. nov.

(Figs. 3–9, Table 1–2)

urn:lsid:zoobank.org:act:BCAACF37-E200-4172-A875-C4D5F6FFCEFB

Etymology—Meaning “pickled in salty brine” in Greek from *ephalmos* (ἐφαλμος) in reference to the high post-depositional salt content in the sediments of L-41.

Holotype—CGM 83750, right dentary with canine–M₃.

Referred Specimens—DPC 17627, right dentary with P₄–M₃ and rostrum with canine, dP₄–M₂, and erupting P₄. Specimens were associated and probably represent a single individual;

486 DPC 11990, rostrum with left and right P⁴–M³; DPC 11569A, right dentary with canine, P₂–M₃;
487 DPC 11569B, left dentary with P₂, P₃, M₁–M₃.

488 **Type Locality**—Locality 41 (L-41), Jebel Qatrani Formation, Fayum Depression, Egypt.

489 **Age and Distribution**—Late Eocene, latest Priabonian, ~34 Ma (Seiffert, 2006). Only
490 known from Locality 41, approximately 14.5 km west of Qasr el-Sagha Temple, and 2 km north
491 of the contact between the Qasr el-Sagha Formation and the Jebel Qatrani Formation.

492 **Diagnosis**—Differs from early Oligocene *Masrasector* species by being larger; having
493 relatively narrow talonid basins on the lower molars that taper distally toward the hypoconulids,
494 rather than being buccolingually wide and box-like; having tall lower molar trigonids that are
495 more than twice the height of the talonid, rather than being less than half the height of the
496 trigonid; having relatively small lower molar metaconids, rather than having metaconids that are
497 nearly subequal in height to paraconid; and having preprotocristids and postprotocristids that
498 more closely parallel the long axis of the horizontal ramus, rather than angling steeply lingually.
499 Differs from middle-late Miocene *Dissopsalis* by being smaller; having a pronounced metaconid
500 on M₃ rather than a metaconid that is very reduced or absent; having a larger and more complex
501 M₃ talonid rather than a very reduced M₃ talonid with poorly developed cusps; having
502 preprotocristid and postparacristid oriented somewhat lingually relative to the horizontal ramus
503 rather than being nearly parallel to the long axis of the horizontal ramus; having taller paracones
504 on M¹ and M² that are only slightly shorter than metacones, rather than having reduced
505 paracones that are distinctly shorter than metacones; and having wide upper molar protocones
506 that are more lingually placed relative to paracone, rather than having narrow protocones that are
507 shifted distally relative to the paracones. Differs from early Miocene *Anasinopa* by being
508 smaller; having taller, but mesiodistally short, lower molar trigonids rather than relatively low

509 and long trigonids; having a more buccolingually compressed P₄ rather than a buccolingually
 510 broad P₄; having relatively elongate upper molar metastyles that form a deep and distinct
 511 ectoflexus on M², rather than short metastyles that form a relatively shallow M² ectoflexus;
 512 having more buccolingually compressed paracone and metacone cusps (with elliptical cross-
 513 sections) on the upper molars, rather than having paracone and metacone cusps that are more
 514 connate with rounded cross-sections; and having upper molar paracones that are relatively large,
 515 when compared to the size of the metacone, rather than having paracones that are relatively low
 516 and mesiodistally much shorter than metacones. Differs from early or middle Eocene *Furodon*
 517 by having a relatively short P₄ with a more distinct paraconid; having a P₄ protoconid whose long
 518 axis in buccal view is perpendicular to the alveolar margin, rather than being distally inclined;
 519 having relatively low entocristids, rather than tall entocristids that close the lower molar talonids
 520 lingually, especially on M₃; and having upper molar metacones that are mesiodistally longer and
 521 taller than the paracones. Differs from early or middle Eocene *Glibzegdouia* by having an M₁
 522 metaconid that is shorter than the M₁ paraconid, rather than an M₁ metaconid that is taller than
 523 the M₁ paraconid; having an M₁-M₂ trigonid that is more than twice the height of the talonid,
 524 rather than having an M₁-M₂ trigonid that is low compared to talonid; having M₁-M₂ talonids that
 525 open lingually, rather than closed by a notched entocristid; having indistinct M₁-M₂ entoconids
 526 rather than clear entoconid cusps; having M₁-M₂ trigonids that are buccolingually wider than the
 527 talonids, rather than having M₁-M₂ trigonids that are of the same buccolingual width as the
 528 talonids; and having a shallower M¹ ectoflexus and an elongate metastyle that is of
 529 approximately the mesiodistal length of paracone/metacone base, rather than a deep M¹
 530 ectoflexus with a metastyle that is shorter than the paracone/metacone base. Differs from early
 531 Miocene *Teratodon* by having a P₄ with multiple cusps, rather than a bulbous P₄; having M₁-M₃

trigonids that are more than twice the height of the talonid; having buccolingually narrow upper premolars that are not buccolingually wider than they are mesiodistally long; and having a mesiodistally elongate M² metastyle that parallels the buccal margin, rather than a metastyle that is shorter than the paracone/metacone base that angles lingually from buccal margin.

Description

Rostrum—DPC 11990 (Figs. 3 and 4) is a crushed rostrum referred to *Brychotherium ephalmos*. The specimen preserves most of the anterior part of the cranium, from the premaxilla back to the palatines, along with the left and right P⁴–M³. Like many specimens from L-41, the specimen is crushed and many of the cranial bones are fragmentary, making sutures difficult to interpret. Most of the distortion occurred through mediolateral crushing combined with minor anterior-posterior shear. The left side of the rostrum is better preserved than the right. The rostral remains of DPC 17627 also preserve dP⁴–M³; portions of the lateral and palatal aspects of the left maxilla are relatively undistorted.

The premaxilla preserves the alveoli of I²–I³ and it frames the partially preserved nasal aperture. Though the region is distorted, it is clear that the anterior and posterior borders of the premaxilla incline dorsally and posteriorly and, as such, the nasals were somewhat retracted, leaving the dorsal face of the palatal process of the premaxilla visible in dorsal view. The premaxilla-maxilla suture traces the anterior margin of the canine alveolus. Neither canine is preserved in DPC 11990 but the collapsed alveoli are present and indicate that the root of the canine was wide and arched posteriorly over both roots of P¹ and the anterior root of P². From the nasal aperture, the nasals become broader posteriorly. The nasal does not contact the lacrimal; instead, there is an intervening maxilla-frontal suture. The facial process of the maxilla

is broad, and perforated by the infraorbital foramen dorsal to the anterior root of P³. The maxilla does not contribute to the anterior margin of the orbit; instead the dorsoventrally tall lacrimal has a broad facial process that extends anteriorly at least as far as the distal root of P⁴. A prominent lacrimal tubercle is present on the anterior margin of the orbit, and a wide lacrimal canal is completely contained within the orbit. The anterior margin of the orbit is positioned above the distal root of M¹. The inferior margin of the orbit is formed by the jugal, which has a broad contact with the lacrimal, excluding the maxilla from the orbital margin. The jugal process of the maxilla is preserved along with fragments of the jugal. The zygomatic arch was robust and dorsoventrally deep. The dorsal portion of the orbital margin is formed by the frontal, which contacts the lacrimal dorsal to M¹. No postorbital process protrudes from the frontal. The linea temporalis on the frontal has a low relief and trends medially from a lateral position near the superior orbital margin toward the origin of the sagittal crest.

In ventral view, the palatal processes of the maxilla preserve the large alveolus of the canine, two P¹ alveoli, two P² alveoli, and two P³ alveoli. The rostral portion of the palate is narrow, but the palate expands laterally near the distal root of P³. The maxilla contacts the palatine midway between the protocones of M¹ and M². A distinct palatine torus is present just distal to the M³ protocone. The internal choana originates posterior to M³. As the choana opens distally, it is framed by the left and right palatines, which trend laterally.

Upper Dentition—The alveoli of I² and I³ are preserved in the premaxilla, but it is difficult to discern whether an I¹ alveolus is present. The diameter of the I³ alveolus is approximately twice the size of the I² alveolus, while the diameter of the canine root and alveolus is approximately twice the diameter of the I³ alveolus. DPC 17627 preserves the crown of the canine, which has crenulated enamel and is buccolingually compressed. The collapsed

alveolus of the canine is preserved in DPC 11990 and it arches posteriorly toward the nasal. P¹ had two roots, and the mesial root was smaller than the distal root and set very close to the root of the canine. The crown of P¹ would have been close to, or in contact with, the base of the canine. P² and P³ also had two roots though the anterior alveolus of P³ is not well preserved. The premolars, from P¹ to the anterior root of P³, were in the same anteroposterior plane and the margins of the maxilla holding these teeth were parallel. At the posterior root of P³ the palate flares laterally and broadens distally.

P⁴ is the only premolar whose crown is preserved. The parastyle is buccolingually compressed, forming a crista that connects with the preparacrista. A thin buccal cingulum surrounds the parastyle and runs along the base of the paracone to the base of the metastyle. The preprotocrista connects the base of the parastyle to the protocone, forming a distinct mesial shelf along the base of the paracone. The protocone is mesiodistally wide and connate, though much lower than the paracone, and the preprotocrista and postprotocrista form a broad equilateral triangle around the base of the paracone. The protocone is shifted slightly mesially relative to the paracone. The paracone is ellipsoid in cross-section and the postparacrista tapers to a sectorial blade that connects with the buccolingually compressed metastyle. The metastyle forms a distinct carnassial notch with the postparacrista, and the metastyle rises distally from the notch to approximately one-third the height of the paracone.

DPC 17627 represents a subadult individual and provides insight into an earlier ontogenetic stage than that of DPC 11990. The specimen preserves the right P⁴, which has fully erupted, and the left dP⁴, which still has its roots. The left M³ was erupting into occlusion. The parastyle of dP⁴ is wide and shelf-like, leaving space between the base of the paracone and the cusp of the parastyle. The parastyle connects the wide buccal cingulum to the preprotocrista. A

large paraconule forms a distinct crest along the preprotocrista, which slopes to the protocone where the paraconule and protocone form a notch. The protocone is large and triangular and almost rises to the point of divergence between the paracone and metacone. No lingual cingulum is evident along the base of the protocone. The protocone is shifted slightly mesially, as it is on P⁴. The postprotocrista slopes to a small metaconule, which is very reduced compared to the paraconule. The postprotocrista terminates at the base of the metacone rather than coursing along the base of the metastyle. The paracone and metacone are heavily worn, though the cross-sections of both indicate that the cusps were buccolingually compressed, especially the postparacrasta and the premetacrasta, which together form a distinct notch where the cusps diverge. The postmetacrasta forms a carnassial notch with the long metastyle. The metastyle is subequal in mesiodistal length to the mesiodistal length of the paracone/metacone base. The buccal face of the metastyle slopes steeply to the thin buccal cingulum, which traces the alveolar margin without forming an ectoflexus. The metastyle of dP⁴ contacts the parastyle of M¹ at its mesial-most point. In DPC 11990, the metastyle of P⁴ also contacts the mesial-most point of M¹. M¹ is generally similar to dP⁴. The parastyle forms a broad shelf between the apex of the parastyle and the base of the paracone. The parastyle is connected to the broad buccal cingulum, which forms a very slight ectoflexus near the base of the paracone. The buccal cingulum rises slightly along the base of the paracone then slopes distally along the base of the metacone and terminates at the base of the metastyle. The preprotocrista terminates at the base of the paraconule, forming a distinct notch between the paraconule and protocone, and a preparaconule crista courses from the apex of the paraconule to the parastyle, forming a broad mesial cingulum. The protocone rises to a prominent cusp that is equal in height to the divergence between the paracone and metacone; it has a more mesial position, relative to the paracone, than the

protocone of P⁴. There is no lingual cingulum. The postprotocrista slopes steeply to the metaconule, which is not as mesiodistally broad as the paraconule, though still distinct. The metaconule does not have a postmetaconule crista connecting to the metastyle; instead, the postmetaconule crista abuts the lingual face of the metacone. The paracone is buccolingually compressed with a distinctly elliptical cross-section. The apex projects mesially and overhangs the parastylar region. The postparacrista is blade-like and, in buccal view, meets the premetacrista at a right angle. The metacone is more buccolingually compressed than the paracone near its apex, and is mesiodistally longer. The postmetacrista is blade-like and slopes to a deep carnassial notch at the junction with the metastyle. The mesiodistal length of the sectorial metastyle is subequal to the mesiodistal length of the paracone/metacone base. The lingual face of the metastyle is perpendicular to the palate, while the buccal face of the metastyle slopes more gently to the buccal cingulum.

M¹ contacts M² at the mesial-most point of the parastyle. M² is similar in many ways to M¹, with many of the distinctions between dP⁴ and M¹ expressed even more extremely between M¹ and M². The parastyle of M² is shelf-like with a broad region between the parastyle and paracone, but the parastyle is more buccolingually narrow. M² has a deeper ectoflexus than M¹ though its depth is variable, with the M² ectoflexus on DPC 11990 deeper than the M² ectoflexus on DPC 17627. The paraconule of M² is very pronounced and forms most of the mesial border of a broad talon basin. The protocone projects as far lingually as the protocone of M¹, leaving the protocone buccolingually more elongate than the protocone of M¹. The metaconule of M² is more reduced, compared to the size of the paraconule, than that of M¹. On M² the metaconule only forms a slight ridge. The postmetaconule crista runs along the base of the metacone and terminates at the base of the metastyle. The paracone and metacone are more buccolingually

compressed and the paracone is lower than the metacone, projecting mesially from the metacone. The metacone is relatively wider and its long axis is aligned closer to perpendicular to the palate. As on M^1 , the sectorial postmetacrista forms a deep carnassial notch where it meets the metastyle. The metastyle rises distally from the notch before tapering to its distal-most point. M^3 is reduced primarily to a long parastyle and the paracone and protocone cusps. The parastyle contacts the distal-most point of M^2 . Mesially, the parastyle connects to the preparacrista, forming a steep mesial face. The protocone projects as far lingually as the protocone of M^2 and it frames a deep trigon basin. The protocone rises close to the height of the paracone. The paracone is more connate than the paracone of M^2 , though the postparacrista is buccolingually compressed. The postparacrista terminates at the buccal cingulum, which connects the parastyle to the postprotocrista. The buccal cingulum rises slightly near the distal aspect of the paracone.

Dentary and Lower Dentition—The holotype of *Brychotherium*, CGM 83750, is a right dentary that preserves lower dental row from the canine to M_3 . The cusps of CGM 83750 are worn, particularly the premolars and M_1 . Three other dentary specimens are referred to *Brychotherium ephalmos*: DPC 11569A (right dentary), DPC 11569B (left dentary), and DPC 17627 (left dentary). CGM 83750 as the only specimen with a complete coronoid process and tooth row distal to the canine. There is variation among the dentary specimens referred to *Brychotherium ephalmos*. This description will first refer to the morphology preserved by CGM 83750, then will address the morphological variation present in the referred specimens.

The horizontal mandibular symphysis is rugose and was unfused. The symphysis extends distally to the mesial root of P_3 . There are multiple mental foramina preserved along the buccal aspect of the horizontal ramus. The most rostral mental foramen is ventral to the mesial root of

P₁. The second mental foramen is ventral to the mesial root of P₂ and the third mental foramen is the largest and is ventral to the space between the distal root of P₃ and the mesial root of P₄. The ventral margin of the corpus of the dentary gently curves to the partially preserved angular process then inflects at the midpoint of the coronoid process, forming a convex ventral margin ventral to the dental row. The ventral margin slightly tapers to the canine. The anterior margin of the coronoid process rises at an obtuse angle (~125 degrees) distal to the talonid of M₃. A broad ridge originates on the buccal face of the dentary, ventral to the distal edge of the talonid of M₃. The anterior fibers of the temporalis muscle would have inserted along this margin. The ridge rises to form the anterior margin of the coronoid process. The anterior edge of the masseteric fossa is deeply excavated but the ventral margin of the masseteric fossa is not as well-defined as the anterior portion.

The lower incisors are not preserved. The crown of the canine is worn. The buccal face of the canine is traced by multiple longitudinal ridges of enamel. The mesial root of P₁ is very close to the distal edge of the root of the canine and it sweeps distally with the root canine. The distal root of P₁ parallels the distally swept mesial root of P₁. The crown of P₁ is worn, but a portion of the mesiodistally short talonid is preserved. The crown of P₁ is set at an oblique angle relative to the mesiodistal axis of P₂.

Like P₁, P₂ has two roots. The roots of P₂ are perpendicular to the alveolar margin. In buccal or lingual view, P₂ is an asymmetrical triangle. There is a small, but pronounced paraconid on the mesial portion of the tooth. The paraconid is mesiodistally aligned with the protoconid. The shorter paraconid is linked to the protoconid by a short preprotocristid that rises steeply from the paraconid to the apex of the protoconid. The postprotocristid slopes to a mesiodistally short talonid.

There is no diastema between P_2 and P_3 . Like P_2 , P_3 is asymmetrical in buccal and lingual views with a mesiodistally short preprotocristid and mesiodistally long postprotocristid. The paraconid of P_3 is small, but distinct and in a more lingual position than the protoconid. The protoconid of P_3 is at least twice the height of the paraconid. The postprotocristid is buccolingually compressed and slopes to an indistinct talonid basin. A thin lingual cingulum connects the paraconid to the the talonid.

The crown of P_4 forms an equilateral triangle in lingual view, and, like each of the premolars, bears striated enamel. P_4 is a stout tooth in occlusal view, its buccolingual width about half its mesiodistal length. The paraconid is a small but distinct cusp, with a postparacristid that forms a small notch with the longer preprotocristid. The paraconid is connected to a weak lingual cingulum that terminates at the base of the protoconid. A distal lingual cingulum begins just posterior to the apex of the protoconid. The cingulum forms the lingual margin of a very shallow talonid basin. The talonid of P_4 has a small hypoconulid that connects to the hypoconid. The hypoconid is buccolingually compressed and rises to half the height of the protoconid. The hypoconid forms a distinct notch with the postprotocristid. The preprotocristid and postprotocristid are sectorial, and the apex of the protoconid curves slightly lingually and inclines very slightly distally.

A thin anterior keel on the buccal face of the M_1 paraconid contacts the hypoconulid of P_4 . M_1 is heavily worn on CGM 83750, but is well-preserved on DPC 17627. The protoconid is the tallest of the trigonid cusps, followed by the paraconid and the metaconid. The preprotocristid curves slightly mesially as it runs from the apex of the protoconid to the carnassial notch, where the preprotocristid and postparacristid meet at an angle of approximately 90 degrees. The shearing surface created by the protoconid and paraconid is set at about an angle

of 45 degrees relative to the long axis of the dentary. The apex of the paraconid projects mesially. The metaconid is connate and connects with the base of the paraconid; its apex projects distally and is positioned slightly distal to the apex of the protoconid. A slight depression descends from the junction of the paraconid and metaconid, defining the base of each cusp. The distal face of the trigonid slopes at an obtuse angle (~100 degrees) to the talonid. The talonid basin is about one-third the total mesiodistal length of M_1 . The talonid basin is deep, closed buccally by the hypoconid, and closed lingually by the entocristid. The talonid cusps are crestiform. The entoconid is particularly indistinct, effectively submerged into the entocristid, which slopes distally from the base of the metaconid to meet the apex of the hypoconulid. The hypoconulid is a small cusp that is distinguished from the hypoconid by a weak intervening notch or inflection. The hypoconid is the most pronounced of the talonid cusps, and the cristid obliqua slopes ventrally and lingually toward the base of the protoconid from its apex.

M_2 is mesiodistally longer, buccolingually broader, and taller than M_1 . The contact between M_1 and M_2 is small, with a gap formed between the M_2 paraconid and the distal M_1 talonid. M_1 and M_2 are similar in morphology, but differ in relative proportions. The metaconid is relatively low when compared with the paraconid, and the paraconid is relatively broader at its base, forming a stout cusp. The paraconid apex projects mesially and more lingually than the apex of the metaconid. The talonid basin of M_2 makes up ~40% of the mesiodistal length of the entire tooth, and the talonid basin is only about one-third the height of the protoconid. As on M_1 , the talonid cusps are crestiform and the entoconid is reduced to an undifferentiated entocristid. In buccal view, the angle formed between the alveolar margin and the distal edge of the protoconid is approximately 100 degrees.

M₃ is the tallest tooth in the dentary. It is subequal in mesiodistal length to M₂ though more of its mesiodistal length is occupied by the trigonid. The talonid is ~27% the mesiodistal length of the tooth, and ~25% the height of the protoconid. The paraconid and protoconid on M₃ are taller than the same cusps on M₂ but the metaconids on M₃ and M₂ are almost the same height above the alveolar margin, making the M₃ metaconid proportionally smaller compared to the rest of the trigonid. One distinctive feature of M₃ is the morphology of the preprotocristid, which arcs mesially from the apex of the cusp to the deep carnassial notch. The apex of the protoconid projects distally like the metaconid, and both cusps arch somewhat distally toward the talonid basin. The talonid of M₃ is relatively narrow when compared with the talonids of M₁ and M₂. The hypoconid is proportionally smaller, and the hypoconulid forms a more distinct distal point than it does on the more mesial molars.

Dental Variation—Compared to CGM 83750, which was utilized for most of the description of the lower dentition, DPC 17627 is very similar, though the corpus of the dentary is more gracile than the dentary of CGM 83750. DPC 17627 preserves the two alveoli of P₃ and the distal alveolus of P₂. Like CGM 83750, there is no indication of a diastema between P₂ and P₃. This contrasts with DPC 11569A and DPC 11569B, two specimens that likely represent the right and left dentary of the same individual. Both specimens preserve a diastema between P₂ and P₃ that is half the mesiodistal length of P₃. On DPC 11569A and DPC 11569B the paraconids on P₂–P₄ are very small compared to the paraconids on the same premolars on CGM 83750 and DPC 17627. Finally, the talonid basin of M₃ is relatively smaller and narrower, with less clearly defined cusps than are found on the talonids of M₃ on CGM 83750 and DPC 17627. We do not consider these differences significant enough to designate a new taxon based on the current

sample. Future work in the L-41 collections will further explore morphological variation in the hyaenodont fauna found at this locality.

Body Mass—The average mesiodistal length of the lower molars is 9.57 mm, which yields a body mass estimate of 5.24 kg using the equation of Morlo (1999), and 5.96 kg using the equation of Van Valkenburgh (1990). Using only M_2 length yields an estimate of 6.10 kg, and only M_3 length yields an estimate of 6.20 kg. Carnivorans with a comparable body mass include *Vulpes vulpes* (red fox) and *Taxidea taxus* (American badger).

Comparisons

Rostrum—*Dissopsalis* and *Teratodon*, both Miocene taxa (Barry, 1988; Savage, 1965), are the only demonstrable teratodontines (Solé et al., 2014b; Rana et al., 2015) for which cranial morphology has been described. *Dissopsalis carnifex* is known from the middle to late Miocene of Asia; the holotype was reconstructed and described by Colbert (1933). The fragmentary specimen preserves much of the left and right maxillae as well as the frontal. Colbert (1933) reconstructed the zygomatic arches and much of the posterior skull. As in *Brychotherium*, the palatal margins from P_1 to the anterior root of P_3 of *Dissopsalis* are parallel. P_3 is angled and its buccal margin follows the lateral flare of the maxilla. The infraorbital foramen is positioned dorsal to P_3 in *Dissopsalis*, as it is in *Brychotherium*. Also like *Brychotherium*, the rostral profile of *Dissopsalis*, created by the gently sloping nasals and frontals, is low, and the sagittal crest emerges from the frontal caudal to subtle postorbital “peaks” rather than distinct processes. This differs from late Eocene European taxa like *Hyaenodon* and *Cynohyaenodon*, which have more pronounced postorbital processes and more deeply excavated lineae temporales (Lange-Badré, 1979).

Teratodon enigmae, from the early Miocene of East Africa (Savage, 1965), is also known from the rostrum. KNM-RU 14769 is a fragment of the left maxilla that contains the complete left canine and P¹-P⁴. While the premolars are bulbous and very different from those of *Brychotherium*, the alveolus of the buccolingually compressed canine is similar in morphology to that preserved in DPC 11990. The P¹ of *Teratodon* is also set close to, and slightly lingual of, the upper canine, as is suggested by the disposition of the canine and P¹ alveoli of *Brychotherium*. The holotype of *Teratodon* preserves portions of the rostrum from the premaxilla back to the distal aspect of the palate; in this specimen, too, the anterior root of P¹ is lingual to the canine alveolus.

