

The delayed rise of present-day mammals

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Did the end-Cretaceous mass extinction event, by eliminating non-avian dinosaurs and most of the existing fauna, trigger the evolutionary radiation of present-day mammals? Here we construct, date and analyse a species-level phylogeny of nearly all extant Mammalia to bring a new perspective to this question. Our analyses of how extant lineages accumulated through time show that net per-lineage diversification rates barely changed across the Cretaceous/Tertiary boundary. Instead, these rates spiked significantly with the origins of the currently recognized placental superorders and orders approximately 93 million years ago, before falling and remaining low until accelerating again throughout the Eocene and Oligocene epochs. Our results show that the phylogenetic ‘fuses’ leading to the explosion of extant placental orders are not only very much longer than suspected previously, but also challenge the hypothesis that the end-Cretaceous mass extinction event had a major, direct influence on the diversification of today’s mammals.

Molecular data and the fossil record can give conflicting views of the evolutionary past. For instance, empirical palaeontological evidence by itself tends to favour the ‘explosive model’ of diversification for extant placental mammals¹, in which the orders with living representatives both originated and rapidly diversified soon after the Cretaceous/Tertiary (K/T) mass extinction event that eliminated non-avian dinosaurs and many other, mostly marine², taxa 65.5 million years (Myr) ago^{1,3,4}. By contrast, molecular data consistently push most origins of the same orders back into the Late Cretaceous period^{5–9}, leading to alternative scenarios in which placental lineages persist at low diversity for some period of time after their initial origins (‘phylogenetic fuses’; see ref. 10) before undergoing evolutionary explosions¹¹. Principal among these scenarios is the ‘long-fuse model’¹, which postulates an extended lag between the Cretaceous origins of the orders and the first split among their living representatives (crown groups) immediately after the K/T boundary⁸. Some older molecular studies advocate a ‘short-fuse model’ of diversification¹, where even the basal crown-group divergences within some of the larger placental orders occur well within the Cretaceous period^{4,5–7}.

A partial molecular phylogeny emphasizing divergences among placental orders suggested that over 20 lineages with extant descendants (henceforth, ‘extant lineages’) survived the K/T boundary⁸. However, the total number of extant lineages that pre-date the extinction event and whether or not they radiated immediately after it remain unknown. The fossil record alone does not provide direct answers to these questions. It does reveal a strong pulse of diversification in stem eutherians immediately after the K/T boundary^{4,12}, but few of the known Palaeocene taxa can be placed securely within the crown groups of extant orders comprising Placentalia⁴. The latter only rise to prominence in fossils known from the Early Eocene epoch onwards (~50 Myr ago) after a major faunal reorganization^{4,13,14}. The geographical patchiness of the record complicates interpretations of this near-absence of Palaeocene crown-group fossils^{14–16}: were these clades radiating throughout the Palaeocene epoch in parts of the

world where the fossil record is less well known; had they not yet originated; or did they have very long fuses, remaining at low diversity until the major turnover at the start of the Eocene epoch?

The pattern of diversification rates through time, to which little attention has been paid so far, might hold the key to answering these questions. If the Cretaceous fauna inhibited mammalian diversification, as is commonly assumed¹, and all mammalian lineages were able to radiate after their extinction, then there should be a significant increase in the net per-lineage rate of extant mammalian diversification, r (the difference between the per-lineage speciation and extinction rates), immediately after the K/T mass extinction. This hypothesis, along with the explosive, long- and short-fuse models, can be tested using densely sampled phylogenies of extant species, which contain information about the history of their diversification rates^{17–20}.

Using modern supertree algorithms^{21,22}, we construct the first virtually complete species-level phylogeny of extant mammals from over 2,500 partial estimates, and estimate divergence times (with confidence intervals) throughout it using a 66-gene alignment in conjunction with 30 cladistically robust fossil calibration points. Our analyses of the supertree indicate that the principal splits underlying the diversification of the extant lineages occurred (1) from 100–85 Myr ago with the origins of the extant orders, and (2) in or after the Early Eocene (agreeing with the upturn in their diversity known from the fossil record^{4,13,14}), but not immediately after the K/T boundary, where diversification rates are unchanged. Our findings—that more extant placental lineages survived the K/T boundary than previously recognized and that fewer arose immediately after it than previously suspected—extend the phylogenetic fuses of many extant orders and indicate that the end-Cretaceous mass extinction event had, at best, a minor role in driving the diversification of the present-day mammalian lineages.

