

1 **Dispersal ability predicts evolutionary success among mammalian carnivores**

2 **Authors:** S. Faurby^{1,2,*}, L. Werdelin³, A. Antonelli^{1,2,4}

3 **Affiliations:**

4 ¹Department of Biological and Environmental Sciences, University of Gothenburg, Box 461, SE
5 40530, Göteborg, Sweden

6 ²Gothenburg Global Biodiversity Centre, Box 461, SE 40530 Göteborg, Sweden

7 ³Swedish Museum of Natural History, Department of Palaeobiology, Box 50007, SE 10405
8 Stockholm, Sweden

9 ⁴Royal Botanic Gardens, Kew, TW9 3AE, Richmond, Surrey, UK

10 *Correspondence to: Soren.Faurby@bioenv.gu.se

11

12 **Abstract**

13 Understanding why some clades contain more species than others is a major challenge in evolutionary
14 biology, and variation in dispersal ability and its connection to diversification rate may be part of the
15 explanation. Several studies have suggested a negative relationship between dispersal capacity and
16 diversification rate among living mammals. However, this pattern may differ when also considering
17 extinct species, given known extinction biases. The colonization of new areas by various lineages may
18 be associated with both diversity increases in those colonising lineages and declines in the lineages
19 already present. Past diversity declines are, however, effectively impossible to infer based on
20 phylogenies of extant taxa, and the underlying process may, therefore, be difficult to determine. Here
21 we produce a novel species-level phylogeny of all known extant and extinct species of the order
22 Carnivora and related extinct groups (1,723 species in total) to show that there is instead a positive
23 relationship between dispersal rate and diversification rate when all extinct species are included.
24 Species that disperse between continents leave more descendant species than non-dispersers, and
25 dispersing species belong to lineages that at the time of dispersal were diversifying faster than the
26 average non-disperser. Our study showcases the importance of combining fossils and phylogenies to
27 better understand evolutionary and biogeographic patterns.

28

29 **1 Introduction**

30 Clades from across the tree of life vary widely in both diversification rate and in the dispersal capacity
31 of the species they comprise, but the extent to which the variation in the two is coupled remains
32 unclear. Among extant vertebrates, a limited number of clades show substantially higher
33 diversification rates than others (1). The fossil record also shows that vertebrate classes vary widely in
34 how many families of equal ages they contain (2). The variation in dispersal capacity among extant
35 vertebrates is equally evident. Some species have colonised nearly the entire world. At one extreme,
36 the range of the wild horse (*Equus ferus*) spanned five continents including northern Africa, the whole
37 of Eurasia and most of the Americas until the end of the last ice age (3). At the other extreme, we find
38 the lemur genus *Eulemur* in Madagascar, where even minor rivers have restricted the migration of
39 individuals sufficiently to result in individual species that are endemic to small areas between
40 neighbouring rivers (4). Interestingly, the clades encompassing these two examples have identical
41 numbers of species (12; *sensu* [3]), at least when the extinct Late Pleistocene species of horses are
42 included (Equidae: *Equus*, *Haringtonhippus*, and *Hippidion*). These two clades also have similar ages
43 (the most recent common ancestor [MRCA] of the lemur genus is ~4.5 million years [My] old
44 following (4); the MRCA of the horses is ~6 My following [5]). Taken together, there is thus no
45 universal relationship between dispersal rate and diversification rate.

46 There are, however, strong arguments for why a relationship between dispersal rate and
47 diversification rate should be expected. A negative correlation between the two rates may be generated
48 under purely neutral models (see e.g. [6]). This is because the *in situ* per area speciation rates would
49 normally increase with decreasing dispersal rates, since populations of poorly dispersing organisms
50 can more readily become isolated from each other and eventually speciate. While a negative
51 relationship is most likely based on neutral models, arguments could also be made for a positive
52 relationship. Increased dispersal rate could potentially increase diversification rate by increasing the
53 total area occupied by the clade, but empirical support for such an effect is limited (7).

54 While neutral models are thus likely to predict a negative relationship, a positive
55 relationship between diversification and dispersal rates may be the expected outcome of non-neutral

56 models based on interspecific competition (hereafter non-neutral models). A common pattern is a wax-
57 and-wane model with increases followed by decreases in diversity within each clade (e.g. 8, 9). If this
58 is driven by competition, it should produce increased diversity for species with higher dispersal rates,
59 both at the time of diversity increase and the time of diversity decline. During the period of increased
60 diversity, species with a higher dispersal rate would be faster at colonizing all the areas formerly
61 occupied by the species of a clade that they are outcompeting. During their global decline, species
62 with a higher dispersal ability would be able to survive in peripheral regions by escaping direct contact
63 with their competitors.

64 Although the expectations for non-neutral models have not been explicitly tested, there
65 is anecdotal support based on distribution data, at least when fossils are included. The clearest
66 examples come from the isolated archipelago of New Zealand, where both the Tuatara (*Sphenodon*
67 spp.) and the only known non-flying mammal native to those islands (an unnamed Miocene species
68 often referred to as the Saint Bathans mammal) represent the last remnants of formerly far more
69 diverse and widespread clades (1, 10). There is also evidence of large geographic ranges for some
70 rapidly diversifying lineages, presumably in their expanding phase, such as the Pacific flying foxes
71 (*Pteropus spp.*) (11), but the latter pattern could be generated under both a neutral and a non-neutral
72 model. The expectations from these non-neutral models are also seen in macro-evolutionary analyses
73 of the fossil record. Among mammalian carnivores, there is evidence that the decline in some older
74 clades may be causally related, through increased competition, to the net diversification of younger
75 clades (12, 13).

76 To reliably tease apart the different mechanisms operating under the neutral and non-
77 neutral models, we may need data on both the diversification rate at the time of dispersal and on the
78 number of descendants each species leaves after dispersal. If diversification rate is increased through
79 increased colonization rate, good dispersers would leave more descendant species than poor
80 dispersers, but they would be unlikely to have a high diversification rate at the time of dispersal in
81 their source area, as discussed above. On the other hand, if non-neutral models prevail, better
82 competitors would both be diversifying faster in their source area and leaving a larger number of

83 descendant species after successful colonization. The required information to test these predictions
84 has, to the best of our knowledge, not yet been assembled.

85 With few but increasing exceptions (e.g 13, 14), macro-evolutionary studies to date
86 have been based on phylogenies comprised solely of extant species, where the amount of information
87 often makes it impossible to determine if clades are in diversity decline, or show positive yet density-
88 dependent diversification (15). It has even been suggested that estimation of extinction rates relying
89 solely on extant taxa may not be possible (16, 17). Such problems may be avoided for analyses relying
90 solely on fossil data (18). On the other hand, the exclusion of a phylogenetic tree in such analyses
91 usually only allows for comparison of the diversification rates within pre-defined taxonomic entities
92 like families (see e.g. (13)), unlike tree-based analyses where comparisons can be made between any
93 named or unnamed clades. A combined approach based on phylogenetic trees but also incorporating
94 all suitable fossils may, therefore, be optimal for inferring macro-evolutionary patterns (14, 19, 20).

95 Here we test the relationship between diversification and transcontinental dispersal
96 rates in mammals by combining the advantages of tree-based and fossil-based methods. We build and
97 analyse a complete species-level phylogeny of all extant and extinct species of mammalian carnivores
98 and related extinct groups (Carnivoramorpha, Hyaenodonta, and Oxyaenidae). Our results provide
99 unequivocal evidence that species with high dispersal capacity both had a higher diversification rate at
100 the time of dispersal and left more descendant species than the species that did not disperse between
101 continents. These results suggest that the underlying process is best explained by a non-neutral,
102 competition-driven model.

103

104 **2 Results**

105 **2.1 Diversity accumulation**

106 We found a nearly continuous increase in diversity across the entire carnivore phylogeny, both
107 globally and within continents, for both phylogenetic and taxonomic diversity (Fig. 1). There were
108 only three main exceptions: 1) Diversity in North America initially peaked at the early Eocene climatic
109 optimum and then decreased in the interval 50 to 45 million years ago (Ma). Given that the majority of
110 species at that time were confined to this continent, a similar decrease was also seen in global

111 diversity. 2) Diversity in both North America and Eurasia decreased over the last ~10 My. 3) There
112 was a decline in phylogenetic (but not species) diversity in Eurasia between approximately 40 to 35
113 Ma. Similar results were obtained independently of the length of the time bins being analysed and
114 showed only limited variation across the 100 trees (Fig. 2).
115 These results were based on the assumption of complete sampling. However, the increase in diversity
116 through time could be partially caused by an increase in sampling intensity towards the present. We
117 showed through simulations that this is very unlikely. Our simulations showed very limited effects of
118 incomplete sampling on the observed patterns when using empirically derived sampling intensities
119 (Figure S1).

120

121 **2.2 Higher evolutionary success of dispersers**

122 We estimated the evolutionary success of dispersers using two novel metrics, which we refer to as *pre-*
123 *dispersal success* and *post-dispersal success* (Fig. 3). *Pre-dispersal success* measures the
124 diversification rate of lineages at the time of their dispersal, whereas *post-dispersal success* measures
125 how many species the dispersing lineages diversify into.

126

127 **2.2.1 Pre-dispersal success**

128 Our analyses of *pre-dispersal success* suggest that the dispersing species belong to clades that, at the
129 time of dispersal, were diversifying faster than non-dispersers (Tables 1, S1-S2). This pattern was
130 observed irrespective of whether comparisons were to all species alive in the time interval, or only to
131 species occurring on the source continents in the time interval (which we refer to as *global* and
132 *continental pre-dispersal success*). We estimated dispersal within time bins rather than in continuous
133 time, but the results were independent of the length of these bins. The best model for *continental pre-*
134 *dispersal success* showed a difference in success between dispersers and non-dispersers depending on
135 the target continent. In particular, the model showed a substantially smaller difference between
136 dispersers and non-dispersers for species colonizing South America. The best model for *global pre-*
137 *dispersal success* showed temporal variation, where the difference in success between dispersing and
138 remaining lineages was smaller for older dispersal events. In both cases, however, both models had

139 lower AIC than the model without any spatial or temporal variation. Thus, the two analyses only
140 disagreed on whether spatial or temporal variation was most important.

141 Our analyses assumed complete sampling of all extinct species but we tested the
142 consequences of this assumption through simulations. For this, we modelled scenarios of no difference
143 in diversification patterns between dispersers and non-dispersers and assessed if spatial patterns in
144 sampling would create a false signal with such a difference. These simulations showed that the
145 patterns of *pre-dispersal success* were not caused by incomplete sampling (Table S3-S4). The
146 simulations of *global pre-dispersal success* found no significant difference in success between
147 dispersers and non-dispersers and found no support for any spatial or temporal variation in the
148 difference between dispersers and non-dispersers. The simulations of *continental pre-dispersal*
149 *success* also found no significant difference in success between dispersers and non-dispersers. They
150 did, however, recover weak support based on AIC for models with temporal, but not spatial, variation
151 in the difference between dispersers and non-dispersers. Even then, the estimated effect size for
152 temporal variation was not significantly different from zero. If sampling effort did have an effect on
153 spatial or temporal variation in our results, the effect size must have been minimal.

154

155 **3.2.2 Post-dispersal success**

156 Our results clearly demonstrate that dispersing lineages leave more descendant lineages than lineages
157 that remain within the source continents (Table 2). This applies to both *continental* and *global post-*
158 *dispersal success* (i.e. comparisons to all other species on the target continent or all species alive at the
159 time of dispersal). This pattern – that dispersers leave more descendant lineages – remained constant
160 irrespective of the length of the analysed time bin and how long after the dispersal the number of
161 descendant species was counted (Tables S5-S6). The model with spatial variation was, however, only
162 supported for *continental* (but not *global*) *post-dispersal success* and similar, although weaker, support
163 for spatial variation was also recovered when we simulated incomplete sampling (Table S7). We,
164 therefore, focus our discussion solely on the strong evidence for higher *post-dispersal success* rather
165 than on any more detailed spatial or temporal patterns regarding the magnitude of this success.

166

167 **3 Discussion**

168 Our results unequivocally show a positive correlation between diversification rate and dispersal in
169 carnivores. The analyses are based on the first species-level phylogeny of carnivores that includes all
170 suitable fossils and all extant species. These results contradict an expected neutral pattern of a trade-
171 off between diversification rate and dispersal, as has been suggested based on analyses of
172 contemporary mammals (6).

173

174 **3.1 Diversity accumulation**

175 The occasional periods of diversity decline detected by our analyses lend biological credence to our
176 results, since a monotonous increase in diversity could point towards a pattern driven by insufficient
177 fossil information. All three declines detected clearly match previous knowledge. The first two
178 declines were likely climatically driven. If carnivores throughout their history have had lower diversity
179 in higher latitudes, similar to what we see today (21), we should expect to see diversity declines during
180 times of global temperature decline, particularly in North America and Eurasia, which have the highest
181 proportions of non-tropical areas. In this regard, the first early decline in North America coincides
182 with a period of Eocene cooling (22) and is temporally similar to a time period recently found to have
183 a low overall mammalian diversity in North America (23). Secondly, the declines in North America
184 and Eurasia during the last 10 My may be explained by the overall climatic cooling during this time
185 period (24).

186 In contrast, the third decline in phylogenetic diversity in Eurasia may not have been
187 climatically driven. Instead, it probably reflects the so-called ‘Grande Coupure’, where the formerly
188 isolated European fauna was replaced by an immigrant Asian fauna (e.g. 25). The cause of the Grande
189 Coupure is not entirely known (25) but if it represents biotic replacement driven by competition,
190 which is one of the hypotheses (25), it may indicate that such processes are important for carnivores in
191 general.

192

193 **3.2 Neutral or non-neutral models**

194 Our results for *pre-dispersal success* and *post-dispersal success* clearly suggest that dispersal rate and
195 diversification rate are linked in carnivores. As previously noted, the pattern for *post-dispersal success*
196 could be the result of either neutral or non-neutral models or both, but the higher *pre-dispersal success*
197 among good dispersers is only expected under the non-neutral models.

198 Support for a non-neutral model is further evident in the temporal variation in *pre-*
199 *dispersal success*. We find an increasing effect for recent dispersals, where the number of free niches
200 would be expected to be lower. This matches the expectations of this model – the non-neutral model
201 would only generate a relationship between *pre-dispersal success* for dispersers and non-dispersers if
202 dispersal to other continents required the displacement of lineages already there. There should be
203 smaller differences if there are free niches open to any coloniser. This non-neutral model, therefore,
204 contrasts with the frequently found priority effects in community ecology where the first coloniser is
205 nearly always more successful (26).

206 The spatial patterns also support non-neutral models (Table 1). We find elevated *pre-*
207 *dispersal success* for dispersers to North America and a near-random pattern for dispersers to South
208 America, which matches our expectations. Under non-neutral models, we only expect elevated *pre-*
209 *dispersal success* for dispersers if these are invading already occupied niches. The South American
210 continent lacked placental carnivores until the mid-Miocene (27), and all invading carnivores would
211 have initially encountered empty ecological niches. The pattern of elevated *pre-dispersal success* in
212 North America is expected because our analyses suggest that carnivores originated in North America.
213 Our results also show that the clade has consistently been highly diverse in that continent (Fig. 1). This
214 North American origin is clear from Oxyaenidae, which is one of the three earliest diverging clades we
215 analyze (28). The origin of the two other clades (Carnivoramorpha and Hyaenodonta) has previously
216 been considered to be Eurasian or African, but even studies suggesting a non-North American origin
217 for these clades have suggested extremely rapid dispersal to, and substantial diversification within,
218 North America (29, 30).

219 Our results partially contradict earlier work which suggested that dispersal from North
220 America to Eurasia – but not in the opposite direction – was associated with high diversification rate
221 (31). Our results suggest the opposite and we found both higher increases in both *pre-dispersal* and

222 *post-dispersal success* for dispersers to North America compared to dispersers to the other continents
223 (Tables 1–2). The reason for this difference may partly be a function of the non-phylogenetic approach
224 of Pires et al (31), meaning that the different outcomes of multiple dispersals within the same family
225 could not be distinguished.

226 As a minor point of uncertainty, we note that we treat the carnivore niche in South
227 America as unoccupied, although it was occupied prior to the arrival of the placental carnivores by the
228 Sparassodonta (Metatheria; sister group to marsupials). It is still unknown if the Sparassodonta went
229 extinct independently of the arrival of placental carnivores, or if they were driven to extinction by
230 competitive replacement (32). Non-placental lineages seem, however, to be inherently inferior
231 competitors to placental carnivores, likely due to effects related to their lack of deciduous teeth (33,
232 34, 35). It, therefore, seems plausible that if the Sparassodonta were still extant when the carnivores
233 arrived then any member of the group that arrived there may have been able to outcompete them.

234

235 **3.3 Implications**

236 Our results suggest a model of consistent competitive replacement among carnivore clades, although
237 the generality of the observed pattern remains unclear. The methodology we employed was possible
238 because carnivores have a well-understood fossil history, which is why the effects of incomplete
239 sampling were deemed minor (Tables S3–S4, S7; Fig. S1). Furthermore, carnivores are a particularly
240 useful group to study for this purpose because there is strong phylogenetic conservatism in their niche,
241 with few other taxa competing with them. They are thus nearly a monophyletic ecological guild,
242 although there are exceptions to this; some species within the group, such as the giant and red pandas,
243 for instance, are predominantly herbivorous (3). Until the Eocene, carnivores shared the carnivorous
244 niche with other mammalian species of uncertain placement, such as Arctocyonidae or Cimolestidae
245 (36), but even then, carnivores plausibly comprised the majority of the guild (12). Arguably, the only
246 other large monophyletic mammalian group that behaves like an ecological guild is bats, but they are
247 noteworthy for having a particularly scarce fossil record among mammals (37). It may therefore not be
248 possible at present to directly replicate our analyses using other clades and thereby directly test the
249 generality of the patterns reported here.

250 Despite the difficulties in applying our methodology to other clades, we find it unlikely
251 that the patterns we report here would be taxon-specific. Taxon specificity could have explained why
252 our results appear to run counter to some studies showing lower diversification rates for species with
253 higher dispersal rates (6, 7). We think, however, that the apparent differences are instead a
254 consequence of the taxonomic scale of the analyses and the inclusion or exclusion of fossil taxa. A
255 lower diversification rate in highly dispersing lineages has been recovered in analyses at the subfamily
256 or family level, whereas our estimates here are conducted at the species level. Direct competition may
257 be strongest between the most closely related species in the case of mammals (38), which is also what
258 would be expected for any traits with phylogenetic conservatism. This would explain the apparent
259 conflict between this and earlier analyses of mammals. Earlier analyses at the subfamily level have
260 suggested a negative relationship between dispersal and diversification rate in mammals (6), whereas
261 in a species-level analysis we here recover a positive relationship between the two.

262 We are not implying that competition is not frequent between distantly related taxa, as
263 is increasingly being acknowledged (39). However, competition may be expected to be linked to
264 physiological or morphological traits, which are generally more similar for closely related species.
265 There are many examples of convergent evolution within mammals (e.g. 40, 41), but even so, recently
266 diverged species will be more similar than a random pair of species under most evolutionary models.
267 They must, therefore, be expected to rely more on the same resources and the same environmental
268 conditions than random members of a larger clade.

269 If the pattern we recover is driven by non-neutral biotic interactions, it may only be
270 observable because we included fossil species in our analyses. When species are driven to extinction
271 by other species it may be on too fast a time scale for us to see it clearly based only on extant species
272 in their native ranges. The only clear contemporary evidence for biologically caused extinctions or
273 declines comes from the invasion biology literature (e.g. 42). Competition-driven extinctions could
274 leave signals on the phylogenies of the extant species but, as we noted in the introduction, such
275 declines may be extremely difficult to detect based on phylogenies of extant species only (15, 16, 17).
276 Even in the few situations where declines can be detected, methods solely relying on contemporary
277 species can logically only give a signal if the declining lineages still have at least one extant species.

278 Some of the clearest cases of clade competition, such as the bone-crushing dogs (Borophaginae) being
279 driven to extinction by related and extant modern dogs (Caninae) (13), are thus impossible to infer
280 without fossils.

281 In summary, our analysis of a novel species-level phylogeny of all extant and extinct
282 carnivores shows that: 1) lineages that disperse between continents are generally those that diversify
283 more quickly; and 2) lineages that colonise new continents leave more descendant species than
284 lineages already present there. These results are only likely to have emerged because we combined
285 fossil and phylogenetic information, highlighting the need to incorporate both sources of information
286 whenever possible.

287

288 **4 Methods**

289 **4.1 Method summary**

290 We analysed all extant and extinct species of mammalian carnivores and related extinct groups
291 (Carnivoramorpha, Hyaenodonta, and Oxyaenidae). Herein we refer to this entire clade as
292 ‘carnivores’. We revisited the taxonomy of all fossil and extant members of the group and accepted,
293 1723 species (314 of which are extant). We based our analyses on records in the Paleobiology
294 Database (PBDB; <https://paleobiodb.org/>) and the New and Old Worlds Database of fossil mammals
295 (<http://www.helsinki.fi/science/now/>; NOW), but supplemented these with data from the original
296 literature for 128 species that we consider valid but which, at least when we were collecting data,
297 lacked any records in either of the two databases.

298 We constructed the phylogeny of all extant and extinct species of carnivores using a tip
299 dating approach under a fossilised birth-death model in MrBayes 3.2 (43). We did this in a two-step
300 procedure combining a backbone tree with a number of smaller phylogenies at lower taxonomic levels.
301 This procedure is similar to that used to construct phylogenies focusing on other large clades (e.g. 44,
302 45), but it has previously only been used to generate all-taxon phylogenies of all extant species within
303 a clade. This is the first time it has been expanded to include all extant and extinct species within the
304 focal clade. The placement of species without genetic or morphological data was facilitated by a
305 number of constraints based on taxonomy and suggested relationships from taxonomic treatments.

306 These trees only give species origination time, but the information from these was combined with
307 extinction times generated by the Bayesian program PyRate (46), which estimated likely extinction
308 times based on the temporal distribution of all known records of each species. The resulting phylogeny
309 is attached as appendix 1 giving 1000 trees from the posterior distribution of trees We included
310 pinnipeds to improve the usability of the phylogeny for other researchers, but here we discarded them
311 for all analyses for this paper due to our focus on terrestrial species.

