the TIMETREE of LIFE

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Whales and even-toed ungulates (Cetartiodactyla)

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Abstract

Whales and even-toed ungulates are grouped into ~24 families within the mammalian Order Cetartiodactyla. Recent phylogenetic analyses of molecular and morphological data robustly support most interfamilial relationships, including a nested position of whales within the order. However, resolution among basal clades of toothed whales and groupings within Ruminantia remain elusive. The fossil record of Cetartiodactyla is rich and has inspired many molecular clock studies. The cetartiodactyl timetree suggests that the earliest divergences among living species may have occurred in the Cretaceous (146–66 million years ago, Ma) and that the majority of splits among families were in the Oligocene (34–23 Ma).

Whales (Cetacea) and even-toed ungulates ("Artiodactyla," not a natural group) are represented by ~290 extant species (*1*), and have been grouped into 20–25 families within the placental Order Cetartiodactyla (Fig. 1). Extinct diversity is well represented in the clade, with about six extinct genera for every genus that contains extant species (*2*). This rich fossil record has facilitated molecular clock analyses (*3–14*), but phenotypic diversity in the group is extensive and has confounded systematic studies. Cetartiodactylans range in body size from the tiny ~4 kg mouse deer, *Tragulus javanicus*, to the enormous 190,000 kg Blue Whale, *Balaenoptera musculus* (*1*). It is often difficult to assess homology of structures in organisms that are as divergent as these in terms of anatomical organization, mass, and ecological specialization. Among taxa with living representatives, McKenna and Bell (*2*) recognized 11 families of Cetacea and 10 families of "Artiodactyla." Three additional family-level groups (Eschrichtiidae, Neobalaenidae, and Kogiidae) are commonly accepted. Here I review the phylogenetic relationships and divergence times of the families of Cetartiodactyla (Fig. 2).

The systematic database for Cetartiodactyla is large. Nuclear genome sequences are completed or in progress for members of four cetartiodactyl families. Mitochondrial (mt) genomes have been sequenced from 18 families (*11, 13, 15*), insertions of transposons have been scored from most families (*7, 16, 17*), and cladistic analysis of paleontological data sets is at an advanced stage (*18–25*). Perhaps most importantly, several large matrices of fossil and molecular data have been compiled (*26–29*). Studies based on these combined data sets permit direct synthesis of DNA sequence data with temporal information from the fossil and geological record.

Given the wealth of systematic evidence, there are some areas of strong congruence between analyses of morphological and molecular data sets. Suina, a grouping of Suidae (pigs) and Tayassuidae (peccaries), is robustly supported by both DNA sequences and phenotypic characters (*3, 14, 16, 20, 23–25, 27, 28, 30–33*). Likewise, a cluster of species that "chew the cud," Ruminantia, has been consistently supported by diverse analyses, in combination with Pecora, a subclade of Ruminantia (*3, 9, 14, 16, 18, 20, 23, 27, 28, 30–35*). Pecora includes all extant cetartiodactylans with prominent cranial appendages (Bovidae = antelopes and cattle, Cervidae = antlered deer, Giraffidae = giraffes, and Antilocapridae = pronghorn
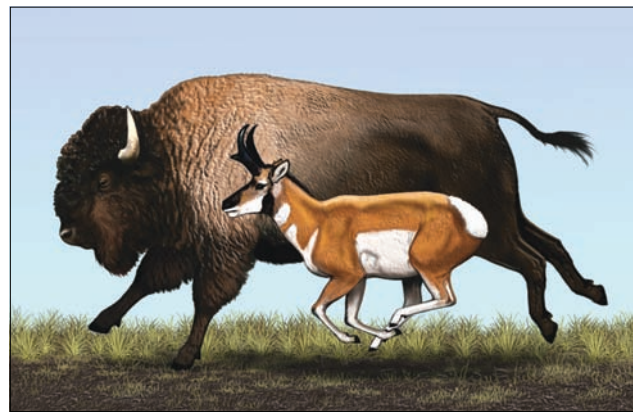