A supertree with divergence times for extant mammals

The supertree contains 4,510 of the 4,554 extant species recorded in ref. 23, making it 99.0% complete at the species level (Fig. 1; see also

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Supplementary Fig. 1 and Supplementary Table 1). Most major clades have complete taxonomic coverage and all are more than 90% complete except for Afrosericida (tenrecs and golden moles; 78.6%). The supertree is 46.7% resolved compared to a fully bifurcating tree, with poorly resolved areas being generally found closer to the tips of the tree, particularly within Muridae and other rodent families (Supplementary Table 1). Roughly 63% of the 2,108 nodes in the tree were dated on the basis of one or more estimates from molecular sequence data and/or cladistically robust fossil estimates (Supplementary Table 2).

The two earliest splits in the phylogeny established Monotremata by 166.2 Myr ago, and then Marsupialia and Placentalia by 147.7 Myr ago (Table 1). After nearly 50 Myr without the origination of any further extant groups, all four placental superorders (Afrotheria, Euarchotheria, Laurasiatheria and Xenarthra) arose within 2.4 Myr of

one another around 100 Myr ago. This period seems to mark the start of a temporal hotspot of eutherian diversification: nearly all extant placental orders originated by 85 Myr ago, and all had appeared by 75 Myr ago, some 10 Myr before the K/T boundary. This interval of rapid eutherian radiation from 100–85 Myr ago is also notable for many other events in Earth history (for example, the rise of angiosperms; general reduction in worldwide temperatures to the Campanian low at 75 Myr ago; the Cenomanian/Turonian boundary ocean anoxic event at 93.5 Myr ago), but whether the co-occurrence is more than coincidence is beyond the scope of this work. The phylogeny suggests that 43 placental lineages with extant descendants survived the K/T boundary, nearly twice as many as previously identified⁸. This taxic diversity is consistent with the hypothesis that placentals diversified ecologically in the Cretaceous period (model 5 of ref. 11), although phylogenies alone are mute