312 We inferred the ancestral areas of all nodes based on a DEC
313 (dispersal-extinction-cladogenesis) model in BiogeoBEARS (47). We used a DEC rather than the
314 DEC +j model since the underlying mathematical properties of the DEC +j model have been
315 questioned (48). Following the estimation of ancestral areas for all nodes, we inferred dispersal events
316 and times along branches.

317 We assessed changes in global and continental diversity by plotting species and
318 phylogenetic diversity (49) (i.e. the sum of branch lengths). Following this, we analysed the
319 evolutionary success (estimated as their diversification rate) of dispersers at the time of their dispersal
320 (*pre-dispersal success*) and the number of descendant species they left behind after a set time (*post-*
321 *dispersal success*).

322 The analyses related to phylogenetic diversity and diversification rate are only
323 meaningfully interpretable for ultrametric trees. For simplicity, extinction was therefore dealt with in
324 time intervals rather than in continuous time and on trees sliced at various ages, only counting the
325 species (internal or external branches) extant at that point in time. Hence, when using 0.5 My time
326 intervals, two species that went extinct 1.2 and 1.4 Ma were assumed to have survived until 1.0 Ma
327 and would both be included as extant for a tree sliced at 1.0 Ma. To test the effect of this procedure on
328 the results, all analyses were conducted with time intervals of 0.25, 0.5 or 1.0 My duration.

329 We estimated *pre-dispersal success* based on diversification rate (DR) (45). We sliced
330 the tree at the end of each time interval throughout the Cenozoic and calculated the DR of all lineages
331 alive at that time. For all intercontinental dispersal events occurring in the following time interval, we
332 then identified the lineage at the beginning of the interval that would evolve into the disperser during
333 the interval. This could be either the same species or one of its ancestors, which would be the case for

334 founder speciation occurring within the time interval. We then calculated the logarithm of the ratio
335 between the diversification rate of the disperser and the median diversification rate for either all
336 lineages alive in the time interval (*global pre-dispersal success*) or the subset of these that was found
337 on the same continent the disperser originated in (*continental pre-dispersal success*). This calculation
338 is outlined in Fig. 3.

339 We estimated *post-dispersal success* by comparing the tree at the time before dispersal
340 with the tree sliced a number of million years afterwards. For each lineage alive at the first time
341 interval, we identified how many species it had diversified into a few million years later (which was 0
342 if the lineage had gone extinct in the meantime). We then calculated the ratio between the number of
343 species in the dispersing lineage and the mean for either all other species (*global post-dispersal*
344 *success*) or all species from the continent dispersed to (*continental post-dispersal success*). In both
345 cases, we square-root-transformed the *post-dispersal success* to improve normality. Separate analyses
346 of *post-dispersal success* were conducted on trees sliced after 3, 5, and 7 My.

347 Although we have included all known species, an unknown number of extinct species
348 may be missing from the fossil record, which may influence our results, especially since the fraction of
349 missing species is likely to vary in time and space. In order to understand the influence of missing taxa
350 on our results, we, therefore, simulated a number of random phylogenies. We then simulated
351 incomplete sampling on those phylogenies based on spatial and temporal sampling effort estimated in
352 the PyRate analyses described above. Following this, we repeated all analyses described above on both
353 the full and the sampled phylogenies in order to directly measure the effect of incomplete sampling on
354 our results.

355 A detailed explanation of all steps can be found in the supplementary materials and
356 methods.

357

358 **References**

359 1) Alfaro, M.E. et al. Nine exceptional radiations plus high turnover explain species diversity in
360 jawed vertebrates. *Proc. Natl Acad. Sci. USA* **106**, 13410–13414 (2009)

- 361 2) Sepkoski, J. A factor analytic description of the Phanerozoic marine fossil record.
362 *Paleobiology* **7**, 36-53 (1981).
- 363 3) Faurby, S. et al. PHYLACINE 1.2: The phylogenetic atlas of mammal
364 macroecology *Ecology* **99**, 2626 (2018)
- 365 4) Markolf, M. & Kappeler, P. M. Phylogeographic analysis of the true lemurs (genus *Eulemur*)
366 underlines the role of river catchments for the evolution of micro-endemism in Madagascar.
367 *Front. Zool.* **10**, 70 (2013)
- 368 5) Heintzman, P.D. et al. A new genus of horse from Pleistocene North America. *eLife* **6**, e29944
369 (2017)
- 370 6) Faurby, S. & Antonelli, A. Evolutionary and ecological success is decoupled in mammals. *J.*
371 *Biogeogr.* **45**, 2227–2237 (2018)
- 372 7) Weeks, B. C. & Claramunt, S. Dispersal has inhibited avian diversification in Australasian
373 archipelagos. *Proc. R. Soc. B* **281**, 20141257 (2014)
- 374 8) Quantal, T. B. & Marshall, C. R. How the Red Queen drives terrestrial mammals to extinction.
375 *Science* **341**, 290–292 (2013)
- 376 9) Žliobaitė, I., Fortelius, M. & Stenseth, N. C. Reconciling taxon senescence with the Red
377 Queen’s hypothesis. *Nature* **552**, 92–95 (2017)
- 378 10) Worthy, T. H. et al. Miocene mammal reveals a Mesozoic ghost lineage on insular New
379 Zealand, southwest Pacific. *Proc. Natl Acad. Sci. USA* **103**, 19419–19423 (2006)
- 380 11) Upham, N., Esselstyn, J. A. & Jetz, W. Ecological causes of uneven diversification and
381 richness in the mammal tree of life. *bioRxiv* <https://doi.org/10.1101/504803> (2019)
- 382 12) Valkenburgh, B. V. Major patterns in the history of carnivorous mammals. *Annu. Rev. Earth*
383 *Planet. Sci* **27**, 463–493 (1999)
- 384 13) Silvestro, D., Antonelli, A., Salamin, N. & Quental, T. B. The role of clade competition in the
385 diversification of North American canids. *Proc. Natl Acad. Sci. USA* **112**, 8684–8689 (2015)
- 386 14) Cantalapiedra, J. L., Prado, J. L., Hernández Fernández, M. & Alberdi, M. T. Decoupled
387 ecomorphological evolution and diversification in Neogene–Quaternary horses. *Science* **355**,
388 627–630 (2017)

- 389 15) Quantal, T. B. & Marshall, C. R. The molecular phylogenetic signature of clades in decline.
390 *PLoS One* **6**, e25780 (2011)
- 391 16) Rabosky, D. L. Extinction rate should not be estimated from molecular phylogenies. *Evolution*
392 **64**, 1816–1824 (2010)
- 393 17) Louca, S. & Pennell, M. W. Phylogenies of extant species are consistent with an infinite array
394 of diversification histories. bioRxiv doi.org/10.1101/719435 (2019)
- 395 18) Silvestro, D., Schnitzler, J., Liow, L. H., Antonelli, A. & Salamin, N. Bayesian estimation of
396 speciation and extinction from incomplete fossil occurrence data. *Syst. Biol.* **63**, 349–367
397 (2014)
- 398 19) Fritz, S.A. et al. Diversity in time and space: wanted dead and alive. *Trends Ecol. Evol.* **28**,
399 509–516 (2013)
- 400 20) Slater, G. J. & Harmon, L. J. Unifying fossils and phylogenies for comparative analyses of
401 diversification and trait evolution. *Methods Ecol. Evol.* **4**, 699–702 (2013)
- 402 21) Sandom, C. et al. Mammal predator and prey species richness are strongly linked at
403 macroscales. *Ecology* **94**, 1112–1122 (2013)
- 404 22) Bohaty, S. M. & Zachos, J. C. Significant Southern Ocean warming event in the late middle
405 Eocene. *Geology* **31**, 1017–1020 (2003)
- 406 23) Brodie, J. F. Environmental limits to mammal diversity vary with latitude and global
407 temperature. *Ecol. Lett.* **22**, 480–485 (2019)
- 408 24) Zachos, J., Pagani, M., Sloan, L., Thomas, E. & Billups, K. Trends, rhythms and aberrations
409 in global climate 65 Ma to present. *Science* **292**, 686–693 (2001)
- 410 25) Costa, E., Garces, M., Saez, A., Babrera, L. & López-Blanco, M. The age of the “Grande
411 Coupure” mammal turnover: New constraints from the Eocene–Oligocene record of the
412 Eastern Ebro Basin (NE Spain). *Palaeogeography, Palaeoclimatology, Palaeoecology* **301**,
413 97–107 (2011)
- 414 26) Fukami, T. Historical contingency in community assembly: Integrating niches, species pools,
415 and priority effects. *Annu. Rev. Ecol. Evol. Syst.* **46**, 1–23 (2015)

- 416 27) Webb, S.D. The great American biotic interchange: patterns and processes. *Ann. Missouri*
417 *Bot. Gard.* **93**, 245–275. (2006)
- 418 28) Chester, S. G. B., Bloch, J. I., Secord, R. & Boyer, D. M. A new small-bodied species of
419 *Palaeonictis* (Creodonta, Oxyaenidae) from the Paleocene Eocene thermal maximum. *J.*
420 *Mamm. Evol.* **17**, 227–243 (2010)
- 421 29) Borths, M. R., Holroy, P. A. & Seiffert, E. R. Hyainailourine and teratodontine cranial
422 material from the late Eocene of Egypt and the application of parsimony and Bayesian
423 methods to the phylogeny and biogeography of Hyaenodonta (Placentalia, Mammalia). *PeerJ*
424 **4**, e2639 (2016)
- 425 30) Solé, F., Smith, T., De Bast, E., Codrea, V. & Gheerbrant, E. New carnivoraforms from the
426 latest Paleocene of Europe and their bearing on the origin and radiation of Carnivoraformes
427 Carnivoramorpha, Mammalia). *J. Vert. Paleontol.* **36**, e1082480 (2016)
- 428 31) Pires, M. M., Silvestro, D. & Quental, T. B. Continental faunal exchange and the
429 asymmetrical radiation of carnivores. *Proc. R. Soc. B* **282**, 20151952 (2015)
- 430 32) Prevosti, F. J., Forasiepi, A. & Zimicz, N. The Evolution of the Cenozoic Terrestrial
431 Mammalian Predator Guild in South America: Competition or Replacement? *J. Mamm. Evol.*
432 **20**, 3–21 (2013)
- 433 33) Werdelin, L. Jaw geometry and molar morphology in marsupial carnivores: analysis of a
434 constraint and its macroevolutionary consequences. *Paleobiology* **13**, 342– 350 (1987)
- 435 34) Croft, D.A. Do marsupials make good predators? Insights from predator–prey diversity ratios.
436 *Evol. Ecol. Res.* **8**, 1193–1214 (2006)
- 437 35) Faurby, S. & Svenning, J. C. The asymmetry in the Great American Biotic Interchange in
438 mammals is consistent with differential susceptibility to mammalian predation. *Glob. Ecol.*
439 *Biogeogr.* **25**, 1443–1453 (2016)
- 440 36) Halliday, T. J. D., Upchurch, P. & Goswami, A. Resolving the relationships of Paleocene
441 placental mammals. *Biol. Rev.* **92**, 521 – 550 (2015)
- 442 37) Barnosky, A. D. et al. Has the Earth’s sixth mass extinction already arrived? *Nature* **471**, 51–
443 57 (2011)

- 444 38) Cooper, N., Rodríguez, J. & Purvis, A. A common tendency for phylogenetic overdispersion
445 in mammalian assemblages. *Proc. R. Soc. B* **275**, 2031–2037 (2008)
- 446 39) Wilcox, T. M., Schwartz, M. K. & Lowe, W. H. Evolutionary community ecology: Time to
447 think outside the (taxonomic) box. *Tr. Ecol. Evol.* **33**, 240–250 (2018)
- 448 40) Chikina, M., Robinson, J. D. & Clark, N. L. Hundreds of genes experienced convergent shifts
449 in selective pressure in marine mammals. *Mol. Biol. Evol.* **33**, 2182–2192 (2016)
- 450 41) Mazel, F. et al. The geography of ecological niche evolution in mammals. *Curr. Biol.* **27**,
451 1369–1374 (2017)
- 452 42) Burbidge, A. A. & Manly, B. F. J. Mammal extinctions on Australian islands: causes and
453 conservation implications. *J. Biogeogr.* **29**, 465–473 (2002)
- 454 43) Ronquist, F. et al. MrBayes 3.2: efficient Bayesian phylogenetic inference and model choice
455 across a large model space. *Syst. Biol.* **61**, 539–542 (2012)
- 456 44) Faurby, S., Svenning, J. C. A species–level phylogeny for all extant and Late Quaternary
457 extinct mammals using a novel hierarchical Bayesian approach that accounts for topological
458 uncertainty. *Mol. Phylogenetics Evol.* **84**, 14–26 (2015)
- 459 45) Jetz, W., Thomas, G. H., Joy, J. B., Hartmann, J. K. & Mooers, A. O. The global diversity of
460 birds in space and time. *Nature* **491**, 444–448 (2012)
- 461 46) Silvestro, D., Salamin, N. & Schnitzler, J. PyRate: a new program to estimate speciation and
462 extinction rates from incomplete fossil data. *Methods Ecol. Evol.* **5**, 1126–1131 (2014)
- 463 47) Matzke, N. J. BioGeography with Bayesian (and Likelihood) evolutionary analysis in R
464 scripts. Retrieved from [https://cran.r-](https://cran.r-project.org/web/packages/BioGeoBEARS/BioGeoBEARS.pdf)
465 [project.org/web/packages/BioGeoBEARS/BioGeoBEARS.pdf](https://cran.r-project.org/web/packages/BioGeoBEARS/BioGeoBEARS.pdf) (2013).
- 466 48) Ree, R. H. & Sanmartin, I. Conceptual and statistical problems with the DEC+J model of
467 founder-event speciation and its comparison with DEC via model selection. *J Biogeogr* **45**,
468 741–749 (2018)
- 469 49) Faith, D. P. Conservation evaluation and phylogenetic diversity. *Biol. Conserv.* **284**, 1–10.
470 (1992)

471

472 **Supplementary Materials:**

473 Supplementary materials and methods

474 Tables S1-S9.

475 Figures S1-S2.

476 Appendix 1: The produced phylogeny of all carnivores

477 Appendix 2. A description of our treatment of all the individual fossil records

478

479 **Acknowledgments: Funding:** Funding for this work was provided through a Wallenberg Academy

480 Fellowship from the Knut and Alice Wallenberg Foundation, by the Swedish Research Council

481 (B0569601, 2015-04587, and 2017-03862), the Swedish Foundation for Strategic Research and the

482 Royal Botanic Gardens, Kew. **Author contributions:** SF, LW, and AA designed the study. SF and LW

483 performed the taxonomic cleaning for all records. SF conducted all analyses. SF led the writing of the

484 paper with input from LW and AA. All authors approved the submitted version. **Competing interests:**

485 Authors declare no competing interests. **Data and materials availability:** The produced phylogeny is

486 added as an appendix. All scripts used for running individual analyses are available from the authors

487 upon request.

488

Table 1: Pre-dispersal success.

Pre-dispersal success was estimated as the logarithm of the ratio between the diversification rate of the dispersing lineage dispersers and the median of the dispersal rates of the remaining species alive at the time of dispersal (see Fig. 3). Separate analyses were conducted comparing the dispersers with either all species alive (*global pre-dispersal success*) or only the species alive in the source continent (*continental pre-dispersal success*).

The p-values for node age and for global rate are the probability of the estimate in question being greater than 0. For models with different patterns depending on continental source and target, the p-value is based on the probability of being different from the estimated global rate.

This table only lists the results for the simplest model, and models preferred by AIC for either global or *continental pre-dispersal success*. The results from the remaining models are provided in the supplementary material (Tables S1–S2). Values are only given for time intervals of 0.5 million years, but results are similar for the other two intervals (Tables S1–S2).

| | <i>Continental pre-dispersal success</i> | <i>Global pre-dispersal success</i> |
|---|--|-------------------------------------|
| Simplest model | | |
| Global | 0.0835 (0.0194) ^{***} | 0.1205 (0.0205) ^{***} |
| ΔAIC | 5.973 | 6.178 |
| Temporal variation | | |
| Global | 0.1122 (0.0259) ^{***} | 0.1636 (0.0272) ^{***} |
| Age before present | -0.0018 (0.0012) [‘] | -0.0027 (0.0013) [*] |
| ΔAIC | 4.079 | 0.000 |
| Variation between target continent | | |
| To Africa | 0.1160 (0.0373) | 0.1468 (0.0372) |
| To Eurasia | 0.0453 (0.0343) | 0.1050 (0.0362) |
| To North America | 0.1260 (0.0360) | 0.1420 (0.0370) |
| To South America | 0.0017 (0.0503) | 0.0423 (0.0528) |
| ΔAIC | 0.000 | 5.873 |
| ‘ 0.10>P>0.05 * 0.05>P>0.01 ** 0.01>P>0.001 *** 0.001>P | | |

489

490

Table 2: Post-dispersal success.

Post-dispersal success is estimated as the square root of the ratio between the number of descendants for each dispersing lineage alive 5 million years (My) after dispersal divided by the mean number of descendants for any species alive at the time of dispersal (see Fig. 3). Separate analyses were conducted comparing the dispersers with either all species alive then (*global post-dispersal success*) or only the species alive in the target continent (*continental post-dispersal success*). P-values for node age and for global rate are the probability of the estimate in question being higher than 1 (the null expectation). For models with different patterns depending on continental source and target, the p-value is based on the probability of being different from the estimated global rate.

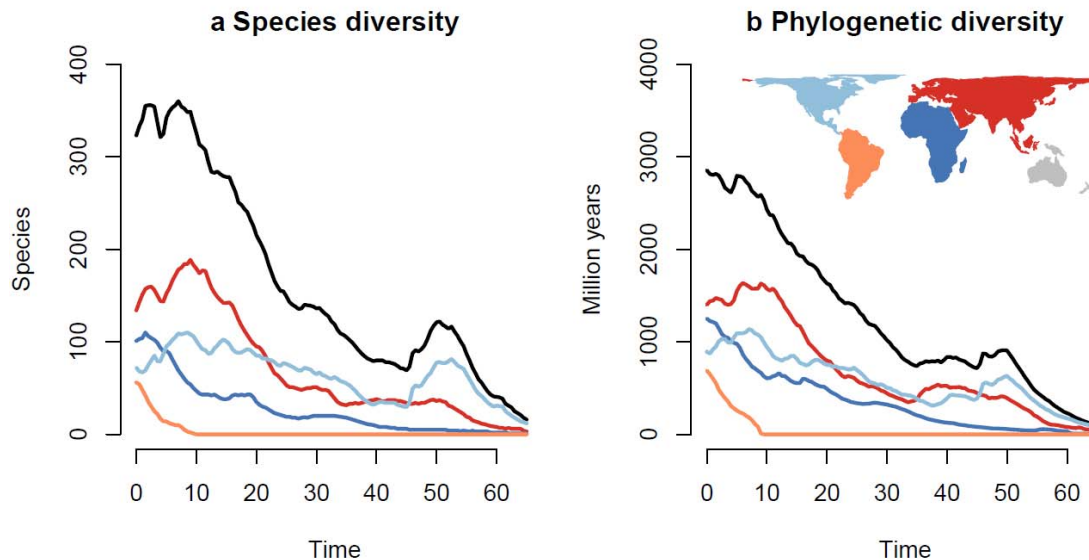
Values are only given for time intervals of 0.5 My and only based on the number of species alive after 5 My, but results are similar for time intervals of 0.25 and 1.00 and after 3 or 7 My (Tables S5–S6). This table only lists the results for the simplest model, and models preferred by AIC for either *global* or *continental post-dispersal success*. The results from the remaining models are provided as supplementary material (Tables S5–S6).

| | <i>Continental post-dispersal success</i> | <i>Global post-dispersal success</i> |
|---|---|--------------------------------------|
| Simplest model | | |
| Global | 1.4433 (0.0730) ^{***} | 1.4606 (0.0730) ^{***} |
| ΔAIC | 5.792 | 0.000 |
| Variation between source and target continent | | |
| Africa to Eurasia | 1.2666 (0.1727) | 1.3557 (0.1777) |
| Eurasia to Africa | 1.3607 (0.1206) | 1.3991 (0.1184) |
| Eurasia to North America | 1.6677 (0.1282) [‘] | 1.5767 (0.1243) |
| North America to Eurasia | 1.4238 (0.1487) | 1.4572 (0.1428) |
| North to South America | 1.1263 (0.2925) | 1.4005 (0.2835) |
| ΔAIC | 0.000 | 1.685 |
| ‘ 0.10>P>0.05 * 0.05>P>0.01 ** 0.01>P>0.001 *** 0.001>P | | |

491

Figure 1: Temporal changes in diversity.

Change in species and phylogenetic diversity through time globally (in black) and separately per continent (different colours). Lines represent median values across 100 trees for 0.5-million-year time intervals. The variation between trees and between lengths of the study interval can be seen in Fig. 2.



492

Figure 2: Variation in diversification rate among trees.

Plots of diversity through time for 100 trees drawn from the Bayesian phylogenetic analysis. Results for each tree are drawn as separate lines with results for different sample periods shown in different colours. Due to the strong consistency of results between trees and between lengths of the intervals many lines are drawn on top of each other.