Limited comparisons can also be made with *Indohyaenodon* from the early Eocene of India (Rana et al., 2015), *Tritemnodon* from the early Eocene of North America (Gunnell, 1998), *Paroxyaena* from the late Eocene of Europe (Lavrov, 2007), *Apterodon macrognathus* from the early Oligocene of Egypt (Lewis & Morlo, 2010), and *Pterodon dasyuroides* from the late Eocene of Europe (Lange-Badré, 1979). Each of these taxa has a long, narrow rostrum with a broad nasal aperture. The nasals do not project prominently over the aperture and the nasals widen slightly as they approach the nasal-frontal suture. The frontal in each of these taxa does not exhibit a distinct postorbital process, but instead a postorbital peak (*Pterodon*) or subtle bump (*Apterodon*, *Paroxyaena*). The linea temporalis (= supraorbital boss in Rana et al., 2015) is demarcated, but not deeply excavated (it is particularly subtle in *Apterodon* and *Paroxyaena* and more distinct in *Indohyaenodon* and *Pterodon*). Along the anterior orbital margin, the lacrimal has a particularly broad facial wing in *Pterodon*, *Apterodon*, and *Paroxyaena*, as it does in *Brychotherium*.

The fragmentary palatines of *Brychotherium* indicate that the internal choanae open distal to M³ and are delimited ventrally by a rugose palatine torus, comparable to the palatine construction of *Paroxyaena* and *Tritemnodon*. The internal choanae of *Pterodon dasyuroides* and *Apterodon macrognathus* open more caudally. In *P. dasyuroides* and *A. macrognathus* the palatines are fused along the midline posterior to the dentition. The palatines of *Apterodon* are fused for more of their length than those of *P. dasyuroides*, forming a palatine tube that extends to the basicranium. Colbert (1933) reconstructed the palatines of *Dissopsalis* as a long, fused palatine tube, likely based on comparisons to the skull of North American *Hyaenodon*, which also has a *Apterodon*-like tube (Mellett, 1977). The palatine morphology of *Dissopsalis* is, in fact, largely unknown.

Upper Dentition—Like the teratodontines *Dissopsalis* and *Anasinopa*, *Brychotherium* has distinct paracones and metacones on the upper molars that are fused at their bases, but diverge well before their apices. In all three taxa, the paracone and metacone are buccolingually compressed, giving them an elliptical cross section, and the paracone is the smaller of the two cusps. The apex of the metacone projects perpendicular to the plane of the hard palate, while the smaller paracone projects mesially. This differs from hyainailourines (e.g., *Pterodon dasyuroides*, *Kerberos*, and “*Pterodon*” *africanus*), which fuse the paracone and metacone near the apices of the cusps. In hyainailourines, the paracone is the taller of the two cusps and would have been the leading piercing cusp during mastication. The paracone/metacone morphology of Teratodontinae is comparable to the arrangement of these cusps in *Hyaenodon* and *Eurotherium* which, like teratodontines, had metacones that were taller than paracones. However, in *Hyaenodon* and *Eurotherium*, the cusps are not as divergent; rather, in *Hyaenodon*, the paracone projects perpendicular to the plane of the hard palate, like the metacone, and is almost

completely fused to the metacone, essentially forming part of the premetacrista (a state evident in unworn upper molars, such as the M¹ of the subadult AMNH 75646). *Apterodon* also has distinct paracones and metacones as in teratodontines, but these cusps are more circular in cross-section and diverge closer to the buccal margin.

The molar paracones are more distinct in *Brychotherium* than in *Dissopsalis*, and the molar protocones of *Brychotherium* are more triangular and project lingually, rather than being elongate and shifted far mesially as in *Dissopsalis*. The trigon basins of *Brychotherium* more closely resemble those of *Anasinopa*, though the paraconules and metaconules of *Brychotherium* are relatively well-developed. The deep ectoflexus and large parastyle of the M¹⁻² of *Brychotherium* set the new genus apart from *Anasinopa* and *Dissopsalis*. *Teratodon* has small, tritubercular molars and a distinct ectoflexus on M². The M¹⁻² metastyles of *Brychotherium* are mesiodistally longer than the parastyles whereas the para- and metastyles on the M² of *Teratodon* are subequal in length. *Indohyaenodon* also has an elongate, arching M² metastyle, like *Brychotherium*, but its protocone is more mesiodistally broad. The P⁴ paracone of *Indohyaenodon* is more buccolingually compressed than that of *Brychotherium* and its P⁴ protocone is less distinct. P⁴ in *Kyawdawia*, from the middle Eocene of Myanmar (Egi et al., 2005) is also more compressed buccolingually, and the metastyle is taller and more sectorial than that of *Brychotherium*. The M² paracone and metacone of *Kyawdawia* are both buccolingually compressed and the mesiodistally elongate metacone is only slightly taller than the paracone. The M² ectoflexus of *Kyawdawia* has the same degree of lingual curvature as that of *Brychotherium* and the same well-defined buccal cingulum. The M¹ of middle Eocene *Furodon* shares many features with *Brychotherium*, including an elongate metastyle, buccolingually compressed and apically divergent paracones and metacones, a broad talon basin with a large

paracone, and a prominent and only slightly mesially oriented protocone. *Koholia* is from the late early Eocene and is the oldest Afro-Arabian hyaenodontidan known from its upper dentition. The P⁴ protocone of *Brychotherium* is mesiodistally wider than the P⁴ protocone of *Koholia*, and the P⁴ metastyle of *Brychotherium* is mesiodistally short compared to the elongate metastyle of *Koholia*, which is the same mesiodistal length as the paracone. The M¹ parastyle of *Koholia* is buccolingually wide, with space formed between the apex of the parastyle and the base of the paracone. The M¹ parastyle in *Brychotherium* is buccolingually narrow and cingulum-like. Like in *Brychotherium*, the M¹ paracone and metacone of *Koholia* have distinct apices, but the paracone and metacone are more fully fused in *Koholia* and the paracone is distinctly taller than the metacone. On the M¹ of *Brychotherium* the metacone is slightly taller than the paracone.

Lower Dentition—Solé et al. (2014b) recovered *Furodon* as a hyainailourine with *Pterodon* and *Akhnatenavus*, with *Furodon* as the only member of this clade with a prominent metaconid. The phylogenetic analyses presented below do not support the Solé et al. (2014b) hypothesis and instead resolve *Furodon* in a close relationship to metaconid-bearing teratodontines. *Brychotherium* and *Furodon* share many features, including their comparable size, relatively tall trigonids, low metaconids, and wide talonid basins with poorly defined talonid cusps. They primarily differ in the morphology of P₄, the protoconid of which projects perpendicular to the alveolar margin in *Brychotherium*, and in occlusal view curves lingually. The lower molar paraconids also project more lingually in *Brychotherium* than they do in *Furodon*, the talonid basins are buccolingually more broad, and the molar hypoconulids are larger.

The oldest teratodontine in the analyses of Solé et al. (2014b) and Rana et al. (2015) is *Glibzegdouia*, an early or middle Eocene taxon from Algeria. The M₁ metaconid of *Glibzegdouia*

is subequal in height to the paraconid, and the talonid basins of M_{1-2} are lined with distinct entoconids, hypoconulids, and hypoconids, unlike the poorly differentiated talonid cusps of *Brychotherium*. The talonid basin also occupies more than 50% of the total mesiodistal length of the molars of *Glibzegdouia*. The talonid is proportionally smaller and shorter in *Brychotherium*.

Masrasector aegypticum is a teratodontine from Quarry G (early Oligocene) in the Fayum succession (Simons & Gingerich, 1974). Like *Brychotherium*, *M. aegypticum* has broad talonid basins with indistinct talonid cusps. The smaller *M. aegypticum* is further differentiated from *Brychotherium* in having buccolingually broad premolars and a more tightly packed trigonid, with the paraconid apex perpendicular to the alveolar plane, rather than projecting lingually as it does in *Brychotherium*. The other possible teratodontine from the Fayum, *Metasinopa*, differs from *Brychotherium* in having a much deeper mandibular corpus, a more reduced talonid on M_3 , and much smaller M_2 - M_3 metaconids, particularly on M_3 where the metaconid barely connects to the paraconid. The reduction of the M_3 metaconid is even more extreme in *Dissopsalis* and *Anasinopa*; the paraconid and protoconid of both taxa are divergent and form an obtuse carnassial notch between the preprotocristid and postparacristid and the metaconid is reduced to a very low or absent cusp (especially in *Dissopsalis*). Both *Dissopsalis* and *Anasinopa* have broad and lingually closed talonids on M_1 and M_2 and reduced talonids on M_3 , with the talonid on *Dissopsalis* reduced to a small distal projection from the M_3 trigonid. These features contrast with the connate metaconid, well-developed talonid, and more acute carnassial notch found on the M_3 of *Brychotherium*.

Lahimia, from the middle Paleocene of Morocco (Solé et al., 2009), and *Boualitomus*, from the early Eocene of Morocco (Gheerbrant et al., 2006), are both small hyaenodontidans that Solé et al. (2014b) and Rana et al. (2015) classified as part of Koholiinae. Like *Brychotherium*,

they both retain lower molar metaconids that are slightly lower than the paraconids and distinct talonids with indistinct talonid cusps. They differ from *Brychotherium* in their much smaller size, and by having molars that are mesiodistally subequal in length to each other. *Brychotherium*, like many hyaenodontidans including *Masrasector* and *Pterodon*, but unlike *Lahimia* and *Boualitomus*, has molars that increase in length distally.

Indohyaenodon and *Kyawdawia*, part of Indohyaenodontinae in Solé et al. (2014b) and Rana et al. (2015), have buccolingually broad talonids that are lingually closed by the entocristid, rather than lingually open as the talonid is in *Brychotherium*. Both taxa also have distinct buccal cingulids on the lower molars that originate from the anterior keel. In *Brychotherium* the anterior keel is small and does not connect to any cingulid. The metaconid is much lower than the paraconid on M₃ in *Indohyaenodon*, *Kyawdawia*, and *Brychotherium*, but the metaconid is subequal to the height of the paraconid on M₁ in the indohyaenodontines and is lower than the paraconid in *Brychotherium*. *Indohyaenodon* and *Brychotherium* also share relatively gracile dentaries that are only a little deeper dorsoventrally than the crown height of M₃.

HYAENODONTIDA Solé, 2013

HYAINAILOURINAE Pilgrim, 1932

AKHNATENAVUS Holroyd, 1999

Type Species—*Akhnatnavus leptognathus* Holroyd, 1999.

Emended Generic Diagnosis (modified from Holroyd, 1999)—Differs from “*Pterodon*” *africanus* and “*Pterodon*” *phiomensis* by being smaller and by having more buccolingually compressed lower premolars; narrow, mesially shifted M¹⁻² protocones; and more buccolingually compressed and elongate M¹⁻² metastyles. Differs from *Metapterodon* by being smaller, retaining

a talonid on M₃ rather than having no talonid, having distinct M¹⁻² paracone and metacone cusps rather than being completely fused into a single cusp, having more lingually projecting M¹⁻² protocones rather than having small protocones that are close to the paracone bases, and having distinct M¹⁻² parastyles with spaces between the parastyle and the base of the paracone rather than the parastyles forming only a small projection. Differs from *Pterodon dasyuroides* by having smaller talonids on molars, a reduced M³ that does not project lingually as far as the M² protocone, and narrower M¹⁻² protocones with preprotocrista and postprotocrista nearly parallel rather than protocones that are mesiodistally broad and triangular. Differs from *Apterodon* by having fused paracone and metacone cusps on M¹⁻², molar paraconids that are much shorter than the protoconids, mesiodistally short molar talonids, and M¹⁻² metastyles that are mesiodistally longer than the mesiodistal length of the paracone and metacone bases. Differs from *Brychotherium* by having M¹⁻² paracones that are taller than metacones and narrow, simple M¹⁻² protocones rather than triangular protocones with metaconule and paraconule cusps.

AKHNATENAVUS NEFERTITICYON Borths, Holroyd, and Seiffert, sp. nov.

(Figs. 10–15, Table 3)

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Etymology—Meaning “Nefertiti’s dog,” in reference to Nefertiti, the wife of Akhnaten, who is known from an exceptional cranial specimen.

Holotype—CGM 83735, cranium with canine, P²-M³.

Referred Specimens—DPC 13518, M¹; DPC 18242, palate with partial canine, alveoli for P¹, and P²-M²; DPC 7765, dentary with P₂-M₃ (Described by Holroyd, 1999)

Type Locality—Jebel Qatrani Locality 41 (L-41), Jebel Qatrani Formation, Fayum Depression, Egypt.

Age—late Eocene, latest Priabonian, ~34 Ma (Seiffert, 2006)

Geographic Distribution—Only known from Locality 41.

Diagnosis—Differs from *Akhnatenavus leptognathus* by being smaller and by having mesiodistally shorter diastemae between the premolars. Rostrum is inferred to be relatively shorter in *A. nefertiticyon* than is implied by the elongate dentary of *A. leptognathus* which has wide diastemae between adjacent premolars. P_3 in *A. nefertiticyon* is distally inclined and relatively buccolingually wider than P_3 in *A. leptognathus*. P_4 in *A. nefertiticyon* is taller than P_4 in *A. leptognathus* and P_4 paraconid height is subequal to the mesiodistal length of the tooth rather than shorter than the mesiodistal length. M_1 – M_3 have weak to absent ectocingulids and the talonid is reduced in *A. nefertiticyon* compared to the slight ectocingulids and better developed cusp-bearing talonids of *A. leptognathus*.

Description

Cranium—CGM 83735 is a complete cranium that was dorsoventrally crushed, with the left portion of the skull folded medially. The best preserved portions of the cranium are the right palate and dentition, the right squamosal, the nuchal crest, the posterior aspect of the sagittal crest, portions of the parietals, and the anterior portion of the frontal. A complete atlas is preserved on the right basicranial region and a rib is preserved attached to the right parietal.

The atlas is preserved in dorsal view with deep facets for articulation with the occipital condyles visible in ventral view, along with the vertebral foramina and the articular facets for the axis. The left articular facet for the axis, visible in Fig. 10A and Fig. 11A, is broad and not as

concave as the facets for the occipital condyles. The rugose dorsal tubercle is preserved along the dorsal arch, which is craniocaudally wide, approximating the dorsoventral diameter of the vertebral foramen. Fragments of the right transverse process suggest that the structure swept laterally before curving caudally. The proximal portion of a rib is preserved in caudal view with a deep costal groove along its body. It is mediolaterally broad, likely a first or second rib.

The nasals are relatively well-preserved, though the nasal aperture is not. Originating rostrally from a slight lateral expansion, the nasals narrow posteriorly and then expand laterally superior to the infraorbital foramen. The nasal-frontal suture reaches its posterior-most point at the midline of the cranium, and the suture trends at a 45-degree angle to the nasal-maxilla suture along the lateral border of the nasal. The facial portion of the maxilla is rostrally elongate. The maxilla is perforated by the infraorbital foramen, which is dorsal to the distal root of P³. The maxilla flares laterally posterior to the infraorbital foramen. The rugose maxillary portion of the maxilla-jugal suture indicates that the jugal formed the inferior margin of the orbit. The large lacrimal formed the anterior portion of the orbital rim. The orbital margin of the lacrimal has a dorsoventrally elongate lacrimal tubercle. The facial wing of the lacrimal is extensive, reaching from the anterior orbital margin, which is superior to the mesial root of M², anteriorly to the distal root of P⁴. The frontal forms the superior margin of the orbit and preserves the deeply excised linea temporalis, which leads to the sagittal crest. The sagittal crest tracks the interparietal suture to the nuchal crest. The sutures of the bones that form the nuchal crest are not clear, though the occipital forms the lateral portions of the nuchal crest in *Pterodon dasyuroides* and *Apterodon macrognathus*, and the parietals form the medial portions of the crest near the sagittal crest. There are suggestions of a suture in these regions of the skull of *Akhmatavenus*, which are indicated in Fig. 11. The entire nuchal crest stands prominently above the cranial vault

with the tallest portion of the sagittal crest bridging the space between the posterior aspect of the cranial portion of the parietal and the apex of the nuchal crest. The crest curves laterally, then recurves medially towards the foramen magnum, with the supraoccipital forming a clover-leaf-shape in caudal view. The exoccipital curves laterally from the ventral extension of the nuchal crest and supraoccipital. The occipital condyle is dorsoventrally elongate, though its relationship to the foramen magnum is difficult to interpret.

The left mandibular (or glenoid) fossa indicates that the mandibular condyle was mediolaterally wide and dorsoventrally short, with the width of the condyle about three times the height. A large postglenoid foramen is preserved posterior to the mandibular fossa. The right zygomatic process of the squamosal has an anteroposteriorly broad origin. The zygomatic process is dorsoventrally tall and robust near the mandibular condyle and it tapers as it trends rostrally. The fragmentary jugal would have formed a short contact with the inferior margin of the squamosal and continued the zygomatic arch to the inferior orbit and the contact of the jugal with the maxilla. The palatal portion of the maxilla is rugose and deeply embayed between the protocones. The maxilla-palatine suture is not easily traced, but the posterior margin of the palate is marked by a torus between the distal-most molars. The palatines extend posterior to the torus; though they are broken and the morphology of the internal choanae is obscured. The ventral face of the left palatine preserves a broken suture, evidence that the right and left palatine formed a suture posterior to the last upper molar, and diverged approximately mid-cranium.

Upper Dentition—The upper right canine is preserved in CGM 83735. The root is ~1.5 times the length of the crown and is widest just dorsal to the enamel-dentine junction. The enamel is longitudinally striated and the crown is round in cross-section rather than dorsoventrally depressed. The two roots of P¹ are preserved in DPC 18242 and the tooth is

crowded close to the mesial margin of the alveolus of the canine. P² also has two roots and there is a small gap between P¹ and P². P² is mesiodistally longer than P¹. The buccolingual width of P² is about half its mesiodistal length. The tooth has no parastyle or buccal cingulum. The paracone is recurved, and a convex curve is formed between the metastyle and the apex of the paracone. The metastyle is short, <25% the mesiodistal length of the tooth, and buccolingually compressed. The mesiodistal length of P³ is subequal to the length of P². A small gap separates the two premolars. A very small parastyle is present on P³. Like P², the paracone sweeps distally and a buccolingually compressed metastyle protrudes from P³. The metastyle is offset from the mesiodistal axis of the paracone where the palate widens laterally, posterior to the infraorbital foramen. A slight lingual shelf is present, though it is not developed into a distinct protocone as is present on P⁴. P⁴ is mesiodistally longer than P³. The parastyle forms a prominent mesial cusp and the metastyle is an elongate, buccolingually compressed blade that is more than half the mesiodistal length of the base of the paracone. The buccolingually compressed paracone sweeps distally and the postparacrista forms a deep carnassial notch with the arching metastyle. The protocone cusp is buccolingually shorter than its mesiodistal width and is lined mesially by a cingulum-like preprotocrista and lined distally by the postprotocrista, which runs along the base of the paracone and metastyle.

The metastyle of P⁴ is braced buccally by the parastyle of M¹ where the teeth are in contact. The parastyle of M¹ is a broad cingulum-like shelf with a small and distinct apex, and there is no space between the apex of the parastyle and the base of the paracone. A thin buccal cingulum traces the base of the paracone and metastyle. The ectoflexus is very slightly distal to the metacone. The parastyle cusp is in line with the preparacrista, which is a buccolingually compressed, sectorial blade. The apex of the paracone is slightly taller than the metacone. The

metacone is also buccolingually compressed but its base is mesiodistally elongate compared to the base of the paracone. The groove that distinguishes the fused paracone and metacone is visible in buccal and lingual view. The postmetacrista is thinner and mesiodistally longer than the preparacrista. The sectorial blade on the metacone forms a deep carnassial notch with the metastyle. The elongate metastyle is half the mesiodistal length of the tooth. From the carnassial notch the metastyle traces a convex, then concave, line to the distal-most point of the tooth. The protocone is broad with a distinct preprotocrista, a small paraconule, and no metaconule. The protocone is buccolingually as broad as it is mesiodistally wide and it has a strong mesial deviation relative to the paracone. The protocone is shifted so far mesially that it is lingual to the metastyle of P⁴. M¹ contacts M² lingual to the parastylar apex. M² is mesiodistally longer than M¹. Compared with M¹, M² has a larger parastyle that projects buccally. This gives M² a deeper ectoflexus than M¹. M² is taller than M¹ and the cleft between the paracone and metacone is more faint, though the apex of the paracone and metacone are both distinct, with the paracone slightly taller than the metacone. The protocone is buccolingually longer than its mesiodistal width, making the protocone on M² appear slenderer than the protocone on M¹. The protocones on both molars are subequal in width, though the protocone of M² does not angle as far mesially as the protocone of M¹. M³ contacts the lingual face of the metastyle of M². The tooth is not buccolingually wide, only reaching the lingual-most point of the metacone of M². The paracone is very small and the entire tooth is mesially angled. This does not appear to be postmortem distortion, but the natural orientation of the small terminal molar.

Body Mass—The mesiodistal length of the lower molars was measured between the postprotocrista of adjacent molars, which yielded an average molar length of 12.45 mm for DPC 18241 and 12.0 for CGM 83735. Using Morlo (1999), the body mass estimate for DPC 18241 is

~15.8 kg and for CGM 83735 is ~13.86 kg. Using Van Valkenburgh (1990), M_2 length ($M_2 = 13.1$ mm) yields estimates of 17.6 kg and 17.2 kg and only M_3 length ($M_3 = 13.4$ mm) yields an estimate of 17.4 kg and 18.3 kg. The average estimated body mass is ~16.7 kg, within range of *Gulo gulo* (wolverine), *Lynx lynx* (Eurasian lynx), and *Canis simensis* (Ethiopian wolf) (body mass estimates from Finarelli & Flynn, 2009).

Comparisons

Akhnatenavus nefertiticyon shares many cranial and dental features with species placed in Hyainailourinae by Polly (1996), Solé et al. (2014b) and Solé et al. (2015). Most notably, *Pterodon dasyuroides*, *Hemipsalodon*, and *Megistotherium* each also have distinctive, wedge-shaped nuchal crests that trend medially toward the foramen magnum, a feature also preserved in *A. nefertiticyon*, the oldest Afro-Arabian hyainailourine known from cranial material. *Apterodon macrognathus* also has this narrowed nuchal crest, which inclines caudally like the nuchal crest of *Akhnatenavus nefertiticyon*. This morphology contrasts with the broad nuchal crest of *Hyaenodon* and *Eurotherium*, which trends laterally toward the mastoid process (see Solé et al., 2015:Fig. 5). Another cranial feature shared by *A. nefertiticyon* and the other hyainailourines is the extensive facial wing of the lacrimal, which reaches from the anterior margin of the orbit to the distal root of P^4 . A rostrally extensive lacrimal is also shared with *Brychotherium*. More difficult to determine is the extent of palatine fusion in *A. nefertiticyon*, a feature that differs between *Pterodon dasyuroides*, which has palatines that diverge closer to the M^3 than the mandibular fossa, and *Megistotherium*, which has palatines that are fused through the middle section of the cranium and only diverge close to basicranium. *A. nefertiticyon* does share the dorsoventrally deep zygomatic process of the squamosal with *Megistotherium*. The zygomatic

arch is not completely preserved in *Pterodon dasyuroides*, but is preserved in *Apterodon macrognathus* and *Kerberos langebadrae*, both of which have dorsoventrally deep zygomatic arches that form robust attachment sites for the masseter muscle. Unlike *Apterodon* but like *Kerberos*, *Akhnatenavus* has distinct temporal lines leading to the origin of the sagittal crest. These deep lines, which indicate the anterior origin of the temporalis muscle, are comparable in depth to the lines preserved on the frontals of *Pterodon dasyuroides*. “*Pterodon*” *africanus* is known from a rostral specimen (SMNS 11575) that was sculpted into a complete cranium (Schlosser, 1911). The anterior portion of the skull preserves the broad nasal aperture and gently sloping nasals that are shared with *Pterodon dasyuroides*, *Kerberos*, and *Akhnatenavus*. It also preserves the slight postorbital eminence or subtle peak noted in *Brychotherium*. There is no indication of distinct, *Hyaenodon*-like postorbital processes in *Akhnatenavus*. Instead, the neurocranium is elongate along the anteroposterior axis with very slight waisting in the middle region of the skull as it is in *Apterodon* and *Pterodon dasyuroides*. The neurocranium of *Hyaenodon* and *Eurotherium* is hourglass-shaped in dorsal view, going from an expanded postorbital frontal to a narrow parietal around the sagittal crest, to a posteriorly expanded squamosal-parietal region.

Compared to the atlas preserved with CGM 83735, the atlas of *Megistotherium* (NHM M21902) has much broader transverse processes than *A. nefertiticyon* would have had, based on what is preserved along the fractured lateral margin of the *A. nefertiticyon* atlas. NHM M9472 is an atlas attributed to “*Pterodon*” *africanus*, which shares with *Akhnatenavus* transverse processes that are less robust than those of *Megistotherium*. The transverse processes of “*Pterodon*” *africanus* and *Akhnatenavus* sweep laterally, perpendicular to the vertebral foramen, and then caudally, rather than sweeping cranially before trending laterally as they do in

Megistotherium. The dorsal arch of each hyainailourine atlas is craniocaudally long and thick compared to the much narrower dorsal arch of *Hyaenodon* (AMNH 8775; BSPG 1898 IV 32).