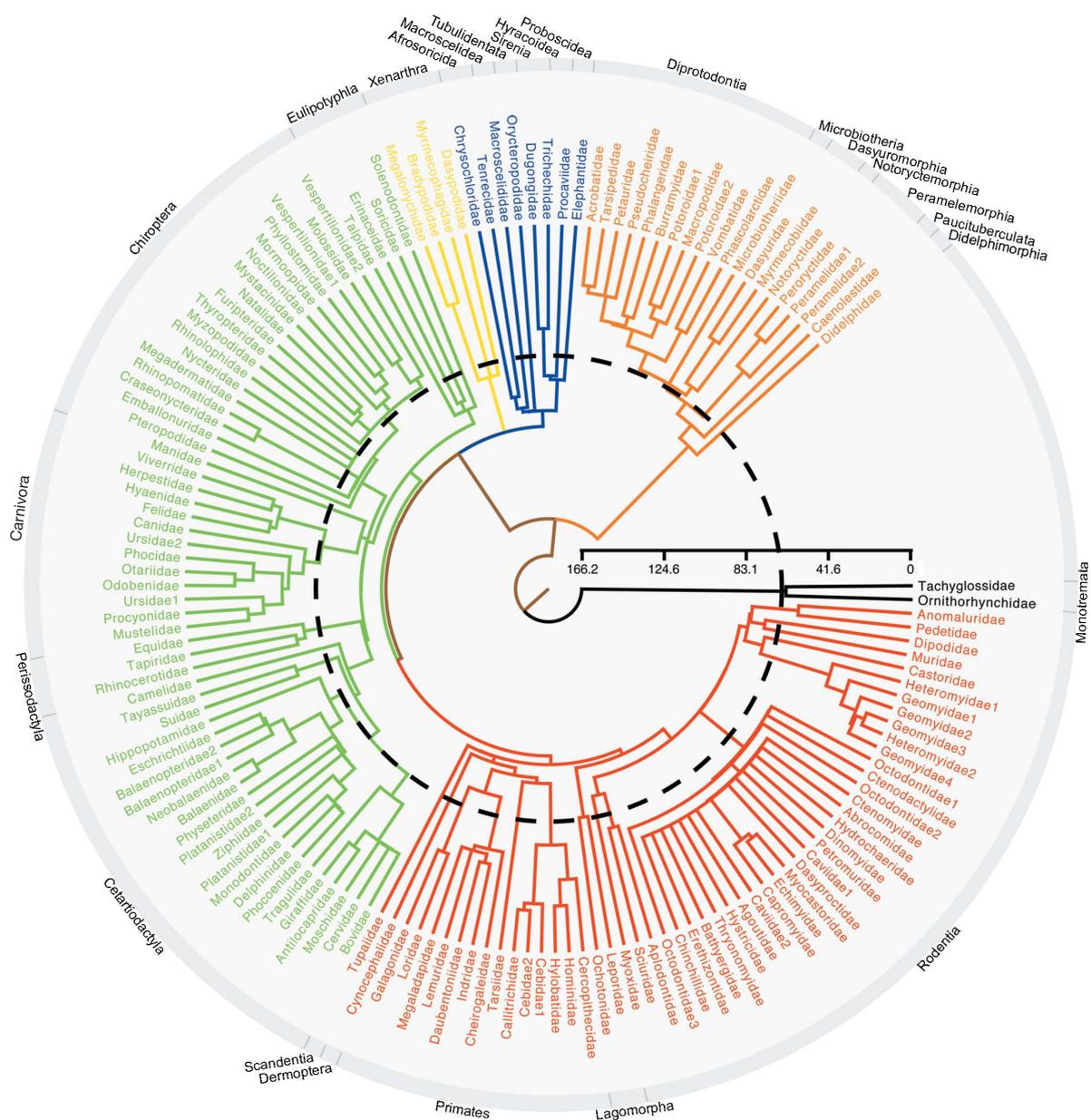


Figure 1 | Partial representation of the mammalian supertree showing the relationships among the families (following ref. 23). All orders are labelled and major lineages are coloured as follows: black, Monotremata; orange, Marsupialia; blue, Afrotheria; yellow, Xenarthra; green, Laurasiatheria; and red, Euarchotheria. Families that were reconstructed as non-

monophyletic are represented multiple times and numbered accordingly. Branch lengths are proportional to time, with the K/T boundary indicated by a black, dashed circle. The scale indicates Myr. The base tree was drawn using FigTree v1.0 (<http://evolve.zoo.ox.ac.uk/software.html?id=figtree>).

Table 1 | Divergence times for major mammalian lineages.

Taxon	Crown-group size	Time of origin	Time of basal diversification	Waiting time to first split	
				Absolute	Percentage
Mammalia	4,510	N/A	166.2 (fixed)	N/A	N/A
Monotremata	3	166.2 (fixed)	63.6 ± 11.4	102.6	61.7
Placentalia	4,249	147.7 ± 5.5	101.3 ± 7.4	46.4	31.4
Euarchothoglires	2,302	98.9 ± 2.7	94.5 ± 2.0	4.4	4.4
Rodentia	1,969	91.8 ± 1.3	85.3 ± 3.0	6.5	7.1
Lagomorpha	79	91.8 ± 1.3	66.8 ± 5.1	25.0	27.2
Primates	233	91.3 ± 2.6	87.7 ± 2.7	3.6	3.9
Dermoptera	2	91.3 ± 2.6	13.0 ± 5.2	78.3	85.8
Scandentia	19	94.3 ± 2.3	32.7 ± 2.6	61.6	65.3
Laurasiatheria	1,851	98.9 ± 2.7	91.8 ± 2.6	7.1	7.2
Cetartiodactyla	290	87.3 ± 1.5	74.1 ± 3.1	13.2	15.1
Perissodactyla	17	87.3 ± 1.5	58.2 ± 4.9	29.1	33.3
Carnivora	268	84.9 ± 3.6	67.1 ± 3.8	17.8	21.0
Pholidota	7	84.9 ± 3.6	19.9 ± 20.7	65.0	76.6
Chiroptera	915	88.7 ± 2.0	74.9 ± 3.3	13.8	15.6
Eulipotyphla	354	91.8 ± 2.6	84.2 ± 2.1	7.6	8.3
Xenarthra	29	101.1 ± 3.3	72.5 ± 5.1	28.6	28.3
Afrotheria	67	101.3 ± 7.4	93.4 ± 3.0	7.9	7.8
Afrosoricida	39	91.2 ± 2.6	85.2 ± 4.2	6.0	6.6
Macroscelidea	15	91.2 ± 2.6	50.7 ± 7.6	40.5	44.4
Tubulidentata	1	93.2 ± 3.0	N/A	N/A	N/A
Sirenia	4	75.9 ± 3.9	52.2 ± 14.4	23.7	31.2
Hyracoidea	6	75.9 ± 3.9	19.1 ± 0.8	56.8	74.8
Proboscidea	2	77.8 ± 3.6	19.5 ± 12.1	58.3	74.9
Marsupialia	258	147.7 ± 5.5	82.5 ± 11.1	65.2	44.1
Diprotodontia	109	63.6 ± 0.6	54.5 ± 1.7	9.1	14.3
Microbiotheria	1	63.6 ± 0.6	N/A	N/A	N/A
Dasyuromorphia	61	58.5 ± 8.0	32.8 ± 20.0	25.7	43.9
Notoryctemorphia	2	58.5 ± 8.0	9.3 ± 0.9	49.2	84.1
Peramelemorphia	18	66.8 ± 5.2	36.2 ± 5.6	30.6	45.8
Paucituberculata	5	73.8 ± 2.7	33.3 ± 6.9	40.5	54.9
Didelphimorphia	62	82.5 ± 11.1	56.1 ± 10.9	26.4	32.0