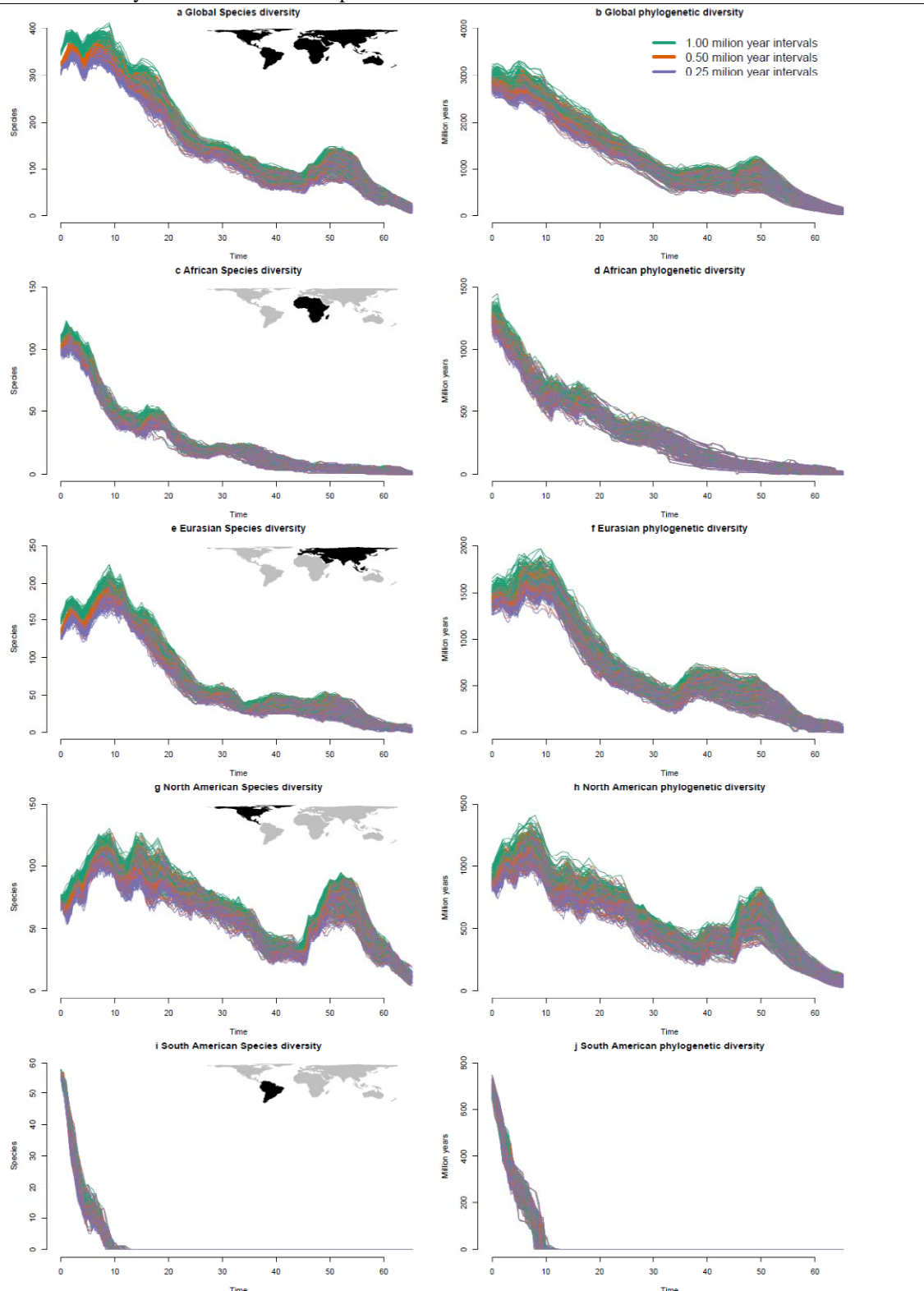
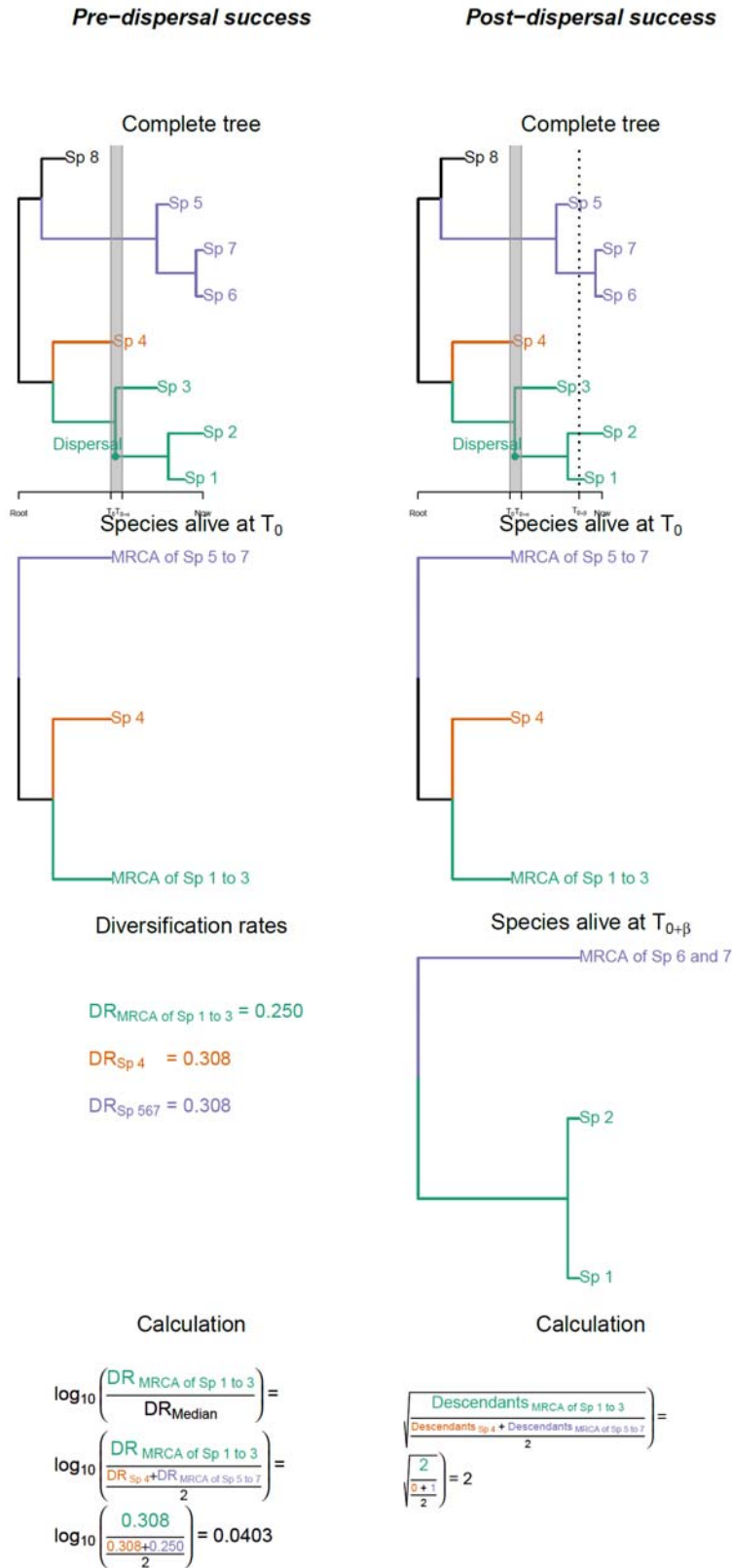


Figure 3: Estimation of dispersal success.



In the example above, one dispersal event happened within the interval from T_0 and $T_{0+\alpha}$, where α represents the time interval, which in our case was 0.25, 0.5 or 1.0 million years (My).

Both *Pre-dispersal success* and *Post-dispersal success* are calculated on the same tree.

The panels on the right illustrate how *Pre-dispersal success* is calculated. In order to improve understanding, we have used the same colours on each panel to show corresponding parts of trees or equations.

The two first panels show the entire tree, and a tree of just the species alive at time T_0 . The third panel shows DR rates estimated as in (44) for the species alive at T_0 . The fourth shows the calculation of *Pre-dispersal success*, which we define as the logarithm to the ratio between the DR of the dispersing lineage and the median of the remaining lineages (see the methods section for details).

The panels on the left illustrate how *Post-dispersal success* is calculated. In order to improve understanding, we have used the same colours on each panel to show corresponding parts of trees or equations.

The first panel shows the entire tree. This is identical to the tree for *Pre-dispersal success* except that a stippled line has been added at time $T_{0+\beta}$. β here represents a pre-defined length of time (in our case 3, 5 or 7 My). *Post-dispersal success* compared the trees at T_0 and $T_{0+\beta}$ and how many descendant species, each species alive at T_0 has diversified into. The next two panels show the trees of the species alive at T_0 and $T_{0+\beta}$ respectively. The last panel illustrates the calculation of *Post-dispersal success*, which we defined as the square root of the ratio between the number of descendants of the dispersing lineage and the mean number of descendants for any lineage from time T_0 alive at time $T_{0+\beta}$. Note that we here only look at the descendants alive at this time point and not all descendants. This, for instance, means that the taxon “*MRCA of Sp 5 to 7*” has only diversified into one species at time $T_{0+\beta}$ (“*MRCA of Sp 6 and 7*”) because Sp 5 is already extinct by then and the split between Sp 6 and Sp 7 happens at a later stage (see the methods section for details).

494

495

496

Supplementary materials

497

498 **5 Supplementary materials and methods**

499 **5.1 Phylogeny**

500 **5.1.1 Input data**

501 We downloaded all records of carnivores identified at least to genus level from the Paleobiology
502 Database (PBDB; <https://paleobiodb.org/>) on October 10, 2016 and the New and Old Worlds Database
503 of fossil mammals New and Old Worlds Database of fossil mammals
504 (<http://www.helsinki.fi/science/now/>; NOW), on September 30, 2016. We defined the focal clade as
505 Carnivoramorpha (Carnivora and Miacoidea) + Creodonta (Hyaenodonta and Oxyaenidae). Hereafter,
506 we refer to this entire clade as ‘carnivores’ and use the term ‘Carnivora’ when referring exclusively to
507 the extant order.

508 We revisited the taxonomy of all named species to generate a consistent list matching
509 current knowledge of extinct mammals, as well as the taxonomy of species surviving at least until the
510 Late Pleistocene (hereafter ‘extant carnivores’). For the latter, we followed the taxonomy of the
511 Phylacine V 1.2 database (3). Phylacine follows the International Union for Conservation of Nature
512 (IUCN) version 2016-3 for extant species and extinct species with extinction dates post 1500 AD, and
513 an updated version of the database of Faurby and Svenning (44) for species that went extinct between
514 the Late Pleistocene and 1500 AD. The resulting dataset had 7,551 useable records from NOW (6,285
515 records assigned to a species and 1,266 only to genus, while 94 records from the database were not
516 assignable to any of the genera we accept and were therefore excluded) and 7,984 useable records
517 from PBDB (6,755 records assigned to species and 1,229 only to genus, while 123 were not assignable
518 to any of our genera and therefore excluded).

519 Our combined dataset consisted of 1,723 species after cleaning, 314 of which are
520 extant. Among the species that went extinct prior to the Late Pleistocene, 631 were included in both
521 NOW and PBDB, 382 only had records in the NOW Database, and 268 only had records in PBDB. An
522 additional 128 species were manually added since they were not included in either of the databases at
523 the time of original download (October 10, 2016, and September 30, 2016 for the PBDB and NOW

524 databases, respectively; see Table S8). We included a few forms as separate species entities although
525 not formally described as such. Five genera had records only identified at the genus level from North
526 America. For our analyses, we treat these as distinct species, such as “*Parailurus* NorthAmerica”.
527 Although species designation for these has not formally been made, morphological differences have
528 generally been noted (50), which makes species designation plausible. Finally, we treat the records of
529 two small species (*Palaeogale minuta* and *Palaeogale sectoria*) from North America and Eurasia as
530 distinct continental endemics, since both persist on both continents for many million years and it
531 seems biologically implausible for them to maintain population coherence (i.e., gene flow) during that
532 time interval. A full breakdown of records by database can be found in the attached Excel spreadsheet
533 ‘Database summary’.

534

535 **5.1.2 Phylogenetic and dating analyses**

536 The phylogeny of all extant and extinct species of carnivores was constructed using a tip dating
537 approach under a fossilised birth-death model in MrBayes 3.2 (43). The phylogeny was created by
538 combining a backbone phylogeny with 17 smaller phylogenies (for Amphicyonidae, Barbourfelidae,
539 Canidae, Eupleridae, Felidae, Herpestidae, Hyaenodontidae, Hyaenidae, Mustelidae, Nimravidae,
540 Oxyaenidae, *Palaeogale*, Percrocutidae, Pinnipedia, Ursidae, Viverravidae and Viverridae). This
541 procedure requires that all the smaller phylogenies have a known number of species. For two families
542 (Miacidae and Stenoplesictidae) that were not constrained to be monophyletic (see next section), we,
543 therefore, included all species in the backbone phylogeny. Two chains were run for both the backbone
544 and the 17 smaller phylogenies until the average standard deviation of split frequencies was lower than
545 0.03, but for a minimum of 10 million generations. The analyses were further inspected with Tracer
546 1.6 (51) to ensure that the Effective Sample Size of the post burn-in for the overall model tree
547 likelihood for the two chains combined was at least 200.

548 The priors for the analyses were based on earlier tip dating analyses across all mammals
549 from Ronquist et al (52). In particular, we set a uniform prior of the root between 56.3 and 88.0 Ma,
550 representing the span between the oldest fossil in the database and the estimated divergence time
551 between the MRCA of Hyaenodontidae and Carnivora and their combined outgroup, following

552 Ronquist et al. (52). We further penalised long ‘ghost lineages’ (i.e. lineages existing for very
553 extended time periods without leaving any fossil evidence) in all analyses using the prior “prset
554 fossilizationpr = beta(100,1)” as also suggested by Ronquist et al (52). For all phylogenetic
555 reconstructions, we assumed that all species are included in the analyses. While we have included all
556 known species in the phylogeny, we acknowledge that a fraction of undescribed species must be
557 missing, but this fraction cannot be reliably estimated with any available method.

558 The backbone phylogeny was constructed based on morphological data for extinct
559 clades and a combination of morphological and genetic data for extant ones. All morphological data
560 were analysed under an MK-model conditioned to only include variable sites and incorporating
561 gamma rate heterogeneity. The morphological data were based on the matrix by Wesley-Hunt and
562 Flynn (53) but supplemented by numerous studies (see Table S9). We added new data for four key
563 taxa representing taxonomic groupings not included in previous analyses (*Percrocuta* sp,
564 *Ginsburgsmilus napakensis*, *Barbourofelis* sp, and *Oxyaena forcipata*) (all four coded by LW). This
565 morphological matrix was supplemented with genetic data from Meredith et al (54). To facilitate the
566 merging of the smaller phylogenies with the backbone phylogeny, we added the oldest known species
567 of each family (in this and all other cases we use the ages as listed in the original data source) to the
568 backbone analysis, with all characters coded as missing data. The 17 smaller phylogenies were for the
569 most part constructed based on one or more morphological data matrices, with genetic data also
570 included for the extant families. Depending on the family, the genetic data were either based almost
571 entirely on a single source although with supplemented searches for missing data of missing species
572 from NCBI, or on NCBI searches for each species (a list of sources can again be found in Table S9).

573 We made a number of modifications to the nexus files before running MrBayes. We set
574 the best nucleotide substitution model and partition scheme for the genetic data as the optimal one
575 based on AIC as inferred by Partitionfinder 1.1 (55) for both the overall and the smaller phylogenies.
576 We set the age of all fossil taxa and all extant species without genetic data to the age of the oldest
577 known record. Six of the species not included in either NOW or PBDB (*Amphicynodon brachyrostris*,
578 *Amphicynodon cephalogalinus*, *Amphicynodon chardini*, *Amphicynodon crassirostris*, *Phoberogale*
579 *minor* and *Filholictis filholi*) come from undated deposits. The first five were given uniform priors

580 between the age of the oldest and youngest species in the genus, whereas the sixth (*Filholictis filholi*)
581 is from a monospecific genus and was given a uniform prior between the youngest and oldest member
582 of the subfamily. For all genera constrained to be monophyletic (see next section), we set the
583 minimum age of the genus to the age of the oldest record in the genus (whether identified to species or
584 not). We did this using a uniform prior on the node age, with a maximum age equal to the rootage of
585 the family. We set the prior on the age of all tips representing fossil species and all extant species
586 lacking genetic data as a uniform prior ranging between the minimum and maximum ages of the oldest
587 known fossil of the species. These are intended to inform the origination time for the species lacking
588 genetic data. For all later analyses, they are treated in the same way as the extant taxa.

589 We merged the smaller trees with the backbone phylogeny while keeping the dating
590 information for both sets, as described below. For the 17 smaller phylogenies, we set a uniform prior
591 of the rootage between the oldest known fossil in the group and the upper 95% HPD (Highest
592 Posterior Density) for the stem age of the group from the backbone phylogeny. The backbone and the
593 smaller phylogenies were merged so that there was the same correlation between the stem and crown
594 age as between the age of the stem age and the next internal branch in the phylogeny. That is, since
595 Felidae and Barbuoufelidae are sister families, the phylogenies were merged so the correlation
596 between the stem and rootage of Felidae is the same as the correlation between the stem age of Felidae
597 and the age of the MRCA (Most Recent Common Ancestor) of Felidae and Barbuoufelidae.

598 For some trees, the resulting family-level clades had crown ages slightly older than the
599 stem ages of the overall tree, and we, therefore, needed to recalibrate the family level trees to avoid
600 negative branch lengths. This was done for all problematic trees (i.e. family level trees with crown
601 ages slightly older than the stem ages from the backbone tree) so that all branch lengths in the new tree
602 were proportional to the branches in the original tree, and the rootage was equal to the stem age of the
603 backbone tree minus 0.01.

604

605 **5.1.3 Constraints**

606 Similar to the assumption of other complete phylogenies, where a number of species lack genetic or
607 morphological data (e.g. 44, 45), we assumed taxonomic clades to be monophyletic unless there is

608 good evidence against it. This meant that we carefully inspected the paleontological literature
609 regarding each taxonomic unit to judge if they are generally understood to comprise monophyletic
610 entities (all taxonomic constraints are shown in the attached Excel spreadsheet ‘Database summary’).

611 At the highest level Carnivoramorpha, Hyaenodonta, and Oxyaenidae were each
612 constrained to be monophyletic. Within Carnivoramorpha, Carnivora and Viverravidae, but not
613 Miacidae (which is a paraphyletic assembly; see e.g. 53), were constrained to be monophyletic. Within
614 Carnivora, all taxa were constrained to be either Caniformia or Feliformia. Within Caniformia, we
615 constrained the monophyly of Amphicyonidae, Canidae, Musteloidea, Pinnipedia, and Ursidae and
616 assumed *Lycophocyon hutchisoni* to be outside any of the major lineages. Within Feliformia we
617 constrained the monophyly of Barbourofelidae, Eupleridae, Felidae, Herpestidae, Hyaenidae,
618 Nimravidae, Percrocutidae, Prionodontidae, and Viverridae, but not Stenoplesictidae (which again is
619 generally considered a paraphyletic assemblage; see e.g. 56). This means that we assumed that each
620 genus normally assigned to Stenoplesictidae, as well as *Palaeogale*, was outside any of the major
621 lineages listed above. We further constrained Percrocutidae as sister to Hyaenidae following (57) and
622 Felidae as sister to Barbourofelidae following (58). The morphological dataset started by Wesley-Hunt
623 and Flynn (53) was designed to determine the relatedness between basal taxa and on its own (i.e.
624 without genetic data added) produces improbable relationships between more derived members of
625 extant families within Carnivora. (53). Both Percrocutidae and Barbourofelidae are only known from
626 Miocene fossils, meaning that the morphological matrix may be suboptimal to infer their placement,
627 but unlike the extant families, their relationship cannot be inferred by adding genetic data to the
628 analysis.

629 At a lower level, we constrained most subfamilies and genera to be monophyletic, but
630 deviated from this in a number of cases for three main reasons: 1) Some of the earliest described
631 genera within families and subfamilies, e.g. *Lutra* for otters, have served as waste-baskets for a
632 number of frequently poorly-defined fossil taxa (59). Many fossil forms within such genera, as well as
633 other poorly known taxa, were therefore allowed to be placed freely within the family or subfamily
634 instead of being constrained to their genera; 2) Other species of uncertain phylogenetic placement
635 belong to distinct genera, but are rarely included in the newer taxonomic treatments and were therefore

636 not constrained to be within otherwise constrained subfamilies or tribes; and 3) Taxonomy does not
637 always imply genus-level monophyly. For some taxa, there is evidence that named genera are nested
638 within other named genera and we, therefore, allowed such nesting when supported. For example, this
639 is the case for *Neovison* (the American mink and the extinct sea mink), which phylogenetically may be
640 nested within *Mustela* (weasels) (60).

641 In addition to these taxonomic constraints, we also employed a number of constraints
642 based on stated likely relationships in taxonomical treatments. Finally, we employed a number of
643 biogeographical constraints within lineages or species and often enforced that there would only be a
644 single intercontinental dispersal within a lineage unless there are data to suggest otherwise. A full
645 breakdown of family, subfamily and genus level constraints can be found as part of appendix 2, which
646 contains information on all fossil records and our treatment of them, while a full list of additional
647 constraints and the relevant sources can be found in Table S10.

648

649 **5.1.4. Extinction times**

650 The procedure described above only gives the origination times of all lineages, but not the extinction
651 times. To estimate the actual extinction times for all taxa we used the Bayesian program PyRate (45).
652 We did this independently for each continent, which means that we treat a species occurring on
653 multiple continents as two distinct populations that may go extinct independently of each other, rather
654 than as a coherent group of sub-populations with ongoing gene flow.

655 Firstly, we combined fossil records from NOW and PBDB, keeping as many records as
656 possible while avoiding duplicate records. For each species, we initially accepted all records in either
657 NOW or PBDB (whichever had most records of the species in question). We then examined all
658 records of the other database for the same species, one by one, to assess if they were clearly distinct (in
659 which case they were added) or potential duplicates (in which case they were not). If the latitude and
660 or longitude rounded to the nearest degree was different from all records already accepted, and/or if
661 the age of the record was non-overlapping with accepted records with the same latitude and longitude,
662 we added the record. If there was only one record already accepted with identical latitude and
663 longitude and overlapping age, we considered the old and new ones to be potential duplicates and

664 retained the one with the most precise dating. However, we discarded the new record if there was more
665 than one already accepted record with the identical latitude and longitude and overlapping age.