Dentally, *Akhnatenavus* shares with other hyainailourines a fused, buccolingually compressed upper molar paracone and metacone, with the paracone taller than the metacone. This arrangement differs from the partially fused paracone and metacone of Teratodontinae, which have taller metacones than paracones, and Hyaenodontinae, which have fused paracones and metacones, but the metacone is the taller of the two cusps and the paracone is fused to the mesial aspect of the metacone. *Akhnatenavus* differs from “*Pterodon*” *africanus* and “*Pterodon*” *phiomensis* primarily in size, but there are dental distinctions, particularly in the overall robusticity of the dentition of “*Pterodon*” *africanus*. P⁴ in “*Pterodon*” *africanus* (NHM M21897) has a short, shelf-like protocone compared to the lingually projecting P⁴ protocone of *Akhnatenavus*. Like *Akhnatenavus*, the parastyle of M² is better developed than the parastyle of M¹ and the ectoflexus is slightly deeper, though not as lingually excavated as that of *Akhnatenavus*. The paracones of each preserved premolar and molar of “*Pterodon*” *africanus* sweep distally at stronger angles than the paracones of *Akhnatenavus*. “*Pterodon*” *syrtos* from Quarry M, an early Oligocene locality in the Fayum (Holroyd, 1999), differs from the other Afro-Arabian “*Pterodon*” species and *Akhnatenavus* by reducing the parastyles to thin mesial cingula.

Even greater differences in robusticity are evident between *Akhnatenavus* and the large early Miocene *Hyainailouros napakensis* (NHM M19090) and *Megistotherium*. In the early Miocene taxa, the buccolingual width of the molars and mesiodistal length of the molars are closer to subequal. Like *Akhnatenavus*, the protocone of M¹ in *Hyainailouros* crosses the transverse plane of the P⁴ metastyle and the protocone of M² is narrower and more lingually

oriented than the protocone of M^1 . The upper dentition of *Megistotherium* is not well-preserved, but the skull does preserve the alveoli, which indicate that small gaps were present between P^1 and P^2 , and between P^2 and P^3 . These short diastemata are also present between these teeth in *Akhnatenavus*. In all hyainailourines discussed so far, including *Pterodon dasyuroides*, the upper molar paracone and metacone are distinguishable by a shallow buccal and lingual groove that runs between them. This differs from the condition in *Metapterodon*, a genus known from the early Oligocene (Holroyd, 1999) through the Miocene (Lewis & Morlo, 2010), which has completely fused the paracone and metacone and it is very difficult to distinguish the two cusps from one another. The metastyle, paracone, and metacone of *Metapterodon* are buccolingually compressed into delicate, blade-like structures. The protocone and parastyle are much more reduced than they are in *Akhnatenavus*, “*Pterodon*” *africanus*, and *Pterodon dasyuroides*.

Akhnatenavus differs from the European hyainailourines *Pterodon dasyuroides* and *Kerberos* in the reduction of M^3 , which, in the European taxa, retains a distinct protocone that projects as far lingually as the protocone of M^2 . *Kerberos* and *P. dasyuroides* also have prominent paracones on M^3 , and a sectorial parastyle. The distinction between M^1 and M^2 in *P. dasyuroides* is not as clear as it is in *Akhnatenavus*. In *P. dasyuroides*, the parastyle of M^1 is a distinct cusp and it forms a slight ectoflexus and the protocones of the two molars are shifted mesially at similar angles. The contact between M^1 and M^2 in *P. dasyuroides* is small, with the distal-most point of the metastyle of M^1 touching the mesial-most point of the parastyle of M^2 , where the buccolingually more broad parastyle of the M^2 in *Akhnatenavus* buccally embraces the metastyle of M^1 .

PHYLOGENETIC RESULTS

Maximum Parsimony

The maximum parsimony analysis recovered 650 most parsimonious trees (MPT) each with a length of 1029 steps, a consistency index (CI) of 0.187, and a retention index (RI) of 0.613 with three parsimony uninformative characters. The character-taxon matrix contains 41.5% missing data with individual OTUs ranging from a minimum of 0% missing data (*Hyaenodon horridus*) to 84% missing data (*Koholia*) with a median of 40% of missing data across all OTUs. Synapomorphies for the clades in the strict consensus are listed in Table S3 with a single lined arrow indicating an ambiguous synapomorphy and double lined arrow indicating an unambiguous synapomorphy. With regard to the species described here, the strict consensus tree (Fig. 16) does not uphold a monophyletic Teratodontinae (leaving the lower-level position of *Brychotherium* uncertain), and relationships among African and Asian species are largely unresolved; only some hyainailourines (i.e., a strictly African clade including “*Pterodon*,” *Akhnatenavus*, and Miocene *Isohyaenodon*, *Leakitherium*, and *Megistotherium*, forming one branch of a trichotomy that also includes North American *Hemipsalodon* and European *Kerberos*) and Apterodontinae (*Apterodon* + *Quasiapterodon*) are retained as clades within a large polytomy that includes all other hyainailourines, teratodontines, indohyaenodontines, koholiines, North American *Tritemnodon* and *Pyrocyon*, and European *Paroxyaena*.

We also show the Adams consensus of the 650 MPTs in Fig. 16, with alphanumeric codes listed to the left of the relevant node, Bremer values indicated to the right of the node, and bootstrap support for the node (if >50%) in italics below the Bremer support value. The

1171 agreement subtree is shown next to the Adams consensus tree in Fig. 17 with OTUs recovered
 1172 consistently in the same phylogenetic position indicated with black text and connecting branches.

1173 The ~~Adam's~~ consensus suggests that the species that break down into a polytomy at the
 1174 base of node P31 (koholiines, *Masrasector aegypticum*, *Pyrocyon*, and *Tritemnodon*) contribute
 1175 to irresolution within P31. This is further corroborated by the structure of the agreement subtree
 1176 which does not recover these OTUs at P31 in a consistent phylogenetic position. In the Adams
 1177 consensus and agreement subtree, Apterodontinae joins an expanded Hyainailourinae that
 1178 includes the aforementioned taxa as well as European *Pterodon dasyuroides*, African
 1179 *Metapterodon*, and Asian *Orienspterodon*. In the Adams consensus the most basal position ever
 1180 occupied by *Brychotherium* in the MPTs is as at the same level as *Anasinopa*, *Dissopsalis* and
 1181 *Furodon*. The remaining teratodontines (*Glibzegdouia*, *Masrasector ligabuei*, and *Teratodon*)
 1182 form another clade in the Adams consensus (P33). *Akhnatenavus nefertiticyon* is the sister taxon
 1183 of *Akhnatenavus leptognathus* in all MPTs (P45); the monophyly of the genus is supported by
 1184 four unambiguous synapomorphies and a Bremer value of 2, and is consistently nested within
 1185 Hyainailourinae in a polytomy with “*Pterodon*” *africanus*, “*Pterodon*” *phiomensis*, and Miocene
 1186 hyainailourines (P44).

1187 Apterodontinae (P39; Bremer = 4) is unambiguously supported by 13 synapomorphies,
 1188 and *Apterodon* (P40; Bremer = 5) is unambiguously supported by four synapomorphies (Table
 1189 S3). Hyainailourinae (P43; Bremer = 1) is unambiguously supported by 23 synapomorphies
 1190 (Table S3). A clade that contains exclusively Afro-Arabian hyainailourines (P44; Bremer = 1;
 1191 i.e., excluding North American *Hemipsalodon*, European *Kerberos*, and more basal taxa) is
 1192 united by four unambiguous synapomorphies (Table S3), the clade formed by the Miocene
 1193 hyainailourines *Isohyaenodon*, *Leakitherium*, and *Megistotherium* (P47; Bremer = 4) is

unambiguously supported by five synapomorphies, and *Megistotherium* and *Leakitherium* (P48; Bremer = 2) are united by one unambiguous synapomorphy.

The closest sister taxa of P31 are *Prototomus*, *Sinopa*, Limnocyoninae, and a *Galecyon-Gazinocyon* clade, all of which break down into a polytomy with P31 at the base of node P22 in the strict consensus; on the Adams consensus tree, *Prototomus phobos* and *Sinopa* are sister taxa of P31. The sister taxon of P21 is *Arfia*, a North American genus from the early Eocene whose monophyly is well-supported (Bremer = 8; Bootstrap = 90%). Limnocyoninae (P23; Bremer = 1) is unambiguously supported by eight synapomorphies, and, within that subfamily, the genus *Prolimnocyon* (P24), which includes late Paleocene *Prolimnocyon chowi* from Asia and early Eocene *Prolimnocyon atavus* from North America, is supported by a Bremer value of 3. *Sinopa* (P30), like *Prolimnocyon*, is known from species in North America (*Sinopa grangeri*) and Asia (*Sinopa jilinia*), and is unambiguously supported by four synapomorphies. Node P20, which joins *Arfia* with P22, is supported by a Bremer value of 1 and seven unambiguous synapomorphies (Table S3).

The sister taxa of P20 are almost entirely European, including early Eocene *Lesmesodon* and *Morlodon* and a large clade of “proviverrines” and hyaenodontines (P4) whose relationships are well-resolved in the strict consensus. As this is the first phylogenetic analysis of Hyaenodontida to sample extensively from Hyaenodontinae as well as other African and Asian hyaenodontidan subfamilies, the relationships within clade P4 are worthy of additional discussion. Clade P4 is supported by a Bremer value of 1 and nine unambiguous synapomorphies (Table S3) and includes *Proviverra* as its basal-most taxon. The placements of each consecutive “proviverrine” sister taxon of hyaenodontines are supported by a Bremer value of 1, and include, from the basal node P5 (supported by seven unambiguous synapomorphies, see Table S3),

Allopterodon; a *Eurotherium* + *Leonhardtina* clade (clade P7, branching off at node P6, which is supported by four unambiguous synapomorphies); a *Boritia-Parvagula* clade (P10, supported by three unambiguous synapomorphies, branching off at node P9); *Quercytherium* (P12, supported by a Bremer value of 6, bootstrap of 60, and eight unambiguous synapomorphies; branching off at node P11); *Cynohyaenodon* (branching off at node P13; supported by three synapomorphies); *Preregidens* (branching off at node P14, supported by seven unambiguous synapomorphies); *Matthodon* (branching off at node P15, supported by eight unambiguous synapomorphies); and *Oxyaenoides* (branching off at P16, nine unambiguous synapomorphies). The placement of *Oxyaenoides* close to hyaenodontines is strikingly different from the placement found by Rana et al. (2015) in which it was placed on the other side of the hyaenodontidan tree, closer to hyainailourines than apterodontines. Hyaenodontinae (P17) is a relatively well-supported clade (Bremer = 8; Bootstrap = 63) in which middle Eocene *Propterodon* species fall into a polytomy as the sister taxon of late Eocene/early Oligocene *Hyaenodon* (P18). Hyaenodontinae is unambiguously supported by 12 synapomorphies. *Hyaenodon* is well-supported as a clade (P18; Bremer = 6; Bootstrap = 79%) and is unambiguously supported eight synapomorphies.

The sister group of all other hyaenodontidans is early Eocene European *Eoproviverra* (P1). Hyaenodontida (P1) has a Bremer support of 2 and Bootstrap support of 50% and is unambiguously supported by six synapomorphies. Outside of Hyaenodontida, the closest relatives among the non-hyaenodontidan species sampled is a *Cimolestes-Tinerhodon* clade (P56), which is supported by a Bremer value of 2 and three unambiguous synapomorphies.

Bayesian Phylogenetic Inference

The “allcompat” (majority-rule plus compatible groups) topology recovered through standard Bayesian analysis is shown in Fig. 18 with posterior probabilities (PP) indicated to the right of the relevant node and the alphanumeric code used in this discussion to the left of the relevant node. The results of the parsimony character optimization onto the “allcompat” tree are listed in Table S3.

Teratodontinae (B47) is recovered as a moderately supported clade (PP = 0.70), unlike the parsimony analysis, which collapsed all teratodontines into an unresolved polytomy. *Brychotherium* is placed as the sister taxon of *Dissopsalis* (B53; PP = 0.35) as part of a larger, very weakly supported clade (B51; PP = 0.16) with *Furodon* and *Anasinopa* (as in clade P37 on the Adams consensus derived from the parsimony analysis). The sister taxon of B51 (B48; PP = 0.39) includes *Masrasector*, *Glibzegdouia*, and *Teratodon* and resembles clade P39 in the parsimony Adams consensus, but in the Bayesian analysis both species of *Masrasector* are included in Teratodontinae, though the genus is not monophyletic; instead, *Masrasector ligabuei* is the sister taxon to a clade B49 (PP = 0.40) that includes *Masrasector aegypticum* from Egypt and *Teratodon* + *Glibzegdouia* (B50; PP = 0.16).

Akhnatenavus nefertiticyon is strongly supported (B67; PP = 0.93) as the sister taxon of *Akhnatenavus leptognathus*. *Akhnatenavus* is placed as the sister clade to the more deeply nested Afro-Arabian hyainailourines, including African “*Pterodon*” species and Miocene hyainailourines (B68; PP = 0.42). *Akhnatenavus* + B68 (B66) is only moderately supported (PP = 0.44), and is followed by the successive non-African sister taxa *Hemipsalodon* (branching off at B65, PP = 0.50) and *Kerberos* (branching off at B64, PP = 0.50). Successively more inclusive clades subsume African *Metapterodon* (at node B63, PP = 0.38), European *Pterodon*

dasyuroides (at node B62, PP = 0.42), African *Koholia* (at node B61, PP = 0.36), Asian *Orienspterodon* (at node B60, PP = 0.32), and European *Paroxyaena* (at node B58, PP = 0.29).

The weakly supported clade formed by Apterodontinae and Hyainailourinae (B54, PP = 0.28) was called Hyainailouridae by Solé et al. (2015). Apterodontinae (B55) is strongly supported as a clade (PP = 0.79) with *Quasiapterodon* as the sister taxon of *Apterodon*, a strongly supported genus (PP = 0.94) with *Apterodon macrognathus* recovered as the basal-most species, and *Apterodon gaudryi*, from the early Oligocene of Europe being the sister taxon of *Apterodon langebadrae*, from the early Oligocene of Afro-Arabia (at node B57; PP = 0.92).

The oldest African hyaenodontidans, *Lahimia* and *Boualitomus*, form a strongly supported clade (B40; PP = 0.89) as they did in the parsimony analysis, but have no special relationship to teratodontines or hyainailourines to the exclusion of various other species from the Eocene of Asia, Europe, and North America. For instance, *Tritemnodon*, from the early Eocene of North America, is placed closer to teratodontines and hyainailourids, and with moderate support (B41; PP = 0.56), followed by successive taxa referred to Indohyaenodontinae by Solé et al. (2014b) and Rana et al. (2015). The clades that successively include the paraphyletic “indohyaenodontines” *Indohyaenodon* (B42; PP = 0.37), *Kyawdawia* (B43; PP = 0.32), and *Paratritemnodon* (B44; PP = 0.33) are weakly supported, as is the more deeply nested clade that includes early Oligocene African *Metasinopa fraasi* (B45; PP = 0.31) as the sister taxon of the weakly supported (PP = 0.21) clade that contains Teratodontinae, Apterodontinae, and Hyainailourinae (B46).

The composition of the clade that contains *Arfia*, *Sinopa*, Limnocyoninae, Indohyaenodontinae, Teratodontinae, Apterodontinae, and Hyainailourinae (B23; PP = 0.42) is identical in taxonomic composition to clade P20 except for the inclusion of *Preregidens*. The

earliest divergences are among predominantly North American taxa. The sister group of all other members of B23 (B24) contains the two species of *Prototomus*, *Sinopa* (B27; PP = 0.85), and *Arfia* (B28; PP = 1.0). In the parsimony analysis, *Prototomus minimus*, an earliest Eocene species from Europe (Smith & Smith, 2001), was recovered in a more basal position in Hyainailourinae than *Prototomus phobos*, an early Eocene species from North America (Zack, 2011), but the Bayesian analysis places both *Prototomus* species as sister taxa of an *Arfia-Sinopa* but with weak support (B24; PP = 0.24 and B25; PP = 0.26). Successively more exclusive clades leading to the common node of the clade containing hyainailourids, teratodontines, and koholiines (B39) first exclude Limnocyoninae (node B33, PP = 0.22), followed by a *Galecyon-Gazinocyon* clade (node B37, PP = 0.27), *Preregidents* (node B38, PP = 0.36) and *Pyrocyon*.

As in the parsimony analysis, *Tinerhodon* is recovered as the sister taxon of *Cimolestes* (B74; PP = 0.59) outside of Hyainailourinae. The Hyainailourinae + *Tinerhodon* + *Cimolestes* clade (B73) is strongly supported (PP = 0.95), as is Hyainailourinae (B1, PP = 1.0). The basal nodes of Hyainailourinae are different from the basal polytomy recovered using parsimony analysis (P1) with several early Eocene taxa from Europe (*Eoproviverra*, *Lesmesodon* + *Parvagula*, and *Morlodon*) representing successive sister taxa of more deeply nested hyainailourines. As in the parsimony analysis, *Eoproviverra* is the sister taxon of all other hyainailourines (B1) but, in contrast, the Bayesian analysis recovers successively more exclusive clades that first subsume *Lesmesodon* + *Parvagula* (B2, PP = 0.75) and then *Morlodon* (B4, PP = 0.15). The sister group of *Morlodon* is a weakly supported clade (B5, PP = 0.13) that diverges into Proviverrinae/Hyainailourinae (B6, PP = 0.13) and the clade already discussed above (B23) of predominantly North American, Asian, and Afro-Arabian taxa.

The basal nodes in the Proviverrinae/Hyaenodontinae clade (B6) are weakly supported (B7, PP = 0.15; B8, PP = 0.26; B9, PP = 0.33; B11, PP = 0.38) and the branching order differs from that in the parsimony analysis. In the Bayesian analysis, *Quercytherium* is more basal than *Eurotherium* and *Leonhardtina* (the latter of which also do not form a clade as in the parsimony analysis), and *Preregidens* is not recovered in Proviverrinae + Hyaenodontinae. *Cynohyaenodon* is the sister taxon to several strongly supported and successively more nested clades containing derived hyaenodontines and derived “proviverrines,” including clades with *Leonhardtina* (B12 = 0.87), *Eurotherium* (B13 = 0.92), *Matthodon* (B15, PP = 0.94), and *Oxyaenoides* (B16, PP = 0.96) as successive sister taxa of Hyaenodontinae. As in the parsimony analysis, *Propterodon* is not monophyletic, with *Propterodon morrissi* being the sister group of all other hyaenodontines including *Propterodon tongi*; the *P. tongi* + *Hyaenodon* clade (B19) is moderately supported (PP = 0.53). *Hyaenodon* (B20) is strongly supported (PP = 1.0) and the two early Oligocene species from Asia, *Hyaenodon neimongoliensis* and an undescribed *Hyaenodon* species from Ergiliyn Dzo, are successive sister taxa to latest Eocene *Hyaenodon minor* from Europe and the late Eocene/early Oligocene *Hyaenodon horridus* from North America.

Tip-Dating Bayesian Inference

The “allcompat” topology recovered using the Bayesian tip-dating method is shown in Fig. 19 with branches color-coded to indicate relative percent change per million years (% change/Ma). The alphanumeric code to the left of the relevant node corresponds with this discussion and posterior probabilities (PP) are italicized and placed to the right or below the relevant node. Table S4 contains the statistics generated by the tip-dating analysis most relevant to this study: median and mean age, median and mean relative rates, posterior probabilities, and

the 95% confidence interval for the youngest and oldest age estimates for each node. Each taxon is shown with the full estimated age range drawn from the literature (Table S2) and the mean age for each taxon, as recovered with tip-dating Bayesian analysis, is indicated in the Fig. 19. Some taxa are reconstructed with a median divergence date that postdates the earliest possible age for the taxon (see *Eurotherium* in Fig. 19), but the mean estimated age for each taxon always postdates the median estimated divergence date. Divergence dates discussed below are mean age estimates. The results of the parsimony character optimization onto the “allcompat” tip-dating tree are listed in Table S3.

In order to perform the tip-dating analysis and place a prior on the age of Hyaenodontida, that clade had to be explicitly defined. Because *Tinerhodon* was recovered as the sister taxon of *Cimolestes* using both parsimony and standard Bayesian analysis, *Tinerhodon* was excluded from Hyaenodontida in the tip-dating analysis. *Tinerhodon*, *Cimolestes*, and *Maelestes* were recovered as the sister group of Hyaenodontida (T73; PP = 0.63). *Tinerhodon* and *Cimolestes* are estimated to have split from each other during the Late Cretaceous (~73 Ma). Hyaenodontida is estimated to have originated in the Late Cretaceous at ~68.5 Ma.

As in the parsimony and standard Bayesian analyses, the monophyly of *Akhnenavenus* is strongly supported (T67; PP = 0.95), and the divergence between the two species is reconstructed as having occurred ~37 Ma (late Eocene). Also like the parsimony and standard Bayesian analyses, *Akhnenavenus* is the sister clade to the rest of the Afro-Arabian hyainailourines (T66; PP = 0.44), a clade that is estimated to have originated in the late middle Eocene (~42 Ma). Evolutionary rates in the hyainailourine clade are relatively slow (<1.0% change/Ma) and the branch supporting *Akhnenavenus* (T67) is only moderately faster (~1.37% change/Ma) than the evolutionary rates of neighboring branches. Hyainailourinae as a whole (T62) is strongly

supported (PP = 0.72) and is estimated to have originated in the middle Eocene (~47 Ma); it is taxonomically identical to Hyainailourinae as recovered by the standard Bayesian analysis (B62). A *Pterodon dasyuroides* + *Metapterodon* clade (T63; PP = 0.44) is the sister group of all other hyainailourines. Successively more nested clades include *Kerberos* (T64; PP = 0.23) and *Hemipsalodon* (T65; PP = 0.28) as sister taxa of Afro-Arabian hyainailourines. There is weak support for the placement of *Akhnatonavus* as the sister clade of the rest of Hyainailourinae (T66; PP = 0.44). As in the Bayesian analysis, African “*Pterodon*” is paraphyletic with respect to the Miocene hyainailourines *Isohyaenodon*, *Leakitherium*, and *Megistotherium*, the monophyly of which is strongly supported (T70, PP = 0.99); this result is consistent with both the parsimony (node P51) and standard Bayesian analyses (node B70).

As in the standard Bayesian analysis, *Brychotherium* is nested within Teratodontinae (T48; PP = 0.50), but in contrast to the results from the parsimony and standard Bayesian analyses, *Brychotherium* is the sister taxon of a (*Teratodon*, (*Masrasector*, (*Anasinopa*, *Dissopsalis*))) clade (T49, PP = 0.38) that is estimated to have diverged at ~45 Ma. *Anasinopa* and *Dissopsalis* are strongly supported as sister taxa (T52; PP = 0.79) in a clade that is estimated to have originated ~27 Ma (middle Oligocene). Teratodontinae as a whole is estimated to have appeared ~58 Ma (late Paleocene), with *Glibzegdouia* and *Furodon* as its most basal members. The stem leading to the clade *Glibzegdouia* + T48 (T47) has a moderate rate of evolutionary change (1.04% change/Ma) and is the last of the basal teratodontine branches to change at a moderate rate. All more derived teratodontine branches show slower rates except for the *Brychotherium* (1.4% change/Ma) and *Dissopsalis* branches (1.34% change/Ma).

The clade that includes Apterodontinae and Hyainailourinae plus *Koholia*, *Tritemnodon*, and *Paroxyaena* (T53) is weakly supported (PP = 0.29) and is estimated to have originated

during the Paleocene (~59 Ma) along a branch that was marked by rapid evolutionary change (2.71% change/Ma). The clade *Tritemnodon* + *Koholia* (T54) is weakly supported (PP = 0.39) and is the sister group of the larger Apterodontinae + Hyainailourinae + *Paroxyaena* clade (T55, which is supported by a PP of 0.35). *Paroxyaena* is robustly supported (T56; PP = 0.98) as a clade. *Paroxyaena* is estimated to have diverged from Apterodontinae + Hyainailourinae during the Ypresian (T55; ~54.5 Ma). The clade Apterodontinae + Hyainailourinae (T57) is estimated to have diverged during the Ypresian (~53 Ma); the stem leading to this clade is reconstructed as having had a relatively fast evolutionary rate (2.81% change/Ma).