Hierarchical nesting of taxa is indicated using an indented taxonomy. Divergence times are in Myr ago ± 95% confidence intervals. Waiting times indicate the temporal gap (phylogenetic-fuse length) between the time of origin and of the basal diversification of the existing members of the crown group, both in absolute (Myr) and relative terms (percentage, relative to time of origin). See also Supplementary Table 2.

about ecological diversity¹². Marsupialia did not diversify until 82.5 Myr ago, nearly 20 Myr after placentals, with four lineages crossing the K/T boundary. Diversification of the surviving Monotremata is even later, with the single lineage that crossed the boundary first diversifying shortly thereafter (63.6 Myr ago).

Purely on the basis of the timings of the interordinal and first intraordinal splits, all three diversification models are present in mammals (Table 1). The short-fuse model is found for all placental crown groups that include at least 29 species, where the basal splits within these clades occur shortly after their origins (average fuse length = 13.6 Myr or 14.8%), and average some 10 Myr before the K/T boundary (77.5 Myr ago; range = 66.8–87.7 Myr ago). Crown-group marsupials instead approximate the explosive model, with the K/T boundary being within the confidence intervals of the dates of origin of most orders (although two orders did arise significantly earlier and most intraordinal divergences are significantly later). Finally, the long-fuse model characterizes Monotremata, the depauperate placental super-order Xenarthra, and the less diverse extant placental orders. For many of these groups, the long fuses (average = 57.3 Myr or 60.9%) reflect that these taxa have often been more diverse in the past, with the present crown group encompassing little of their early evolutionary history (for example, Proboscidea, Perissodactyla, Monotremata).

The tempo of mammalian diversification

To identify times of unusually rapid net diversification ('evolutionary explosions'), we use lineages-through-time plots¹⁷ to gain insight into the history of mammalian diversification rates. If speciation and extinction rates have been constant through time, the logarithm of the number of phylogenetic lineages with extant descendants should rise linearly with time for much of a clade's history¹⁹, with a slope that estimates the net rate of diversification, r . An increase in slope at the K/T boundary would indicate that r rose at that point, whereas a step-like increase would signify a burst of speciation¹⁸. Lineages-through-time plots from the supertree (Fig. 2a), however, show no evidence of any significant

upturn in r at any time around the K/T boundary. This result is confirmed by two-tailed γ -tests²⁰, which show that no significant temporal trend in r exists for mammals as a whole from the origin of crown-group mammals to 50 Myr ago ($\gamma = -0.575$, $P = 0.56$), with placental diversification actually slowing significantly over this period ($\gamma = -2.084$, $P = 0.04$). However, the placental data are more consistent with a step-change in diversification rate than a gradual trend (corrected Akaike information criterion, $AIC_c = 232.21$ and 239.04 , respectively; evidence weight for step-change = 96.8%), with the rate decrease inferred to have taken place at 85 Myr ago. Although marsupials do show a jump at the K/T boundary, the number of lineages involved (from three to six lineages) is very small, making firm conclusions difficult (see Supplementary Results).