Fig. 1 An antilocaprid (*Antilocapra americana*; foreground) and a bovid (*Bison bison*; background). Credit: painting by C. Buell (J. Gatesy, copyright).
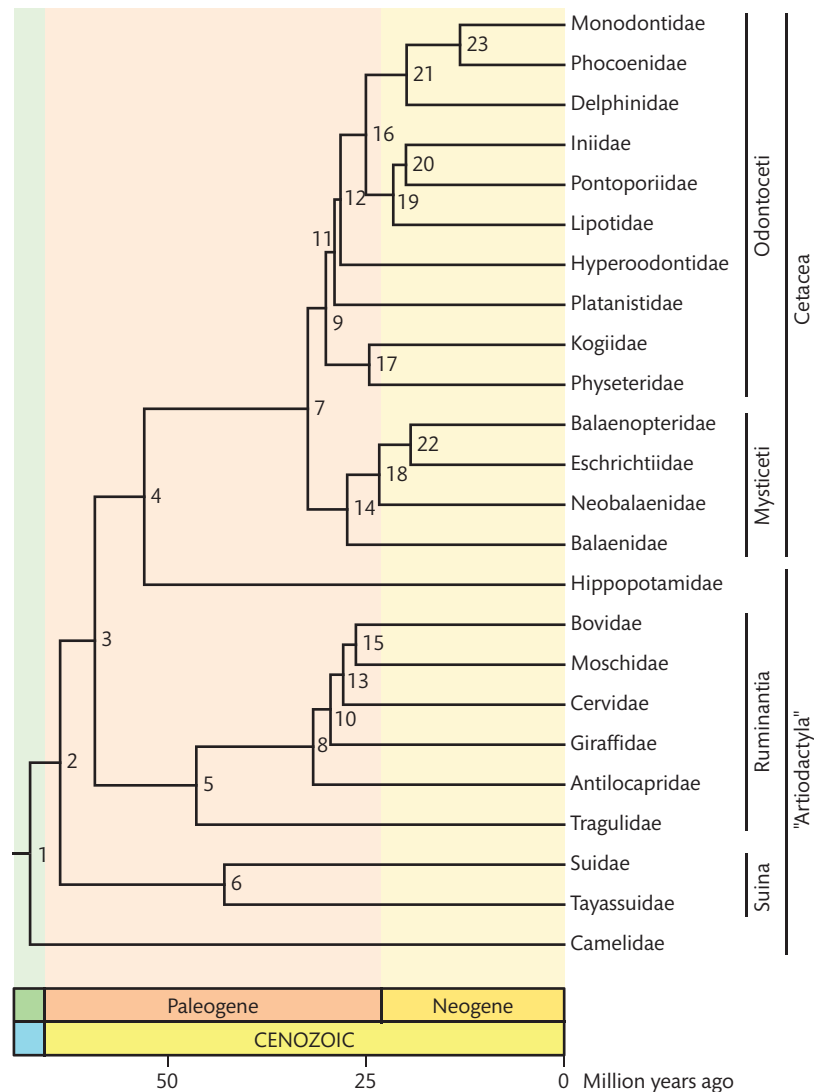
Fig. 2 A timetree of whales and even-toed ungulates (Cetartiodactyla). Divergence times are shown in Table 1. Hyperoodontidae = Ziphiidae.

antelopes), as well Moschidae (musk deer), which may be hornless primitively (*28*) or secondarily (*9, 18*). DNA data and the phenotypic evidence also generally agree in supporting Cetacea (whales), Odontoceti (toothed whales), Mysticeti (baleen whales), Eschrichtiidae (Gray Whale) + Balaenopteridae (rorqual baleen whales), Physeteroidea (Physeteridae = Giant Sperm Whale and Kogiidae = Dwarf and Pygmy Sperm Whales), Iniidae (Amazon River Dolphin) + Pontoporiidae (Franciscana Dolphin), and Delphinoidea (Delphinidae = oceanic dolphins, Phocoenidae = porpoises, and Monodontidae = Beluga and Narwhal) (*4–8, 10, 11, 13–17, 19, 20, 22, 23, 26–33, 36, 37*).

Despite this consensus, sharp conflicts between molecules and morphology have emerged over the past 20 years. Non-monophyly of "Artiodactyla," even-toed ungulates, is perhaps the most striking molecular incongruence with traditional mammalian taxonomy. Multiple nuclear gene sequences (*5, 6, 10, 30, 31*), mt genomes (*11*), and insertions of transposons (*16*) support a close relationship between Cetacea and Hippopotamidae (hippos), which is closest to Ruminantia (Fig. 2). The clusters render "Artiodactyla" paraphyletic, in contrast to most cladistic analyses of phenotypic data that favor a monophyletic grouping of even-toed ungulates (*20, 21, 25, 28*; but see *23, 24*). Recently discovered hindlimbs

Table 1. Divergence times (Ma) and their confidence/credibility intervals (CI) among whales and even-toed ungulates (Cetartiodactyla).