Apterodontinae (T59) has robust support (PP = 0.99) and is estimated to have originated during the Lutetian (middle Eocene, ~43 Ma). *Quasiapterodon* is recovered as the sister taxon to the genus *Apterodon* on a branch characterized by a moderate relative evolutionary rate (~1.54% change/Ma). The monophyly of *Apterodon* is weakly supported (T59; PP = 0.47) and the three species sampled here are estimated to have first diverged during the Bartonian (late middle Eocene, ~40.6 Ma).

Hyainailourinae, Apterodontinae, Indohyaenodontinae, and Teratodontinae form a very weakly supported Hyainailouroidea clade (T41; PP = 0.09) that is estimated to have originated during the early Paleocene (~65 Ma). The common stem shows a fast relative evolutionary rate (2.94% change/Ma). This large clade (T41) includes two major sub-clades with early divergences: Indohyaenodontinae + Teratodontinae (T42) and Hyainailourinae + Apterodontinae (T53). The indohyaenodontine/teratodontine clade (T42; PP = 0.15) is estimated to have originated in the early Paleocene (~63 Ma). Unlike in the standard Bayesian analysis, Indohyaenodontinae (T43; PP = 0.30) is monophyletic and its origin is placed in the middle Paleocene (~60 Ma).

A major difference between the standard Bayesian and tip-dating Bayesian allcompat topologies is the structure of relationships near the origin of Hyaenodontida. In the tip-dating analysis, *Eoproviverra* is not recovered as the sister taxon to all other hyaenodontidan clades. Instead, *Eoproviverra* is nested within the very weakly supported clade Hyaenodontidae (T8; PP = 0.11) as the sister taxon of *Proviverra* (T14; PP = 0.54). Based on the tip-dating results, the earliest split in Hyaenodontida gave rise to two large clades: one originated ~68 Ma (T2) and includes the *Sinopa* clade (T3) and Hyaenodontidae, and the other originated ~68 Ma (T29) and includes Limnocyoninae, the *Galecyon* clade, the *Lahimia* clade, and Hyainailouroidea. In each of these major hyaenodontidan clades, the earliest diverging clades are predominantly composed of North American taxa once classified as “proviverrines” though these early-diverging relationships have very weak support (T2; PP = 0.06 and T29; PP = 0.17).

The *Sinopa* clade (T3) includes *Arfia* (T5; PP = 1.0), *Prototomus*, and *Sinopa* (T7; 0.97) and is sister clade to the predominantly European clade Hyaenodontidae (T8; PP = 0.11), which includes European “Proviverrinae” and Hyaenodontinae. The branch supporting Hyaenodontinae has a rapid relative evolutionary rate (3.21% change/Ma) and an estimated origin of ~66.7 Ma. The oldest taxa in Hyaenodontinae are from the earliest Eocene, and multiple, unsampled, rapidly diverging lineages are reconstructed as originating during the Paleocene.

In the tip-dating analysis topology *Parvagula*, *Lesmesodon*, and *Morlodon* are recovered within Hyaenodontidae, though all PP support for these early-diverging relationships is very weak (T9; PP = 0.12, T11; PP = 0.06; T12; PP = 0.10). The composition of the clade defined by the divergence of *Cynohyaenodon* (T15; PP = 0.26) at ~62 Ma is identical in taxonomic composition to clade B9 in the standard Bayesian analysis, and only differs in topology in the placement of *Quercytherium* (T17; PP = 1.0) and *Leonhardtina* (T19; PP = 0.37). During the late

Paleocene and early Eocene, along the branch that includes *Matthodon* (T21) and the branch that includes *Oxyaenoides* (T22), relatively rapid evolutionary changes took place (T21; 5.22% change/Ma, T22; 5.27% change/Ma) before the origin of the clade that includes Hyaenodontinae (T24; PP = 0.98) in the early Eocene (~49.4 Ma). The stem supporting Hyaenodontinae (T24) has a fast relative evolutionary rate (3.49% change/Ma). The relationships within Hyaenodontinae are the same as in the standard Bayesian analysis. The results of this analysis place the origins of *Hyaenodon* (T26) in the late middle Eocene (~40.9 Ma).

The most rapid median evolutionary rate in the tip-dating analysis is reconstructed along the branch supporting the clade that includes all Afro-Arabian hyaenodontidans, the *Galecyon* clade and Limnocyoninae (T29; PP = 0.17; 8.45% change/Ma). The clade composed of predominately North American taxa (*Galecyon* clade and Limnocyoninae; T30; PP = 0.10) that originated in the earliest Paleocene (~65.4 Ma) and is sister to the larger, very weakly supported clade that includes all Afro-Arabian taxa (T37; PP = 0.03). Within the Afro-Arabian clade (T37) the oldest hyaenodontidan in the analysis, *Lahimia*, is recovered as the sister taxon of *Boualitomus* (T39; PP = 0.96), a relationship supported by a branch with a very rapid evolutionary rate (4.75% change/Ma). *Lahimia* + *Boualitomus* (T39), is not closely related to *Koholia* and thus Koholiinae is not recovered by tip-dating analysis. Instead *Lahimia* + *Boualitomus* is the sister clade to *Preregidens* + *Pyrocyon* (T40; PP = 0.12) and these four taxa form the sister clade of the very weakly supported Hyainailouroidea (T41; PP = 0.09).

BIOGEOGRAPHIC RESULTS

Biogeographic reconstructions on the maximum parsimony topology

As described above, three methods of biogeographic analysis were applied to the maximum parsimony strict consensus tree: parsimony optimization of geographic areas (PO), likelihood optimization of geographic areas (LO), and Bayesian Binary MCMC (BBM). The biogeographic reconstruction for each node in the strict consensus parsimony topology is presented in Table S5 and the continental area designated for each OTU and the results of the BBM analysis are shown in Fig. 20. The pie chart over each node represents the probability that the clade originated from each continental area.

The root node of Hyaenodontida (P1) is unambiguously reconstructed with Europe as the origin for the entire clade using parsimony optimization (PO). A European origin for Hyaenodontida is strongly supported by likelihood optimization (LO = 93.92%) and Bayesian Binary MCMC analysis (BBM = 99.68%). Node P2 supports a polytomy comprised of *Morlodon*, *Lesmesodon*, a clade of “Proviverrinae” and Hyaenodontinae (P4), and the clade (P20) that includes *Arfia* (P21), Limnocyoninae (P23), *Galecyon* + *Gazinocyon* (P26), *Sinopa* (P30), *Prototomus*, “Koholiinae,” “Indohyaenodontinae,” “Teratodontinae,” Apterodontinae, and “Hyainailourinae” (P31) is reconstructed, like the root of Hyaenodontida, with an unambiguous origin in Europe (PO) with strong support from the other biogeographic methods (LO = 99.73%; BBM = 99.79%). Within the “Proviverrinae”/Hyaenodontinae clade (P4), all stem nodes and constituent clades [*Leonhardtina* and *Eurotherium* (P7), *Boritia* and *Parvagula* (P10), *Quercytherium* (P12)] are unambiguously reconstructed as originating in Europe with strong support from all biogeographic methods. A dispersal to Asia is implied at the basal node of Hyaenodontinae (P17), with the node shared by *Propterodon* and *Hyaenodon* unambiguously reconstructed in Asia, which is highly likely using LO (98.31%) and BBM (96.77%). *Hyaenodon*

is also unambiguously Asian in origin (LO = 97.51%, BBM = 99.9%) with subsequent dispersals to North America (*Hyaenodon horridus*) and Europe (*Hyaenodon minor*).

The common node (P20) that unites *Arfia* (P21) as the sister clade to P22 (a clade that includes Limnocyoninae, *Galecyon* + *Gazinocyon*, “Koholiinae,” “Teratodontinae,” Apterodontinae, and “Hyainailourinae”) is unambiguously resolved with a North American origin (LO = 89.89%; BBM = 82.38%) and a small likelihood of an origin in Europe (LO = 8.63%; BBM = 17.53%). This reconstruction implies a dispersal of hyaenodontidans from Europe to North America. Node P22 unites a polytomy comprised of the unambiguously North American Limnocyoninae (P23; LO = 99.90%; BBM = 99.99), the unambiguously North American *Galecyon* clade (P26; LO = 99.76%; BBM = 99.99%), North American *Prototomus phobos*, European *Prototomus minimus*, and clade P31 (“Koholiinae,” “Indohyaenodontinae,” Apterodontinae, “Hyainailourinae”). P22 is unambiguously North American in origin with a high likelihood of this origin using the other biogeographic methods (LO = 99.72%; BBM = 92.47%). Multiple dispersals to Afro-Arabia, North America, and Europe are implied at node P31, which supports a large polytomy that includes taxa categorized as “Teratodontinae” (*Brychotherium*, *Dissopsalis*, *Anasinopa*, *Glibzegdouia*, *Metasinopa*, and *Teratodon*) in Solé et al. (2014b) and Rana et al. (2015); as “Koholiinae” (*Koholia*, *Lahimia*, *Boualitomus*, and *Metapterodon*) in Solé et al. (2014b); as “Indohyaenodontinae” (*Indohyaenodon*, *Kyawdawia*, *Paratritemnodon*) in Solé et al. (2014b); as “Hyainailourinae” (*Paroxyaena*, *Pterodon dasyuroides*, and *Orienspteron*) in Solé et al. (2015); and as “Sinopaninae” (*Pyrocyon* and *Tritemnodon*) in Rana et al. (2015). The polytomy at node P31 also includes Apterodontinae (P39), a clade unambiguously resolved with an Afro-Arabian origin (LO = 99.81%; BBM = 99.99%) and a clade of hyainailourines (P43) that includes *Akhnatnavus* that is unambiguously Afro-Arabian in origin (LO = 84.85%; BBM

= 86.65%). This large polytomy, P31, has a contradictory biogeographic reconstruction. Parsimony optimization unambiguously recovers an Afro-Arabian origin for the clade, implying a dispersal from North America to Afro-Arabia between node P22 and node P31. Likelihood optimization also supports Afro-Arabia as the most likely continent of origin for P31. However, BBM analysis only resolves an Afro-Arabian origin for P31 as 9.83% likely. More likely, according to the BBM analysis, is a North American origin (75.85%) or European origin (11.84%) with multiple dispersals between each of the continents. What is certain, according to the maximum parsimony topology, is at least two lineages dispersed to Afro-Arabia — Apterodontinae (P39) and a subset of hyainailourines (P43)— and radiated there with the lineage leading to *Apterodon gaudryi* (P40) dispersing from Afro-Arabia to Europe, the lineage leading to *Kerberos* (P43) dispersing from Afro-Arabia to Europe, and the lineage leading to *Hemipsalodon* (P43) dispersing from Afro-Arabia to North America. Direct dispersal between Afro-Arabia and North America, as implied at multiple nodes in the P31 clade, is unlikely and these dispersals likely passed through Europe or Asia but this strict consensus topology is not well-resolved enough to offer insight into which dispersal routes were most likely followed by hyaenodontidans between North America and Afro-Arabia.

Biogeographic reconstructions on the “allcompat” Bayesian topology

The results of each method for reconstructing biogeography on the Bayesian “allcompat” topology [parsimony optimization (PO), likelihood optimization (LO), and Bayesian Binary MCMC (BBM)] are listed in Table S6 and the results of BBM are shown in Fig. 21 imposed on the standard Bayesian topology. The root node of Hyaenodontida (B1) is unambiguously resolved as European using parsimony optimization and is strongly supported as such by the

other methods (LO = 96.36%; BBM = 99.86%). The clade *Parvagula* + *Lesmesodon* (B3) is unambiguously European in origin (LO = 99.74%; BBM = 99.86%), as is the common node of *Parvagula* + *Lesmesodon* and the rest of Hyaenodontida (B2; LO = 99.74%; BBM = 99.99%), and the clade that unites Proviverrinae/Hyaenodontinae, *Sinopa*, *Arfia*, Limnocyoninae, *Lahimia* + *Boualitomus*, “Indohyaenodontinae,” Teratodontinae, Apterodontinae, and Hyainailourinae (B5; LO = 97.55%; BBM = 99.89%). Proviverrinae/Hyaenodontinae (B6) is also unambiguously European (LO = 99.84%; BBM = 100%) and every node more deeply nested in the clade is as strongly supported with a European origin until node B16, which supports *Oxyaenoides* as the sister clade to Hyaenodontinae. *Oxyaenoides* + Hyaenodontinae (B16) is unambiguously reconstructed as having originated in Europe (LO = 75.25%; BBM = 99.58%) though LO also recovers a 19.26% probability of an Asian origin for the clade. Hyaenodontinae (B18; *Propterodon* + *Hyaenodon*) is unambiguously resolved with an Asian origin (LO = 98.63%; BBM = 97.61%). *Hyaenodon* (B20) is also unambiguously reconstructed with an Asian origin and the clade *H. horridus* + *H. minor* (B22) is ambiguously resolved as having originated either in Asia [the most likely result using LO (39.71%) and BBM (60.24%)], Europe (LO = 26.69%; BBM = 20.62%), or North America (LO = 32.87%; BBM = 18.85%).

The clade that contains *Sinopa*, *Arfia*, Limnocyoninae, *Lahimia* + *Boualitomus*, “Indohyaenodontinae,” Teratodontinae, and Hyainailouridae (B23) is ambiguously reconstructed as having originating in either Europe (LO = 53.19%; BBM = 45.35%) or North America (LO = 76.72%; BBM 23.18%). The *Sinopa*-*Arfia*-*Prototomus* clade (B24) is ambiguously reconstructed with either a European (LO = 54.25%; BBM = 73.51%) or North American (LO = 44.83%; BBM = 26.32%) origin, with its more deeply nested clade (B25) being unambiguously of North American origin (LO = 88.53%; BBM = 98.11%). The clade containing Limnocyoninae (B30) is

the sister clade to “Indohyaenodontinae,” Teratodontinae, Apterodontinae, and Hyainailourinae (B29) and is unambiguously North American in origin (LO = 89.74%; BBM = 96.25%), as is Limnocyoninae (B30; LO = 97.61%; BBM = 99.83%) and *Gazinocyon* + *Galecyon* (B34; LO = 98.99%; BBM = 99.96%). *Preregidens* is reconstructed as having dispersed from North America to Europe. The common ancestor of *Lahimia* + *Boualitomus* is unambiguously Afro-Arabian (B40; LO = 98.57%; BBM = 99.42%), but a dispersal from North America to Afro-Arabia is reconstructed along their common stem.

A dispersal from North America to Asia is reconstructed at the node uniting *Indohyaenodon* with other indohyaenodontines, Teratodontinae, Apterodontinae, and Hyainailourinae; their common node is unambiguously reconstructed as Asian (LO = 91.23%; BBM = 98.69%). A subsequent dispersal from Asia to Afro-Arabia is reconstructed between nodes B44 and B45, the latter of which joins African *Metasinopa* to Teratodontinae, Apterodontinae, and Hyainailourinae; B45 is unambiguously reconstructed as being of Afro-Arabian origin (LO = 94.54%; BBM = 98.04%).

Teratodontinae (B47) and all of its internal nodes are unambiguously Afro-Arabian (B47 LO = 99.90%; BBM = 100%), as is the common node that Teratodontinae shares with Apterodontinae and Hyainailourinae (B46; LO = 97.81%; BBM = 99.95%). Apterodontinae (B55) and all internal nodes are also unambiguously Afro-Arabian in origin (LO = 99.14%; BBM = 100%), supporting trans-Tethyan dispersal to Europe to account for the presence of *Apterodon gaudryi* on that landmass.

The biogeographic history of Hyainailourinae and its possible relatives is particularly complex. The node that unites *Paroxyaena* and more deeply nested hyainailourines (B58) is unambiguously Afro-Arabian (LO = 44.01%; BBM = 91.74%) though LO also resolves high

probabilities for a European origin (29.79%) and an Asian origin (23.04%); the most probable reconstructions on the Bayesian topology imply that *Paroxyaena* dispersed from Afro-Arabia to Europe. *Orienspteron* is the next most deeply nested hyainailourine relative and the common node it shares with other hyainailourines (B60) is unambiguously Afro-Arabian in origin using PO, an origin supported by BBM (90.63%), but LO analysis recovers Asia as a more likely center of origin (54.14%) with Afro-Arabia as the second-most probable continent of origin for the clade (30.70%). *Koholia* is the sister group of definitive hyainailourines, and their common node (B61) is unambiguously Afro-Arabian (LO = 62.78%; BBM = 98.07%) with LO recovering a 21.77% probability that this clade originated in Europe. *Pterodon dasyuroides*, a European taxon, is part of the next most deeply nested clade (B62), which has an unambiguous origin in Afro-Arabia, a reconstruction strongly supported by BBM (85.25%), but less probable using LO (17.89%) than a European origin for B62 (81.10%). *Metapterodon*, nested between European *Pterodon dasyuroides* and *Kerberos*, is an Afro-Arabian taxon whose common node with more derived hyainailourines (B63) is unambiguously Afro-Arabian using PO, an origin supported by BBM (94.26%) but, again, LO recovers Europe as the more likely continent of origin for the clade (64.17%) followed by Afro-Arabia (33.47%). The common node for *Kerberos* and all more deeply nested hyainailourines (B64) is unambiguously Afro-Arabian in origin (LO = 33.32%; BBM = 79.06%) but LO resolves the most probable area of origin as Europe (LO = 63.56; BBM = 19.3%). *Hemipsalodon* is sister taxon to an entirely Afro-Arabian clade of hyainailourines and their common node (B65) is unambiguously resolved with an Afro-Arabian origin (LO = 57.79%; BBM = 81.24%). *Akhnatnavus* (B67) is unambiguously Afro-Arabian (LO = 99.93%; BBM = 99.94%) and the node shared with more deeply nested Afro-Arabian hyainailourines

(B66) is also unambiguously Afro-Arabian (LO = 97.84%; BBM = 99.94%), as are all nodes in the Afro-Arabian hyainailourine clade.

Biogeographic reconstructions on the tip-dating topology

The tip-dating topology differs from the standard Bayesian topology in a number of ways that change the biogeographic reconstructions of ancestral nodes within Hyainailourinae when parsimony optimization (PO), likelihood optimization (LO), and Bayesian Binary MCMC (BBM) methods are applied to the tree. The inclusion of specific divergence dates and branch lengths from tip-dating analysis also alter some biogeographic hypotheses based on the parsimony and standard Bayesian topologies. The results of each method are listed in Table S7 and the results of BBM analysis are shown over the corresponding nodes in Fig. 22.

Unlike in the standard Bayesian topology, Hyainailourinae (T1) is unambiguously resolved with an origin in North America (LO = 69.57%; BBM = 83.96%). Hyainailourinae is split into two major clades, one that includes Hyainailourinae (T2) and one that includes Hyainailouroidea (T29). Node T2 is unambiguously North American in origin (LO = 76.46%; BBM = 62.24%) though there is a high probability of a European origin for T2 (LO = 26.97%; BBM = 36.85%). Node T29 is also unambiguously North American (LO = 72.05%; BBM = 87.75%) with the next-most likely origin for the node that includes Hyainailouroidea in Afro-Arabia (LO = 15.54%; BBM = 8.17%).

The larger clade that contains Hyainailourinae (T2) includes a predominately North American *Sinopa* clade (T3) that is unambiguously North American in origin (LO = 84.88%; BBM = 87.7%) and a predominately European clade with “Proviverrinae” and Hyainailourinae (T8) that is unambiguously European in origin (LO = 92.05%; BBM = 99.67%). Despite the

inclusion of *Prototomus minimus* from Europe and *Sinopa jilinia* from Asia, every node within the *Sinopa* clade (T3) is unambiguously North American in origin (T4; LO = 85.71%; BBM = 70.6%, T5, *Arfia*; LO = 99.79%; BBM = 99.84%, T6; LO = 93.46%; BBM = 98.56%, T7, *Sinopa*; LO = 91.89%; BBM = 97.51%) implying dispersal from North America to Europe in the lineage that includes *Prototomus minimus*, and dispersal from North America to Asia in the lineage that includes *Sinopa jilinia*.

The sister clade of the *Sinopa* clade, Hyaenodontidae (T8), is unambiguously European in origin (LO = 92.05%; BBM = 99.67) and all of the nodes and clades contained within Hyaenodontidae are unambiguously European in origin (T8–T22; LO >92%; BBM >99%) except for the nodes defined as part of Hyaenodontinae (T24). During the early Eocene, the ancestor of Hyaenodontinae (T24) dispersed from Europe to Asia and the origin of Hyaenodontinae (T24) is unambiguously in Asia (LO = 96.32%; BBM = 97.72%). The taxonomically diverse genus *Hyaenodon* (T26) is also unambiguously Asian in origin (LO = 96.59%; BBM = 99.99%). The biogeographic scenario surrounding the dispersal of *Hyaenodon* to North America (represented in this analysis by *H. horridus*) and to Europe (*H. minor*) is ambiguous with the common ancestor of these species most likely originating in Asia (LO = 52.32%; BBM = 59.83%) before dispersal to North America and Europe, though there is support for this common ancestor originating in Europe (LO = 24.92%; BBM = 21.82%) or North America (LO = 22.02%; BBM = 18.06%).

As stated above, the large clade that includes Limnocyoninae, the *Galecyon* clade, and Hyainailouroidea (T29) is unambiguously North American in origin. The clade composed largely of North American taxa, *Galecyon* clade + Limnocyoninae (T30), is unambiguously North America in origin (LO = 95.99%; BBM = 99.88%) and all nodes contained within the *Galecyon*

clade and Limnocyoninae (T31–T36) unambiguously originate in North America (LO >95%; BBM >99%). This reconstruction indicates Asian *Prolimnocyon chowi* is the result of a dispersal event from North America to Asia during the late Paleocene.

The *Galecyon* clade + Limnocyoninae clade (T30) is sister to the large clade that includes all Afro-Arabian taxa (T37). This node is ambiguously reconstructed as either Afro-Arabian or North American in origin, though an Afro-Arabian origin is more likely (LO = 48.27%; BBM = 73.37%) than a North American origin (LO = 43.31%; BBM = 24.21%). This reconstruction indicates the ancestor of *Lahimia*, Indohyaenodontinae, Teratodontinae, Apterodontinae, and Hyainailourinae likely dispersed to Afro-Arabia from North America in the Late Cretaceous. Direct dispersal between these continents seems unlikely and the implications of this dispersal are discussed below.

The clade that contains the oldest known hyaenodontidan, *Lahimia*, along with *Preregidens*, *Pyrocyon*, and *Boualitomus* (T38) has an ambiguous origin in Afro-Arabia (LO = 51.97%; BBM = 79.77%) or North America (LO = 39.72%; BBM = 16.66%), though an Afro-Arabian origin is more likely. This result implies the ancestors of North American *Pyrocyon* and European *Preregidens* (T40) independently dispersed from Afro-Arabia (LO = 29.76%; BBM = 49.78%) or the common ancestor of these taxa dispersed from Afro-Arabia to North America (LO = 49.78%; BBM = 48.95%) or from Afro-Arabia to Europe (LO = 18.56%; 37.57%). The clade that includes *Lahimia* and *Preregidens* (T38) is the sister clade of Hyainailouroidea (T41). Hyainailouroidea is unambiguously Afro-Arabian in origin (LO = 66.14%; BBM = 94.99%). The clade that includes Indohyaenodontinae and Teratodontinae (T42) also unambiguously originated in Afro-Arabia (LO = 68.48%; BBM = 94.1%). Indohyaenodontinae (T43) is unambiguously Asian in origin (LO = 82.18%; BBM = 96.4%) implying the ancestor of indohyaenodontines

1649 dispersed from Afro-Arabia to Asia during the Paleocene or early Eocene. Afro-Arabian
 1650 *Metasinopa fraasi* is nested within Indohyaenodontinae as the sister taxon of *Paratritemnodon*.
 1651 *Paratritemnodon* + *Metasinopa* (T45) is unambiguously Asian in origin (LO = 96.36%; BBM =
 1652 96.83%), indicating the ancestor of *Metasinopa* dispersed from Asia to Afro-Arabia during the
 1653 Eocene. The sister clade of Indohyaenodontinae (T43) is Teratodontinae, a clade that includes
 1654 *Brychotherium* and is entirely composed of Afro-Arabian taxa. Every node in Teratodontinae is
 1655 unambiguously Afro-Arabian in origin (T46–T52; LO > 95%; BBM > 99%).