Regression models in which r is a smooth function of time substantiate these findings (Fig. 2b). The temporal variation in r before 25 Myr ago is highly significant ($\chi^2_9 = 31.3$, $P < 0.001$). There is a peak at 93.1 Myr ago coincident with the Cenomanian/Turonian boundary, after which r declined to a minimum around the K/T boundary. After the latter, r remained low until the late Palaeocene, after which it increased more or less continuously until the Miocene epoch. Net diversification rates did not rise suddenly at any time around the K/T event: no significant rate difference exists between the latest Cretaceous (Maastrichtian) and earliest Tertiary (Danian) (general linear model with Poisson errors: $z = 0.479$, degrees of freedom = 104, $P = 0.63$). Results from parallel analyses broken down according to the major lineages of mammals or based on the 95% confidence interval dates are very similar (see Supplementary Results and Supplementary Figs 2–4).

The supertree therefore contains no evidence that the diversification rate of the extant mammalian lineages increased soon after non-avian dinosaurs went extinct. Although there is strong palaeontological evidence that mammalian diversity, driven by a massively elevated rate of speciation, generally rose rapidly immediately after the K/T boundary⁴, there is in fact no conflict between the palaeontological

and neontological interpretations of the known facts. Most diversifications immediately after the K/T boundary were in groups such as multituberculates, plesiadapiforms and 'archaic' ungulates⁴, as plots of the numbers of genera known in each sub-epoch indicate (Fig. 2c). These groups declined or went extinct early in the Cenozoic era and so are barely, if at all, represented in the phylogeny of living species. The continuing low rates of extant mammalian diversification through this period imply that the dearth of Palaeocene crown-group fossils is a real reflection of the low diversity of those clades. The low rates are also consistent with (but not direct evidence for) the hypothesis that extant lineages were inhibited in some manner by the diversity of the predominantly Palaeocene groups, and only started to diversify with the decline of the latter (Fig. 2c). However, like most other proposed competitive exclusion scenarios (for example, see refs 24, 25), this conjecture is based purely on the negative correlation of taxon diversities rather than direct evidence of exclusion.