666 Secondly, we ran PyRate analyses separately for records from South America, North
667 America, Asia, Europe, and Africa, with an additional separate analysis for Pinnipeds (since marine
668 species may have different fossilization potential than terrestrial ones). Sampling intensity (i.e. the
669 product of the number of specimens fossilizing and the fraction of fossils that are identified and placed
670 in the available databases) is a vital component determining how long after the youngest record the
671 true extinction time is likely to have been. Sampling intensity may vary between continents and
672 between marine and terrestrial species. For each continent (and for pinnipeds) we ran 20 separate
673 PyRate analyses, further allowing for variable sampling intensity in each epoch, for example as a
674 consequence of different amounts of exposed rocks of different ages. The analyses of African and
675 South American records (which had fewer records) were run for 10 million generations, whereas all
676 others were run for 20 million generations. Not all analyses converged but we generally used the
677 results from 10 separate chains, where the effective sample size for all key parameters was high (i.e.
678 all parameters related to the overall process but not necessarily the speciation or extinction time of
679 each species, which are treated as individual parameters, had an effective sample size above 200). The
680 exception for this was Europe, where convergence by these criteria was only seen in four chains and
681 only these four were therefore used in the subsequent analyses.

682 Finally, we combined the estimated extinction dates from the PyRate analyses with the
683 origination times estimated from the phylogenetic analyses. We first sampled random generations
684 across the different PyRate analyses (with the same number of samples for each). Following this, we
685 combined the results from a random PyRate generation with a random tree from the posterior
686 distribution. By doing this, we estimated the extinction time for every species on one continent
687 independently of their extinction time on other continents, which means that we consider them to
688 represent separate distinct populations rather than meta-populations with ongoing gene flow. We
689 treated Eurasia as a continent for all downstream analyses rather than as the distinct continents of
690 Europe and Asia. In doing this we set the Eurasian extinction date as the latest of the inferred
691 European and Asian extinction dates.

692

693 **5.2 Data analyses**

694 **5.2.1 Dispersal inference**

695 The first analytical step was an estimation of the dispersal dynamics between continents. For this and
696 all further analyses we discarded pinnipeds (which were just included in the datamining elements to
697 maximise the use of our created phylogeny for future evolutionary studies) and thus only analysed
698 terrestrial species. We estimated ancestral geographic range for all nodes with a DEC
699 (dispersal-extinction-cladogenesis) model in BiogeoBEARS (47), using the trees with origination time
700 as described above. We used a DEC rather than the frequently used DEC +j model since the
701 underlying mathematical properties of the DEC +j model have been seriously questioned (48).

702 We manually specified settings in BiogeoBEARS to match the study system. We did
703 not allow dispersal to South America prior to 10 million years ago (Ma). The oldest carnivore fossils
704 from the continent within our database are two records of the procyonid genus *Amphinasua* dated to
705 6.8–9 Ma; i.e. the Huayquerian South American Land Mammal Age (SALMA). By doing this we
706 assume that at most one SALMA (the Chasicoan, 9–10 Ma) could lack fossils, even though carnivores
707 actually could be present. We only allowed dispersal between adjoining continents (Africa/Eurasia,
708 Eurasia/North America, and North America/South America). Finally, we allowed the dispersal rate in
709 the Pleistocene (and Holocene) to be potentially higher than the pre-Pleistocene dispersal rate but
710 otherwise kept a single constant dispersal rate. BiogeoBEARS does not generally allow temporal
711 variation in dispersal rates, unless the relative temporal rates are manually specified, but we allowed
712 the dispersal rate in the Pleistocene to be different from the pre-Pleistocene rate by setting the
713 Pleistocene rate as $d_{\text{Pleistocene}} = d_{\text{Pre-Pleistocene}} * 2^w$, with w being a free parameter estimated by
714 BiogeoBEARS.

715 As a second step, we transformed the probabilistic ancestral states at all nodes of the
716 DEC analysis into binary presence/absences by sampling values based on the estimated probabilities.
717 This was done starting with the most terminal nodes. While sampling ancestral nodes, we only
718 sampled among states that were reasonable considering the states of the descendant nodes. Thus, if the

719 estimated ancestral state of two daughter nodes was inferred to be Eurasia and North America, the
720 ancestral area of their direct ancestor was restricted to combinations of one or both of these two areas.

721 Finally, we estimated dispersal times between continents. Whenever mechanistically
722 plausible (e.g. if the ancestor lived in North America and the daughter species lived in Eurasia and
723 North America) dispersal was inferred to be at the time of speciation. When this was not the case, the
724 necessary dispersal events (and potential required extinction events) were placed equidistant from each
725 other on the relevant branches.

726 We acknowledge that the procedure of assigning areas to nodes and branches can be
727 seen as a violation from the DEC model the data was estimated under, but we consider these violations
728 biologically justifiable. Our estimation procedure means that we can infer jump dispersal whenever it
729 is possible. These do not exist under a standard DEC model, but due to mathematical problems with
730 the extension that explicitly incorporates jump dispersal (DEC+j model), we preferred to use this
731 workaround. If we instead had used stochastic mapping to infer ancestral areas, we would have
732 drastically overestimated the magnitude of dispersal events – especially ones taking place along long
733 branches. This is because the only way to generate the frequent range changes that can be seen for
734 rapidly diversifying clades without having jump dispersal in the model is by having unrealistically
735 high dispersal rates within lineages. To get an idea of the magnitude of this issue, we estimated
736 ancestral areas through stochastic mapping ten times for each of the 100 trees. We found that the
737 smallest overestimation among all these 1,000 replicates was 47% while the median overestimation
738 was 71%. The overestimation of dispersal events based on stochastic mapping would be particularly
739 problematic for our analyses, due to its concentration on longer branches, which would produce biased
740 results in our analyses of the relationship between dispersal rate and diversification.

741

742 **5.2.2 Statistical analyses**

743 We conducted a number of separate analyses on 100 separate trees from the posterior distribution.
744 These analyses dealt with the dispersal dynamics between continents, the build-up of diversity and the
745 macro-evolutionary success of intercontinental dispersers relative to other species. In all cases

746 described below, we analysed the patterns in standard regression analyses with the results from each of
747 the 100 trees weighted equally.

748 Some analyses (related to phylogenetic diversity and diversification rate) are only
749 meaningfully interpretable for ultrametric trees. For simplicity, extinction was therefore dealt with in
750 time intervals and on trees sliced at various ages, rather than in continuous time, counting only the
751 species (internal or external branches) extant at that time point. Hence, when using 0.5-million-year
752 time intervals, two species that went extinct 1.2 and 1.4 Ma would both be included as extant for a tree
753 sliced at 1.0 Ma (but extinct in a tree sliced at 0.5 Ma). All analyses were conducted with time
754 intervals of 0.25, 0.5 or 1.0 million years duration in order to test the effect of this procedure on the
755 results.

756 In the simplest analyses, we calculated species diversity and phylogenetic diversity (49)
757 (i.e. the sum of the branch lengths in the tree) for all species alive in each time interval globally or on
758 each continent. In two other sets of analyses, we tested whether dispersing species were diversifying
759 faster than others were. The first of these sets of analyses, which we call *pre-dispersal success*,
760 investigated if species that disperse belong to lineages that, at their time of dispersal, diversified faster
761 than the other lineages present at that point in time. The second, which we call *post-dispersal success*,
762 investigated if species that disperse leave more descendant species than species that do not disperse.

763 We estimated *pre-dispersal success* based on the diversification rate (DR) (45). We
764 sliced the tree at the end of each time interval throughout the Cenozoic and calculated the DR of all
765 lineages alive at that time. For all intercontinental dispersal events occurring in the following time
766 interval, we then identified the lineage representing the disperser (this could be either the same species
767 or one of its ancestors). We then calculated the logarithm of the ratio between the diversification rate
768 of the disperser and the median diversification rate for either all lineages alive in the time interval
769 (*global pre-dispersal success*) or the subset of these that was found on the same continent the disperser
770 originated in (*continental pre-dispersal success*). This calculation is outlined in Fig. 3.

771 We estimated *post-dispersal success* by comparing the tree at the time before dispersal
772 with a tree sliced a number of million years afterwards. For each lineage alive at the first time interval,
773 we identified how many species they had diversified into a few million years later (this would be 0 if

774 the lineage had gone extinct in the meantime). We then calculated the ratio between the number of
775 species in the dispersing lineage and the mean for either all other species (*global post-dispersal*
776 *success*) or all species from the continent dispersal is to (*continental post-dispersal success*). In both
777 cases, we square-root transformed the *post-dispersal success* to improve normality. For this measure,
778 we used square-root rather than log transformation and means rather than medians, because zero
779 descendants for both the dispersing and non-dispersing lineages are common. Zero descendants for the
780 dispersing lineages could otherwise require taking the logarithm to zero, while zero descendants for
781 the non-dispersers (if occurring for more than half the species) would otherwise require dividing by
782 zero. Dispersal events were ignored for these analyses if they occurred so recently that the time period
783 a few million years later than that which we compare them to would be in the future. Separate analyses
784 of *post-dispersal success* were conducted on trees sliced after 3, 5, and 7 My (with all dispersal events
785 occurring within the last 3, 5, or 7 My ignored).

786

787 **5.2.3 Simulations**

788 All analyses described in 5.2.2 implicitly assume complete sampling. Although we have included all
789 known species, an unknown number of extinct species may be missing from the fossil record, which
790 can influence our results. This is especially so since the fraction of missing species is expected to vary
791 in time and space. In order to understand the influence of missing taxa on our results, we, therefore,
792 simulated a number of random phylogenies. We then simulated incomplete sampling on those
793 phylogenies, then repeated all analyses described in 5.2.2 on both the full and the sampled
794 phylogenies.

795 We simulated trees based on a stage-dependent speciation and extinction model. More
796 specifically, we simulated trees based on a seven-class ClaSSE (Cladogenetic State change Speciation
797 and Extinction) model (61) modified into a four-area version of the normally two-area GeoSSE model
798 (62) using Diversitree (63). In this version, each species was given seven potential character states 1:
799 S, 2; SN, 3: N, 4: NE, 5: E, 6: EA, 7: A (where S means South America, N means North America, E
800 means Eurasia and A means Africa). The model included five parameters: sympatric speciation rate
801 (λ_1) present in all classes; jump dispersal speciation (λ_2) for single area classes; allopatric speciation

802 (λ_3) for two area classes; local extinction rate (ϵ); and dispersal rate (δ) only between adjoining
803 regions. The model is outlined in Fig. S2.

804 We generated plausible trees of the same size as the empirical ones using a rejection
805 sampler to obtain a distribution of trees resembling the empirical ones in shape and geographic ranges.
806 We obtained the ClaSSE parameter values by randomly drawing them from the following uniform
807 distributions: $\lambda_1 \sim U(0, 0.2)$, $\lambda_2 \sim U(0, 0.05)$, $\lambda_3 \sim U(0, 3)$, $\delta \sim U(0, 0.1)$, and $\epsilon \sim U(0, 0.4)$. We
808 generated phylogenetic trees and geographic ranges at each random draw. The rejection sampler
809 included three summary statistics: 1) the fraction of all taxa that are extant; 2) the total number of
810 dispersals; and 3) the number of extant species occurring on more than one continent. Phylogenetic
811 trees and geographic ranges were only accepted if all summary statistics met the condition:

812 $x_{sim}/x_{emp} \in [2/3, 1.5]$, where x_{sim} is the statistic obtained from the simulation (e.g. the total number
813 of dispersals) and x_{emp} is the corresponding value obtained from the empirical data. We repeated the
814 simulation until 100 trees were accepted. The branch lengths of these trees were then multiplied by the
815 appropriate factors to have root ages corresponding to those of the 100 empirical trees.

816 We simulated geographic and spatial variation in preservation rate for each of these
817 random trees based on estimated sample intensity at each epoch as inferred from the PyRate analysis
818 (see 4.1.4). We assumed complete sampling of extant species. Sample intensity for the PyRate analysis
819 was estimated separately for Asia and Europe, due to the large difference in paleontological research
820 conducted in the two continents. For all biogeographical analyses, however, we used a combined
821 Eurasia since the borders between the two are poorly defined and a large fraction of species have
822 ranges spanning both continents. For the simulations (which are intended to mimic the
823 biogeographical analyses), we, therefore, used a combined value for Eurasian sampling. This was
824 estimated as the mean of the European and Asian sampling weighted by the contemporary diversity of
825 carnivores in the two continents. No pre-Miocene South American carnivores exist in the empirical
826 trees and therefore we cannot use empirical values for this continent for the Paleocene, Eocene, and
827 Oligocene. We instead used the mean estimate for Africa and Eurasia (corresponding to substantially
828 lower estimated sampling effort than North America). Estimation of sample intensity in PyRate can be

829 imprecise for very shallow time intervals such as the Holocene (Daniele Silvestro, pers. comm.). We,
830 therefore, used the Pleistocene value for both the Pleistocene and Holocene.

831 We carried out one round of random sampling based on the preservation rate defined
832 above for each continent, separately for each branch. We first assessed sampling on all external
833 branches on all continents and accepted presence whenever sampling was simulated to have taken
834 place. After this, we assessed internal branches ranked in order of increasing number of descendants.
835 Whenever an internal branch occurred on, and was sampled in, a continent where none of its occurring
836 descendants were sampled, we considered a random descendant species on the relevant continent as
837 sampled instead. The logic of this treatment can be understood by looking at a small clade of two
838 species, with a long internal branch and an extinction of both species nearly immediately after
839 speciation. In such cases, the probability of sampling both species would be limited but it is more
840 likely that we would sample the lineage before speciation. If we only looked at sampling in external
841 branches, we would thus drastically underestimate the diversity resulting from incomplete sampling.

842 In order to test the importance of incomplete sampling, we repeated all analyses from
843 5.2.2 on both the full random trees and the random trees with simulated sampling. After this, we
844 assessed if the effects we observed in the empirical trees matched the differences between the
845 simulated trees with incomplete and complete sampling, in which case extreme care would be needed
846 in the interpretation of the results.

847

848 **Additional references**

849 50) Tedford, R. H. & Gustafson, E. P. First North American record of the extinct panda

850 *Parailurus*. *Nature* **265**, 621–623 (1977)

851 51) Rambaut, A., Drummond, A. J., Xie, D., Baele, G. & Suchard, M. A. Posterior summarization

852 in bayesian phylogenetics using Tracer 1.7. *Syst. Biol.* **67**, 901–904 (2018)

853 52) Ronquist, F., Lartillot, N. & Phillips, M. J. Closing the gap between rocks and clocks using

854 total–evidence dating. *Philos. Trans. Royal Soc. B* **371**, 20150136 (2016)

- 855 53) Wesley-Hunt, G., & Flynn J. J. Phylogeny of the Carnivora: basal relationships among the
856 carnivoramorphans, and assessment of the position of Miacoidea relative to Carnivora. *J. Syst.*
857 *Palaeontol.* **3**, 1–28 (2005)
- 858 54) Meredith, R. W. et al. Impacts of the Cretaceous Terrestrial Revolution and KPg extinction on
859 mammal diversification. *Science* **334**, 521–524 (2011)
- 860 55) Lanfear, R., Calcott, B., Ho, S. Y. W. & Guindon, S. PartitionFinder: combined selection of
861 partitioning schemes and substitution models for phylogenetic analyses. *Mol. Biol. Evol.* **29**,
862 1695–1701 (2012)
- 863 56) Werdelin L. & Peigne, S., in *Cenozoic Mammals of Africa*. (eds. Werdelin, L., & Sanders W.
864 J.) 603–658 2010. (University of California Press, 2010)
- 865 57) Figueirido, B., Tseng, Z. J. & Martin-Serra, A. Skull shape evolution in durophagous
866 carnivorans. *Evolution* **67**, 1975–1993 (2013)
- 867 58) Morlo, M., Peigné, S. & Nagel, D. A new species of *Prosansanosmilus*: implications for the
868 systematic relationships of the family Barbourfelidae new rank (Carnivora, Mammalia).
869 *Zool. J. Linn. Soc.* **140**, 43.61 (2004)
- 870 59) Willemsen, G. A revision of the Pliocene and Quaternary Lutrinae from Europe. *Scripta*
871 *Geologica* **101**, 1-115 (1992)
- 872 60) Koepfli, K. P. et al. Molecular systematics of the Hyaenidae: relationships of a relictual
873 lineage resolved by a molecular supermatrix. *Mol. Phylogenet. Evol.* **38**, 603–620 (2006)
- 874 61) Goldberg, E. E. & Igić, B. Tempo and mode in plant breeding system evolution. *Evolution* **66**,
875 3701–3709 (2012)
- 876 62) Goldberg, E. E., Lancaster, L. T. & Ree, R. H. Phylogenetic inference of reciprocal effects
877 between geographic range evolution and diversification. *Syst. Biol.* **60**, 451–465 (2011)
- 878 63) Fitzjohn, R. G. Diversitree: comparative phylogenetic analyses of diversification in R.
879 *Methods Ecol. Evol.* **6**, 1084–1092 (2012)
- 880 64) Cirot, E. & Bonis, L. Révision du genre *Amphicynodon*, carnivore de l'Oligocène.
881 *Palaeontographica Abteilung A* **220**, 103-130 (1992)

- 882 65) Wang, X. & Tedford, R. H. The Status of genus *Nothocyon* Matthew, 1899 (Carnivora): an
883 Arctoid not a Canid. *J. Vert Paleontol.* **12**, 223–229 (1992)
- 884 66) Kordikova, E. G., Heizmann, E. P. J. & Mavrin, A. V. Early Miocene Carnivora of Aktau
885 Mountains South Eastern Kazakhstan. *Palaontologische Zeitschrift* **74**, 195–204 (2000)
- 886 67) Peigné, S. & Heizmann, P. J. The amphicyonidae (mammalia: carnivora) from Ulm-
887 Westtangente MN2, Early Miocene), Baden-Würteemberg, Germany: systematics and
888 ecomorphology. *Stuttgarter Beiträge zur Naturkunde. Serie B, Geologie und Paläontologie*
889 **343**, 1–131 (2003)
- 890 68) Ginsburg, L. Les faunes de mammifères terrestres du Miocène moyen des Faluns du bassin de
891 Savigné-sur-Lathan (France). *Geodiversitas* **23**, 381–394 (2001)
- 892 69) Hunt, R. M. Long-legged pursuit carnivorans (Amphicyonidae, Daphoeninae) from the early
893 Miocene of North America. *Bull. Am. Mus. Nat. Hist.* **318**, 1–95 (2009)
- 894 70) Raza, S. M., Barry, J. C., Meyer, G. E. & Martin, L. Preliminary report on the geology and
895 vertebrate fauna of the Miocene Manchar Formation, Sind, Pakistan. *J. Vert. Paleontol.* **4**,
896 584–599 (2010)
- 897 71) Rybczynski, N., Dawson, M. R. & Tedford, R. H. A semi-aquatic Arctic mammalian
898 carnivore from the Miocene epoch and origin of Pinnipedia. *Nature* **458**, 1021–1024 (2009)
- 899 72) Hartstone-Rose, A. , Kuhn, B. F., Nalla, S., Werdelin, L. & Berger, L. R. A new species of fox
900 from the *Australopithecus sediba* type locality, Malapa, South Africa. *T. Roy. Soc. S. Afr.* **68**,
901 1–9 (2013)
- 902 73) Werdelin, L. A new genus and species of Felidae (Mammalia) from Rusinga Island, Kenya,
903 with notes on early Felidae of Africa. *Estudios Geológicos* **67**, 217–222 (2012)
- 904 74) Peigne, S. *Proailurus*, l'un des plus anciens Felidae (Carnivora) d'Eurasie : systématique et
905 évolution. *Bulletin du Museum National d'Histoire Naturelle Toulouse* **135**, 125–134 (1999)
- 906 75) Salesa, M. J., Anton, M., Morales, J. & Peigne, S. Systematics and phylogeny of the small
907 felines (Carnivora, Felidae) from the Late Miocene of Europe: A new species of Felinae from
908 the Vallesian of Batallones (MN 10, Madrid, Spain). *J. Syst. Palaeontol.* **10**, 87–102 (2012)

- 909 76) Spassov, N. & Geraads, D. A new felid from the Late Miocene of the Balkans and the contents
910 of the genus *Metailurus* Zdansky, 1924 (Carnivora, Felidae). *J. Mamm. Evol.* **22**, 45–56
911 (2015)
- 912 77) Solé, F., Falconnet, J. & Yves, L. New proviverrines (Hyaenodontida) from the early Eocene
913 of Europe; phylogeny and ecological evolution of the Proviverrinae. *Zool. J. Linn. Soc.* **171**,
914 878–917 (2014)
- 915 78) Zack, S. P. New species of the rare early Eocene creodont *Galecyon* and the radiation of early
916 Hyaenodontidae. *J. Paleontol.* **85**, 315–336 (2011)
- 917 79) Solé, F. et al. A New Large Hyainailourine from the Bartonian of Europe and Its Bearings on
918 the Evolution and Ecology of Massive Hyaenodonts (Mammalia). *PLoS ONE* **10**, e0141941.
919 (2015)
- 920 80) Egi, N. et al. Proviverrine hyaenodontids (Creodonta: Mammalia) from the Eocene of
921 Myanmar and a phylogenetic analysis of the proviverrines from the Para-Tethys area. *J. Syst.*
922 *Palaeontol.* **3**, 337–358 (2005)
- 923 81) Schmidt-Kittler, N. et al. European reference levels and correlation tables. *Münchner Geo*
924 *wissenschaftliche Abhandlungen A* **10**, 13–31 (1987)
- 925 82) Lavrov, A. V. New Species of *Paroxyaena* (Hyaenodontidae, Creodonta) from Phosphorites
926 of Quercy, Late Eocene, France. *Paleontol. J.* **41**, 298–311 (2007)
- 927 83) Werdelin, L. & Solounias, N. The Hyaenidae: taxonomy, systematics and evolution. *Fossils*
928 *and Strata* **30**, 1–104 (1991)
- 929 84) Werdelin, L. & Lewis, M. E. New species of *Crocota* from the early Pliocene of Kenya, with
930 an overview of early Pliocene hyenas of eastern Africa. *J. Ver. Paleontol.* **28**, 1162–1170
931 (2008)
- 932 85) Wang, X. & Qui, Z. Late Miocene Promephitis (Carnivora, Mephitidae) from China. *J. Ver.*
933 *Paleontol.* **24**, 721–731 (2004)
- 934 86) Spaulding, M., Flynn, J. J. & Stucky, R. K. A new basal Carnivoramorphan (Mammalia) from
935 the ‘Bridger B’ (Black’s Fork member, Bridger Formation, Bridgerian Nalma, middle Eocene)
936 of Wyoming, USA. *Palaeontology* **53**, 815–832 (2010)