1656 The sister clade of Indohyaenodontinae + Teratodontinae that includes *Koholia*,
 1657 *Tritemnodon*, *Paroxyaena*, Apterodontinae, and Hyainailourinae (T53) is unambiguously Afro-
 1658 Arabian in origin (LO = 74.41%; BBM = 94.75%). This clade contains taxa from North America
 1659 (*Tritemnodon*, *Hemipsalodon*), Europe (*Paroxyaena*, *Apterodon gaudryi*, *Pterodon dasyuroides*,
 1660 and *Kerberos*), and Asia (*Orienspteron*) but all nodes within the clade are unambiguously
 1661 reconstructed with an Afro-Arabian origin (T53–T71) using parsimony optimization except T56,
 1662 the node that supports the monophyly of *Paroxyaena*. This is evidence that most of the dispersal
 1663 scenarios that concern apterodontines and hyainailourines involve dispersal events from Afro-
 1664 Arabia to the northern continents. *Koholia* + *Tritemnodon* (T54) is likely Afro-Arabian in origin
 1665 (LO = 76.29%; BBM = 89.02%) and the ancestor of *Tritemnodon* dispersed from Afro-Arabia to
 1666 North America during the early Eocene. The ancestor of *Paroxyaena* dispersed from Afro-
 1667 Arabia (T55; LO = 68.57%; BBM = 83.19%) to Europe (T56; LO = 98.48%; BBM = 99.62%)
 1668 during the early Eocene. Apterodontinae (T58) originated in Afro-Arabia (LO = 96.49%; BBM =
 1669 99.94%), indicating the ancestor of European *Apterodon gaudryi* (T60) dispersed from Afro-
 1670 Arabia to Europe during the late Eocene or early Oligocene.

The common node for Hyainailourinae and *Orienspteron* (T61) is unambiguously Afro-Arabian in origin (LO = 62.37%; BBM = 80.23%), implying the lineage that includes *Orienspteron* dispersed from Afro-Arabia to Asia during the middle Eocene. Hyainailourinae (T62) is unambiguously Afro-Arabian (LO = 58.70%; BBM = 63.42%) though there some support for a European origin for Hyainailourinae (LO = 34.95%; BBM = 34.61%). The common node shared by European *Pterodon dasyuroides* and Afro-Arabian *Metapterodon kaiseri* (T63) is unambiguously Afro-Arabian, a result supported by BBM (59.9%). The LO analysis resolves this node as more likely European in origin (63.02%) and an Afro-Arabian origin for *Pterodon dasyuroides* + *Metapterodon* is resolved by LO as less likely (33.07%). This result complicates the dispersal of *Pterodon dasyuroides*, but it does not eliminate the possibility that the common ancestor of *P. dasyuroides* dispersed from Afro-Arabia to Europe during the middle Eocene. *Kerberos*, a European hyainailourine, is the sister taxon of the clade that includes North American *Hemipsalodon* and Afro-Arabian hyainailourines, and the common node (T64) is unambiguously Afro-Arabian in origin. The Afro-Arabian origin of T64 is supported by LO (59.2%) but not BBM (41.5%), which resolves Europe as a slightly more likely origin (55.85%) of the clade. This further supports the hypothesis that there were hyainailourines dispersing between Afro-Arabia and Europe in the middle Eocene, though the direction of this dispersal is ambiguous when all three biogeographic methods are applied to the tip-dating topology. Node T65 supports *Hemipsalodon* as the sister taxon of a clade of Afro-Arabian hyainailourines. The origin of T65 is unambiguously Afro-Arabian (LO = 66.97%; BBM = 61.13%), though there is also support for a European (LO = 22.34%; BBM = 17.88%) or North American (LO = 9.65%; BBM = 20.61%) origin for the clade.

Akhnatenavus (T67) is unambiguously Afro-Arabian in origin (LO = 99.9%; BBM = 100%) as is the common node (T66) shared with more deeply nested Afro-Arabian hyainailourines (LO = 97.58%; BBM = 99.92%). All Afro-Arabian hyainailourine clades more deeply nested than clade T66 are unambiguously resolved with an origin in Afro-Arabia with LO probabilities greater than 99% and BBM probabilities equal to 100%. Ultimately, according to the tip-dating analysis, Afro-Arabia is the center of hyainailouroidean radiation beginning in the Paleocene and is most likely the continent of origin for the ancestors of Indohyaenodontinae, Teratodontinae, Apterodontinae, and Hyainailourinae.

DISCUSSION

Phylogenetic position of *Brychotherium* and Teratodontinae

In both the standard Bayesian analysis and the Adams consensus derived from the parsimony analysis, *Brychotherium* was placed in the same clade as *Dissopsalis*, *Anasinopa*, and *Furodon* (P37, B51) to the exclusion of other teratodontines (Figs. 18, 16). The close relationship of *Brychotherium* with *Dissopsalis* and *Anasinopa* is not particularly surprising, because Solé et al. (2014b) also included *Brychotherium* in their analysis based on the descriptions and images of more fragmentary specimens provided by Holroyd (1994) in her doctoral dissertation, and found a well-supported (Bremer = 4) *Anasinopa-Brychotherium-Dissopsalis* clade as part of a similarly robust Teratodontinae (Bremer = 4) that also included *Masrasector*, *Teratodon*, and *Glibzegdouia*. The placement of early or middle Eocene *Furodon* as a derived teratodontine in the analyses presented here is more surprising, as this result differs from the parsimony-based results of Solé et al. (2014b) and Rana et al. (2015), both of which found *Furodon* to be a basal

hyainailourine. It is particularly noteworthy that the standard Bayesian analysis places *Furodon* deep within Teratodontinae as the sister taxon of Miocene *Anasinopa*, requiring an extensive ghost lineage for the *Anasinopa* branch through most of the Eocene and Oligocene. Similarly extensive ghost lineages are also required by the topology recovered by Rana et al. (2015), who found Miocene *Anasinopa* and *Dissopsalis* to be paraphyletic with respect to Paleogene teratodontines, and with the oldest teratodontine in their analysis (*Glibzegdouia*) being the most deeply nested. Such long ghost lineages, and near-inversions of the expected relationship between node age and stratigraphic succession, hints at the possibility of a misplaced root for teratodontines in those analyses.

The tip-dating analysis presented here (Fig. 19) instead places *Furodon* as the sister taxon of all other teratodontines, diverging from the other species in the late Paleocene or early Eocene, a result that is more consistent with the stratigraphic succession of species. In the tip-dating topology, Miocene *Anasinopa* and *Dissopsalis* are strongly supported (PP = 0.79) as sister taxa, with Oligocene species of *Masrasector* weakly situated as the clade's sister group, again significantly reducing the lengths of the ghost lineages implied by the other methods and previous studies. Tip-dating analysis also resolves *Glibzegdouia* and *Brychotherium* as tips of lineages that diverged from other teratodontines during the early and middle Eocene, respectively. This more basal position for *Brychotherium* is comparable to the position occupied by *Brychotherium* among "Afroasian proviverrines" in the study of Egi et al. (2005, in which *Brychotherium* is referred to as "African *Sinopa*"). The weakly supported, very basal teratodontine placement of *Furodon* is not radically inconsistent with the parsimony-based results of Rana et al. (2015), which placed Teratodontinae as the sister clade to Hyainailourinae, and *Furodon* as the basal-most sister group of Hyainailourinae, implying that basal-most

hyainailourines and teratodontines might be very similar morphologically. Solé et al.'s (2014b) analysis placed *Furodon* far from Teratodontinae, at the base of Hyainailourinae in a hyainailourine-koholiine clade; note, however, that Solé et al. (2014b) sampled far fewer taxa than did Rana et al. (2015), and the expanded sampling of Rana et al. might help to explain why their results are more consistent with those presented here.

The position of “Indohyaenodontinae” (*Indohyaenodon*, *Kyawdawia*, *Paratritemnodon*, and possibly *Metasinopa*, an African genus that is consistently placed in the same vicinity as “indohyaenodontines”) relative to Teratodontinae differs using each method, and has also been unstable in previous studies that have included these taxa. Solé et al. (2014b) found Indohyaenodontinae to be the sister group of *Apterodon* + Sinopaninae (which, in their analysis, includes *Sinopa*, *Tritemnodon*, *Pyrocyon*, and *Prototomus*), while Rana et al. (2015) found that “indohyaenodontines” were paraphyletic with respect to (Apterodontinae, (Teratodontinae, Hyainailourinae)). Neither of these analyses sampled *Metasinopa*. The parsimony analysis presented here did not resolve relationships among indohyaenodontines, but in the Adams consensus *Indohyaenodon*, *Kyawdawia*, *Paratritemnodon*, and the *Brychotherium* “teratodontine” clade + *Paroxyaena* (P36) fall into a polytomy at the base of a node (P35) shared with Apterodontinae + Hyainailourinae (P38), and tip-dating analysis supports the hypothesis that indohyaenodontines are more closely related to Teratodontinae than they are to Apterodontinae + Hyainailourinae. The ambiguous position of “indohyaenodontines” and teratodontines bears similarities to the “Afroasian proviverrine” clade recovered by Egi et al. (2005), which included *Dissopsalis* + *Anasinopa* as the sister clade of (*Paratritemnodon*, (*Masrasector*, *Kyawdawia*)). The fact that expanded sampling of taxa and characters, first by Rana et al. (2015), and now by this study, congruently recovers

“indohyaenodontines” and teratodontines close to Apterodontinae and Hyainailourinae suggests that the still poorly documented “indohyaenodontines” are likely to be of great importance for understanding the origin and dispersal of multiple Paleogene Afro-Arabian lineages.

Phylogenetic position of *Akhnatenavus* and Hyainailourinae

In every phylogenetic analysis performed in this study, *Akhnatenavus nefertiticyon* was placed as the sister taxon of early Oligocene *Akhnatenavus leptognathus*. This *Akhnatenavus* clade was recovered by every analysis as a sister group of Oligo-Miocene Afro-Arabian hyainailourines, either as the exclusive sister clade to the younger Afro-Arabian hyainailourines (standard Bayesian inference B66 and tip-dating Bayesian inference T66) or as part of a basal polytomy with those taxa and “*Pterodon*” *africanus* (parsimony analysis P48). In every analysis, North American *Hemipsalodon* and European *Kerberos* were recovered as sister taxa to the Afro-Arabian clade that includes *Akhnatenavus*, with European *Pterodon dasyuroides* and African *Metapterodon kaiseri* occupying even more basal positions in Hyainailourinae. In Solé et al. (2014b) *Akhnatenavus* was placed as the sister taxon to *Megistotherium*, with Afro-Arabian *Pterodon* species being that clade’s sister group. Rana et al. (2015) found no resolution among hyainailourines, with *Akhnatenavus* falling into a polytomy that also included *Hyainailouros*, *Koholia*, *Metapterodon*, *Oxyaenoides*, and *Pterodon* (note that, in this analysis, *Oxyaenoides* is placed with hyaenodontines). In their description of *Kerberos*, Solé et al. (2015) performed a phylogenetic analysis that included Hyainailourinae and found “*Pterodon*” *phiomensis* to be the sister group of an unresolved clade that included *Akhnatenavus*, *Isohyaenodon*, and *Hyainailouros*. Ultimately, earlier phylogenetic studies and the results presented in this study have supported Holroyd’s (1999) decision to erect the genus *Akhnatenavus* rather than keeping

1785 *A. leptognathus* as a species within the genus *Pterodon*, as was originally done by Osborn
1786 (1909).

1787 *Pterodon* is not monophyletic in any of the analyses. *Pterodon dasyuroides* (the type
1788 species of *Pterodon*) was consistently placed in a more basal position than either “*Pterodon*”
1789 *africanus* or “*Pterodon*” *phiomensis*. Furthermore, “*Pterodon*” *africanus* and “*Pterodon*”
1790 *phiomensis* were not recovered as sister taxa using any method in this study. This result is
1791 consistent with the results of Solé et al. (2015) in which *Pterodon dasyuroides* was also placed at
1792 a basal node in Hyainailourinae, with “*Pterodon*” *africanus* in a more deeply nested position, and
1793 “*Pterodon*” *phiomensis* even more deeply nested as the sister taxon to the clade that includes
1794 *Akhnatenavus*. Other studies that have included *Pterodon* have combined multiple species of
1795 *Pterodon* — the *Pterodon* OTUs in Solé et al. (2014b) and Rana et al. (2015) were a
1796 combination of African “*P.*” *africanus*, “*P.*” *phiomensis*, and “*P.*” *syrtos*, while *Pterodon* in
1797 Polly (1996) combines *P. dasyuroides* and “*P.*” *africanus*. The results of Solé et al. (2015) and
1798 the present study strongly suggest that the separate species included in *Pterodon* need to be
1799 reexamined and analyzed as separate OTUs in all future phylogenetic analyses, and that revision
1800 of the genus is in order. In his discussion of “Hyaenodontinae” (which then included *Pterodon*,
1801 *Apterodon*, *Metapterodon*, and *Hyaenodon*), Savage (1965) synonymized North American
1802 *Hemipsalodon* with *Pterodon*. Mellett (1969) disputed this, arguing that *Hemipsalodon* was
1803 distinct from *Pterodon*, though they do share dental and cranial similarities. The results of Solé
1804 et al. (2015) and the analysis presented here support the distinction between these taxa.

1805 In both Bayesian analyses, the major sister clade to Hyainailourinae is Apterodontinae,
1806 and this clade is also found in the Adams consensus derived from the parsimony analysis.
1807 However, in some cases, other taxa that are not distinctly apterodontine or hyainailourine

(*Koholia*, *Orienspterodon*, *Paroxyaena*) intervene or form sister clades of either subfamily. In the parsimony-based Adams consensus (P39) the consecutive sister clades of Hyainailourinae are *Orienspterodon* and Apterodontinae alone — *Quasiapterodon* and *Apterodon* — and the latter is well supported (Bremer = 4), whereas in the standard Bayesian analysis *Koholia*, *Orienspterodon*, and *Paroxyaena* intervene between Hyainailourinae and Apterodontinae as stem members of the former clade; again, Apterodontinae is well supported (PP = 0.79). In the tip-dating analysis, *Koholia*, *Tritemnodon*, and *Paroxyaena* shift to a position along the stem of Hyainailouridae, outside of Apterodontinae and Hyainailourinae, and *Orienspterodon* is the sister taxon of Hyainailourinae. This is the first time that *Orienspterodon* has been included in a phylogenetic analysis and it supports the conclusions of Egi, Tsubamoto & Takai (2007), who advocated for a close relationship between hyainailourines and *Orienspterodon* rather than a close relationship between *Orienspterodon*, *Paratritemnodon*, and *Kyawdawia*, as was suggested by Lewis & Morlo (2010).

Grohé et al. (2012) undertook the first phylogenetic analysis of Apterodontinae and found that species of *Apterodon* formed a polytomy with *Quasiapterodon* and *Metasinopa*. They did not include any hyainailourines in their analysis and the sister clade to their Apterodontinae was *Paratritemnodon* + *Kyawdawia*; both of those Asian taxa are clearly in the phylogenetic neighborhood of Apterodontinae, but the results of the current analysis indicate that hyainailourines are probably even more critical for any phylogenetic evaluation of apterodontine relationships. Solé et al. (2014b) performed the first phylogenetic analysis that included *Apterodon* alongside hyainailourines. Their study was limited to dental characters, and *Apterodon* was recovered as the sister clade to Sinopaninae, an assemblage whose monophyly was not recovered by any of the analyses presented here. More recently, Solé et al. (2015)

illustrated cranial features that are shared by Apterodontinae and Hyainailourinae, and elevated this group to Hyainailouridae, but these features were not converted into characters for their phylogenetic analysis, which recovered Apterodontinae and Hyainailourinae in a polytomy with *Lahimia* and *Boualitomus*. Cranial characters sampled from Polly (1996) were integrated into the analysis performed by Rana et al. (2015) and that study placed Apterodontinae as the sister clade to Teratodontinae + Hyainailourinae. The cranial features illustrated by Solé et al. (2015) were converted into characters for the character-taxon matrix presented here. The matrix also includes cranial characters from Polly (1996), and several new characters, and the “hyainailourid” hypothesis (Apterodontinae as the sister clade to Hyainailourinae) is supported, though it is disrupted in the parsimony analysis by the occasional incursion of “wildcard” taxa. For the sake of improved communication, we support and encourage the future use of the family-level nomen Hyainailouridae, which we recommend for the clade that includes *Apterodon macrognathus*, *Megistotherium osteothlastes*, and their last common ancestor. Furthermore, given the consistent placement of Teratodontinae as a major sister group of Hyainailouridae using all phylogenetic methods, we propose the use of the superfamily Hyainailouroidea for the clade that includes *Apterodon macrognathus*, *Megistotherium osteothlastes*, *Dissopsalis pyroclasticus*, and their last common ancestor.

One of the more problematic genera that may or may not fall within Hyainailouridae as defined above is middle-late Eocene *Paroxyaena*. In his discussion of the genus, Lavrov (2007) suggested that *Paroxyaena* was more closely affiliated with *Pterodon* and *Hemipsalodon* than with *Hyaenodon*, and that *Hemipsalodon*, *Paroxyaena*, and *Pterodon* belong to a distinct Paroxyaenini. Solé et al. (2015) placed *Hemipsalodon* in Paroxyaenini with *Paroxyaena*. All analyses performed in this study found a monophyletic *Paroxyaena*, but not Paroxyaenini as

defined by Solé et al. (2015); instead, *Paroxyaena* is situated in different positions depending on the method used. In the parsimony analysis, *Paroxyaena* can only be placed as a member of a clade that also includes hyainailouroids (P31), the relationships of which are largely unresolved, while standard Bayesian inference places *Paroxyaena* along the stem of Hyainailourinae (B58), and tip-dating analysis places *Paroxyaena* as a sister taxon of Hyainailouridae (T55). As a taxon with a long and narrow cranial vault, indistinct postorbital processes, and partially fused paracones and metacones the phylogenetic position of *Paroxyaena* close to or within Hyainailouridae seems likely. The M¹⁻² paracone and metacone of *Paroxyaena* are more divergent than most hyainailourids and the morphology of the molars may be one source of instability for the genus in the character-taxon matrix used in this analysis.

Phylogeny of Hyaenodontida

In this analysis the possible basal hyaenodontidan *Tinerhodon*, a late Paleocene taxon from Morocco, was found to be more closely related to *Cimolestes* than to Hyaenodontida, though it should be noted that outgroup sampling is limited and this relationship will need to be reevaluated again as the matrix used here is eventually expanded to include other non-hyaenodontidans. *Tinerhodon* was considered by McKenna & Bell (1997) to be part of Cimolestidae, but Gheerbrant et al. (2006) disputed its cimolestid affinities, suggesting that it was a basal hyaenodontidan based on comparisons to *Boualitomus*. Subsequent studies (Solé, 2013; Solé, Falconnet & Yves, 2014a; Solé et al., 2014b; Solé et al., 2015) found *Tinerhodon* to be the sister group of Hyaenodontida while Rana et al. (2015) found *Tinerhodon* to be the sister taxon of *Lahimia* + *Boualitomus*, a clade that occupied multiple positions in their analysis. None of the analyses performed here recover *Lahimia* and *Boualitomus* in such a basal position, and

1877 none place *Tinerhodon* as the sister taxon to Hyaenodontida to the exclusion of *Cimolestes*.
 1878 *Tinerhodon* has large metaconids that project well above the paraconids, well-developed talonid
 1879 cusps that include an additional cusp along the entocristid, and wide talonids basins, characters
 1880 not shared with *Boualitomus* and *Lahimia*; the placement of these taxa in separate clades is
 1881 consistent with the gross morphology of the dentition. Currently, *Tinerhodon* is only known from
 1882 isolated lower teeth, and more morphological information from upper teeth would help to further
 1883 test the phylogenetic position of this Afro-Arabian taxon, as it may either have important
 1884 biogeographic implications for Hyaenodontida, or be of no relevance to the clade.

1885 Crochet (1988) erected the subfamily Koholiinae to contain *Koholia*, which was, at the
 1886 time, the oldest-known Afro-Arabian hyaenodontidan. Solé et al. (2009) added *Boualitomus* and
 1887 *Lahimia* to Koholiinae based on wear patterns inferred from the fragmentary upper dentition of
 1888 *Koholia* that were used to reconstruct the lower dentition and make comparisons to *Lahimia*.
 1889 Solé et al. (2014b) later found a monophyletic Koholiinae that also included *Metapterodon*,
 1890 which together were placed as the sister clade to Hyainailourinae. None of the phylogenetic
 1891 analyses presented here recover a monophyletic Koholiinae. Instead, *Koholia* is either in an
 1892 unresolved position relative to other hyainailouroids (using parsimony), closely affiliated with
 1893 Hyainailourinae (using standard Bayesian inference), or is a sister group of Hyainailouridae to
 1894 the exclusion of Teratodontinae (using Bayesian tip-dating). The monophyly of *Lahimia* +
 1895 *Boualitomus*, on the other hand, is strongly supported in both Bayesian analyses, in which it is
 1896 placed outside of Hyainailouroidea. The other alleged “koholiine,” *Metapterodon* (the only
 1897 “koholiine” known from upper and lower dentitions), is placed with hyainailourines in both
 1898 Bayesian analyses, with tip-dating suggesting a close relationship with *Pterodon dasyuroides*; a
 1899 placement with hyainailourines is also present in the parsimony-based Adams consensus.

The tip-dating approach employed here (a first for Hyaenodontida) is of particular interest given the great age of *Lahimia*, because some have proposed an African origin of hyaenodontidans solely on the basis of the antiquity of *Lahimia*; however, in practice, the expected phylogenetic pattern that would support such an African origin (i.e., paraphyly of multiple African taxa with respect to non-African taxa) has not been found in any phylogenetic analysis that included these species. Even using tip-dating, *Lahimia* was consistently highly nested within Hyaenodontida, a result consistent with Rana et al. (2015), who also found *Lahimia* deeply nested in some MPTs. This result might be expected based on the dentition of *Lahimia* — the lower molar metaconids are subequal in height to the paraconid, unlike taxa such as *Cimolestes*, *Tinerhodon*, and *Eoproviverra*, which have taller metaconids than paraconids. The talonid basin of *Lahimia* is also very narrow compared to the trigonid, and reduced compared to taxa positioned more basally in the analyses presented here. A deeply nested *Lahimia* nevertheless implies multiple, unsampled ghost lineages of hyaenodontidans reaching into the earliest Paleocene and Late Cretaceous. In the tip-dating analysis, *Lahimia* + *Boualitomus* was resolved in a more basal position than it is in standard Bayesian and Parsimony analysis, supported by a very relatively rapidly evolving branch, though all basal branches (except the branch supporting the *Sinopa* clade + Hyaenodontidae) are rapidly evolving. These rapid basal rates are consistent with an explosive radiation of hyaenodontidans during the Paleocene, and we interpret this to be an adaptive radiation, that may have involved filling vacant carnivore niche space on multiple continents before evolutionary rates slowed in the early Eocene, indicative of more stable, occupied niche space (e.g., Simpson, 1953).

One of the clades consistently resolved as more basal than *Lahimia* and *Boualitomus* and all other Afro-Arabian taxa is Proviverrinae/Hyaenodontinae, a clade supported by rapidly

evolving branches that emerge very early in the evolution of Hyaenodontida. A close relationship between Hyaenodontinae and some European proviverrines was first demonstrated by Polly (1996) when *Eurotherium* was resolved as the sister taxon to *Propterodon* + *Hyaenodon*. Contra Solé (2013) and Solé, Falconnet & Yves (2014a) who found *Proviverra* and *Eurotherium* were part of a monophyletic Proviverrinae, Polly (1996) proposed *Proviverra* as the sister taxon to all more deeply nested hyaenodontidans and *Eurotherium* as closely related to *Propterodon* and *Hyaenodon*. Rana et al. (2015) were the first to include *Propterodon* and *Hyaenodon* in a phylogenetic analysis since Polly (1996); they also included many more proviverrines than Polly (1996) and found a monophyletic, entirely European Proviverrinae as the sister clade to Hyaenodontinae. *Proviverra* is the most deeply nested proviverrine in their analysis and *Eurotherium* is also deeply nested. The entire clade Hyaenodontinae + Proviverrinae in Rana et al. (2015) is deeply nested within Hyaenodontida, with a stem including North American “sinopanines” and Limnocyoninae, *Arfia*, and possibly *Lahimia* placed even more basally, near the root of Hyaenodontida. The results presented in this analysis resolve Proviverrinae near the root of Hyaenodontida (Parsimony and standard Bayesian analysis) or as a paraphyletic group of stem taxa relative to Hyaenodontinae. *Eoproviverra* is resolved by parsimony and standard Bayesian analysis as the sister group of all other Hyaenodontida, but is more deeply nested when evolutionary rates are incorporated into the analysis.