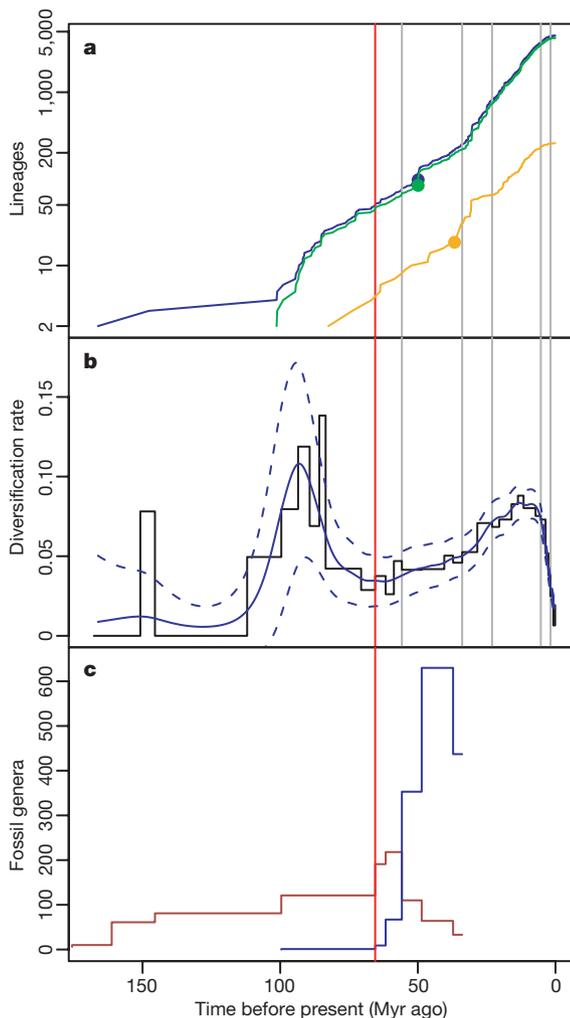


Figure 2 | Temporal patterns of mammalian diversification. **a**, Lineages-through-time plot for all (blue), placental (green) and marsupial (orange) mammals. Filled circles indicate when resolution in the phylogeny dropped below 85%. **b**, Net diversification rates: stepped line, rate in each age or sub-epoch; solid blue curve, rate inferred from a GAM of rate against time ($\chi^2 = 241.5$, estimated degrees of freedom = 14.75, $P \ll 0.001$, adjusted $R^2 = 77.6\%$, deviance explained = 20.3%); dashed curves, 95% confidence intervals. **c**, Counts of mammalian genera in each sub-epoch (Late Triassic to Late Eocene) according to the Unitaxon database (based on ref. 42). Red and blue lines represent genera whose families diversified predominantly before or after the Palaeocene/Eocene boundary, respectively. Throughout, the red vertical line is the K/T boundary and grey lines separate Cenozoic epochs.

510

Conclusions

As unquestionably useful as molecular data have been for untangling mammalian evolutionary history²⁶, no current molecular phylogeny is sufficiently complete to provide a clear view of dynamics so far in the past. Our analysis of a near-complete, species-level phylogeny of extant mammals sheds new light on how one of the best-known mass extinctions in Earth history affected their macroevolutionary dynamics. In particular, we challenge the widely accepted importance of the K/T extinction event for the origin and diversification of extant mammalian lineages. The pulse of mammalian diversification immediately after the K/T event was mainly or wholly in groups that declined subsequently or died out, without contributing markedly to those lineages with extant descendants, for which the diversification rate remained flat across the boundary. Only selected marsupial orders agree with the explosive model to any extent, and then only in their times of origin. Instead, the pivotal macroevolutionary events for extant mammalian lineages occur either well before the boundary (significant decrease in diversification rate at approximately 85 Myr ago, after establishment and initial radiations of the placental superorders and major orders at approximately 93 Myr ago) or well afterwards, from the Early Eocene onwards (when net diversification began to accelerate). The supertree and fossil record provide different parts of this picture, attesting to the value of using both approaches together: the supertree provides no information about the dynamics of extinct lineages, whereas the fossil record probably underestimates the timing of crown-group diversification in the past. Together, both lines of evidence indicate that the phylogenetic fuses throughout mammals, but especially in placentals, are much longer than previously suspected.

Therefore, the demise of the non-avian dinosaurs, and the K/T mass extinction event in general, do not seem to have had a substantial direct impact on the evolutionary dynamics of the extant mammalian lineages. What, then, was delaying the diversification of present-day mammals? Clearly, the priority is to identify why net rates of diversification remained low for so long after the major lineages became established. Time lags are also known for other groups^{10,27}; however, our values are much longer. Future tests are needed to see whether the time lag might involve inhibition by not only the Cretaceous fauna, but also by the major Palaeocene mammal groups. Net diversification rates might also have been shaped in part by abiotic factors that were more favourable for the modern groups: r starts to rise at around the time of the Cenozoic thermal maximum and subsequent Early Eocene Climatic Optimum (approximately 55–50 Myr ago)²⁸. Discriminating among all these scenarios will be demanding, requiring a highly integrative approach combining phylogenetic, palaeontological, palaeoclimatic and geographical data at both regional and global scales.

METHODS

The supertree was constructed in a hierarchical framework, combining pre-existing supertrees for Carnivora, Chiroptera, 'Insectivora' (split into Afrosoricida and Eulipotyphla) and Lagomorpha with new ones for the remaining groups, including the base supertree of all extant families (see Supplementary Table 1). All new supertrees were built using an explicit source tree collection protocol²⁹ to minimize both data duplication (for example, where the same data set underlies more than one source tree) and the inclusion of source trees of lesser quality (for example, taxonomies or those based on appeals to authority). Species names in the source trees were standardized to those found in ref. 23, and extinct taxa (following the 2004 IUCN Red List; <http://www.redlist.org>) were pruned from the final supertree. All supertrees were obtained using Matrix Representation with Parsimony (MRP^{30,31}), with the parsimony analyses for the new supertrees being performed in PAUP* v4.0b10 (ref. 32).

