

# Supporting Online Material

## Supporting Text: Rapprochement in dating the early branching of modern mammals

It is important to distinguish the meaning of nodes in the tree (Fig. S1): successive branching of the subclass Metatheria (marsupials), and the superorders Afrotheria (elephants, hyraxes, sea cows, aardvarks), Xenarthra (sloths, anteaters), Euarchontoglires (rodents, rabbits, primates), and Laurasiatheria (whales, hooved mammals, carnivores, bats, insectivores). After those deep, *superordinal*, branching events, the individual *orders* differentiated and radiated.

Many estimated molecular dates for these five basal branching points (Table S1) of the subclasses and superorders are broadly in accord with fossil evidence. The split of Metatheria from Eutheria at 130-150 Ma predates the oldest distinctive metatherian (S1) and eutherian fossils (S2), but falls within the age range of undifferentiated therian mammals. The molecular dates for divergences of Afrotheria in the interval 90-107 Ma, of Xenarthra in the interval 90-102 Ma, and of Euarchontoglires and Laurasiatheria in the interval 85-95 Ma (Table S1) are all essentially within the Late Cretaceous. The Late Cretaceous fossil record of African and South American mammals is limited, so the divergences of Afrotheria and Xenarthra are hard to assess from fossils (S3). There are, however, placental mammals belonging to extinct families from the interval from 100-65 Ma (S1) from other parts of the world, some of which have not been assigned to superorders. However, the divergence of Euarchontoglires and Laurasiatheria is documented by fossils: zalmalestids (related to rodents and rabbits) and zhelestids (archaic ungulates) from Uzbekistan, dated at 85-90 Ma (S4), represent these two clades respectively.

Current molecular dates (Table S1; Fig. S1) place the differentiation of the mammalian orders in the interval 50-83 Ma. Four orders apparently began to diverge before the end of the Cretaceous, the primates at 70-83 Ma, the lipotyphlans (insectivores) at 73-79 Ma, the xenarthrans (edentates) at 66-72 Ma, and the rodents at 70-74 Ma. These younger dates for rodents (S5, S6) contradict earlier suggestions that the group was polyphyletic and had long Cretaceous roots (S7), although there are as yet no confirmed Late Cretaceous rodent fossils.

There are also some latest Cretaceous lipotyphlans, but other Late Cretaceous fossils that have been assigned to modern mammalian orders have been incorrectly identified or wrongly dated (S5).

Fig. S1

Major branches in the tree of modern mammals, showing known fossil ranges (heavy line), relationships, and estimated molecular dates (thin line). Fossil dates are taken from refs. S1, S8, and relationships and molecular dates from ref. S9. Abbreviations: Eoc, Eocene; Mio, Miocene; Oli, Oligocene; Pal, Paleocene; P, Pliocene

Supporting References

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Fig. 2. Major branches in the tree of modern mammals, showing known fossil ranges (heavy line), relationships, and estimated molecular dates (thin line). Fossil dates are taken from refs. 49, 65, and relationships and molecular dates from ref. 67. Abbreviations: Eoc, Eocene; Mio, Miocene; Oli, Oligocene; Pal, Paleocene; P, Pliocene

Table S1. Estimated ages (Ma) of branching points in lower parts of the tree of placental mammals. Dates of origin of major clades are given for Theria (all modern mammals except the monotremes), Eutheria (= placental mammals), with successive branching of the Afrotheria (represented by the elephant), Xenarthra (represented by the sloth), split of the crown group of the Euarchontoglires (rodents, rabbits, primates) and Laurasiatheria (even- and odd-toed ungulates, whales, carnivores, bats, insectivores), and dates for intraordinal diversification, using rodents and primates as examples. \* = Human/ rodent dates. Other abbreviations as for Figure 1.

Data source	Theria	Eutheria	Eutheria	Crown-group Eutheria	Modern orders	Ref.
	Marsupial/Placental	Human/Elephant	Human/Sloth	Human/Cow	Rodents Primates	
Fossil	131 ± 7	87 ± 3	87 ± 3	87 ± 3	60 ± 5    65 ± 5	
	<i>S1,S4,S8,S10</i>					
G/P	238 ± 20			*123 ± 11		<i>S11</i>
G (mtDNA)	154 ± 21			*134 ± 16		<i>S12</i>
G (20-48G, rRNA)				90 ± 8		<i>S13</i>
G (mtDNA)	140 ± 20			*124 ± 18		<i>S14</i>
G (12S rRNA)		103 ± 5		103 ± 7	98 ± 12	<i>S15</i>
G (658G)	173 ± 12	105 ± 7	129 ± 18	92 ± 1	110 ± 3	<i>S7</i>
G (mtDNA)		169 ± 24	169 ± 24	95 ± 9		<i>S16</i>
P (104E)				*96 ± 4		<i>S17</i>
G (12S rRNA, 3G)					75	<i>S18</i>
G (18G)		90 ± 18	90 ± 22	85 ± 17		<i>S3</i>
G (15G, 3 mtG)		105 ± 5	94 ± 6	84 ± 5		<i>S19</i>
G (3G)				85	65	<i>S5</i>
G (12 mtG)	130	95	95	95	70	<i>S20</i>
G (19G, 3 mtG)		107 ± 5	102 ± 8	94 ± 6	74 ± 6    77 ± 7	<i>S21</i>