Solé (2013) and Solé, Falconnet & Yves (2014a) proposed multiple clades within “proviverrines” including Sinopaninae (including *Sinopa*, *Prototomus*, *Tritemnodon*, and *Galecyon*), Arfianinae (synonymous with the genus *Arfia*), and Proviverrinae. Rana et al. (2015) did not recover a monophyletic Sinopaninae, instead placing *Prototomus* as a group that is paraphyletic with respect to all non-arfianine, non-limnocyonine hyaenodontidans; the remaining

“sinopanines” were placed as basal stem members of a Hyaenodontinae + Proviverrinae clade. None of the methods employed here support a monophyletic Sinopaninae, and the positions of the "sinopanine" taxa are highly variable depending on the method applied. *Tritemnodon*, a North American taxon with partially fused upper molar paracones and metacones, and paracones that are taller than metacones, is placed along the stem of Hyainailouroidea using standard Bayesian analysis and as a stem hyainailourid (as the sister taxon of *Koholia*) using tip-dating. The *Galecyon* + *Gazinocyon* clade occupies more basal positions, in close phylogenetic proximity to Limnocyoninae. Both Bayesian methods place *Sinopa* in a clade with *Arfia* and *Prototomus*. In the standard Bayesian analysis, this clade is more closely related to Hyainailouroidea than to Hyaenodontinae, but tip-dating places *Sinopa*, *Prototomus*, and *Arfia* in a sister clade relationship with Hyaenodontinae. Clearly these Eocene North American taxa are vital for understanding the evolution of major radiations of hyaenodontidans and further study of these taxa is required as demonstrated by Zack & Rose (2015).

Biogeographic History of Hyaenodontida

Each topology and each biogeographic method yielded consistent biogeographic origins for several constituent clades within Hyaenodontida. Proviverrinae/Hyaenodontinae is unambiguously European in origin and Hyaenodontinae unambiguously originates in Asia. Across all analyses, Limnocyoninae, *Sinopa*, and the clade *Gazinocyon* + *Galecyon* originated in North America. Teratodontinae, Apterodontinae, and derived Hyainailourinae (from the node shared with *Akhnatnavus*) are unambiguously Afro-Arabian in origin, but the biogeographic origins of Hyainailouridae and Hyainailouroidea are uncertain. Most significantly, the origin of Hyaenodontida across all analyses is reconstructed with an ancestral area in either Europe or

1969 North America and an Afro-Arabian origin is not likely for Hyaenodontida using any of the
 1970 methods or topologies employed in this analysis. The nodes closest to the root of Hyaenodontida
 1971 are weakly supported, but the earliest Afro-Arabian taxon (*Lahimia*) and earliest Asian taxon
 1972 (*Prolimnocyon chowi*) are consistently recovered in deeply nested positions. A European or
 1973 North American origin of Hyaenodontida is problematic because hyaenodontidans are unknown
 1974 in Europe and North America before the Paleocene/Eocene boundary (Gingerich & Deutsch,
 1975 1989; Gunnell, 1998; Zack, 2011; Solé, 2013), though, unlike North America, the Paleocene of
 1976 Europe is still not well sampled. Tip-dating analysis indicates that the Paleocene was a period of
 1977 rapid evolution for Hyaenodontida when many of the major hyaenodontidan clades originated.
 1978 This explosive radiation is not fully captured in the fossil record. It also remains the case that
 1979 Asia and Afro-Arabia are particularly poorly sampled, with some geological intervals, like the
 1980 late Paleocene, only represented by a few, sparse localities (Meng, Zhai & Wyss, 1998; Seiffert,
 1981 2010) that may yet yield important fossils for understanding the origins of Hyaenodontida. Asia,
 1982 in particular, is situated as a kind of keystone between the other continental areas and very early
 1983 dispersals to North America or Europe from Asia may explain the sudden Paleocene/Eocene
 1984 emergence of the group in the Europe and North America, which shared a connection as
 1985 indicated by common hyaenodontidan taxa (*Arfia*, *Galecyon*, *Prototomus*) between the
 1986 continents. Another confounding factor in understanding the possible European roots of
 1987 Hyaenodontida is the fragmentary biogeography and and geography of Europe during the early
 1988 Paleocene and early Eocene with different faunal zones spread across the continent (Hooker,
 1989 2010; Solé, 2013; Solé, Falconnet & Yves, 2014a) with unsampled or isolated regions possibly
 1990 serving as the center of origin for early Hyaenodontida.

One goal of this study was to test the Afro-Arabian origin hypothesis for Hyaenodontida advocated by multiple authors (Gingerich & Deutsch, 1989; Gheerbrant et al., 2006; Morlo et al., 2013; Solé et al., 2014b), which has never been tested using a phylogenetic analysis and explicit biogeographic method with assumptions defined. The most recent argument for an Afro-Arabian origin hypothesis was based on the discovery of *Lahimia*, and the assumption that this taxon is basal within Hyaenodontida or represents an early-diverging clade (“Koholiinae”) from Hyaenodontida (Grohé et al., 2012; Morlo et al., 2013; Solé et al., 2014b). The study by Rana et al. (2015) and the results presented here do not support *Lahimia* as a particularly basal hyaenodontidan, but rather as a basal member of the clade that ultimately gave rise to Hyainailouroidea. Notably, *Lahimia* and *Boualitomus* were consistently recovered at more basal nodes than Asian “indohyaenodontines,” whose placements either within, or basal to, Hyainailouroidea indicate that they may be critically important for understanding the biogeographic origins of Hyainailouroidea and its Afro-Arabian sub-clades. Across all topologies, *Lahimia* and *Boualitomus* represent an independent dispersal to Afro-Arabia from taxa with North American or European roots.

Multiple dispersal events within Hyainailouridae are required given the topologies presented here, but the directions of most are not yet clear due to phylogenetic ambiguity at the base of the clade. All analyses support a dispersal from Afro-Arabia to Europe that led to *Apterodon gaudryi*. Both Bayesian analyses support a dispersal from Afro-Arabia to Asia to account for the presence of *Orienspterodon* in Myanmar, and the Bayesian topologies support four separate dispersals during the middle Eocene from Afro-Arabia to account for the presence of *Kerberos*, *Paroxyaena*, and *Pterodon dasyuroides* in Europe, and *Hemipsalodon* in North America. Perhaps the lineage that led to *Hemipsalodon* crossed through Europe, following the

same dispersal pathway used by *Kerberos*, a closely related European taxon; it is also possible, given the very weak statistical support for the paraphyly of *Hemipsalodon*, *Kerberos*, and *Pterodon dasyuroides* with respect to Afro-Arabian taxa, that additional material of these species will reveal that they are in fact a monophyletic radiation derived from a single out-of-Africa Eocene dispersal.

The biogeographic history of Teratodontinae, Apterodontinae, and Hyainailourinae is complicated by the differences between the tip-dating topology and the standard Bayesian and maximum parsimony topologies. Instead of occupying stem positions relative to the Afro-Arabian clades, the indohyaenodontines are weakly supported as closely related only to Teratodontinae in the tip-dating tree, implying that the common ancestor of Indohyaenodontinae dispersed from Afro-Arabia to Asia during the late Paleocene or early Eocene and the ancestor of *Metasinopa* dispersed from Asia to Afro-Arabia at some point after the late early Eocene (late Ypresian). Dispersal from Asia to Afro-Arabia during the Ypresian is possible in multiple mammalian lineages, potentially but not unambiguously including the zegdomyid-like ancestor of anomaluroid rodents, the ancestor of caenopithecine adapiform primates, and the ancestor of more crownward strepsirrhine primates (Seiffert, 2012), though dispersal from Europe is also possible (see below). If the ancestors of *Metasinopa* and *Orienspterodon* dispersed from Asia during the middle Eocene this would coincide with the interval when hystricognathous rodents and anthropoid primates also likely dispersed from Asia to Afro-Arabia, and when the anomaluroid rodent *Pondaungimys* dispersed from Afro-Arabia to Asia (Sallam et al., 2010; Seiffert, 2012; Marivaux et al., 2015).

Using BBM, the common node of “Indohyaenodontinae” + Hyainailouroidea is reconstructed as North American (parsimony; P31), Asian (standard Bayesian, B42), or North

American (tip-dating, T53). These conflicting reconstructions make it difficult to confidently assert the ultimate origins of these clades, though there is evidence of dispersal between Afro-Arabia and Europe as initially proposed in early studies of Fayum Hyaenodontida (Andrews, 1904, 1906; Osborn, 1909; Schlosser, 1911). Gheerbrant & Rage (2006) note a minor exchange event from Europe to Afro-Arabia near the Lutetian/Bartonian boundary that includes caenopithecine adapiform and anchomomyin primates, and the European origin of African caenopithecines was supported by the phylogenetic analyses of Seiffert et al. (2015). The dispersal of the ancestor of *Paroxyaena* from Afro-Arabia to Europe (as supported by both Bayesian analyses) may have occurred during this interval, following the same dispersal route as *Kerberos*, *Hemipsalodon*, and *Pterodon dasyuroides*. The successful dispersal of hyainailourines to Europe and North America from Afro-Arabia during the middle Eocene has interesting implications for the structure of the hypercarnivorous niche at the time of the dispersal because the hypercarnivorous niche was already occupied on both continents by early species of *Hyaenodon* (Mellet, 1977; Lange-Badré, 1979).

Multiple relationships recovered in the tip-dating analysis support exchange between North America and Europe near the PETM (Paleocene-Eocene Thermal Maximum), as suggested by Smith & Smith (2001). The divergence between North American *Pyrocyon* and European *Preregidens* reaches across the PETM, as does the divergence between *Prototomus minimus* and *Prototomus phobos*, and the divergence of the clade *Arfia*, *Sinopa*, and *Prototomus* from a node reconstructed with likely European and North American origins (T2). The connection between North America and Europe during this interval is further supported by the European species of *Arfia*, *A. gingerichi*, that was not included in this analysis (Smith & Smith, 2001). There is also a species of *Galecyon*, *G. galus*, from Europe (Solé, Falconnet & Yves,

2014a). The *Galecyon* lineage stretches across the PETM and the ancestor of *Galecyon* likely originated before this interval and dispersed between Europe and North America.

The nodes supporting *Prolimnocyon chowi* and *Sinopa jilinia*, both Asian taxa, are reconstructed with North American origins, evidence of exchange from North America to Asia during the late Paleocene and early Eocene. Exchange between Europe and Asia is implied by the close relationship between Hyaenodontinae, reconstructed with an Asian origin, and *Oxyaenoides*, reconstructed with a European origin. The West Siberian Sea was a major epicontinental seaway that separated Europe from Asia, limiting direct fauna exchange between these continents, but early Eocene exchange likely occurred, as documented in Perissodactyla (Hooker & Dashzeveg, 2003), Primates (Smith, Rose & Gingerich, 2006), and Rodentia (Badiola et al., 2009). The ancestor of Hyaenodontinae may have dispersed directly from Europe to Asia during this interval. Alternatively, Rana et al. (2015) recovered Hyaenodontinae as the sister clade to a monophyletic Proviverrinae. The stem of this clade includes North American taxa and Hyaenodontinae is ambiguously resolved with a North American or European origin. Further analyses will test the sister-taxon relationships to Hyaenodontinae. *Hyaenodon* is resolved with an Asian origin across all analyses with dispersal to Europe and North America during the late Eocene, and endemic radiations of the genus occurred after dispersal in Europe (Bastl, Nagel & Peigné, 2014) and North America (Mellet, 1977).

The Evolution of Hypercarnivory within Hyaenodontida

The dental specializations of hyaenodontidans — such as extended postparacristids and preprotocristids, elongate metastyles, and buccolingually compressed metacones — indicate that the group was adapted, like modern carnivorans, to a primarily faunivorous diet (Van

Valkenburgh, 1999). But just as some lineages of carnivorans are more dentally specialized for carnivory than others, so too were some lineages of hyaenodontidans. Hypercarnivory in modern carnivores is used to refer to animals that acquire 70% or more of their calories from meat, in contrast to generalist carnivores, which eat 50%–60% meat and complete the diet with plant matter and invertebrates (Van Valkenburgh, 1988, 1989). Dental adaptations correlate with the dietary shift from generalist to hypercarnivore, including the mesiodistal lengthening of the carnassial complex, reduction and simplification of the talonid, reduction of the protocone, and loss of the metaconid (Holliday, 2010).

The first attempts to classify subgroups within Hyaenodontida were based on the degree of specialization in the dentition, particularly in the morphological specialization of the carnassial complex. “Proviverrinae” contained the less dentally specialized, or generalist taxa, and “Hyaenodontinae” contained the more specialized, hypercarnivorous taxa (Matthew, 1909, 1915). The distinction between “Proviverrinae,” the hyaenodontidans with prominent metaconids and unfused paracones and metacones, and “Hyaenodontinae,” the hyaenodontidans with no metaconids and fused paracones and metacones, was utilized through most of the 20th century (Matthes, 1952; Savage, 1965; Van Valen, 1965; Barry, 1988). In this scheme, *Pterodon* and *Hyaenodon* were closely related based on their hypercarnivorous dentition (Barry, 1988). The genus *Pterodon* was defined by a groove between the paracone and metacone while *Hyaenodon* was recognized by its apparent fusion of these cusps (Savage, 1965). The arrangement caused some debate over how to classify taxa that did not neatly fit the dichotomy, like *Apterodon*, which has a reduced metaconid but separated paracones and metacones (Van Valen, 1965; Szalay, 1967) and *Dissopsalis*, which has long, sectorial metastyles and metacones but retains the metaconid on M₂ and has a paracone that is reduced and not entirely fused to the metacone

(Barry, 1988). Using cranial and postcranial characters, Polly (1996) demonstrated that *Hyaenodon* and *Pterodon* evolved specialized, hypercarnivorous shearing dentition (lost the metaconid and fused the paracone and metacone) independent of one another, and each lineage arose from separate “proviverrine” ancestors. In Polly (1996), *Dissopsalis* is the sister taxon to Hyainailourinae, with its elongate metastyle and prominent metacone reflecting the possible ancestral condition that led to the fused paracone and metacone of *Pterodon*, while *Eurotherium* is the sister taxon to *Propterodon* + Hyaenodontinae, with its divergent paracone and metacone possibly reflecting the ancestral morphology of its sister clade. Solé et al. (2015) detailed additional cranial features that distinguish Hyainailourinae from Hyaenodontinae, further emphasizing the ancient divergence of the two lineages with specialized, or hypercarnivorous dentition. With the separate origins of *Hyaenodon* and *Pterodon* supported by the present study and by Rana et al. (2015), the morphology of the carnassial complex in each lineage is worthy of reexamination.

Originally, the dental adaptations of *Pterodon* and *Hyaenodon* were assumed to be part of an evolutionary sequence. *Pterodon*, with incompletely fused paracones and metacones, was viewed as the ancestral condition for *Hyaenodon* (Matthew 1915; Van Valen, 1967), which completely fused the paracone and metacone. However, carnivorous mammals have not adapted to hypercarnivory in the exact same way in every lineage that has evolved specialized shearing dentition, particularly in the arrangement of the metacone and paracone. Furthermore, with the establishment of Hyainailourinae and Hyaenodontinae as functionally convergent clades, it is possible to recognize that these two lineages converged on hypercarnivory through fundamentally different arrangements of the paracone, metacone, and metastyle, which in turn affects the occlusal morphology of the lower molars.

In Carnivora the carnassial complex is formed between P⁴ and M₁. The upper carnassial blade stretches between the elongate metastyle of P⁴ and the buccolingually compressed postparacrista. This differs from the arrangement of the carnassials in carnivorous metatherians, which adapted the tricusate molars into the upper carnassial rather than the bicusate premolars. Borhyaenoid metatherians were the dominant carnivores in South America from the Paleocene through the Pliocene (Rose, 2006), and, like hyaenodontidans, borhyaenoids formed a shearing carnassial complex between multiple upper and lower molars rather than one carnassial complex between a premolar and molar as in Carnivora. In borhyaenoids (i.e., Miocene *Pseudolycopsis* and *Lycopsis*) the upper carnassial is formed through mesiodistal elongation of the metacone and metastyle rather than the paracone and metastyle as in carnivorans (Van Valen, 1967; Muizon & Lange-Badré, 1997). The paracone apex in borhyaenoids is distinct from the metacone, and much shorter than the taller shearing metacone. Borhyaenoids are not closely related to Dasyuromorphia, the Australian radiation of carnivorous marsupials that includes *Thylacinus*, but dasyuromorphians converged on the same shearing morphology as borhyaenoids. In Dasyuromorphia the paracone is retained as a distinct, reduced cusp and the metacone is mesiodistally elongate and buccolingually compressed, forming the tallest cusp of the trigon. The postmetacrista is sharp and slopes to meet the sectorial metastyle. This borhyaenoid and dasyuromorphian-style carnassial, with an augmented metacone and reduced paracone, is the same carnassial arrangement exhibited by many hyaenodontidans, including *Hyaenodon*, *Eurotherium*, *Dissopsalis*, and *Brychotherium* (Fig. 23). *Hyaenodon* differs from *Eurotherium*, *Dissopsalis*, and *Brychotherium* in the degree of fusion between the paracone and metacone. In *Hyaenodon*, the paracone is a small, vestigial structure that fuses to the mesial metacone. *Hyaenodon* upper molars are often heavily worn but, in recently erupted M¹, the distinct, small

paracone is easily distinguished and it is even more evident in dP⁴. The paracone typically forms a small ridge on the mesial surface of M² though it is easily worn away. *Eurotherium*, a middle Eocene taxon in the Proviverrinae/Hyaenodontinae clade, represents the likely ancestral morphology of the upper dentition of *Hyaenodon*, with the metacone more mesiodistally elongate and taller than the paracone. *Oxyaenoides* is the sister taxon to Hyaenodontinae and it also has a derived hypercarnivorous dentition with a tall metacone and extended metastyle. In *Eurotherium*, *Oxyaenoides*, and *Hyaenodon*, the paracone apex parallels the metacone apex, pointing ventrally. The arrangement of the upper molar carnassial cusps differs from the likely ancestral condition of the upper dentition, exemplified by *Proviverra* in Fig. 23. In *Proviverra*, the paracone and metacone are subequal in height and not buccolingually compressed. Rana et al. (2015) resolved Proviverrinae as the sister clade to Hyaenodontinae. In this scenario, metacone-dominated hypercarnivorous carnassials are convergent in Hyaenodontinae and in Proviverrinae.

The arrangement of the paracone and metacone are fundamentally different in Hyainailourinae. Instead of the metacone forming the tallest piercing cusp, the paracone is the tallest cusp, and this arrangement is exemplified by *Pterodon dasyuroides* and *Akhnatenuvus* in Fig. 23. Muizon & Lange-Badré (1997) noted the difference in paracone height in *Hyaenodon* and *Pterodon* but they did not place the distinction into a larger phylogenetic context. In hyainailourines, the metacone is fused to the distal face of the paracone. The postmetacrista becomes homologous to the P⁴ postparacrista in Carnivora. The paracone is also the tallest cusp of the trigon in *Tritemnodon*, an early Eocene taxon from North America and, based on the results of this analysis, probably part of the clade that includes Apterodontinae and Hyainailourinae. The trigons of *Tritemnodon* differ from those of *Pterodon* and *Akhnatenuvus* by

retaining a distinct apex on the metacone and a wider notch between the metacone and paracone. This arrangement represents the likely ancestral condition to the hyainailourine carnassial complex. Apterodontinae shares a taller paracone than metacone with Hyainailourinae.

Teratodontinae was consistently recovered in this study as part of the sister clade to the Apterodontinae and Hyainailourine. However, the dentition of Teratodontinae is arranged more like the dentition of borhyaenoids and derived proviverrines/hyaenodontines than it is like hyainailourines. In *Brychotherium* the metacone is slightly taller than the paracone and the metacone more mesiodistally elongate than the paracone. In *Dissopsalis* the metacone is much taller and more elongate than the tiny paracone, which points slightly mesially rather than directly perpendicular to the alveolar plane. The recovery of *Dissopsalis* as part of a separate clade from Hyainailourinae differs from Polly (1996) whose topology recovered a sister-taxon relationship between *Dissopsalis* and Hyainailourinae. The topologies presented in this study imply that *Dissopsalis* provides evidence for yet another (third) convergence upon specialized hypercarnivory in Hyaenodontida.

The different arrangements of the upper carnassial influence the morphology of the trigonid on the lower molars. In Hyaenodontinae, the paraconid is almost mesial to the protoconid and the postparacristid and preprotocristid are nearly parallel to the mandibular corpus, reflecting the morphology of the postmetacrista and metastyle, which nearly parallel the alveolar margin. In Hyainailourinae, the paraconid is set lingual relative to the protoconid, giving the postparacristid and preprotocristid carnassial an oblique shearing angle relative to the mandibular corpus. This trigonid arrangement shears past a postmetacrista that is slightly lingually inflected at the carnassial notch, accommodating the wide base of the paracone.

Through biogeographic analysis and tip-dating analysis, the evolution of hypercarnivory in Hyaenodontinae, Proviverrinae, Hyainailourinae, and Teratodontinae can be reconstructed in place and time. These conclusions are a preliminary discussion of evolutionary trends inferred from this novel topology, and more detailed ancestral state reconstructions based on dental morphology would be an appropriate direction for future studies. Solé, Falconnet & Yves (2014a) observed a general increase in body size and dental specialization in Proviverrinae through the Eocene, a trend supported by this analysis, which recovers the clade that includes *Eurotherium* as European in origin and dentally specialized like Hyaenodontinae. Hyaenodontinae is even more specialized than *Eurotherium*, and likely originated in Asia during the early Eocene. Then the hypercarnivorous *Hyaenodon* dispersed from Asia to Europe and North America where endemic radiations occurred (Mellet, 1977; Bastl, Nagel & Peigné, 2014). Hyainailourinae likely originated in Afro-Arabia and the carnassial morphology dominated by the paracone rather than the metacone also likely originated in Afro-Arabia. Hypercarnivory evolved a second time in Afro-Arabia in the lineage that lead to *Dissopsalis* and *Anasinopa*, which both possess carnassials dominated by metacones that were taller than paracones. Given the time-calibrated tip-dating topology, this lineage diverged from *Masrasector*, a less dentally specialized taxon, during the late Eocene, and *Dissopsalis* diverged from *Anasinopa*, a less-specialized carnivore, during the late Oligocene. *Dissopsalis* is at the end of the most rapidly evolving branch of any hyaenodontidan taxon in the Oligocene or Miocene at 1.34% change/Ma (followed by *Quasiapterodon* at 1.13% change/Ma and *Isohyaenodon* at 1.03% change/Ma). The increased rate of morphological change in *Dissopsalis* is expected to have slightly predated, or coincided with, the arrival of Carnivora in Afro-Arabia. This may reflect a general trend to hypercarnivory that left generalist niche space open for the earliest carnivoran immigrants like

amphicyonids and the ancestors of *Miopriodon* to exploit (Rasmussen & Gutierrez, 2009), or rapid morphological change through the evolution of *Dissopsalis* may reflect niche specialization in carnivores as immigrant taxa crowded the carnivorous niche (Van Valkenburgh, Wang & Damuth, 2004). The last-surviving hyaenodontidans of the Miocene — *Isohyaenodon*, *Megistotherium*, and *Dissopsalis* — were each highly specialized carnivores, and each lineage may have been ecologically vulnerable to extinction as an apex carnivore (Van Valkenburgh, 2007) and morphologically unable to explore novel morphospace with such specialized dentitions, as demonstrated in studies that examine the ecological and morphological flexibility of hypercarnivores and their generalist sister taxa (Holliday & Stepan, 2004; Holliday, 2010). These data can now be used to explore the timing and the ecological context of hypercarnivorous specialization in Hyaenodontida across four continents and can be compared to the timing and location of dental specialization in the other Paleogene carnivore lineages, such as Oxyaenida, Carnivoramorpha, and Mesonychia.

CONCLUSIONS

The character-taxon matrix utilized for this analysis sampled from each hyaenodontidan lineage that has been proposed, both to place the newly described latest Eocene species *Brychotherium ephalmos* and *Akhnatenavus nefertiticyon* in a phylogenetic context, and to rigorously test the hypothesis that Hyaenodontida first arose in Afro-Arabia. All three phylogenetic methods used here supported the monophyly of the clades Apterodontinae, Hyainailourinae, Limnocyoninae, *Galecyon* + *Gazinocyon*, as well as the clade that includes Hyaenodontinae and some European “proviverrines” (sensu Solé, 2013). Teratodontinae was not

recovered in every MPT, but is supported by a majority of them and in both the standard Bayesian and Bayesian tip-dating analyses. *B. ephalmos* is one of the most completely known teratodontines, and is either deeply nested with Miocene taxa (parsimony and standard Bayesian results) or is a basal form that branched off from other teratodontines in the middle Eocene (tip-dating results). *Akhnatenavus* is resolved by all methods as a basal member of a hyainailourine clade that also includes Oligocene African “*Pterodon*” and younger Miocene hyainailourines.