Recognizing that fossils provide minimum divergence-time estimates³³, divergence times throughout the supertree were either estimated by a combination of fossil and/or molecular dates under the assumption of a local molecular clock³⁴ (1,322 of 2,108 nodes) or interpolated from these empirically dated nodes using a pure birth model³⁴ (786 nodes) using the Perl scripts relDate v.2.2 and chronoGrapher v1.3.3, respectively (<http://www.personal.uni-jena.de/~b6biol2/>). The interpolated dates were not used in any of the statistical analyses reported

here. Because of the crucial nature of fossil calibration points, we restricted ourselves to fossils placed within crown groups of major lineages (generally orders) on the basis of one or more shared derived features as demonstrated in robust cladistic analyses. The 30 fossil dates so obtained represented minimum age constraints for their respective nodes (Supplementary Table 3). The root of the mammalian tree (age of the crown group) was estimated at 166.2 Myr ago based on the Middle Jurassic (Bathonian) Malagasy fossil *Ambondro mahabo*³⁵.

Relative molecular date estimates were obtained by fitting sequence data to the topology of the supertree under a maximum-likelihood framework in PAUP* to determine the branch lengths (following ref. 36). Sequence data were mined from the mammal section of GenBank release 144 (15 October 2004) using the Perl script GenBankStrip v2.0 (<http://www.personal.uni-jena.de/~b6biol2/>). Individual gene data sets were post-processed to retain only those sampled for at least 50 species and meeting minimum length and quality requirements before alignment (see Supplementary Methods). The final data set consisted of 51,089 base pairs from 66 genes (32 nuclear DNA, 19 transfer RNA and 15 other mitochondrial DNA), distributed across a total of 2,182 mammalian species (Supplementary Table 4). Representative outgroup sequences from the chicken (*Gallus gallus*) and/or either of the African or western clawed frogs (*Xenopus laevis* and *Xenopus tropicalis*, respectively) were added to each data set. Variation among the relative molecular date estimates provided by each gene was used to establish 95% confidence intervals for each divergence time estimate (see Supplementary Methods).

Two-tailed γ -tests²⁰ based on a lineages-through-time plot¹⁷ of the dated supertree were used to test the significance of any trends in the net diversification rate, r , over time in placentals, marsupials and mammals as a whole; under the null distribution, γ has a standard normal distribution. This test requires the tree to be highly resolved²⁰; we therefore used it only for the time window in which our tree is more than 85% resolved (before 50 Myr ago for placentals and all mammals, Fig. 2a; all dates within this portion of the tree were also estimated directly, rather than interpolated). On finding a trend within placentals, we compared the goodness-of-fit of linear and stepwise regression models to test whether the change in r was gradual or sudden. An additional test used only those lineages for which neither the beginning nor end dates were interpolated, and which did not start at a polytomy. These lineages can be informative about dynamics over a wider range of times (here, from the root of the tree up to about 25 Myr ago, after which point artefacts become increasingly important; see Supplementary Methods). Survival analysis³⁷ was used to estimate r within each geological age (pre-Pleistocene) or sub-epoch (Pleistocene). Temporal constancy in rate was tested by modelling r (as estimated from the number of speciation events per unit branch length within 0.1-Myr bins) as a function of time using generalized additive models (GAMs)³⁸. All analyses were repeated using the 95% confidence interval dates. All statistical analyses were performed in R³⁹ using the packages ape⁴⁰ and mgcv⁴¹.

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Supplementary Information is linked to the online version of the paper at www.nature.com/nature.

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Author Contributions O.R.P.B.-E. developed data and computer protocols underlying the supertree and dating analyses, contributed to or performed many of the supertree analyses, generated the molecular data set and dated the supertree, and wrote major portions of the manuscript; M.C. helped develop data protocols,

contributed source trees and performed many of the intraordinal supertree analyses, and helped write parts of the manuscript; K.E.J. contributed source trees, developed data protocols, collected the fossil database and performed associated analysis; R.D.E.M. provided relevant palaeontological information and first appearance dates of major clades, and collected the fossil database and performed associated analysis; R.M.D.B. contributed to and performed selected supertree analyses, and provided relevant palaeontological information; R.G. developed protocols for and performed supertree construction and macroevolutionary analyses, and contributed to the writing of the manuscript; S.A.P. developed data protocols, collected source trees for and built the cetartiodactyl and perissodactyl

portions of the supertree; R.A.V. provided source trees for Primates; J.L.G. provided source trees and ideas for comparative tests; and A.P. developed, conceived and performed the macroevolutionary analyses, wrote the corresponding sections of the manuscript and developed data protocols. All authors provided comments on the manuscript.