| Timetree | | Estimates | | | | | | | | | | | | | | |
| Node | Time | Refs. (3, 11) | Ref. (4) | | Refs. (7, 9) | | Ref. (8)(a) | | Ref. (8)(b) | | Ref. (10)(a) | | Ref. (10)(b) | | Refs. (13, 14) | |
		Time	Time	CI	Time	CI	Time	CI	Time	CI	Time	CI	Time	CI	Time	CI
1	67.3	–	–	–	–	–	67.3	73–63	64.1	68–60	63.8	65–62	55.3	60–51	74.1	77–71
2	63.5	–	–	–	–	–	63.5	68–59	62.5	66–57	60.5	62–59	50.7	56–46	71.6	74–70
3	59.1	–	–	–	–	–	59.1	63–55	57.7	63–55	55.7	57–54	44.1	49–39	65.9	68–63
4	52.9	53.3	–	–	–	–	52.9	55–52	52.9	55–52	52.4	54–52	39.8	45–35	59.5	62–57
5	46.3	–	–	–	46.3	55–39	–	–	–	–	–	–	–	–	–	–
6	42.8	42.8	–	–	–	–	–	–	–	–	–	–	–	–	49.7	64–36
7	32.3	–	47.5	54–42	32.3	37–27	27.4	33–22	25.5	31–22	29.6	34–25	20.3	25–16	–	–
8	31.6	–	–	–	31.6	36–28	–	–	–	–	–	–	–	–	–	–
9	30.0	32.1	45.5	51–41	30.0	35–25	–	–	–	–	–	–	–	–	–	–
10	29.4	–	–	–	29.4	33–26	22.0	28–17	–	–	–	–	–	–	–	–
11	28.9	–	–	–	28.9	34–24	–	–	–	–	–	–	–	–	–	–
12	28.2	–	–	–	28.2	33–23	–	–	–	–	–	–	–	–	–	–
13	27.8	–	–	–	27.8	30–25	–	–	–	–	–	–	–	–	–	–
14	27.3	20.9	31.0	36–26	–	–	–	–	–	–	–	–	–	–	27.3	29–25
15	26.2	–	–	–	26.2	29–24	–	–	–	–	–	–	–	–	–	–
16	25.0	22.4	–	–	25.0	30–20	–	–	–	–	–	–	–	–	–	–
17	24.5	24.5	37.0	42–32	–	–	–	–	–	–	–	–	–	–	–	–
18	23.3	17.6	–	–	–	–	–	–	–	–	–	–	–	–	23.3	26–21
19	21.5	–	–	–	21.5	26–17	–	–	–	–	–	–	–	–	–	–
20	19.9	18.4	23.0	26–20	19.9	24–16	–	–	–	–	–	–	–	–	–	–
21	19.8	16	24.5	28–22	19.8	24–16	–	–	–	–	–	–	–	–	–	–
22	19.3	14.7	21.5	26–18	–	–	–	–	–	–	–	–	–	–	19.3	22–16
23	13.1	12.8	20.0	22–18	13.1	17–9	–	–	–	–	–	–	–	–	–	–

Note: Node times in the timetree are from refs. (3, 7, 8(a), 9, 11, 13). For ref. (8), times are included from (a) Bayesian analysis of mitochondrial and nuclear DNA from ref. (5), and (b) Bayesian analysis of mitochondrial genome data translated into amino acids. For ref. (10), times are included from (a) Bayesian analysis of mitochondrial and nuclear DNA from ref. (6) using all calibrations, and (b) Bayesian analysis of mitochondrial and nuclear DNA from ref. (6) using all calibrations except those within Cetartiodactyla.

from Eocene whales (*21, 38*) show that early cetaceans had a paraxonic tarsus with a typical "artiodactyl" ankle (*39*), but such characters provide support for a grouping of Cetacea with "Artiodactyla," but not within "Artiodactyla" (*21, 25, 28*). Additional conflicts between morphology and molecules include monophyly vs. paraphyly of Balaenoidea (Balaenidae = right whales and Neobalaenidae = Pygmy Right Whale) (*11, 13, 15, 17, 22, 29, 37*), monophyly vs. non-monophyly of Phocoenidae + Monodontidae (*4, 7, 11, 15, 22, 28, 32, 36*), monophyly vs. polyphyly of river dolphins (Iniidae, Pontoporiidae, Lipotidae = Chinese River Dolphin, and Platanistidae = Indian River Dolphin) (*4, 7, 11, 15, 22*), monophyly vs. polyphyly of Selenodontia (Ruminantia and Camelidae = camels), and monophyly vs. non-monophyly of Suiformes (Suina and Hippopotamidae) (*3, 5, 6, 10, 11, 16, 20, 21, 23, 25, 28, 30–32*). Molecular resolutions of these conflicts are shown in Fig. 2.