All analyses also recovered the origin of Hyaenodontida as having occurred on northern continents, either Europe or North America. Proviverrinae/Hyaenodontinae is consistently recovered as an early-diverging branch with European origins. The earliest diverging nodes in Hyaenodontida also include largely North American clades like *Arfia* and *Limnocyoninae*. A hyaenodontidan origin in Europe or North America is problematic as the group is not known on those landmasses before the PETM, but Asia and Afro-Arabia, both of which have poor Paleocene records and as such have repeatedly been envisioned as the likely home of as-yet unsampled Paleocene hyaenodontidan ghost lineages, have no support as continents of origin based on the branching patterns recovered here. The presence of *Lahimia* in the middle Paleocene of Africa, and *Tinerhodon* in the late Paleocene, are intriguing evidence of early Afro-Arabian hyaenodontidan diversity in Afro-Arabia, but neither is resolved as a sister group of all other hyaenodontidans, or in a basal enough position to influence the geographic reconstruction for the hyaenodontidan root node.

Even with more Paleocene fossils from Asia and Afro-Arabia, tip-dating analysis implies that the early evolutionary history of Hyaenodontida was an explosive adaptive radiation and, without more compelling evidence for the basal branching sequence in the group, it may be difficult to identify the exact geographic origin of the clade with any confidence. The early

evolution of Hyaenodontida apparently echoed the larger-scale trend of K/Pg radiations in mammals (Beck & Lee, 2014) and birds (Lee et al., 2014) in which rapid morphological change occurred over a short period of geological time, potentially leaving little or no time for the accumulation of morphological synapomorphies that might otherwise support basal branches. This rapid period of early radiation led to the establishment of endemic clades on different continents. The early biogeographic history of the group is difficult to unravel, but once the major clades were established, there appears to have been little large-scale exchange of taxa between continents. Immediately after the PETM there were genera common to North America and Europe, but these shared genera did not persist in Europe, and Solé, Falconnet & Yves (2014a) demonstrated that endemic European proviverrines occupied vacant niche space left by genera common to both continents. Dispersal was apparently most likely during the middle and late Paleocene, then only occurred sporadically through the Eocene, mostly as pulses between Afro-Arabia and the northern continents in Hyainailourinae and Apterodontinae. No proviverrine is known to have dispersed from Europe to North America, Afro-Arabia, or Asia. Teratodontines and indohyaenodontines were limited to Afro-Arabia and Asia. Limnocyoninae is a North American clade that dispersed into Asia during the late Paleocene. On each of these continents, different lineages adapted to different carnivorous niches, and hypercarnivory emerged independently at least once in Eurasia and twice in Afro-Arabia.

Description of the new taxa *Brychotherium ephalmos* and *Akhnatenavus nefertiticyon* increases the diversity of the Fayum carnivore fauna and further expands the total faunal diversity of the Afro-Arabia before the continent established a filtered contact with Eurasia through the late Oligocene and early Miocene. Better documentation of endemic clades like Hyainailourinae and Teratodontinae is necessary to understand the ecological context that the

earliest Eurasian immigrant carnivorans encountered. Only with a detailed understanding of the early evolution of Hyaenodontida in Afro-Arabia is it possible to assess the ecological factors that may have led to the ultimate extinction of this widespread and morphologically diverse group of carnivores.

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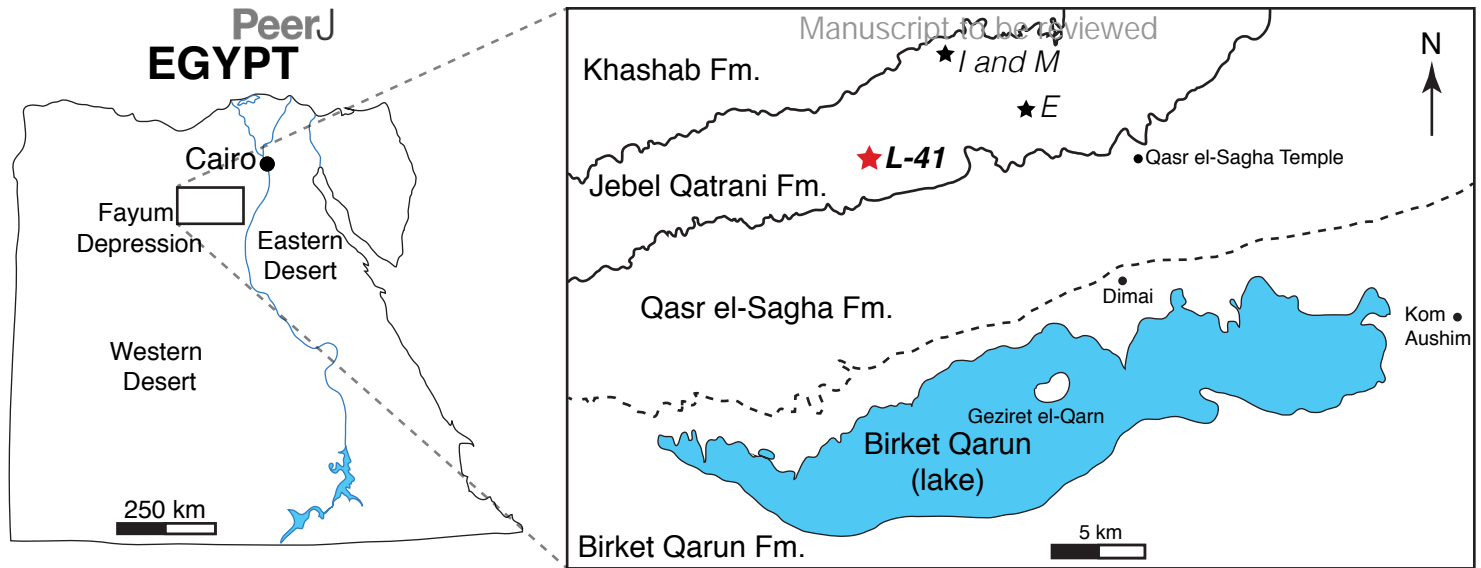
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Figure 1(on next page)

Map of the Fayum Depression, Egypt

A, Map of the Fayum Depression, Egypt. Stars indicate quarries. Red star indicates L-41 (latest Priabonian, ~34 Ma) in the Jebel Qatrani Formation (Fm.). Well-defined formational contacts (Qasr el-Sagha Fm./Jebel Qatrani Fm. and Jebel Qatrani Fm./Khashab Fm.) are indicated by solid lines. The older and more ambiguous formational boundary (Birket Qarun Fm./Qasr el-Sagha Fm.) is indicated by a dashed line. **B**, Fayum field crew excavating at Quarry L-41 by carefully removing sheets of mudstone to expose fossils.

A



B

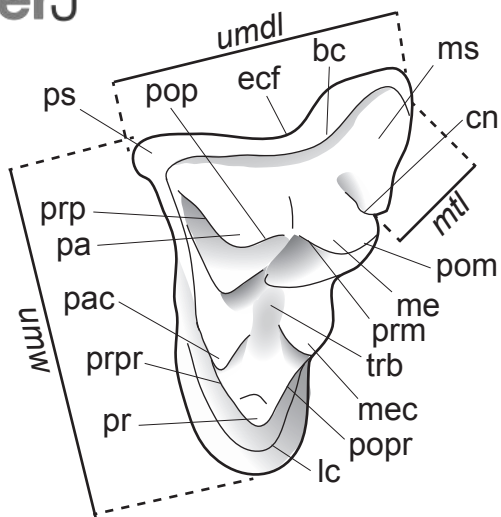


Figure 2(on next page)

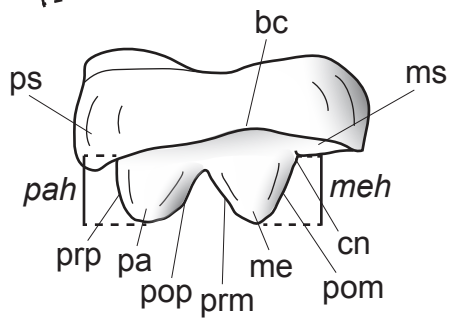
Dental nomenclature used in this study

Upper left M^2 and lower left M_3 of *Proviverra typica* (**A–E**) and *Pterodon dasyuroides* (**F–J**) showing dental terminology and measurements used in this study. **A**, *Proviverra typica* M^2 in occlusal and **B**, buccal views and M_3 in **C**, occlusal **D**, lingual, and **E**, buccal views. **F**, *Pterodon dasyuroides* M^2 in occlusal and **G**, buccal views and M_3 in **H**, occlusal **I**, lingual, and **J**, buccal views. Measurements are indicated in italics. **Abbreviations:** **ak**, anterior keel; **bc**, buccal cingulum; **bcd**, buccal cingulid; **cn**, carnassial notch; **co**, cristid obliqua; **ecf**, ectoflexus; **ed**, entoconid; **ecd**, entocristid; **hd**, hypoconid; **hld**, hypoconulid; **lc**, lingual cingulum; **lmdl**, lower molar mesiodistal length; **meh**, metacone height beyond metastyle; **me**, metacone; **mec**, metaconule; **med**, metaconid; **ms**, metastyle; **mtl**, metastyle mesiodistal length; **pa**, paracone; **pac**, paraconule; **pad**, paraconid; **pah**, paracone height beyond metastyle; **pom**, postmetacrista; **pop**, postparacrista; **popad**, postparacristid; **popr**, postprotocrista; **pr**, protocone; **prd**, protoconid; **prm**, premetacrista; **prp**, preparacrista; **prpr**, preprotocrista; **prprd**, preprotocristid; **ps**, parastyle; **tab**, talon basin; **tadb**, talonid basin; **tall**, talonid mesiodistal length; **talw**, talonid buccolingual width; **trb**, trigon basin; **trdb**, trigonid basin **tril**, trigonid mesiodistal length; **triw**, trigonid buccolingual width; **umdl**, upper molar mesiodistal length; **umw**, upper molar buccolingual width.

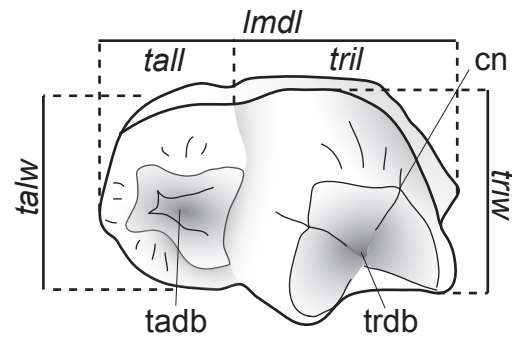
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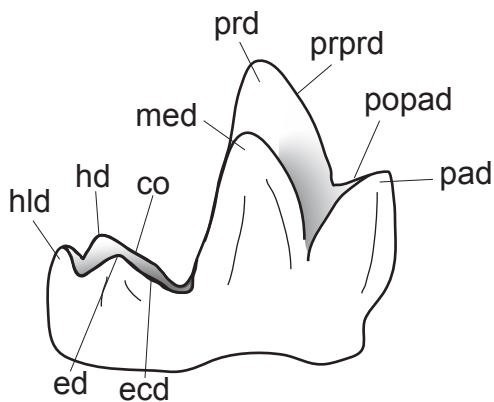
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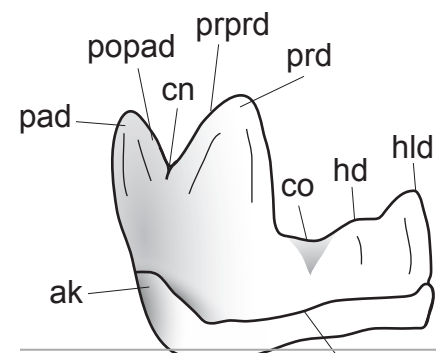
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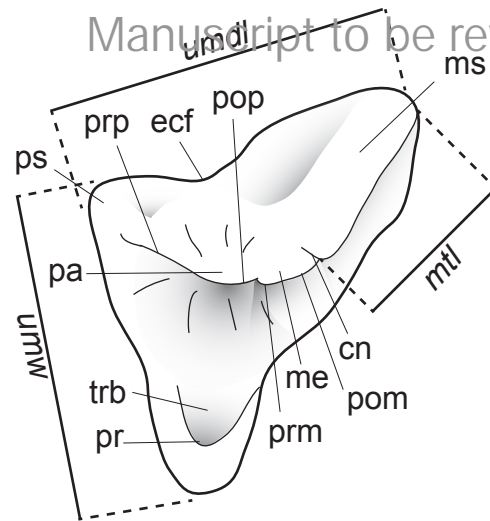
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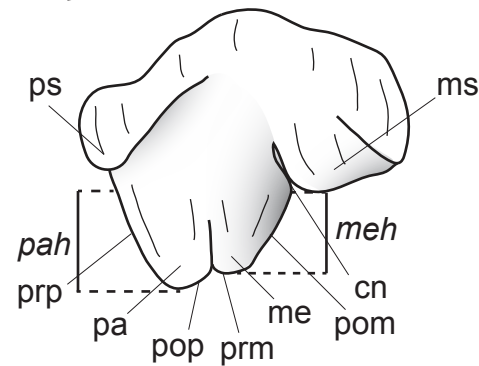
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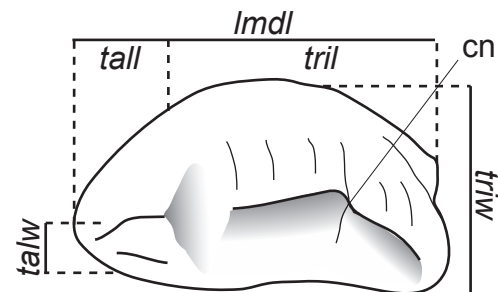
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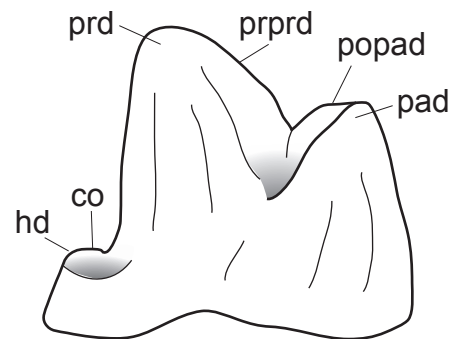
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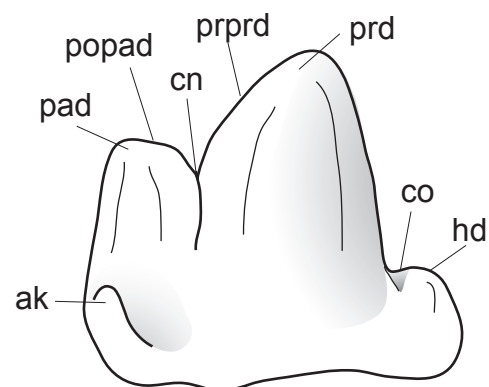


Figure 3(on next page)

Brychotherium ephalmos DPC 11990 rostrum

Brychotherium ephalmos gen. et sp. nov. DPC 11990, rostrum with left and right P⁴-M³ and alveoli for right and left I²-P³. **A**, ventral view; **B**, dorsal view; **C**, left lateral view; **D**, right lateral view. Specimen crushed mediolaterally with left maxilla shifted anteriorly relative to right maxilla.

Figure 4(on next page)

Brychotherium ephalmos DPC 11990 sketch and model

Brychotherium ephalmos gen. et sp. nov. DPC 11990; rostrum with P⁴-M³ with left and right P⁴-M³: and alveolus for right and left I²-P³. Sketch on the left (subscript 1) and digital model on the right (subscript 2): **A**, ventral view; **B**, dorsal view; **C**, left lateral view; **D**, right lateral view. Solid lines indicate definite sutures, dotted lines indicate interpreted sutures that have been obscured by crushing. Digital model is a volume rendering in Avizo based on the model available at MorphoSource.

Figure 5(on next page)

Brychotherium ephalmos holotype DPC 17627 rostrum

Brychotherium ephalmos gen. et sp. nov. DPC 17627, rostrum with left canine, dP⁴-M³ (M³ erupting) and alveolus for dP³ and right P⁴-M²; specimen photographs on the left (subscript 1) and digital model on the right (subscript 2): **A**, occlusal view of left dentition, buccal aspect of right dentition visible; **B**, buccal view of left dentition, protocones of right P⁴-M² and M² paracone and metacone visible; **C**, lingual view of left dentition, buccal aspect of right dentition visible. Postmortem distortion involuted right side of rostrum. Occlusal portions of right dentition protrude through left maxilla. Digital model is a volume rendering in Avizo based on the model available at MorphoSource.

Figure 6(on next page)

Brychotherium ephalmos holotype DPC 17627 dentary

Brychotherium ephalmos gen. et sp. nov. DPC 17627, right dentary with P₄-M₃; specimen photographs on the left (subscript 1) and digital model on the right (subscript 2); **A**, occlusal view; **B**, lingual view; **C**, buccal view. Digital model is a volume rendering in Avizo based on the model available at MorphoSource.

Figure 7 (on next page)

Brychotherium ephalmos holotype CGM 83750 dentary

Brychotherium ephalmos gen. et sp. nov. CGM 83750, right dentary with C-M₃; specimen photos on the left (subscript 1) and digital model images on the right (subscript 2); **A**, occlusal view; **B**, lingual view; **C**, buccal view. Digital model is a volume rendering in Avizo based on the model available at MorphoSource.

Figure 8(on next page)

Brychotherium ephalmos DPC 11569A right dentary

Brychotherium ephalmos gen. et sp. nov. DPC 11569A, right dentary with C, P₂-M₃; specimen photos on the left (subscript 1) and digital model images on the right (subscript 2); **A**, occlusal view; **B**, lingual view; **C**, buccal view. Digital model is a volume rendering in Avizo based on the model available at MorphoSource.

Figure 9(on next page)

Brychotherium ephalmos DPC 11569B left dentary

Brychotherium ephalmos gen. et sp. nov. DPC 11569B, left dentary with C, P₂-M₃; specimen photos on the left (subscript 1) and digital model images on the right (subscript 2); **A**, occlusal view; **B**, lingual view; **C**, buccal view. Digital model is a volume rendering in Avizo based on the model available at MorphoSource.

Figure 10(on next page)

Akhnatenavus nefertiticyon cranium CGM 83735

Akhnatenavus nefertiticyon sp. nov. holotype CGM 83735, cranium with right canine, P³–M³ and alveolus of P² and left P², P⁴, M²; **A**, right lateral view; **B**, dorsal view; **C**, left lateral view. Postmortem distortion mediolaterally crushed the specimen with the left dentition involuted. Specimen also preserves atlas (cervical vertebra 1) appressed to the basicranium and a proximal rib appressed to the right parietal.

Figure 11(on next page)

Akhnatenavus nefertiticyon cranium CGM 83735 labeled

Akhnatenavus nefertiticyon sp. nov. CGM 83735, cranium sketch (subscript 1) and digital model (subscript 2) with right canine, P³-M³ and left P², P⁴, M²; **A**, right lateral view; **B**, dorsal view; **C**, left lateral view. Dotted lines indicate uncertain sutures or boundaries. Unlabeled regions are fragmentary. **Abbreviations:** **l.**, left; **r.**, right; **inf. orb. f.**, infraorbital foramen; **mand. fossa**, mandibular fossa; **r. occ. condyle**, right occipital condyle. Digital model is a volume rendering in Avizo based on the model available at MorphoSource.

Figure 12 (on next page)

Akhnatenavus nefertiticyon CGM 83735 dentition detail

Akhnatenavus nefertiticyon sp. nov. CGM 83735 photographs (subscript 1) and digital model images (subscript 2) of right P³-M³; **A**, occlusal view. DPC 13518, left M¹; **B**, occlusal-lingual view.

Figure 13(on next page)

Akhnatenavus nefertiticyon DPC 18242 cranium

Akhnatenavus nefertiticyon sp. nov., DPC 18242, palate with left P²-M² and P¹ roots and right M¹ and P¹-P⁴ roots; **A**, ventral view; **B**, dorsal view; **C**, left lateral view; **D**, right lateral view. Postmortem distortion involuted the right maxilla and dorsoventrally compressed the cranium.

Figure 14(on next page)

Akhnatenavus nefertiticyon DPC 18242 cranium labeled

Akhnatenavus nefertiticyon sp. nov., DPC 18242, digital model images of palate with left P²-M² and P¹ roots and right M¹ and P¹-P⁴ roots; **A**, ventral view; **B**, dorsal view; **C**, left lateral view; **D**, right lateral view. Postmortem distortion involuted the right maxilla and dorsoventrally compressed the cranium. Digital model is a volume rendering in Avizo based on the model available at MorphoSource.

Figure 15(on next page)

Akhnatenavus nefertiticyon DPC 18242 and DPC 13518 dentition detail

Akhnatenavus nefertiticyon sp. nov., detail from DPC 18242 of left P²-M²; photographs of dental specimen on the left (subscript 1) and digital model images on the right (subscript 2); **A**, occlusal view; **B**, buccal view; DPC 13518, isolated left M¹ in **C**, occlusal; **D**, buccal, and **E**, lingual view. Digital model is a volume rendering in Avizo based on the model available at MorphoSource.

Figure 16(on next page)

Strict and Adams consensus trees

A, Strict consensus tree and **B**, Adams consensus tree of 650 most parsimonious trees (1029 steps, consistency index (CI) = 0.187, retention index (RI) = 0.613, rescaled consistency index (RC) = 0.114). P# corresponds to the node to the right of the label in the strict consensus tree and are used in the discussion of clades and the biogeographic analyses. Bremer support values (range 1–10) right of relevant node in the strict consensus tree. Bootstrap support values (range 50%–100%) right of relevant node and italicized. Only clades supported by greater than 50% bootstrap support are labeled with bootstrap values. Major clades identified by this study are indicated by the round boxes with the name enclosed or overlapping the boundaries of the box. Dashed branches indicate branches recovered in the Adams consensus but not in the strict consensus tree.

A

PeerJ

Manuscript to be reviewed

B

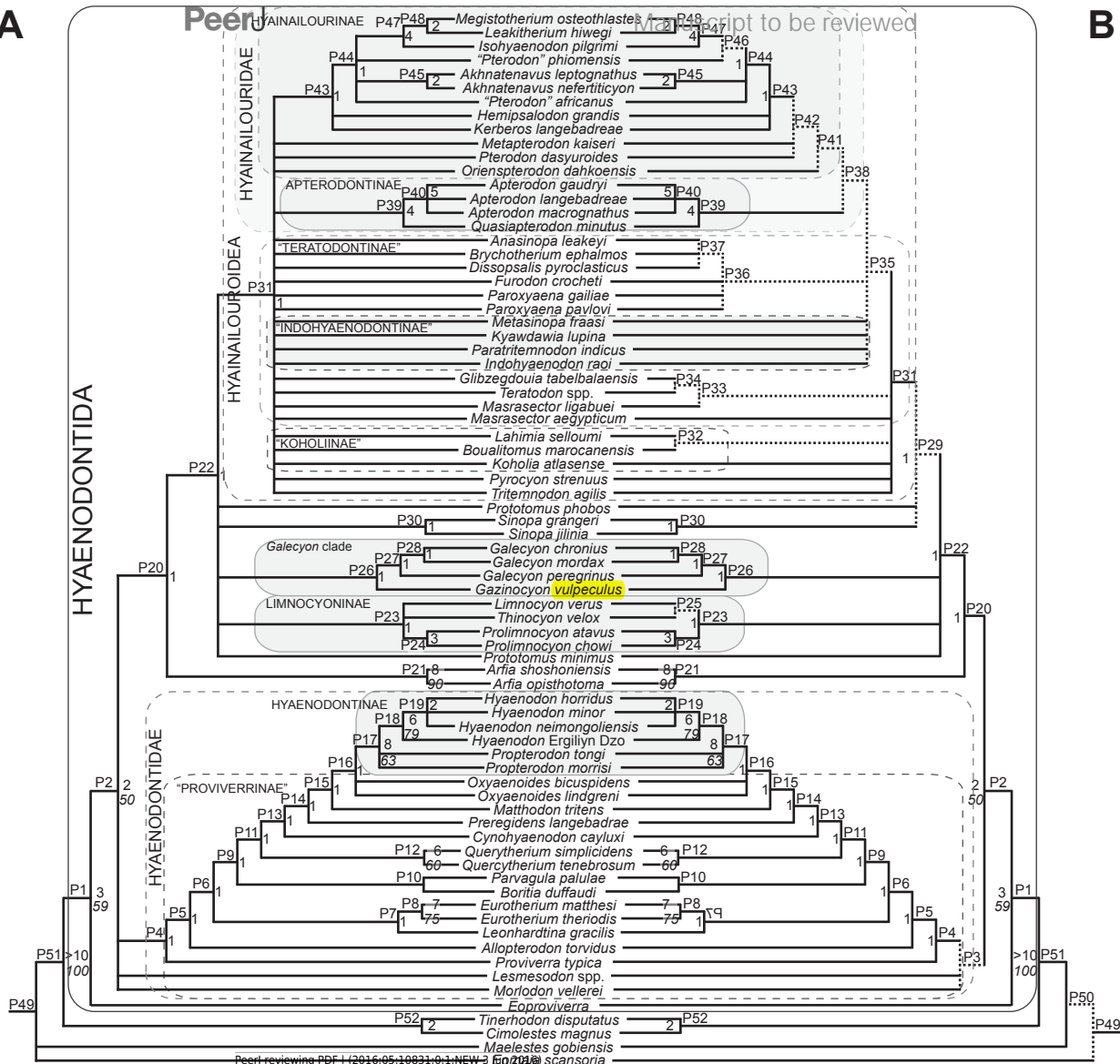


Figure 17 (on next page)

Agreement subtree and Adams consensus

A, Agreement subtree of 650 most parsimonious trees compared with **B**, Adams consensus tree. Taxa colored grey are not part of the agreement subtree. Dashed branch indicates the branch was not recovered in the strict consensus tree.