Author Information Reprints and permissions information is available at www.nature.com/reprints. The authors declare no competing financial interests. Correspondence and requests for materials should be addressed to O.R.P.B.-E. (olaf.bininda@uni-jena.de).

CORRIGENDUM

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The delayed rise of present-day mammals

Olaf R. P. Bininda-Emonds, Marcel Cardillo, Kate E. Jones, Ross D. E. MacPhee, Robin M. D. Beck, Richard Grenyer, Samantha A. Price, Rutger A. Vos, John L. Gittleman & Andy Purvis

Nature 446, 507–512 (2007)

We have discovered a bug in the Perl script relDate v.2.2 that was used in part to date the nodes in the species-level mammalian supertree presented and analysed in our Article. The bug affected all but 80 of the 2,109 published dates, generally causing them to be slightly inflated, with the effect being stronger in more recent nodes. The absolute errors are mostly small (mean and median change of 1.32 and 0.70 million years, respectively), and a strong correlation between the two sets of dates exists ($r = 0.990$); however, 25 dates (all within Chiroptera) do change by more than 10 million years. Four of these dates are associated with the paraphyletic genus *Hipposideros*, whereas the remaining 21 cover most of Molossididae. The errors do not affect the results or overall conclusions of our paper qualitatively.

The Supplementary Information, including the tree files, has now been amended and can be accessed through the Supplementary Information link of the original Article. An additional file with a version of the amended Article can be accessed at <http://www.uni-oldenburg.de/molekularesystematik/> under the 'Publikationen/Publications' link.

CORRIGENDUM

doi:10.1038/nature07432

STING is an endoplasmic reticulum adaptor that facilitates innate immune signalling

Hiroki Ishikawa & Glen N. Barber

Nature 455, 674–678 (2008)

We inadvertently failed to notice that STING protein is encoded by the same gene as the previously described plasma membrane tetraspanner MPYS¹.

1. Jin, L. *et al.* MPYS, a novel membrane tetraspanner, is associated with major histocompatibility complex class II and mediates transduction of apoptotic signals. *Mol. Cell. Biol.* 28, 5014–5026 (2008).

CORRIGENDUM

doi:10.1038/nature07514

A role for clonal inactivation in T cell tolerance to Mls-1^a

Marcia A. Blackman, Hans-Gerhard Burgert, David L. Woodland, Ed Palmer, John W. Kappler & Philippa Marrack

Nature 345, 540–542 (1990)

In this Article, the name of Hans-Gerhard Burgert was incorrectly listed as Hans Gerhard-Burgert.

ADDENDUM

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Genes mirror geography within Europe

John Novembre, Toby Johnson, Katarzyna Bryc, Zoltán Kutalik, Adam R. Boyko, Adam Auton, Amit Indap, Karen S. King, Sven Bergmann, Matthew R. Nelson, Matthew Stephens & Carlos D. Bustamante

Nature 456, 98–101 (2008)

A related manuscript arriving at broadly similar conclusions based on partially overlapping data has recently been published¹. Specifically, 661 of the 3,192 samples from the POPRES collection² analysed in our paper were also analysed by Lao *et al.*¹.

1. Lao, O. *et al.* Correlation between genetic and geographic structure in Europe. *Curr. Biol.* 18, 1241–1248 (2008).
2. Nelson, M. R. *et al.* The population reference sample, POPRES: a resource for population, disease, and pharmacological genetics. *Am. J. Hum. Genet.* 83, 347–358 (2008).

CORRIGENDUM

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Structural basis for specific cleavage of Lys 63-linked polyubiquitin chains

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Nature 455, 358–362 (2008)

In this Fig. 3c of this Article, Asp 324 was incorrectly labelled as Glu 324.