- 937 87) Smith, T. & Smith, R. A new genus of "miacid" carnivoran from the earliest Eocene of Europe
938 and North America. *Acta Palaeontol. Pol.* **55**, 761–764 (2010)
- 939 88) Solé, F. New carnivoraforms from the early Eocene of Europe and their bearings on the
940 evolution of the Carnivoraformes. *Palaeontology* **57**, 963–978 (2014)
- 941 89) Harrison, D. L., Bates, P. J. J., Pearch, M., Michaels, C. & Ward, D. J. New additions to the
942 late middle Eocene mammal fauna of Creechbarrow, Dorset, southern England. *Cainozoic*
943 *Res.* **9**, 65–85 (2012)
- 944 90) Heinrich, R. E., Strait, S. G. & Houde, P. Earliest Eocene Miacidae (Mammalia: Carnivora)
945 from Northwestern Wyoming. *J. Paleontol.* **82**, 154–162 (2008)
- 946 91) Solé, F., Smith, R., Coillot, T., de Bast, E. & Smith, T. Dental and tarsal anatomy of ‘Miacis’
947 latouri and a phylogenetic analysis of the earliest carnivoraforms (Mammalia,
948 Carnivoramorpha), *J. Vert. Paleontol.* **34**, 1–21 (2014)
- 949 92) Raghavan, P., Pickford, M., Patnaik, R. & Gayathri, P. First fossil small-clawed otter,
950 *Amblonyx*, with a note on some specimens of *Lutra*, from the Upper Siwaliks, India. *Estudios*
951 *Geológicos* **63**, 135–146 (2007)
- 952 93) Werdelin, L. & Lewis, M. E. *The Carnivora. Koobi Fora Research Project, Vol. 7.* (California
953 Academy of Sciences, 2013)
- 954 94) Valenciano, A., Abella, J., Göhlich, U. B., Álvarez-Sierra, M. A. & Morales, J. Re-evaluation
955 of the very large *Eomellivora fricki* (Pia, 1939) (Carnivora, Mustelidae, Mellivorinae) from
956 the Late Miocene of Austria. *Palaeontol. Electron.* **20.1.17A**, 1–22 (2017)
- 957 95) Wolsan, M. & Sotnikova, M. Systematics, evolution, and biogeography of the Pliocene stem
958 meline badger *Ferinestrix* (Carnivora: Mustelidae). *Zool. J. Linn. Soc.* **167**, 208–226 (2013)
- 959 96) Lim, J. D. & Martin, L. D. A new fossil mustelid from the Miocene of South Dakota, USA
960 *Naturwissenschaften* **89**, 270–274 (2002)
- 961 97) Cherin, M., Iurino, D. A., Willemsen, G. & Carnevale, G. A new otter from the Early
962 Pleistocene of Pantalla (Italy), with remarks on the evolutionary history of Mediterranean
963 Quaternary Lutrinae (Carnivora, Mustelidae). *Quat. Sci. Rev.* **135**, 92–102 (2016)

- 964 98) Colombero, S., Pavia, M. & Rook, L. *Pannonictis nestii* (Galictinae, Mustelidae), a new
965 element in the vertebrate association of the human site of Pirro Nord (Italy, Early Pleistocene).
966 *Geodiversitas* **34**, 665–681 (2012)
- 967 99) Lim, J. D. & Martin, L. D. A new primitive Leptarctine (Mustelidae) from the North
968 American Miocene. *Neues Jahrbuch für Geologie und Paläontologie*. **2000**, 632–640 (2000)
- 969 100) Morales, J. & Pickford, M. Giant bunodont Lutrinae from the Mio-Pliocene of Kenya
970 and Uganda. *Estudios Geológicos* **61**, 233–246 (2005)
- 971 101) Tseng, Z. J., Wang, X. & Stewart, J. D. A new immigrant mustelid (Carnivora,
972 Mammalia) from the middle Miocene Temblor Formation of central California. *PaleoBios* **29**,
973 13–23 (2009)
- 974 102) Bonis, L. Précisions sur l'âge géologique et les relations phylétiques de *Mustelictis*
975 *olivieri* nov. sp. (Carnivora, Mustelidae), carnassier de l'Oligocène inférieur (MP 22) des
976 phosphorites du Quercy (France). *Geobios* **20**, 55–60 (1997)
- 977 103) Lange, B. Un nouveau Musteline des phosphorites du Quercy *Mustelictis piveteaui*.
978 *Comptes rendus de l'Académie des Sciences de Paris, D* **268**, 2870–2872 (1969)
- 979 104) Barrett, P. Z. Taxonomic and systematic revisions to the North American Nimravidae
980 (Mammalia, Carnivora) *PeerJ* **4**, e1658 (2016)
- 981 105) Peigne, S. New species of *Eofelis* (Carnivora: Nimravidae) from the Phosphorites of
982 Quercy, France. *Comptes rendus de l'Académie des Sciences de Paris, D* **330**, 653–658 (2000)
- 983 106) Averianov, A., Obraztsova, E., Danilov, I., Skutschas, P. & Jin, J. First nimravid skull
984 from Asia. *Sci. Rep.* **6**, 25812. (2016)
- 985 107) Forasiepi, A. M. et al. Carnivorans at the Great American Biotic Interchange: new
986 discoveries from the northern neotropics. *Naturwissenschaften* **101**, 965–974 (2014)
- 987 108) Wolsan, M. & Lange-Badre, B. An arctomorph carnivoran skull from the Phosphorites
988 du Quercy and the origin of procyonids. *Acta Palaeontol. Pol.* **41**, 277–298. (1996)
- 989 109) Hunt, R. M. Evolution of the Aeluroid Carnivora: Diversity of the earliest Aeluroids
990 from Eurasia (Quercy, Hsanda-Gol) and the origins of felids. *Am. Mus. Novit.* **3252**, 1–33
991 (1998)

- 992 110) Peigné, S. & Bonis, L. The genus *Stenoplesictis* Filhol (Mammalia, Carnivora) from the
993 Oligocene deposits of the Phosphorites of Quercy, France. *J. Vert. Paleontol.* **19**, 566–575
994 (1999)
- 995 111) Bonis, L. A new species of *Adelpharctos* (Mammalia, Carnivora, Ursidae) from the late
996 Oligocene of the “Phosphorites du Quercy” (France). *Estudios Geológicos* **67**, 179–186
997 (2012)
- 998 112) Abella, J. et al. *Kretzoiarctos* gen. nov., the oldest member of the giant panda clade.
999 *PLoS ONE* **7**, e48985. (2012)
- 1000 113) Ogino, S., Egi, N., Maung-Thein, Z. M., Htike, T. & Takai, M. New species of
1001 *Agriotherium* (Mammalia, Carnivora) from the late Miocene to early Pliocene of central
1002 Myanmar. *J. Asian Earth Sci.* **42**, 408–414 (2011)
- 1003 114) Soibelzon, L. H. & Schubert, B. W. The largest known bear, *Arctotherium angustidens*,
1004 from the early Pleistocene Pampean region of Argentina: with a discussion of size and diet
1005 trends in bears. *J. Paleontol.* **85**, 69–75. (2011)
- 1006 115) Bonis, L. Ursidae (Mammalia, Carnivora) from the Late Oligocene of the “Phosphorites
1007 du Quercy” (France) and a reappraisal of the genus *Cephalogale* Geoffroy, 1862.
1008 *Geodiversitas* **35**, 787–814. (2013)
- 1009 116) Zhan-Xiang, Q., Tao, D. & Ban-Yue, W. A Late Miocene *Ursavus* skull from Guanghe,
1010 Gansu, China. *Vertebrata Palasiatica* **52**, 265–302 (2014)
- 1011 117) Meehan, T. J. & Wilson, R. W. New Viverravids from the Torrejonian (Middle
1012 Paleocene) of Kutz Canyon, New Mexico and the oldest skull of the Order Carnivora. *J.*
1013 *Paleontol.* **76**, 1091–1101 (2002)
- 1014 118) Beard, K.C. & Dawson, M. R. Early Wasatchian mammals of the red hot local fauna,
1015 uppermost Tuscahoma formation, Lauderdale County, Mississippi. *Ann. Carnegie Mus.* **78**,
1016 193–243 (2009)
- 1017 119) Morales, J. & Pickford, M. A new paradoxurine carnivore from the Late Miocene
1018 Siwaliks of India and a review of the bunodont viverrids of Africa. *Geobios* **44**, 271–277
1019 (2011)

- 1020 120) Tomiya, S. A New Basal Caniform (Mammalia: Carnivora) from the Middle Eocene of
1021 North America and Remarks on the Phylogeny of Early Carnivorans. *PLoS ONE* **6**, e24146
1022 (2011)
- 1023 121) Spaulding, M. & Flynn, J. J. Phylogeny of the Carnivoramorphs: The impact of
1024 postcranial characters. *J. Syst. Palaeontol.* **10**, 653–677 (2012)
- 1025 122) Jian, W. & Zhao-Qun, Z. Phylogenetic analysis on Palaeogale (Palaeogalidae,
1026 Carnivora) based on specimens from Oligocene strata of Saint-Jacques, Nei Mongol.
1027 *Vertebrata Palasiatica* **10**, 310–334 (2015)
- 1028 123) Peigné, S., Salesa, M. J., Anton, M. & Morales, J. A new Amphicyonine (Carnivora:
1029 Amphicyonidae) from the Upper Miocene of Batallones-1, Madrid, Spain. *Palaeontology* **51**,
1030 943–965 (2008)
- 1031 124) Tomiya, S. & Zhijie Tseng, J. Whence the beardedogs? Reappraisal of the Middle to Late
1032 Eocene ‘*Miacis*’ from Texas, USA, and the origin of Amphicyonidae (Mammalia, Carnivora).
1033 *R. Soc. Open Sci.* **3**, 160518 (2016)
- 1034 125) Robles, J. M. et al. New craniodental remains of the barbourofelid *Albanosmilus*
1035 *jourdani* (Filhol, 1883) from the Miocene of the Vallès-Penedès Basin (NE Iberian Peninsula)
1036 and the phylogeny of the Barbourofelini. *J. Syst. Palaeontol.* **11**, 993–1022 (2013)
- 1037 126) Bardeleben, C., Moore, R. L. & Wayne, R. K. A molecular phylogeny of the Canidae
1038 based on six nuclear loci. *Mol. Phylogenet. Evol.* **37**, 815–831 (2005)
- 1039 127) Prevosti, F. J. Phylogeny of the large extinct South American Canids (Mammalia,
1040 Carnivora, Canidae) using a “total evidence” approach. *Cladistics* **26**, 456–481 (2010)
- 1041 128) Slater, G. J. Iterative adaptive radiations of fossil canids show no evidence for
1042 diversity-dependent trait evolution. *Proc. Natl Acad. Sci. USA* **112**, 4897–4902 (2014)
- 1043 129) Johnson, W. E. et al. The late Miocene radiation of modern Felidae: a genetic
1044 assessment. *Science* **311**, 73–77 (2006)
- 1045 130) Rothwell, T. Phylogenetic Systematics of North American *Pseudaelurus* (Carnivora:
1046 Felidae). *Am. Mus. Novit.* **3403**, 1–64 (2003)

- 1047 131) Tseng, Z. T. et al. Himalayan fossils of the oldest known pantherine establish ancient
1048 origin of big cats. *Proc. R. Soc. B* **281**, 20132686 (2016)
- 1049 132) Werdelin, L. & Flink, T. in *Smilodon: The Iconic Sabertooth* (eds Werdelin, L.,
1050 McDonald, H. G. & Shaw, C. A.) 14–29 (Johns Hopkins University Press, 2018)
- 1051 133) Koepfli, K. P. et al. Molecular systematics of the Hyaenidae: relationships of a relictual
1052 lineage resolved by a molecular supermatrix. *Mol. Phylogenet. Evol.* **38**, 603–620 (2006)
- 1053 134) Baskin, J. A. *Bassariscus* and *Probassariscus* (Mammalia, Carnivora, Procyonidae)
1054 from the early Barstovian (middle Miocene). *J. Ver. Paleontol.* **24**, 709–720. (2004)
- 1055 135) Finarelli, J. A. A total evidence phylogeny of the Arctoidea (Carnivora: Mammalia):
1056 relationships among basal taxa. *J. Mamm. Evol.* **15**, 231–259 (2008)
- 1057 136) Robles, J. M. et al. New craniodental remains of *Trocharion albanense* Major, 1903
1058 (Carnivora, Mustelidae), from the Vallès-Penedès Basin (middle to late Miocene, Barcelona,
1059 Spain). *J. Ver. Paleontol.* **30**, 547–562 (2010)
- 1060 137) Wang, X., Carranza-Castañeda, O. & Aranda-Gómez, J. J. A transitional skunk,
1061 *Buisnictis metabatos* sp. nov. (Mephitidae, Carnivora), from Baja California Sur and the role
1062 of southern refugia in skunk evolution. *J. Syst. Palaeontol.* **12**, 291–302 (2014)
- 1063 138) Fulton, T. L. & Strobeck, C. Multiple markers and multiple individuals refine true seal
1064 phylogeny and bring molecules and morphology back in line. *Proc. R. Soc. B* **277**, 1065–1070
1065 (2010)
- 1066 139) Berta, A., Kienle, S., Bianucci, G. & Sorbi, S. A Reevaluation of *Pliophoca etrusca*
1067 (Pinnipedia, Phocidae) from the Pliocene of Italy: Phylogenetic and biogeographic
1068 implications. *J. Ver. Paleontol.* **35**, e889144 (2015)
- 1069 140) Boessenecker, R. W. & Churchill, M. The oldest known fur seal. *Biol. Lett.* **11**,
1070 20140835 (2015)
- 1071 141) Cozzuol, M. A. A “northern” seal from the Miocene of Argentina: implications for
1072 phocid phylogeny and biogeography. *J. Ver. Paleontol.* **21**, 415–421 (2001)

- 1073 142) Kohno, N. Miocene pinniped *Allodesmus* (Mammalia: Carnivora); with special
1074 reference to the "Mito seal" from Ibaraki Prefecture, Central Japan. *Trans. Proc. Palaeontol.*
1075 *Soc. Jpn.* **181**, 388–404 (1996)
- 1076 143) Koretsky, I. A. & Rahmat, S. J. A new species of the subfamily Devinophocinae
1077 (Carnivora, Phocidae) from the central Paratethys. *Rivista Italiana di Paleontologia e*
1078 *Stratigrafia* **121**, 31–47 (2015)
- 1079 144) Tanaka, Y. & Kohno, N. A new Late Miocene odobenid (Mammalia: Carnivora) from
1080 Hokkaido, Japan suggests rapid diversification of basal Miocene Odobenids. *PLoS ONE* **10**,
1081 e0131856 (2015)
- 1082 145) Pages, M. et al. Combined analysis of fourteen nuclear genes refines the Ursidae
1083 phylogeny. *Mol. Phylogenet. Evol.* **47**, 73–83 (2008)
- 1084 146) Wang, X., McKenna, M. C. & Dashzeveg, D. *Amphicticeps* and *Amphicynodon*
1085 (Arctoidea, Carnivora) from Hsanda Gol Formation, Central Mongolia and Phylogeny of
1086 Basal Arctoids with Comments on Zoogeography. *Am. Mu. Novit.* **3483**, 1–57 (2005)
- 1087 147) Morlo, M. & Gunnell, G. F. Small limnocyonines (Hyaenodontidae, Mammalia) from
1088 the Bridgerian middle Eocene of Wyoming: *Thiocyon*, *Prolimnocyon* and *Imdodon* new genus.
1089 Contributions from the Museum of Paleontology, University of Michigan **31**, 43–78 (2003)
- 1090 148) Solé, F. New proviverrine genus from the Early Eocene of Europe and the first
1091 phylogeny of Late Palaeocene-Middle Eocene hyaenodontidans (Mammalia). *J. Syst.*
1092 *Palaeontol.* **11**, 375–398 (2013)
- 1093 149) Hunt, R. M. Evolution of large carnivores during the Mid-Cenozoic of North America:
1094 The temnocyonine radiation (Mammalia, Amphicyonidae). *Bull. Am. Mus. Nat. Hist.* **358**, 1–
1095 153 (2001)
- 1096 150) Hunt, R. M. New amphicyonid carnivorans (Mammalia, Daphoeninae) from the Early
1097 Miocene of Southeastern Wyoming. *Am. Mus. Novit.* **3385**, 1–41 (2002)
- 1098 151) Hunt, R.M. in *Evolution of Tertiary Mammals of North America Volume 1: Terrestrial*
1099 *Carnivores, Ungulates, and Ungulatelike Mammals*. (eds. Janis, C. M., Scott, K. M. & Jacobs,
1100 L. L.) 196–227 (Cambridge University Press, 1998)

- 1101 152) Morales, J., Pickford, M. & Valenciano, A. Systematics of African Amphicyonidae,
1102 with descriptions of new material from Napak (Uganda) and Grillental (Namibia) *J. Iber.*
1103 *Geol.* **42**, 131–150 (2016)
- 1104 153) Wang, X. & Tedford, R. H. Fossil dogs (Carnivora, Canidae) from the Sespe and
1105 Vaqueros formations in Southern California, with comments on relationships of *Phlaocyon*
1106 *taylori*. *Natural History Museum of Los Angeles County, Science Series* **41**, 225–272 (2008)
- 1107 154) Wang, X. New material of *Osbornodon* from the early Hemingfordian of Nebraska and
1108 Florida. *Bull. Am. Mus. Nat. Hist.* **279**, 163–176. (2003)
- 1109 155) Nyakatura, K. & Bininda-Emonds, O. R. P. Updating the evolutionary history of
1110 Carnivora (Mammalia): a new species-level supertree complete with divergence time
1111 estimates. *BMC Biology* **10**, 12 (2012)
- 1112 156) Bininda-Emonds, O. R. P. et al. The delayed rise of present-day mammals *Nature* **446**,
1113 507–512 (2007)
- 1114 157) Werdelin, L., Yamaguchi, N., Johnson, W. E. & O'Brien, S. J. in *Biology and*
1115 *Conservation of Wild Felids* (eds. Macdonald, D. W. & Loveridge, A. J.) 59–82 (Oxford
1116 University Press, 2010)
- 1117 158) Seymour, K. L. *Panthera onca*. *Mammalian Species.* **340**, 1–9 (1989)
- 1118 159) Barnett, R. et al. Evolution of the extinct sabretooths and the American cheetah-like cat.
1119 *Cur. Biol.* **15**, R589–90. (2005)
- 1120 160) Werdelin, L. & Lewis, M. E. A revision of the genus *Dinofelis* (Mammalia, Felidae).
1121 *Zool. J. Linn. Soc.* **132**, 147–258 (2001)
- 1122 161) Patou, M. L. et al. Molecular phylogeny of the Herpestidae (Mammalia, Carnivora)
1123 with a special emphasis on the Asian *Herpestes*. *Mol. Phylogenet. Evol.* **53**, 69–80 (2009)
- 1124 162) Turner, A., Antón, M. & Werdelin, L. Taxonomy and evolutionary patterns in the fossil
1125 Hyaenidae of Europe. *Geobios* **41**, 677–687 (2008)
- 1126 163) de Bonis, L. et al. Hyaenidae (Carnivora) from the late Miocene of Toros-Mena. *J. Afr.*
1127 *Earth Sci.* **58**, 561–579 (2010)

- 1128 164) Morlo, M. & Peigne, S. in *Carnivoran Evolution: New views on phylogeny, form, and*
1129 *function page* (eds. Goswami, A. & A. Friscia) 92–140 (Cambridge university press 2010).
- 1130 165) Sotnikova, M. V. A new species of lesser panda *Parailurus* (Mammalia, Carnivora)
1131 from the Pliocene of Transbaikalia (Russia) and some aspects of ailurine phylogeny.
1132 *Paleontol. J.* **42**, 90–99. (2008)
- 1133 166) Wang, X. New cranial material of *Simocyon* from China, and its implications for
1134 phylogenetic relationship to the Red Panda (*Ailurus*). *J. Vert. Paleontol.* **17**, 184-198 (1997)
- 1135 167) Baskin, J. A. in *Evolution of Tertiary Mammals of North America Volume 1: Terrestrial*
1136 *Carnivores, Ungulates, and Ungulatelike Mammals.* (eds. Janis, C. M., Scott, K. M. & Jacobs,
1137 L. L.) 152–173 (Cambridge University Press, 1998).
- 1138 168) Nagel, D., Stefen, C. & Morlo, M. The carnivoran community from the Miocene of
1139 Sandelzhausen (Germany). *Paläontologische Zeitschrift* **83**, 151–174 (2009)
- 1140 169) Prassack, K. A. *Lontra weiri*, sp. nov., a Pliocene river otter (Mammalia, Carnivora,
1141 Mustelidae, Lutrinae) from the Hagerman Fossil Beds (Hagerman Fossil Beds National
1142 Monument), Idaho, U.S.A. *J. Vert. Paleontol.* **36**, e1149075 (2016)
- 1143 170) Willemsen, G. F. *Megalenhydris* and its relationship to *Lutra* reconsidered. *Hellenic J.*
1144 *Geosci.* **41**, 83–87 (2006)
- 1145 171) Cherin, M. & Rook, L. First report of *Lutra simplicidens* (Carnivora, Mustelidae,
1146 Lutrinae) in the Early Pleistocene of the Upper Valdarno (Italy) and the origin of European
1147 otters. *Ital. J. Geosci.* **133**, 200-203 (2013)
- 1148 172) Valenciano, A. et al. *Megalictis*, the Bone-Crushing Giant Mustelid (Carnivora,
1149 Mustelidae, Oligobuninae) from the Early Miocene of North America. *PloS ONE* **11**,
1150 e0152430 (2016)
- 1151 173) Howell, F. C. & Petter, G. Comparative observations on some middle and upper
1152 Miocene hyaenids, Genera: *Percrocuta* Kretzoi, *Allohyaena* Kretzoi, *Adcrocuta* Kretzoi
1153 (Mammalia, Carnivora, Hyaenidae). *Geobios* **18**, 419–491 (1985)