A

B

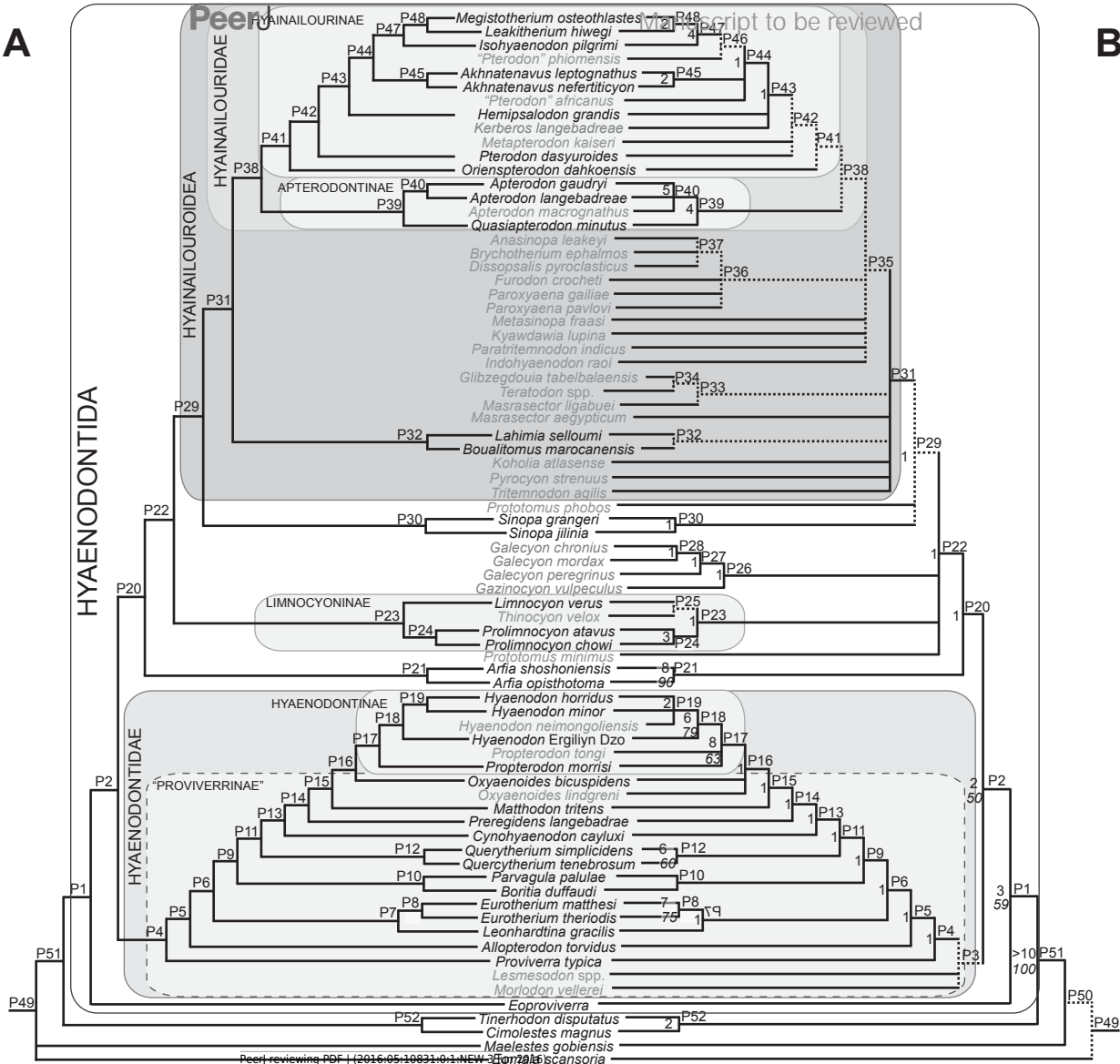


Figure 18(on next page)

Standard Bayesian "allcompat" tree

"allcompat" standard Bayesian tree. B# correspond to the node to the right of the label and are used in the discussion and in the biogeographic analyses to reference the clade. Posterior Probabilities (PP) correspond to the node to the left of value. Strength of PP support summarized by color. Major clades identified by this study are indicated by the round boxes with the clade name enclosed or overlapping the boundaries of the box.

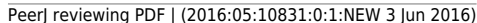


Figure 19(on next page)

Bayesian tip-dating “allcompat” tree

“allcompat” Bayesian tip-dating tree. T# correspond to Table 4 and biogeography results. Posterior probability (PP) shown in italics to the right or below relevant node. Divergence dates represent mean divergence date for clades and taxa. Branch colors correspond to legend for relative median rate (% change/Ma) along branches. Most rapidly evolving clades are shown in warm colors. The mean age recovered by the analysis is shown as a vertical line on the estimated age range for each terminal taxon. See Table S2 for sources of the age ranges used in the tip-dating analysis. Major clades identified by this study are indicated by the round boxes with the clade name enclosed or overlapping the boundaries of the box.

Epoch	Paleocene				Eocene						Oligocene						Miocene																			
Stage	Maastrichtian		Danian		Selandian		Thanetian		Ypresian		Lutetian		Bartonian		Priabonian		Rupelian		Chattian		Aquit.		Burdigalian		Lang.		Serra.		Tortonian		Mess.					
NALMA	Lancian		Puercan		Torrejon.		Tiffanian		CL		Wasatchian		Bridgerian		Uintan		Duchesnean		Chadronian		Whitne.		Geringian		Arikarean		Hemingfordian		Barstov.		Clarendon.		Hemphillian			
European Zones	MP 1–5		MP 6		MP 7–10		MP 11–15		MP 16		MP 17–20		MP 21–24		MP 25		MP 26		MP 27		MP 28		MN 1		MN 2		MN 3		MN 4		MN 5		MN 6		MN 7	

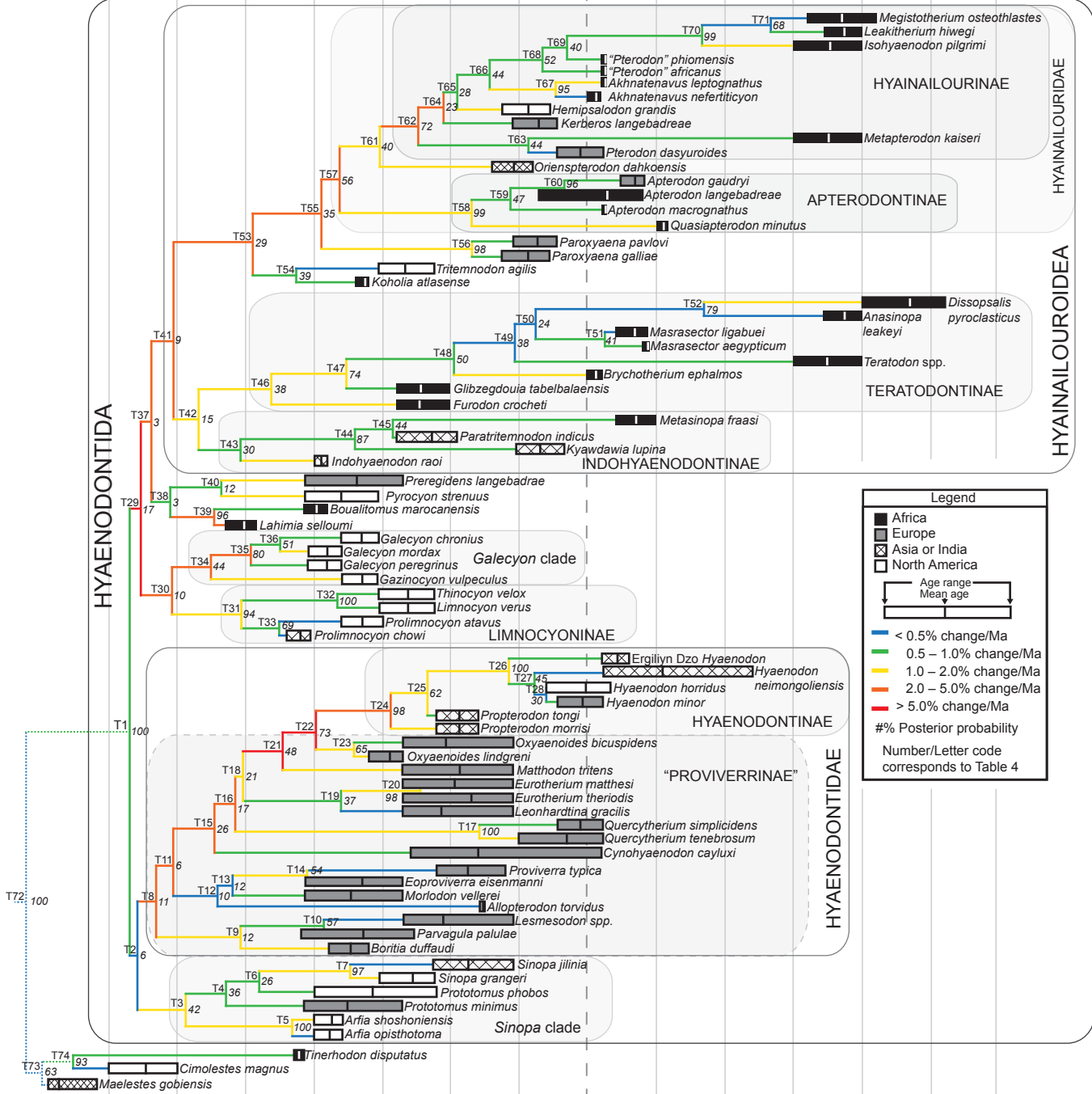


Figure 20(on next page)

BBM biogeographic analysis of strict consensus tree

Results from Bayesian Binary MCMC (BBM) biogeographic analysis performed on the strict consensus tree based on maximum parsimony analysis. Proportion of circle corresponds to likelihood of node originating from continental area. P# corresponds to clade rows in Table S5 where the reconstructed biogeographic origin for each clade is listed using parsimony optimization (PO), and % likelihood for each area using likelihood optimization (LO) and BBM. Green = Afro-Arabia; Purple = Asia; Red = Europe; Blue = North America; Gray = continents without hyaenodontidans.

..... *Branch collapses in strict consensus*



Early Eocene ~50 Ma

Figure 21(on next page)

BBM biogeographic analysis of standard Bayesian tree

Results from Bayesian Binary MCMC (BBM) biogeographic analysis performed on the standard Bayesian “allcompat” consensus tree. Proportion of circle corresponds to likelihood of node originating from continental area. B# corresponds to clade rows in Table S6 where the reconstructed biogeographic origin for each clade is listed using parsimony optimization (PO), and % likelihood for each area using likelihood optimization (LO) and BBM. Green = Afro-Arabia; Purple = Asia; Red = Europe; Blue = North America; Gray = continents without hyaenodontidans.

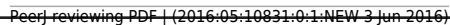


Figure 22 (on next page)

BBM biogeographic applied to Bayesian tip-dating tree

Results from Bayesian Binary MCMC (BBM) biogeographic analysis performed on the Bayesian tip-dating “allcompat” consensus tree. Proportion of circle corresponds to likelihood of node originating from continental area. T# corresponds to clade rows in Table S7 where the reconstructed biogeographic origin for each clade is listed for parsimony optimization (PO), and % likelihood for each area using likelihood optimization (LO) and BBM. Green = Afro-Arabia; Purple = Asia; Red = Europe; Blue = North America; Gray = continents without hyaenodontidans. Red vertical dashed lines indicate dispersal intervals discussed by Gheerbrant & Rage (2006). Gray vertical dashed line indicates age of L-41.

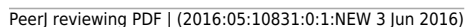


Figure 23(on next page)

Carnassial specialization in Hyaenodontida

Comparison of carnassial specialization in Hyaenodontida. Sketches show M^2 of each taxon (name to the right of the tooth) in buccal view. Mesial direction is to the right of the image; distal direction is to the left. M^1 and M^2 for *Hyaenodon* shown. Schematized tree, including divergence estimates, are based on the tip-dating topology. *Proviverra* represents the unspecialized, condition of the upper molars in Hyaenodontida. *Sinopa* is slightly more specialized with a more buccolingually compressed paracone and metacone. *Eurotherium* represents the more specialized carnivorous dentition with the upper carnassial blade formed between the metacone and metastyle and the paracone is smaller, but unfused to the metacone. *Hyaenodon* represents a very specialized shearing dentition. The metacone is taller than the paracone and the paracone is fused to the mesial aspect of the metacone. Teratodontinae independently evolved specialized carnassial morphology from Hyaenodontinae, but their dental morphology is convergent with the metacone taller than the paracone in Teratodontinae, as expressed in the specialized *Dissopsalis* and less specialized *Brychotherium*. Hyainailourinae also converged on specialized, hypercarnivore-like dentition, but in this lineage the paracone is taller than the metacone and the metacone is fused to the distal aspect of the paracone. While not specialized for hypercarnivorous shearing, *Apterodon* also has taller paracones than metacones. **M**, metacone; **P**, paracone. Timeline abbreviations correspond to the first letter for each stage shown in Figs. 19 and 22.

Paleocene			Eocene				Oligocene		Miocene						
D	S	T	Y	L	B	P	R	C	A	B	L	S	T	M	

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HYAINAILOURINAE

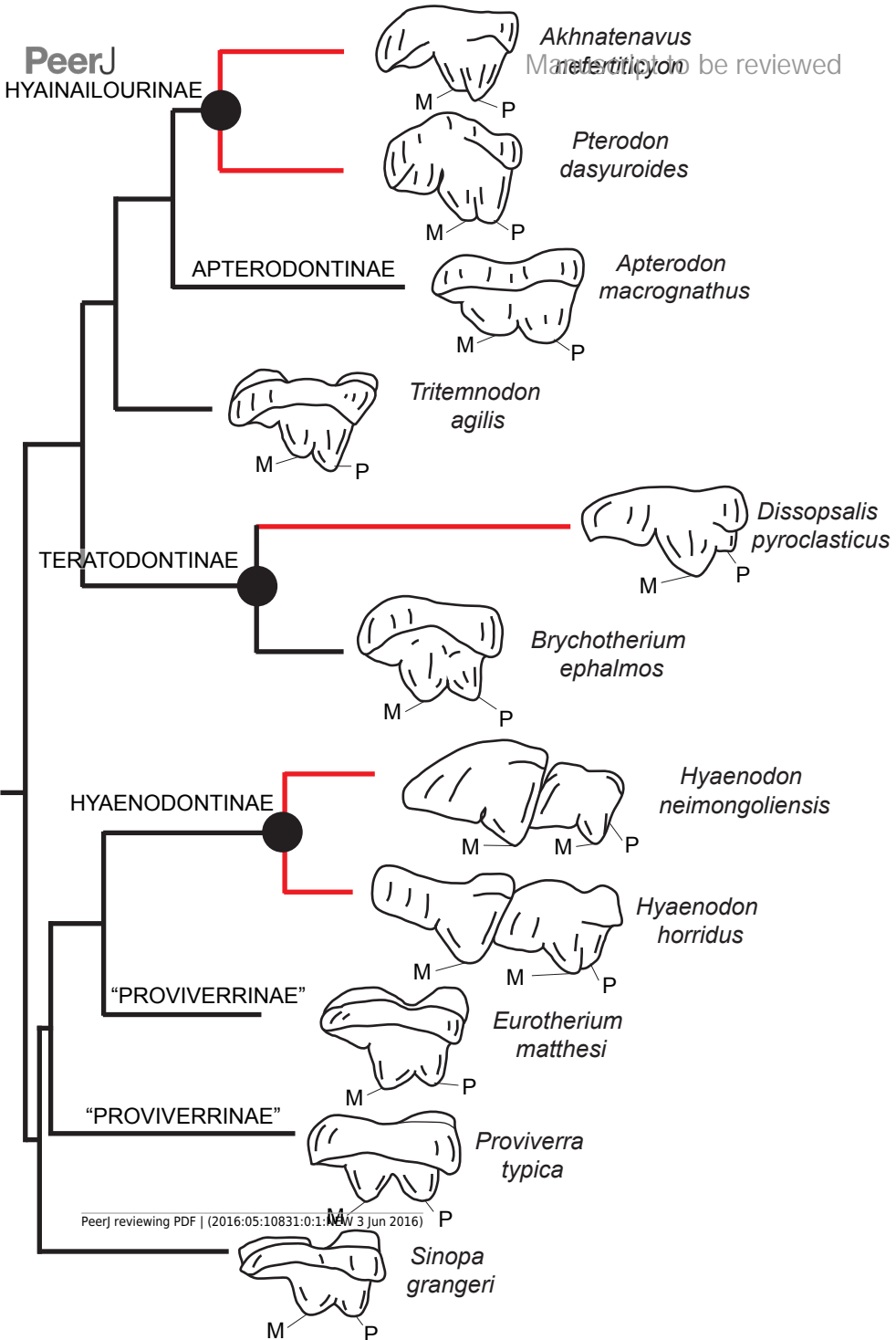


Table 1 (on next page)

Specimen measurements for the upper dentition of *Brychotherium ephalmos*

Length, maximum mesiodistal length; **Width**, maximum buccolingual width; **Metastyle length**, maximum mesiodistal length from base of the paracone (premolars) or metacone (molars); **Paracone Height**, paracone height from alveolar margin to the apex; **Metacone Height**, metacone height from alveolar margin to the apex; **Paracone Length**, paracone mesiodistal length at base of cusp; **Metacone Length**, metacone mesiodistal length at base of cusp.

<i>Brychotherium ephalmos</i>	Element	Length	Width	Metastyle Length	Paracone Height	Metacone Height	Paracone base length	Metacone base length
DPC 11990	p ⁴	7.12	6.53	2.4	—	—	3.72	—
(left side)	M ¹	8.44	7.42	3.87	2.46	3.01	2.21	2.48
	M ²	9.66	9.65	4.35	3.3	4.67	2.3	2.94
	M ³	3.37	11	—	1.93	~0.83	2.03	0.9
DPC 17627	dP ⁴	7.72	5.95	3.36	—	—	1.67	2.75
(left side)	M ¹	8.73	7.05	4.13	2.47	3.21	1.81	2.89
	M ²	9.91	9.82	4.74	3.54	4.55	2.22	3.47

1
2

Table 2 (on next page)

Specimen measurements of the lower dentition of *Brychotherium ephalmos*

Max. length, maximum mesiodistal length; **Max. trigonid length**, maximum mesiodistal length of trigonid; **Max. talonid length**, maximum mesiodistal length of talonid; **Max. trigonid width**, maximum buccolingual width of trigonid; **Max. talonid width**, maximum buccolingual talonid width; **Talonid height**, tallest point on talonid to alveolar margin; **Paraconid height**, apex of paraconid to alveolar margin; **Protoconid height**, maximum height from cristid obliqua to cusp apex. **Std. Dev.**, standard deviation. Measurements preceded by “~” indicate measurement taken from a heavily worn cusp. Summary statistics only include specimens with minimal wear.

<i>Brychotherium ephalmos</i>	Element	Max. length	Max. trigonid length	Max. talonid length	Max. trigonid width	Max. talonid width	Talonid height	Paraconid height	Protoconid height
DPC 17627	P ₄	7.15	5.48	1.49	3.65	3.18	3.54	2.6	6.08
	M ₁	7.56	4.85	2.52	4.18	3.2	2.98	~4.17	5.8
	M ₂	9.55	5.4	3.86	5.1	3.47	3.08	6.23	8.85
	M ₃	10.19	7.22	2.8	5.12	2.31	2.55	7.12	9.48
CGM 83750	C	5.75	—	—	—	—	—	—	—
	P ₁	5.33	3.63	1.45	2.1	2.21	1.52	—	~2.62
	P ₂	6.52	5.06	1.47	3.08	2.85	1.48	2.67	~3.8
	P ₃	6.7	5.45	1.23	3.31	3.13	2.1	1.8	~3.7
	P ₄	7.01	5.21	1.86	3.6	3.57	2.7	2.8	~4.75
	M ₁	6.25	4.24	2.06	3.89	3.49	2.67	~2.16	~3.6
	M ₂	8.17	5.29	2.57	4.61	3.97	2.95	~3.98	~5.95
	M ₃	9.35	6.49	2.97	5.43	3.55	2.69	5.23	7.29
DPC 11569A	C	5.35	—	—	—	—	—	—	—
	P ₂	5.18	4.33	0.81	2.51	1.69	0.61	—	3.4
	P ₃	6.37	5.2	1.02	2.5	1.72	1.07	1.09	~3.10
	P ₄	6.94	5.55	1.41	3.1	2.19	2.37	1.62	5.21
	M ₁	6.06	3.77	2.35	3.02	2.34	2.24	~3.83	~4.33
	M ₂	~7.68	5.07	~2.57	4.13	~2.27	—	4.46	6.52
	M ₃	9.68	6.81	2.81	4.92	2.46	1.93	5.91	8.24
DPC 11569B	C	4.38	—	—	—	—	—	—	—
	P ₂	~4.6	—	1.17	2.31	1.84	0.78	—	—
	P ₃	6.68	5.05	1.68	2.31	2.1	1.31	1.13	3.6
	P ₄	—	—	~1.66	—	2.46	~1.76	—	—
	M ₁	6.16	4.07	2.09	2.73	2.28	2.39	~3.20	~4.95
	M ₂	7.52	4.95	2.62	3.95	2.42	2.88	4.54	6.32
	M ₃	9.07	6.52	2.54	4.69	2.19	1.77	5.87	7.74
Tooth Length		C	P ₁	P ₂	P ₃	P ₄	M ₁	M ₂	M ₃
<i>N</i>		3	1	2	3	3	4	3	4
Mean (Std. Dev.)		5.16 (0.70)	5.33	5.85 (0.95)	6.58 (0.19)	7.03 (0.11)	6.51 (0.71)	8.41 (1.04)	9.57 (0.48)

Table 3 (on next page)

Specimen measurements for the upper dentition of *Akhnatenavus nefertiticyon*

Length, total mesiodistal length; **Width**, total buccolingual width; **Metastyle length**, mesiodistal length from base of the paracone (premolars) or metacone (molars); **Paracone Height**, from alveolar margin to the apex; **Metacone Height**, from alveolar margin to the apex; **Para/Meta base length**, mesiodistal length of base of both paracone and metacone. **Std. Dev.**, standard deviation. Summary statistics only include specimens with minimal wear.

<i>Akhnatenavus nefertiticyon</i>	Element	Length	Width	Metastyle length	Paracone height	Metacone height	Para/Meta base length
DPC 18242	P ²	9.18	4.08	1.37	6.2	—	5.66
(left side)	P ³	10.09	5.22	2.18	6.3	—	6.58
	P ⁴	10.94	8.54	2.96	6.25	—	6.09
	M ¹	14.08	11.08	6.6	5.57	4.63	7.21
	M ²	15.3	12.8	6.9	7.27	6.07	7.44
(right side)	M ¹	13.5	—	5.1	7.37	5.9	5.37
CGM 83735	C	9.95	—	—	—	—	—
(right side)	P ³	10.98	4.44	2.34	—	—	6.03
	P ⁴	11.98	9.15	3.65	—	—	5.71
	M ¹	13.28	9.78	5.33	—	—	5.72
	M ²	15.14	13.5	7.28	—	—	7.04
	M ³	2.49	—	—	—	—	—
(left side)	P ²	9.51	—	2.44	5.95	—	—
	P ⁴	11.79	—	3.49	—	—	—
	M ¹	13.34	—	5.5	—	—	—
	M ²	15.18	—	5.91	7.87	5.54	7.15
DPC 13518	M ¹	14.73	9.5	6.37	5.41	4.41	6.96
Tooth Length		P ²	P ³	P ⁴	M ¹	M ²	M ³
<i>N</i>		2	2	3	5	3	1
Mean (Std. Dev.)		9.35 (0.23)	10.54 (0.63)	11.57 (0.55)	13.79 (0.62)	15.21 (0.08)	2.49