Neither separate nor combined systematic matrices have robustly resolved some interfamilial relationships within Cetartiodactyla. In particular, basal clades of Odontoceti and the five pecoran ruminant families (Bovidae, Cervidae, Giraffidae, Antilocapridae, and Moschidae) have been resistant to hierarchical grouping, and extensive disagreements among characters remain. The topology in Fig. 2 illustrates odontocete phylogeny consistent with the transposon analysis of Nikaido *et al.* (*7*) and ruminant phylogeny according to analysis of mt and nuclear genes by Hassanin and Douzery (*9*). However, these relationships remain highly controversial and are disputed by alternative, large data sets (e.g., *11, 22, 28*). Furthermore, the basal positioning of Camelidae as the closest relative of all other extant cetartiodactylans has been debated, with various molecular and combined matrices favoring different local rearrangements. In general, the conflict here is between mt (*11*) and nuclear data (*5, 6, 10, 16, 30*), with the result favored by the nuclear evidence, the basal position of Camelidae (Fig. 2), prevailing in the most comprehensive compilation of characters to date (*28*; >600 phenotypic and >40,000 molecular characters).

The timetree for Cetartiodactyla is based on six molecular clock analyses (Fig. 2; Table 1). These include four Bayesian analyses of multiple nuclear and/or mt gene sequences (*7–9, 13*), a distance analysis of mt genes (*3*), and a study that utilized maximum likelihood branch lengths for mt genomes (*11*). All six studies employed fossils to establish calibration points. Alternative estimates of time for various nodes are shown in Table 1. The temporal pattern of diversification in the timetree suggests that much of the splitting among cetartiodactyl families (12 of 23 divergences) occurred in the Oligocene. These divergences include the difficult-to-resolve radiations at the base of Odontoceti and at the base of Pecora (Fig. 2). The 95% credibility intervals for estimates of divergence times among all five pecoran families overlap, and speciation events that separate odontocete families also are tightly spaced in time. The earliest branching point within Cetartiodactyla predates the Cretaceous/Paleocene boundary in the timetree, but alternative analyses push multiple nodes to the Cretaceous (*14*) or restrict all nodes to the Cenozoic (66–0 Ma) (*10*), depending on choice of fossil constraints, database, and methodology.

Molecular clock analyses within Cetartiodactyla have been common, in part because extinct taxa have been directly integrated into cladistic studies, and also because extensive genetic data have been compiled for members of this group. However, even with this effort, critical ambiguities remain. For example, the divergence of Cetacea from other cetartiodactylans is a very common calibration point for molecular clock analyses of mammals; van Tuinen (*12*) counted >30 studies that have utilized this divergence, yet the date remains poorly constrained because of the phylogenetic instability of some extinct taxa. The hippopotamid lineage apparently extends back to the Eocene through a paraphyletic series of extinct "anthracotheriids" (*24, 28*), but the identity of the earliest stem cetaceans remains controversial. Based on cranial and dental evidence, the extinct Pakicetidae (~52 Ma) has consistently been placed on the stem lineage of extant Cetacea (*12, 19–21, 23, 26–28*), but the position of Paleocene mesonychids (~62 Ma) remains undetermined. Systematic studies of basicranial characters (*19*), dental characters (*40*), and the largest cetartiodactyl matrix compiled to date (*28*) group Cetacea closer to Mesonychidae than to "artiodactylans," but other data sets entirely exclude Mesonychidae from Cetartiodactyla (*21, 23, 25, 27, 41*). Alternative fossil calibrations have led to very different molecular estimates of time. In particular, divergences within Cetacea (*4, 7, 11*) and at the base of Cetartiodactyla (*8, 10, 12, 14*) differ by 10–15 million years (Table 1).

These discrepancies illustrate the critical importance of robust fossil calibration points in molecular clock studies. Even a group with a well-documented fossil record, such as Cetartiodactyla presents challenges to researchers who wish to time particular divergences using molecular clocks. However, given the wealth of information for Cetartiodactyla, it is very likely that this group will continue to be an exemplar clade for testing

new and improved methods for dating evolutionary events using a combination of diverse systematic data.

Acknowledgment

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