- 1154 174) Paterson, R. S., Rybczynski, N., Kohno, N. & Maddin, H. C. A complete description
1155 and phylogenetic analysis of *Puijila darwini*, a transitional pinniped. *Canadian Society of*
1156 *Vertebrate Anatomy conference abstracts* **2016**, 48 (2016)
- 1157 175) Barnes, L. G. A new genus and species of middle Miocene enaliarctine pinniped
1158 (Mammalia, Carnivora, Otariidae) from the Astoria Formation in coastal Oregon.
1159 *Contributions in Science* **43**, 1–27 (1992)
- 1160 176) Berta, A. A new species of phocoid pinniped *Pinnarctidion* from the early Miocene of
1161 Oregon. *J. Vert. Paleontol.* **14**, 405–413 (2010)
- 1162 177) Hunt, R. M. in *Evolution of Tertiary Mammals of North America Volume 1: Terrestrial*
1163 *Carnivores, Ungulates, and Ungulatelike Mammals.* (eds. Janis, C. M., Scott, K. M. & Jacobs,
1164 L. L.) 174–195 (Cambridge University Press, 1998)
- 1165 178) Soibelzon, L. H., Tonni, E. P. & Bond, M. The fossil record of South American short-
1166 faced bears (Ursidae, Tremarctinae). *J. S. Am. Earth Sci.* **20**, 105–113 (2005)
- 1167 179) García, N. & Arsuaga, J. L. *Ursus dolinensis*: a new species of Early Pleistocene ursid
1168 from Trinchera Dolina, Atapuerca (Spain). *Comptes Rendus de l'Académie des Sciences -*
1169 *Series IIA - Earth and Planetary Science* **332**, 717–725 (2015)
- 1170 180) Russell, R. D. Effects of climate change on mammalian fauna composition and
1171 structure during the advent of North American continental glaciation in the Pliocene. Master
1172 Thesis. The University of Texas at Austin. <http://hdl.handle.net/2152/3226>. (2007).
- 1173 181) Nagel, D. Carnivores from the Middle Miocene deposits of Grund (Lower Austria).
1174 *Annalen des Naturhistorischen Museums in Wien. Serie A für Mineralogie und Petrographie,*
1175 *Geologie und Paläontologie, Anthropologie und Prähistorie* **104**, 297–305 (2002)
- 1176 182) Flunn, J. F. in *Evolution of Tertiary Mammals of North America Volume 1: Terrestrial*
1177 *Carnivores, Ungulates, and Ungulatelike Mammals.* (eds. Janis, C. M., Scott, K. M. & Jacobs,
1178 L. L.) 110–123 (Cambridge University Press, 1998)
- 1179 183) Gunnell, G. F. in *Evolution of Tertiary Mammals of North America Volume 1:*
1180 *Terrestrial Carnivores, Ungulates, and Ungulatelike Mammals.* (eds. Janis, C. M., Scott, K.
1181 M. & Jacobs, L. L.) 91–109 (Cambridge University Press, 1998)

- 1182 184) Solé, F., Gheerbrant, E. & Godinot, M. New data on the Oxyaenidae from the Early
1183 Eocene of Europe; biostratigraphic, paleobiogeographic and paleoecologic implications
1184 *Palaeontol. Electron.* **14**, 13A (2011)
1185

1186 **Table S1: Continental pre-dispersal success.**
 1187 The test statistic is the logarithm of the ratio between the diversification rate at the time of dispersal of
 1188 dispersers and the median of the diversification rates of all species present in the source continent just
 1189 before the dispersal event (see Fig. 1).
 1190 The p-values for the global rate and for the temporal age effect are the probability of being different
 1191 from 0. For models with different patterns depending on the source and or target continent, the p-value
 1192 is based on the probability of being different from the estimated global rate.

| | 1.0-million-year intervals | 0.5-million-year intervals | 0.25-million-year intervals |
|---|--------------------------------|--------------------------------|--------------------------------|
| Simplest model | | | |
| Global | 0.0900 (0.0199) ^{***} | 0.0835 (0.0194) ^{***} | 0.0785 (0.0190) ^{***} |
| AIC | 126.202 | 120.325 | 122.352 |
| Temporal variation | | | |
| Global | 0.1229 (0.0260) ^{***} | 0.1122 (0.0259) ^{***} | 0.1068 (0.0255) ^{***} |
| Age | -0.0021 (0.0012) [‘] | -0.0018 (0.0012) [‘] | -0.0018 (0.0012) [‘] |
| AIC | 123.159 | 118.431 | 120.740 |
| Variation between source continent | | | |
| From Africa | 0.0519 (0.0599) | 0.0487 (0.0577) | 0.0422 (0.0570) |
| From Eurasia | 0.1287 (0.0260) | 0.1226 (0.0260) | 0.1185 (0.0253) |
| From North America | 0.0386 (0.0331) | 0.0303 (0.0330) | 0.0240 (0.0329) |
| From South America | 0.1052 (0.1528) | 0.1002 (0.1439) | 0.0980 (0.1407) |
| AIC | 121.666 | 115.841 | 114.379 |
| Variation between target continent | | | |
| To Africa | 0.1191 (0.0374) | 0.1160 (0.0373) | 0.1137 (0.0366) |
| To Eurasia | 0.0488 (0.0340) | 0.0453 (0.0343) | 0.0379 (0.0337) |
| To North America | 0.1351 (0.0356) | 0.1260 (0.0360) | 0.1214 (0.0346) |
| To South America | 0.0192 (0.0513) | 0.0017 (0.0503) | -0.0009 (0.0495) |
| AIC | 121.745 | 114.352 | 114.924 |
| Variation between source and target continent | | | |
| Africa to Eurasia | 0.0519 (0.0600) | 0.0487 (0.0577) | 0.0422 (0.0570) |
| Eurasia to Africa | 0.1191 (0.0374) | 0.1161 (0.0373) | 0.1137 (0.0366) |
| Eurasia to North America | 0.1372 (0.0368) | 0.1281 (0.0370) | 0.1231 (0.0357) |
| North America to Eurasia | 0.0479 (0.0420) | 0.0439 (0.0428) | 0.0362 (0.0429) |
| North to South America | 0.0192 (0.0513) | 0.0018 (0.0503) | -0.0009 (0.0496) |
| South to North America | 0.1051 (0.1529) | 0.1002 (0.1439) | 0.098 (0.1407) |
| AIC | 124.174 | 116.893 | 117.311 |

‘ 0.10>P>0.05 * 0.05>P>0.01 ** 0.01>P>0.001 *** 0.001>P

1194 **Table S2: Global pre-dispersal success.**

1195 The test statistic is the logarithm of the ratio between the diversification rate at the time of dispersal of
 1196 dispersers and the median of the diversification rates of all species alive globally just before the
 1197 dispersal event (see Fig. 1).

1198 The p-values for global rate and for the temporal age effect are the probability of being different from
 1199 0. For models with different patterns depending on the source and/ or target continent, the p-value is
 1200 based on the probability of being different from the estimated global rate.

| | 1.0-million-year intervals | 0.5-million-year intervals | 0.25-million-year intervals |
|---|--------------------------------|--------------------------------|--------------------------------|
| Simplest model | | | |
| Global | 0.1295 (0.0212) ^{***} | 0.1205 (0.0205) ^{***} | 0.1142 (0.0206) ^{***} |
| AIC | 150.586 | 159.119 | 159.394 |
| Temporal variation | | | |
| Global | 0.1757 (0.0271) ^{***} | 0.1636 (0.0272) ^{***} | 0.1562 (0.0271) ^{***} |
| Age | -0.0029 (0.0013) [*] | -0.0027 (0.0013) [*] | -0.0026 (0.0013) |
| AIC | 141.937 | 152.941 | 147.405 |
| Variation between source continent | | | |
| From Africa | 0.1101 (0.0651) | 0.1010 (0.0612) | 0.940 (0.0631) |
| From Eurasia | 0.1516 (0.0266) | 0.1455 (0.0267) | 0.1414 (0.0266) |
| From North America | 0.1005 (0.0355) | 0.0863 (0.0353) | 0.0759 (0.0353) |
| From South America | 0.0892 (0.1428) | 0.1119 (0.1442) | 0.1122 (0.1416) |
| AIC | 153.595 | 159.794 | 156.610 |
| Variation between target continent | | | |
| To Africa | 0.1476 (0.0368) | 0.1468 (0.0372) | 0.1443 (0.0371) |
| To Eurasia | 0.1131 (0.0373) | 0.1050 (0.0362) | 0.0959 (0.0369) |
| To North America | 0.1508 (0.0369) | 0.1420 (0.0370) | 0.1373 (0.0358) |
| To South America | 0.0710 (0.0528) | 0.0423 (0.0528) | 0.0324 (0.0526) |
| AIC | 154.452 | 158.814 | 157.279 |
| Variation between source and target continent | | | |
| Africa to Eurasia | 0.1100 (0.0651) | 0.1009 (0.0612) | 0.0941 (0.0631) |
| Eurasia to Africa | 0.1476 (0.0368) | 0.1468 (0.0372) | 0.1443 (0.0371) |
| Eurasia to North America | 0.1550 (0.0383) | 0.1440 (0.0385) | 0.1391 (0.0375) |
| North America to Eurasia | 0.1151 (0.0446) | 0.1077 (0.0443) | 0.0972 (0.0449) |
| North to South America | 0.0710 (0.0528) | 0.0443 (0.0529) | 0.0324 (0.0527) |
| South to North America | 0.0892 (0.1418) | 0.1119 (0.1442) | 0.1124 (0.1415) |
| AIC | 156.490 | 161.911 | 159.934 |

[†] 0.10>P>0.05 * 0.05>P>0.01 ** 0.01>P>0.001 *** 0.001>P

1201

1202

1203 **Table S3: Continental pre-dispersal success in simulations.**

1204 Values are given for both the full simulated tree and the simulated incomplete sampling. The difference is
 1205 the median difference between estimates for each tree. In parentheses, we list the number of times where
 1206 this difference is negative (i.e. how many times the value is larger for incomplete sampling than the full
 1207 tree).

1208 The test statistic is the logarithm of the ratio between the diversification rate at the time of dispersal of
 1209 dispersers and the median of the diversification rates of all species in the source continent from just before
 1210 the dispersal event (see Fig. 1).

1211 For models with different patterns based on the source and/ or target continent, the p-value is based on the
 1212 probability of being different from the estimated global rate. The p-value for the difference is based on a
 1213 two-tailed binomial distribution and tests if incomplete sampling is equally likely to lead to larger and
 1214 smaller values than complete sampling.

| | Full tree | Incomplete sampling | Difference |
|--|------------------|---------------------|--|
| Simplest model | | | |
| Global | 0.0192 (0.0149) | 0.0207 (0.0167) | -1.75 x 10 ⁻³ (57/100) |
| AIC | 146.691 | 126.717 | |
| Temporal variation | | | |
| Global | 0.0288 (0.0233) | 0.0316 (0.0256) | -1.75 x 10 ⁻³ (57/100) |
| Age | -0.0007 (0.0010) | -0.0008 (0.0012) | 1.18 x 10 ⁻⁴ (43/100) |
| AIC | 146.503 | 125.441 | |
| Variation between source continent | | | |
| From Africa | NA | NA | NA |
| From Eurasia | 0.0182 (0.0307) | 0.0201 (0.0367) | -6.06 x 10 ⁻³ (61/100)* |
| From North America | 0.0159 (0.0194) | 0.0161 (0.0204) | -7.62 x 10 ⁻⁵ (50/100) |
| From South America | 0.0352 (0.0377) | 0.0450 (0.0451) | -1.15 x 10 ⁻² (66/100)** |
| AIC | 148.964 | 129.271 | |
| Variation between target continent | | | |
| To Africa | -0.0019 (0.0560) | -0.0007 (0.0592) | 1.91 x 10 ⁻³ (47/100) |
| To Eurasia | 0.0323 (0.0283) | 0.0339 (0.0282) | -1.88 x 10 ⁻³ (54/100) |
| To North America | 0.0293 (0.0257) | 0.0376 (0.0310) | -7.93 x 10 ⁻³ (61/100)* |
| To South America | -0.0020 (0.0286) | -0.0035 (0.0291) | 2.30 x 10 ⁻³ (47/100) |
| AIC | 146.629 | 127.837 | |
| Variation between source and target continent | | | |
| Africa to Eurasia | NA | NA | NA |
| Eurasia to Africa | -0.0019 (0.0560) | -0.0070 (0.0592) | 1.91 x 10 ⁻³ (47/100) |
| Eurasia to North America | 0.0238 (0.0362) | 0.0313 (0.0437) | -8.36 x 10 ⁻³ (60/100) [†] |
| North America to Eurasia | 0.0323 (0.0283) | 0.0338 (0.0282) | -1.88 x 10 ⁻³ (54/100) |
| North to South America | -0.0020 (0.0286) | -0.0035 (0.0291) | 2.30 x 10 ⁻³ (47/100) |
| South to North America | 0.0352 (0.0377) | 0.0450 (0.0451) | -1.15 x 10 ⁻² (66/100)** |
| AIC | 148.457 | 129.797 | |
| [†] 0.10>P>0.05 * 0.05>P>0.01 ** 0.01>P>0.001 *** 0.001>P | | | |

1215

1216 **Table S4: Global pre-dispersal success in simulations.**

1217 Values are given for both the full simulated tree and the simulated incomplete sampling. The difference is
 1218 the median difference between estimates for each tree. In parentheses, we list the number of times where
 1219 this difference is negative (i.e. how many times the value is larger for incomplete sampling than the full
 1220 tree).

1221 The test statistic is the logarithm of the ratio between the diversification rate at the time of dispersal of
 1222 dispersers and the median diversification rates of all species alive globally just before the dispersal event
 1223 (see Fig. 1).

1224 For models with different patterns based on the source and/ or target continent, the p-value is based on the
 1225 probability of being different from the estimated global rate. The p-value for the difference is based on a
 1226 two-tailed binomial distribution and tests if incomplete sampling is equally likely to lead to larger and
 1227 smaller values than complete sampling.

| | Full tree | Incomplete sampling | Difference |
|--|------------------|---------------------|--|
| Simplest model | | | |
| Global | 0.0192 (0.0149) | 0.0207 (0.0167) | -1.75 x 10 ⁻³ (57/100) |
| AIC | 146.691 | 126.717 | |
| Temporal variation | | | |
| Global | 0.0288 (0.0233) | 0.0316 (0.0256) | -1.75 x 10 ⁻³ (57/100) |
| Age | -0.0007 (0.0010) | -0.0008 (0.0012) | 1.18 x 10 ⁻⁴ (43/100) |
| AIC | 146.503 | 125.441 | |
| Variation between source continent | | | |
| From Africa | NA | NA | NA |
| From Eurasia | 0.0182 (0.0307) | 0.0201 (0.0367) | -6.06 x 10 ⁻³ (61/100)* |
| From North America | 0.0159 (0.0194) | 0.0161 (0.0204) | -7.62 x 10 ⁻⁵ (50/100) |
| From South America | 0.0352 (0.0377) | 0.0450 (0.0451) | -1.15 x 10 ⁻² (66/100)** |
| AIC | 148.964 | 129.271 | |
| Variation between target continent | | | |
| To Africa | -0.0019 (0.0560) | -0.0007 (0.0592) | 1.91 x 10 ⁻³ (47/100) |
| To Eurasia | 0.0323 (0.0283) | 0.0339 (0.0282) | -1.88 x 10 ⁻³ (54/100) |
| To North America | 0.0293 (0.0257) | 0.0376 (0.0310) | -7.93 x 10 ⁻³ (61/100)* |
| To South America | -0.0020 (0.0286) | -0.0035 (0.0291) | 2.30 x 10 ⁻³ (47/100) |
| AIC | 146.629 | 127.837 | |
| Variation between source and target continent | | | |
| Africa to Eurasia | NA | NA | NA |
| Eurasia to Africa | -0.0019 (0.0560) | -0.0070 (0.0592) | 1.91 x 10 ⁻³ (47/100) |
| Eurasia to North America | 0.0238 (0.0362) | 0.0313 (0.0437) | -8.36 x 10 ⁻³ (60/100) [†] |
| North America to Eurasia | 0.0323 (0.0283) | 0.0338 (0.0282) | -1.88 x 10 ⁻³ (54/100) |
| North to South America | -0.0020 (0.0286) | -0.0035 (0.0291) | 2.30 x 10 ⁻³ (47/100) |
| South to North America | 0.0352 (0.0377) | 0.0450 (0.0451) | -1.15 x 10 ⁻² (66/100)** |
| AIC | 148.457 | 129.797 | |
| [†] 0.10>P>0.05 * 0.05>P>0.01 ** 0.01>P>0.001 *** 0.001>P | | | |

Table S5: Global post-dispersal success.

The test statistic is the square root of the mean number of species alive after a given number of million years (3, 5 or 7) after dispersal, divided by the mean for all species globally. Significance for the estimate is the probability of being different from 1 (the random expectation), for age it is the probability of being different from 0, and for models with different patterns based on the source and/ or target continent, it is based on the probability of being different from the estimated global rate.

| | 3 Million years | | | 5 Million years | | | 7 Million years | | |
|---|----------------------------|----------------------------|-----------------------------|----------------------------|----------------------------|-----------------------------|----------------------------|----------------------------|-----------------------------|
| | 1.0-million-year intervals | 0.5-million-year intervals | 0.25-million-year intervals | 1.0-million-year intervals | 0.5-million-year intervals | 0.25-million-year intervals | 1.0-million-year intervals | 0.5-million-year intervals | 0.25-million-year intervals |
| Simplest model | | | | | | | | | |
| Global | 1.5463 (0.0455)*** | 1.4808 (0.0495)*** | 1.4500 (0.0520)*** | 1.5401 (0.0693)*** | 1.4606 (0.0730)*** | 1.4182 (0.0741)*** | 1.4846 (0.0928)*** | 1.3909 (0.0939)*** | 1.3423 (0.0942)*** |
| AIC | 558.620 | 571.858 | 574.258 | 646.651 | 644.155 | 642.460 | 700.557 | 685.244 | 679.522 |
| Temporal variation | | | | | | | | | |
| Global | 1.5167 (0.0455)*** | 1.4427 (0.0732)*** | 1.4109 (0.0762)*** | 1.5695 (0.0993)*** | 1.4782 (0.1049)*** | 1.4301 (0.1090)*** | 1.5224 (0.1441)*** | 1.4120 (0.1489)** | 1.3600 (0.1492)* |
| Age | 0.0016 (0.0033) | 0.0022 (0.0037) | 0.0022 (0.0038) | -0.0012 (0.0046) | -0.0006 (0.0048) | -0.0004 (0.0050) | -0.0017 (0.0056) | -0.0009 (0.0058) | -0.0008 (0.0057) |
| AIC | 557.176 | 572.007 | 573.035 | 647.353 | 645.788 | 643.953 | 701.968 | 686.662 | 681.166 |
| Variation between source continent | | | | | | | | | |
| From Africa | 1.4552 (0.1200) | 1.3819 (0.1248) | 1.3411 (0.1318) | 1.4119 (0.1694) | 1.3555 (0.1778) | 1.3133 (0.1844) | 1.3539 (0.2250) | 1.2732 (0.2314) | 1.2362 (0.2336) |
| From Eurasia | 1.5800 (0.0577) | 1.5106 (0.0624) | 1.4763 (0.0648) | 1.5725 (0.0837) | 1.4938 (0.0877) | 1.4487 (0.0890) | 1.5377 (0.1155) | 1.4492 (0.1192) | 1.3973 (0.1210) |
| From North America | 1.5275 (0.0794) | 1.4727 (0.0894) | 1.4501 (0.0944) | 1.5318 (0.1240) | 1.4467 (0.1314) | 1.4056 (0.1315) | 1.4459 (0.1569) | 1.3431 (0.1600) | 1.2938 (0.1613) |
| AIC | 555.792 | 569.375 | 572.882 | 647.004 | 645.084 | 645.226 | 703.163 | 687.947 | 682.634 |
| Variation between target continent | | | | | | | | | |
| To Africa | 1.5264 (0.0862) | 1.4464 (0.0885) | 1.4090 (0.0912) | 1.4806 (0.1152) | 1.3990 (0.1184) | 1.3565 (0.1203) | 1.4580 (0.1538) | 1.3993 (0.1583) | 1.3650 (0.1613) |
| To Eurasia | 1.5405 (0.0772) | 1.4700 (0.0838) | 1.4383 (0.0893) | 1.5037 (0.1131) | 1.4262 (0.1183) | 1.3857 (0.1203) | 1.4274 (0.1447) | 1.3312 (0.1475) | 1.2839 (0.1490) |
| To North America | 1.6248 (0.0810) | 1.5622 (0.0851) | 1.5306 (0.0885) | 1.6591 (0.1234) | 1.5781 (0.1241) | 1.5358 (0.1255) | 1.5990 (0.1588) | 1.4831 (0.1614) | 1.4171 (0.1631) |
| To South America | 1.3749 (0.1507) | 1.3526 (0.1628) | 1.3460 (0.1678) | 1.5047 (0.2702) | 1.4004 (0.2834) | 1.3456 (0.2821) | 1.3713 (0.3859) | 1.2702 (0.3997) | 1.2446 (0.4160) |
| AIC | 556.521 | 570.46 | 575.529 | 645.487 | 644.715 | 645.327 | 704.990 | 690.138 | 683.700 |
| Variation between source and target continent | | | | | | | | | |
| Africa to Eurasia | 1.4554 (0.1196) | 1.3819 (0.1245) | 1.3411 (0.1315) | 1.4219 (0.1691) | 1.3557 (0.1777) | 1.3132 (0.1842) | 1.3538 (0.2251) | 1.2731 (0.2316) | 1.2362 (0.2340) |
| Eurasia to Africa | 1.5264 (0.0862) | 1.4464 (0.0885) | 1.4091 (0.0912) | 1.4806 (0.1152) | 1.3991 (0.1184) | 1.3565 (0.1203) | 1.4579 (0.1540) | 1.3993 (0.1583) | 1.3649 (0.1614) |
| Eurasia to North America | 1.6284 (0.0814) | 1.5675 (0.0857) | 1.5368 (0.0893) | 1.6573 (0.1233) | 1.5767 (0.1243) | 1.5312 (0.1257) | 1.5989 (0.1590) | 1.4827 (0.1616) | 1.4167 (0.1634) |
| North America to Eurasia | 1.5829 (0.0945) | 1.5122 (0.1043) | 1.4842 (0.1108) | 1.5392 (0.1355) | 1.4572 (0.1428) | 1.4178 (0.1431) | 1.4570 (0.1707) | 1.3539 (0.1735) | 1.3011 (0.1732) |
| North to South America | 1.3748 (0.1507) | 1.3527 (0.1627) | 1.3460 (0.1678) | 1.5046 (0.2702) | 1.4005 (0.2835) | 1.3458 (0.2822) | 1.3714 (0.3862) | 1.2700 (0.4001) | 1.2447 (0.4164) |
| AIC | 552.733 | 568.98 | 568.980 | 645.240 | 645.840 | 646.678 | 706.231 | 690.988 | 685.240 |

* 0.10>P>0.05 * 0.05>P>0.01 ** 0.01>P>0.001 *** 0.001>P

Table S6: Continental post-dispersal success.

The test statistic is the square root of the mean number of species alive after a given number of million years (3, 5 or 7) after dispersal, divided by the mean for species in the target continent. Significance for the estimate is the probability of being different from 1 (the random expectation), for age it is the probability of being different from 0 and for models with different patterns based on target and/ or source continent it is based on the probability of being different from the estimated global rate.

| | 3 Million years | | | 5 Million years | | | 7 Million years | | |
|---|------------------------------|----------------------------|-----------------------------|------------------------------|------------------------------|------------------------------|----------------------------|----------------------------|-----------------------------|
| | 1.0-million-year intervals | 0.5-million-year intervals | 0.25-million-year intervals | 1.0-million-year intervals | 0.5-million-year intervals | 0.25-million-year intervals | 1.0-million-year intervals | 0.5-million-year intervals | 0.25-million-year intervals |
| Simplest model | | | | | | | | | |
| Global | 1.5321 (0.0463)*** | 1.4666 (0.0494)*** | 1.4361 (0.0517)*** | 1.5197 (0.0699)*** | 1.4433 (0.0730)*** | 1.4018 (0.0739)*** | 1.4622 (0.0952)*** | 1.3695 (0.0956)*** | 1.3203 (0.0953)** |
| AIC | 564.200 | 570.942 | 572.367 | 644.765 | 638.300 | 642.178 | 697.054 | 677.991 | 671.446 |
| Temporal variation | | | | | | | | | |
| Global | 1.4876 (0.0679)*** | 1.4089 (0.0734)*** | 1.3775 (0.0761)*** | 1.5430 (0.1023)*** | 1.4554 (0.1066)*** | 1.4093 (0.1090)*** | 1.5087 (0.1477)*** | 1.4004 (0.1509)** | 1.3468 (0.1485)* |
| Age | 0.0025 (0.0033) | 0.0031 (0.0037) | 0.0032 (0.0039) | -0.0008 (0.0048) | -0.0004 (0.0050) | -0.0002 (0.0051) | -0.0020 (0.0058) | -0.0013 (0.0060) | -0.0012 (0.0059) |
| AIC | 564.603 | 569.47 | 568.672 | 644.363 | 638.872 | 642.141 | 696.491 | 679.063 | 671.775 |
| Variation between source continent | | | | | | | | | |
| From Africa | 1.4041 (0.1199) | 1.3302 (0.1234) | 1.2907 (0.1303) | 1.3310 (0.1674) | 1.2666 (0.1741) | 1.2263 (0.1800) | 1.2344 (0.2187) | 1.1587 (0.2241) | 1.1230 (0.2282) |
| From Eurasia | 1.6068 (0.0603) | 1.5322 (0.0643) | 1.4957 (0.0668) | 1.6058 (0.0888) | 1.5246 (0.0912) | 1.4784 (0.0922) | 1.5818 (0.1227) | 1.4863 (0.1263) | 1.4311 (0.1267) |
| From North America | 1.4560 (0.0832) | 1.4130 (0.0917) | 1.3945 (0.0966) | 1.4491 (0.1272) | 1.3791 (0.1362) | 1.3405 (0.1370) | 1.3552 (0.1654) | 1.2684 (0.1682) | 1.2211 (0.1699) |
| AIC | 556.673 | 563.667 | 566.153 | 643.753 | 638.831 | 640.397 | 693.680 | 676.812 | 668.212 |
| Variation between target continent | | | | | | | | | |
| To Africa | 1.5341 (0.0895) | 1.4484 (0.0915) | 1.4088 (0.0938) | 1.4465 (0.1199) | 1.3607 (0.1207) | 1.3171 (0.1210) | 1.3871 (0.1569) | 1.3221 (0.1607) | 1.2858 (0.1623) |
| To Eurasia | 1.5136 (0.0785) | 1.4472 (0.0850) | 1.4160 (0.0911) | 1.4491 (0.1161) | 1.3761 (0.1232) | 1.3360 (0.1248) | 1.3552 (0.1516) | 1.2667 (0.1541) | 1.2212 (0.1569) |
| To North America | 1.6714 (0.0839) [†] | 1.6016 (0.0879) | 1.5681 (0.0916) | 1.7535 (0.1287) | 1.6694 (0.1278) [†] | 1.6222 (0.1303) [†] | 1.7334 (0.1690) | 1.6065 (0.1723) | 1.5354 (0.1730) |
| To South America | 1.1418 (0.1472)** | 1.1366 (0.1643)* | 1.1379 (0.1695)* | 1.1965 (0.2684) | 1.1262 (0.2927) | 1.0809 (0.2894) | 0.9792 (0.3900) | 0.9267 (0.4108) | 0.9016 (0.4124) |
| AIC | 550.297 | 562.453 | 563.308 | 635.087 | 632.828 | 635.919 | 690.538 | 676.756 | 666.862 |
| Variation between source and target continent | | | | | | | | | |
| Africa to Eurasia | 1.4042 (0.1183) | 1.3303 (0.1222) | 1.2907 (0.1292) | 1.3311 (0.1658) | 1.2666 (0.1727) | 1.2263 (0.1787) | 1.2345 (0.2171) | 1.1588 (0.2232) | 1.1231 (0.2276) |
| Eurasia to Africa | 1.5341 (0.0894) | 1.4484 (0.0914) | 1.4089 (0.0936) | 1.4466 (0.1198) | 1.3607 (0.1206) | 1.3171 (0.1208) | 1.3871 (0.1568) | 1.3220 (0.1607) | 1.2857 (0.1624) |
| Eurasia to North America | 1.6724 (0.0843) [†] | 1.6055 (0.0884) | 1.5729 (0.0922) | 1.7514 (0.1285) [†] | 1.6677 (0.1282) | 1.6212 (0.1308) | 1.7333 (0.1690) | 1.6061 (0.1724) | 1.5351 (0.1732) |
| North America to Eurasia | 1.5677 (0.0971) | 1.5029 (0.1055) | 1.4753 (0.1130) | 1.5002 (0.1395) | 1.4238 (0.1487) | 1.3847 (0.1483) | 1.4048 (0.1791) | 1.3101 (0.1824) | 1.2581 (0.1827) |
| North to South America | 1.1420 (0.1470)** | 1.1366 (0.1641)* | 1.1379 (0.1692)* | 1.1966 (0.2682) | 1.1263 (0.2925) | 1.0810 (0.2892) | 0.9793 (0.3897) | 0.9268 (0.4108) | 0.9014 (0.4126) |
| AIC | 546.753 | 557.481 | 559.768 | 634.213 | 632.508 | 634.331 | 691.426 | 678.12 | 667.401 |

[†] 0.10>P>0.05 * 0.05>P>0.01 ** 0.01>P>0.001 *** 0.001>P

Table S7: Post-dispersal success in simulations.

The test statistic is the square root of the mean number of species alive after 5 million years after dispersal divided by the mean value for all other species globally. Significance for the estimate is the probability of being different from 1 (the random expectation), for age it is the probability of being different from 0 and for models with different patterns based on the source and/ or target continent it is based on the probability of being different from the estimated global rate.

Values are given for both the full simulated tree and the simulated incomplete sampling. The difference is the median difference between estimates for each tree. In parentheses, we list the number of times where this difference is negative (i.e. how many times the value is larger for incomplete sampling than the full tree). The p-value for the difference is based on a two-tailed binomial distribution and tests if incomplete sampling is equally likely to lead to larger and smaller values than complete sampling.

| | <i>Global post-dispersal success</i> | | | <i>Continental post-dispersal success</i> | | |
|---|--------------------------------------|---------------------|--|---|---------------------|--|
| | Full tree | Incomplete sampling | Difference | Full tree | Incomplete sampling | Difference |
| Simplest model | | | | | | |
| Global | 1.0696 (0.0816) | 1.0734 (0.0929) | -6.33 x 10 ⁻⁴ (52/100) | 1.1226 (0.726) | 1.1591 (0.0809) | -3.46 x 10 ⁻² (77/100)*** |
| AIC | 1252.351 | 973.833 | | 1251.687 | 998.474 | |
| Temporal variation | | | | | | |
| Global | 1.0698 (0.1158) | 1.0755 (0.1190) | 5.36 x 10 ⁻³ (47/100) | 1.1317 (0.1105) | 1.1614 (0.1259) | -2.39 x 10 ⁻³ (67/100)*** |
| Age | -0.0001 (0.0038) | -0.0003 (0.0045) | 5.54 x 10 ⁻⁵ (50/100) | -0.0004 (0.0040) | -0.0004 (0.0049) | -4.08 x 10 ⁻⁴ (57/100) |
| AIC | 1253.484 | 974.824 | | 1252.211 | 998.50 | |
| Variation between source continent | | | | | | |
| From Africa | NA | NA | NA | NA | NA | NA |
| From Eurasia | 1.0787 (0.1277) | 1.0734 (0.1725) | 6.90 x 10 ⁻³ (41/100) [†] | 1.1020 (0.1321) | 1.0951 (0.1701) | 1.20 x 10 ⁻² (42/100) |
| From North America | 1.0604 (0.0941) | 1.0669 (0.1025) | -1.67 x 10 ⁻³ (51/100) | 1.1589 (0.0924) | 1.2094 (0.1043) | -4.54 x 10 ⁻² (51/100) |
| From South America | 1.0806 (0.1543) | 1.1042 (0.1765) | -2.23 x 10 ⁻² (59/100) [†] | 1.0148 (0.1597) | 1.0258 (0.1791) | -7.86 x 10 ⁻³ (58/100) |
| AIC | 1254.421 | 973.611 | | 1252.495 | 995.151 | |
| Variation between target continent | | | | | | |
| To Africa | 0.7306 (0.2327) | 0.7528 (0.2874) | -9.21 x 10 ⁻³ (52/100) | 0.9970 (0.2512) | 1.0127 (0.3101) | 1.66 x 10 ⁻² (47/100) |
| To Eurasia | 1.0966 (0.1210) | 1.0825 (0.1236) | 1.84 x 10 ⁻² (37/100) [*] | 1.1913 (0.1198) | 1.2262 (0.1444) | -3.71 x 10 ⁻² (63/100) [*] |
| To North America | 1.1493 (0.1153) | 1.1567 (0.1329) | -3.02 x 10 ⁻³ (51/100) | 1.0794 (0.1236) | 1.0766 (0.1397) | 4.64 x 10 ⁻³ (48/100) |
| To South America | 1.0266 (0.1238) | 1.0477 (0.1291) | -1.64 x 10 ⁻² (62/100) [*] | 1.1297 (0.1273) | 1.1822 (0.1247) | -4.25 x 10 ⁻² (68/100)*** |
| AIC | 1240.512 | 967.294 | | 1253.755 | 991.077 | |
| Variation between source and target continent | | | | | | |
| Africa to Eurasia | NA | NA | NA | NA | NA | NA |
| Eurasia to Africa | 0.7305 (0.2326) | 0.7528 (0.2875) | -9.21 x 10 ⁻³ (52/100) | 0.9970 (0.2512) | 1.0124 (0.3100) | 1.66 x 10 ⁻² (47/100) |
| Eurasia to North America | 1.2061 (0.1433) | 1.2085 (0.1793) | 3.91 x 10 ⁻³ (48/100) | 1.1325 (0.1494) | 1.1219 (0.1842) | 1.42 x 10 ⁻² (42/100) |
| North America to Eurasia | 1.0966 (0.1209) | 1.0825 (0.1236) | 1.84 x 10 ⁻² (37/100) [*] | 1.1913 (0.1198) | 1.2262 (0.1445) | -3.71 x 10 ⁻² (63/100) [*] |
| North to South America | 1.0267 (0.1238) | 1.0477 (0.1291) | -1.64 x 10 ⁻² (62/100) [*] | 1.1297 (0.1273) | 1.1823 (0.1246) | -4.25 x 10 ⁻² (68/100)*** |
| South to North America | 1.0806 (0.1537) | 1.1042 (0.1759) | -2.23 x 10 ⁻² (59/100) [†] | 1.0148 (0.1596) | 1.0257 (0.1790) | -7.86 x 10 ⁻³ (58/100) |
| AIC | 1238.486 | 967.047 | | 1254.992 | 991.629 | |

[†] 0.10>P>0.05 * 0.05>P>0.01 ** 0.01>P>0.001 *** 0.001>P

Table S8: Additional species not in NOW or PBDB.

| Family | Genus | Species | Reference |
|------------------|--------------------------|-----------------------|-----------|
| Amphicyodontinae | <i>Amphicynodon</i> | <i>brachyrostris</i> | 64 |
| Amphicyodontinae | <i>Amphicynodon</i> | <i>cephalogalinus</i> | 64 |
| Amphicyodontinae | <i>Amphicynodon</i> | <i>chardini</i> | 64 |
| Amphicyodontinae | <i>Amphicynodon</i> | <i>crassirostris</i> | 64 |
| Amphicyodontinae | <i>Nothocyon</i> | <i>geismarianus</i> | 65 |
| Amphicyonidae | <i>Askazansoria</i> | <i>mavrini</i> | 66 |
| Amphicyonidae | <i>Haplocyonoides</i> | <i>suevicus</i> | 67 |
| Amphicyonidae | <i>Haplocyonopsis</i> | <i>crassidens</i> | 67 |
| Amphicyonidae | <i>Janvierocyon</i> | <i>pontignensis</i> | 68 |
| Amphicyonidae | <i>Temnocyon</i> | <i>ferox</i> | 69 |
| Amphicyonidae | <i>Vishnucyon</i> | <i>chinjiensis</i> | 70 |
| Barbourofelidae | <i>Afrosmilus</i> | <i>turkanae</i> | 56 |
| Barbourofelidae | <i>Vampyrictis</i> | <i>vipera</i> | 56 |
| Basal Pinnipedia | <i>Puijila</i> | <i>darwini</i> | 71 |
| Canidae | <i>Nyctereutes</i> | <i>terblanchei</i> | 56 |
| Canidae | <i>Vulpes</i> | <i>skinneri</i> | 72 |
| Felidae | <i>Asilifelis</i> | <i>coteae</i> | 73 |
| Felidae | <i>Proailurus</i> | <i>bournonnensis</i> | 74 |
| Felidae | <i>Proailurus</i> | <i>major</i> | 74 |
| Felidae | <i>Styriofelis</i> | <i>vallesiensis</i> | 75 |
| Felidae | <i>Yoshi</i> | <i>garevskii</i> | 76 |
| Herpestidae | <i>Herpestes</i> | <i>debilis</i> | 56 |
| Herpestidae | <i>Herpestides</i> | <i>aequatorialis</i> | 56 |
| Herpestidae | <i>Leptoplesictis</i> | <i>mbitensis</i> | 56 |
| Herpestidae | <i>Leptoplesictis</i> | <i>rangwai</i> | 56 |
| Herpestidae | <i>Suricata</i> | <i>major</i> | 56 |
| Hyaenodontidae | <i>Alienotherium</i> | <i>buxwilleri</i> | 77 |
| Hyaenodontidae | <i>Allopterodon</i> | <i>bulbosus</i> | 77 |
| Hyaenodontidae | <i>Allopterodon</i> | <i>minor</i> | 77 |
| Hyaenodontidae | <i>Cynohyaenodon</i> | <i>cailuxy</i> | 77 |
| Hyaenodontidae | <i>Cynohyaenodon</i> | <i>lautricensis</i> | 77 |
| Hyaenodontidae | <i>Cynohyaenodon</i> | <i>ruetimeyeri</i> | 77 |
| Hyaenodontidae | <i>Cynohyaenodon</i> | <i>trux</i> | 77 |
| Hyaenodontidae | <i>Eurotherium</i> | <i>matthesi</i> | 77 |
| Hyaenodontidae | <i>Galecyon</i> | <i>chronius</i> | 78 |
| Hyaenodontidae | <i>Galecyon</i> | <i>peregrinus</i> | 78 |
| Hyaenodontidae | <i>Hyaenodon</i> | <i>rossignoli</i> | 79 |
| Hyaenodontidae | <i>Kerberos</i> | <i>langebadrae</i> | 79 |
| Hyaenodontidae | <i>Masrasector</i> | <i>ligabuei</i> | 80 |
| Hyaenodontidae | <i>Matthodon</i> | <i>tritens</i> | 77 |
| Hyaenodontidae | <i>Paenoxyaenoides</i> | <i>liguritor</i> | 77 |
| Hyaenodontidae | <i>Paracynohyaenodon</i> | <i>schlosseri</i> | 77 |
| Hyaenodontidae | <i>Parapterodon</i> | <i>lostangensis</i> | 81 |
| Hyaenodontidae | <i>Paroxyaena</i> | <i>galliae</i> | 82 |
| Hyaenodontidae | <i>Paroxyaena</i> | <i>pavlovi</i> | 82 |
| Hyaenodontidae | <i>Praecodens</i> | <i>acutus</i> | 81 |
| Hyaenodontidae | <i>Protoproviverra</i> | <i>palaeonictides</i> | 77 |
| Hyaenodontidae | <i>Quercytherium</i> | <i>simplicidens</i> | 77 |
| Hyaenodontidae | <i>Quercytherium</i> | <i>tenebrosum</i> | 77 |
| Hyaenodontidae | <i>Sivapterodon</i> | <i>lahirii</i> | 79 |

| | | | |
|------------------------|-------------------------|-------------------------|-----|
| Hyanidae | <i>Chasmaporthetes</i> | <i>exitelus</i> | 83 |
| Hyanidae | <i>Crocota</i> | <i>eturono</i> | 84 |
| Hyanidae | <i>Hyaenictitherium</i> | <i>pilgrimi</i> | 83 |
| Hyanidae | <i>Ictitherium</i> | <i>Iberium</i> | 83 |
| Hyanidae | <i>Lycyaena</i> | <i>macrostoma</i> | 83 |
| Hyanidae | <i>Lycyaenops</i> | <i>rhomboideae</i> | 83 |
| Hyanidae | <i>Palinhyena</i> | <i>reperta</i> | 83 |
| Hyanidae | <i>Proteles</i> | <i>amplidentus</i> | 56 |
| Hyanidae | <i>Protictitherium</i> | <i>punixum</i> | 56 |
| Mephetidae | <i>Promephitis</i> | <i>majori</i> | 85 |
| Mephetidae | <i>Promephitis</i> | <i>malustenensis</i> | 85 |
| Mephetidae | <i>Promephitis</i> | <i>qinensis</i> | 85 |
| Miacidae | <i>Dawsonicyon</i> | <i>Isami</i> | 86 |
| Miacidae | <i>Gracilocyon</i> | <i>rosei</i> | 87 |
| Miacidae | <i>Gracilocyon</i> | <i>rundlei</i> | 88 |
| Miacidae | <i>Gracilocyon</i> | <i>solei</i> | 87 |
| Miacidae | <i>Paramiacis</i> | <i>teilharti</i> | 89 |
| Miacidae | <i>Quercygale</i> | <i>angustidens</i> | 88 |
| Miacidae | <i>Quercygale</i> | <i>hastingsiae</i> | 88 |
| Miacidae | <i>Quercygale</i> | <i>helvetica</i> | 88 |
| Miacidae | <i>Quercygale</i> | <i>smithi</i> | 88 |
| Miacidae | <i>Uintacyon</i> | <i>gingerichi</i> | 88 |
| Miacidae | <i>Uintacyon</i> | <i>hookeri</i> | 88 |
| Miacidae | <i>Vassacyon</i> | <i>bowni</i> | 90 |
| Miacidae | <i>Vassacyon</i> | <i>prieuri</i> | 30 |
| Miacidae | <i>Vassacyon</i> | <i>taxidiotis</i> | 88 |
| Miacidae | <i>Xinyuictis</i> | <i>tenius</i> | 90 |
| Miacidae | <i>Zodiocyon</i> | <i>zetesios</i> | 91 |
| Mustelidae | <i>Aonyx</i> | <i>indicus</i> | 92 |
| Mustelidae | <i>Enhydriodon</i> | <i>afman</i> | 93 |
| Mustelidae | <i>Eomellivora</i> | <i>hungarica</i> | 94 |
| Mustelidae | <i>Ferinestrix</i> | <i>rapax</i> | 95 |
| Mustelidae | <i>Leptarctus</i> | <i>bozemanensis</i> | 96 |
| Mustelidae | <i>Leptarctus</i> | <i>timmi</i> | 96 |
| Mustelidae | <i>Lutraeximia</i> | <i>umbra</i> | 97 |
| Mustelidae | <i>Pannonictis</i> | <i>pliocaenica</i> | 98 |
| Mustelidae | <i>Schultzogale</i> | <i>inexpecta</i> | 99 |
| Mustelidae | <i>Sivaonyx</i> | <i>senutae</i> | 100 |
| Mustelidae | <i>Sivaonyx</i> | <i>soriae</i> | 100 |
| Unassigned Musteloidea | <i>Legionarictis</i> | <i>fortidens</i> | 101 |
| Unassigned Musteloidea | <i>Luogale</i> | <i>rusingensis</i> | 56 |
| Unassigned Musteloidea | <i>Mustelictis</i> | <i>olivieri</i> | 102 |
| Unassigned Musteloidea | <i>Mustelictis</i> | <i>piveteaui</i> | 103 |
| Nimravidae | <i>Dinailurictis</i> | <i>bonali</i> | 104 |
| Nimravidae | <i>Eofelis</i> | <i>edwardsii</i> | 105 |
| Nimravidae | <i>Eofelis</i> | <i>giganteus</i> | 105 |
| Nimravidae | <i>Hoplophoneus</i> | <i>villebramarensis</i> | 104 |
| Nimravidae | <i>Maofelis</i> | <i>cantonensis</i> | 106 |
| Nimravidae | <i>Quercylurus</i> | <i>major</i> | 104 |
| Procyonidae | <i>Amphinasua</i> | <i>lutaria</i> | 107 |
| Procyonidae | <i>Chapalmalania</i> | <i>ortognatha</i> | 107 |
| Procyonidae | <i>Cyonasua</i> | <i>argentina</i> | 107 |

| | | | |
|------------------|-----------------------|---------------------|-----|
| Procyonidae | <i>Pseudobassaris</i> | <i>riggsi</i> | 108 |
| Stenoplesictidae | <i>Stenogale</i> | <i>intermedia</i> | 109 |
| Stenoplesictidae | <i>Stenoplesictis</i> | <i>crocheti</i> | 110 |
| Stenoplesictidae | <i>Stenoplesictis</i> | <i>muhoronii</i> | 56 |
| Ursidae | <i>Adelpharctos</i> | <i>ginsburgi</i> | 111 |
| Ursidae | <i>Agriarctos</i> | <i>gaali</i> | 112 |
| Ursidae | <i>Agriarctos</i> | <i>vighi</i> | 112 |
| Ursidae | <i>Agriotherium</i> | <i>myanmarensis</i> | 113 |
| Ursidae | <i>Arctotherium</i> | <i>angustidens</i> | 114 |
| Ursidae | <i>Arctotherium</i> | <i>vetustum</i> | 114 |
| Ursidae | <i>Cephalogale</i> | <i>geoffroyi</i> | 115 |
| Ursidae | <i>Cephalogale</i> | <i>gergoviensis</i> | 115 |
| Ursidae | <i>Cyonarctos</i> | <i>dessei</i> | 115 |
| Ursidae | <i>Filholictis</i> | <i>filholi</i> | 115 |
| Ursidae | <i>Kretzoiarctos</i> | <i>beatrice</i> | 112 |
| Ursidae | <i>Phoberogale</i> | <i>bonali</i> | 115 |
| Ursidae | <i>Phoberogale</i> | <i>minor</i> | 115 |
| Ursidae | <i>Ursavus</i> | <i>tedfordi</i> | 116 |
| Viverravidae | <i>Bryanictis</i> | <i>paulus</i> | 117 |
| Viverravidae | <i>Protictis</i> | <i>minor</i> | 117 |
| Viverravidae | <i>Protictis</i> | <i>simpsoni</i> | 117 |
| Viverravidae | <i>Viverriscus</i> | <i>omnivorus</i> | 118 |
| Viverridae | <i>Civettictis</i> | <i>howelli</i> | 56 |
| Viverridae | <i>Kenyalutra</i> | <i>songhorensis</i> | 56 |
| Viverridae | <i>Legetetia</i> | <i>Nandii</i> | 56 |
| Viverridae | <i>Mioparadoxurus</i> | <i>meini</i> | 119 |

Table S9: Sources for morphological and genetic data within groups.

| Group | Genetic data | Morphological data |
|--|--------------|------------------------------|
| Overall phylogeny | 54 | 30, 53, 91, 120, 121, 122 |
| Carnivora: Amphicyonidae | - | 123, 124 |
| Carnivora: Barbourfelidae | - | 125 |
| Carnivora: Canidae | 126 | 127, 128 |
| Carnivora: Felidae | 129 | 75, 130, 131, 132 |
| Carnivora: Hyanidae | 133 | 83 |
| Carnivora: Musteloidea | 60 | 95, 134, 135, 136, 137 |
| Carnivora: Nimravidae | - | 104 |
| Carnivora: Pinnipedia | 138 | 139, 140, 141, 142, 143, 144 |
| Carnivora: Ursidae (analysed in combination with Amphicyonodontinae) | 145 | 112, 146 |
| Carnivora: Viverridae | - | 119 |
| Creodonta: Hyaenodontidae | - | 29, 147, 148 |

Table S10: Topological constraints.

| Constraint | Source |
|--------------------------|--------|
| Carnivora: Amphicyonidae | |

| | |
|--|--|
| Haplocyoninae paraphyletic | 149 |
| Temnocyon paraphyletic | 149 |
| <i>Temnocyon altigenis</i> , <i>Temnocyon ferox</i> and <i>Temnocyon subferox</i> monophyletic | 149 |
| <i>Daphoenodon</i> and <i>Borocyon</i> sistergenera | 150 |
| <i>Adilophontes</i> sister to <i>Daphoenodon</i> and <i>Borocyon</i> | 150 |
| <i>Pliocyon</i> nested within American species of <i>Cynelos</i> | 151 |
| Asian <i>Amphicyon</i> not enforced to be monophyletic with the rest of the genus | 151 |
| <i>Hecubides</i> , <i>Afrocyon</i> and <i>Myacyon</i> combined considered monophyletic | 152 |
| North American <i>Amphicyon</i> constrained monophyletic | Biogeography |
| North American <i>Cynelos</i> (and <i>Pliocyon</i>) constrained monophyletic | Biogeography |
| <i>Cynodictis</i> sister to all other members of family | Support in preliminary analysis with outgroup 0.91 |
| Carnivora: Barbourfelidae | |
| Overall placement as sister to Felidae | 58 |
| Carnivora: Canidae | |
| <i>Phlaocyon taylori</i> sister to <i>Phlaocyon achoros</i> and <i>Phlaocyon multicuspus</i> | 153 |
| <i>Osbornodon scitulus</i> sister to <i>Osbornodon iamonensis</i> , <i>Osbornodon brachypus</i> and <i>Osbornodon fricki</i> | 154 |
| <i>Vulpes pallida</i> sister to <i>Vulpes chama</i> | 155 |
| <i>Vulpes velox</i> sister to <i>Vulpes macrotis</i> | 155 |
| <i>Vulpes corsac</i> , <i>Vulpes bengalensis</i> and <i>Vulpes ferrilata</i> monophyletic | 156 |
| The two old American species <i>Vulpes kernensis</i> and <i>Vulpes stenognathus</i> basal to all other <i>Vulpes</i> | Biogeography |
| Carnivora: Felidae | |
| <i>Proailurus</i> most basal in family followed by <i>Hyperailurictis</i> | 157 |
| <i>Pseudailurus quadridentatus</i> most basal in Machairodontinae | 157 |
| Miocene members of extant genera (<i>Felis christoli</i> , <i>Lynx longignathus</i> , <i>Lynx proterolyncis</i> , and <i>Puma pardoides</i>) placed freely within the subfamily rather than necessarily within their genus | 157 |
| <i>Felis lunensis</i> sister to <i>Felis silvestris</i> and <i>Felis bieti</i> . | 157 |
| <i>Diamantofelis ferox</i> sister to <i>Namafelis minor</i> | 56 |
| <i>Panthera gombaszoegensis</i> sister to <i>Panthera onca</i> . | 158 |
| <i>Miracinonyx</i> potentially nested within <i>Puma</i> | 159 |
| <i>Dinofelis aronoki</i> sister to <i>Dinofelis piveteaui</i> | 160 |
| <i>Leopardus amnicola</i> sister to <i>Leopardus wiedii</i> | 3 |
| <i>Leopardus guttulus</i> sister to <i>Leopardus tigrinus</i> | 3 |
| Carnivora: Herpestidae | |
| Extant Asian <i>Herpestes</i> monophyletic relative to African species of the genus | 161 |
| <i>Dologale</i> sister to <i>Helogale</i> | 155 |
| <i>Bdeogale jacksoni</i> sister to <i>Bdeogale nigripes</i> | 155 |
| <i>Bdeogale crassicauda</i> sister to <i>Bdeogale omnivora</i> | 155 |
| African <i>Herpestides</i> monophyletic | Biogeography |
| Carnivora: Hyanidae | |
| Relationship between most genera not included in the cladistics analysis based on the taxonomic hypothesis from this source | 162 |
| <i>Werdelinus</i> placed within the clade containing <i>Belbus</i> to <i>Crocota</i> since it was a bone crusher based on the species description. | 163 |
| African <i>Hyaenictis</i> constrained monophyletic | Biogeography |
| African <i>Hyaenictitherium</i> constrained monophyletic | Biogeography |
| Carnivora: Musteloidea: Ailuridae | |

| | |
|--|---|
| Ailurinae (<i>Ailurus</i> , <i>Magerictis</i> , <i>Pristinailurus</i> and <i>Parailurus</i>) and Simocyoninae (<i>Protursus</i> , <i>Protursus</i> and <i>Alopecocyon</i>) each monophyletic and sisters | 164 |
| <i>Parailurus anglicus</i> sister to <i>Parailurus hungaricus</i> | 164 |
| <i>Amphictis</i> paraphyletic and basal to Ailurinae and Simocyoninae | 164 |
| <i>Amphictis prolongata</i> , <i>Amphictis wintershofensis</i> , and <i>Amphictis cuspidata</i> combined monophyletic | 164 |
| <i>Parailurus</i> sister to <i>Ailurus</i> | 165 |
| <i>Magerictis</i> sister to <i>Parailurus</i> and <i>Ailurus</i> | 165 |
| <i>Simocyon marshi</i> sister to <i>Simocyon primigenius</i> | 166 |
| American species of <i>Alopecocyon</i> constrained to be monophyletic | Biogeography |
| Carnivora: Musteloidea: Mephitidae | |
| <i>Brachyopsigale dubius</i> sister to <i>Brachyprotoma obtusata</i> | 167 |
| <i>Conepatus humboldtii</i> sister to <i>Conepatus semistriatus</i> | 155 |
| <i>Spilogale putorius</i> sister to <i>Spilogale angustifrons</i> | 155 |
| American species of the family considered monophyletic | Biogeography |
| Carnivora: Musteloidea: Procyonidae | |
| <i>Procyon cancrivorus</i> most basal in genus (among extant species) | 155 |
| American species of the family considered monophyletic | Biogeography |
| Carnivora: Musteloidea: Mustelidae (family not enforced monophyletic within superfamily) | |
| <i>Namibictis senuti</i> sister to <i>Mellalictis mellalensis</i> sisters | 56 |
| <i>Hoplictis</i> , <i>Ischyriactis</i> , and <i>Laphictis</i> combined monophyletic since they often are called subgenera | 168 |
| <i>Martes occulta</i> , <i>Martes diluviana</i> , <i>Martes paleosinensis</i> , <i>Martes pennanti</i> constrained monophyletic (subgenus <i>Pekania</i>) but not constrained to be within the genus <i>Martes</i> | <i>Pekania</i> outside <i>Martes</i> in 60 |
| <i>Martes gwatkinsii</i> sister to <i>Martes flavigula</i> | 155 |
| <i>Mustela nivalis</i> , <i>M. subpalmata</i> , <i>M. russelliana</i> and <i>M. tonkinensis</i> monophyletic | 3 |
| Tribe Aonychini (<i>Aonyx</i> , <i>Cyrsaonyx</i> , and <i>Limnonyx</i>) monophyletic | 59 |
| Tribe Lutrini (<i>Algarolutra</i> , <i>Lutra</i> (excluding some fossil forms), <i>Lutrogale</i> , <i>Lutravus</i> , <i>Lutraeximia</i> , <i>Mionictis</i> , <i>Paralutra</i> , <i>Pteronura</i> , <i>Sardolutra</i> , <i>Satherium</i> and <i>Siamogale</i>) monophyletic | 59 |
| Enhydriodontini (<i>Enhydriodon</i> , <i>Paludolutra</i> , <i>Sivaonyx</i> and <i>Vishnuonyx</i>) monophyletic | 100 |
| <i>Satherium</i> sister to <i>Pteronura</i> | 169 |
| <i>Algarolutra</i> , <i>Megalenhydris</i> , <i>Sardolutra</i> and <i>Lutraeximia</i> nested within <i>Lutra</i> | 170 |
| <i>Sardolutra</i> sister to <i>Lutra castiglioni</i> | 170 |
| <i>Lutra licenti</i> sister to <i>Lontra</i> | 97 |
| <i>Lutra simplicidens</i> sister to <i>Lutra fatimazohrae</i> | 171 |
| <i>Megalictis frazieri</i> closer related to <i>Megalictis simplicidens</i> than to <i>Megalictis ferox</i> | 172 |
| American species of <i>Aonyx</i> constrained to be monophyletic | Biogeography |
| Carnivora: Nimravidae | |
| <i>Hoplophoneus mentalis</i> sister to <i>Hoplophoneus primaevus</i> | 104 |
| Carnivora: Percrocutidae | |
| Relationship of most species given by ((<i>Dinocrocota salonicae</i> , <i>Dinocrocota senyureki</i>), (<i>Dinocrocota gigantea</i> , <i>Dinocrocota algeriensis</i>)), ((<i>Percrocota abessalomi</i> , <i>Percrocota tobieni</i>), (<i>Percrocota miocenica</i> , (<i>Percrocota tungurensis</i> , <i>Percrocota carnifex</i>))) | 173 |
| African <i>Percrocota</i> constrained monophyletic | Biogeography |
| Carnivora: Pinnepedia | |
| Assignment of <i>Puijila</i> , <i>Semantor</i> , <i>Potamotherium</i> , and <i>Enaliarctidae</i> as basal to other families | 71 |
| Assignment of <i>Kolponomos</i> within the group of basal species mentioned above | 174 |
| <i>Pteronarctos</i> and <i>Pacificotaria</i> sistergenera. <i>Enaliarctos</i> sister to both | 175 |
| <i>Pinnarctidion</i> basal to <i>Desmatophocidae</i> and <i>Phocidae</i> | 176 |

| Carnivora: Ursidae (and Amphicyodontidae) | |
|--|--------------|
| Amphicyodontidae paraphyletic and basal to Ursidae | 146 |
| (<i>Amphicynodon brachyrostris</i> , (<i>Amphicynodon crassirostris</i> , <i>Amphicynodon typicus</i>), (<i>Amphicynodon velaunus</i> , <i>Amphicynodon leptorhynchus</i> , (<i>Amphicynodon teilhardi</i> , (<i>Amphicynodon cephalogalinus</i> , <i>Amphicynodon gracilis</i>))))). <i>Amphicynodon chardini</i> placed freely in the genus | 64 |
| Phoberocyoninae sister to Hemicyoninae | 177 |
| <i>Plionarctos</i> sister to <i>Tremarctos</i> | 178 |
| <i>Arctodus</i> sister to <i>Arctotherium</i> | 178 |
| <i>Arctodus</i> and <i>Arctotherium</i> sister to <i>Plionarctos</i> and <i>Tremarctos</i> | 178 |
| <i>Ursus etruscus</i> basal to <i>U. arctos</i> , <i>U. maritimus</i> and <i>U. spelaeus</i> | 179 |
| <i>Ursus boeckhi</i> basal to remaining <i>Ursus</i> , <i>Helarctos</i> , and <i>Melursus</i> | 180 |
| Carnivora: Viverridae | |
| <i>Euboictis</i> and <i>Legetetia</i> sistergenera | 56 |
| <i>Semigenetta elegans</i> , <i>Semigenetta laugnacensis</i> and <i>Semigenetta sansaniensis</i> considered monophyletic | 181 |
| <i>Arctictis</i> , <i>Arctogalidia</i> , <i>Macrogalidia</i> , <i>Mioparadoxurus</i> , <i>Paguma</i> , <i>Paradoxurus</i> constrained to be monophyletic | 119 |
| <i>Genetta abyssinica</i> sister to <i>Genetta thierryi</i> | 155 |
| <i>Viverra civettina</i> sister to <i>Viverra megaspila</i> | 155 |
| Carnivoramorpha: Viverridae | |
| <i>Ictidopappus</i> most basal in the family (except for perhaps <i>Pappictidops</i> and <i>Pristinictis</i>) | 182 |
| <i>Simpsonictis</i> closer to <i>Viverriscus</i> than any other genus (except for perhaps <i>Pappictidops</i> and <i>Pristinictis</i>) | 182 |
| <i>Bryanictis</i> closer to <i>Intyriictis</i> than any other genus (except for perhaps <i>Pappictidops</i> and <i>Pristinictis</i>) | 182 |
| <i>Bryanictis</i> , <i>Intyriictis</i> , <i>Protictis</i> and <i>Raphictis</i> monophyletic (although <i>Pappictidops</i> and <i>Pristinictis</i> are allowed to be placed freely in the family) | 182 |
| Creodonta: Hyaenodontidae | |
| North American <i>Arfia</i> constrained monophyletic | Biogeography |
| European <i>Prototomus</i> constrained monophyletic | Biogeography |
| Creodonta: Oxyaenidae | |
| Machaeroidinae basal to other subfamilies. | 183 |
| Part of family resolved as (<i>Dipsalodon churchillorum</i> , (<i>Dipsalodon matthewi</i> , (<i>Ambloctonus</i> , (<i>Palaeonictis peloria</i> , (<i>Palaeonictis gigantea</i> , (<i>Palaeonictis occidentalis</i> , <i>Palaeonictis wingi</i>)))))). <i>Sarkastodon</i> and <i>Malfelis</i> free-floating within the subfamily | 183, 184 |
| Part of family resolved as (<i>Dipsalidictis aequidens</i> , (<i>Dipsalidictis krausei</i> , <i>Dipsalidictis platypus</i> , (<i>Dipsalidictis transiens</i> , (((<i>Oxyaena gulo</i> , (<i>Oxyaena forcipata</i> , <i>Oxyaena intermedia</i>)), <i>Oxyaena woutersi</i>), ((<i>Patriofelis ferox</i> , <i>Patriofelis ulta</i>), <i>Protopsalis tigrinus</i>)))))). <i>Sarkastodon</i> and <i>Malfelis</i> free-floating within the subfamily. <i>Oxyaena lupina</i> , <i>Oxyaena pardalis</i> , and <i>Oxyaena simpsoni</i> free-floating within the genus | 183, 184 |

Figure S1: Effect of incomplete sampling on diversity estimates.

The difference in median species and phylogenetic diversity either globally or for individual continents. Due to the limited effect of limited sampling, the two lines are frequently on top of each other and the line for incomplete sampling is therefore stippled to make both lines visible.

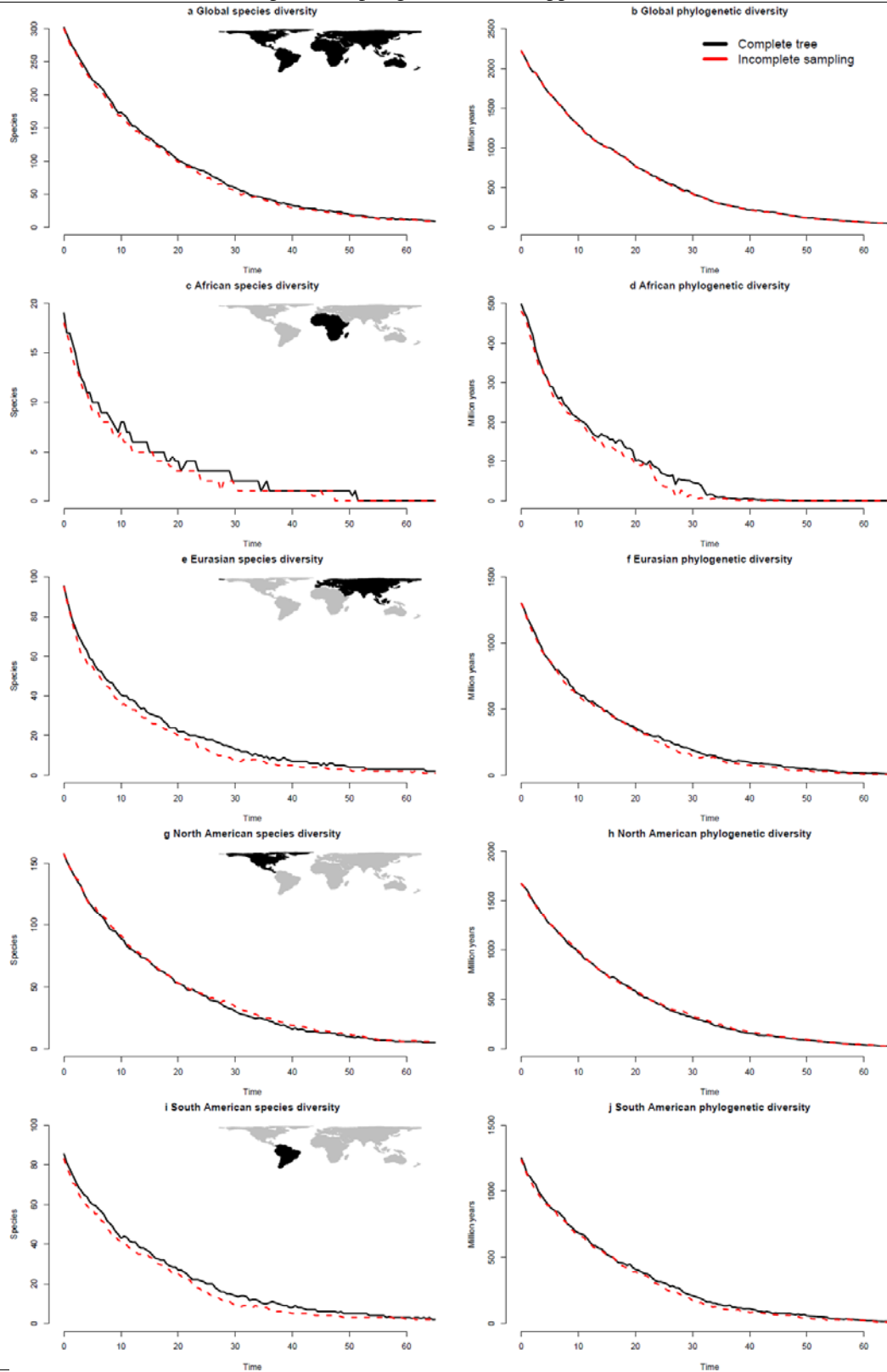


Figure S2: Simulation model.

Schematic drawing of the simulation model, which is a seven classes ClaSSE model transformed into a four-area version of a GeoSSE model. All arrows drawn in full (dispersal rate, extinction rate and allopatric speciation rate) represent cases where the species in question changes class in the ClaSSE model (or completely disappears for extinction from single area classes), whereas stippled lines (sympatric speciation rate and jump dispersal speciation rate) represent cases where the species buds off from another species while the ancestor stays in the region it was before.

