

cetartiodactylans was between the Camelidae and a strongly supported clade of remaining Cetartiodactyla species (PP = 1.0, BP = 100%). Then, Suidae and Ruminantia branched successively. Within Ruminantia, *B. taurus* was the sister group of *Moschus moschiferus*, both of which formed a clade that then clustered with *Elaphurus davidianus* (100% PP and BS). Our results strongly support the idea that the Cetaceans are nested within Artiodactyla as the sister group of Hippopotamidae, with 99% of MP BS, 100% of ML BS, and 1.0 of BI PP values. In addition, the monophyly of Odontoceti (toothed whales), Mysticeti (baleen whales), and Delphinoidea (dolphins) was recovered with significant statistical confidence in all phylogenetic trees. Within Odontoceti, physeteroids (with the dwarf sperm whale of family Kogiidae as a representative) were placed at the most basal position, which is sister to the remaining toothed whales with full statistical support (1.0 PP and 100% BS). In this study, the river dolphins sampled (*Platanista* and *Lipotes*) did not group together, and *Platanista* (Indian River dolphins) branched after the divergence of sperm whales but before beaked whales. In the Delphinoidea, the grouping of *Neophocaena phocaenoides* (Phocoenoidae) with *Delphinapterus leucas* (Monodontidae) also received strong support in all phylogenetic reconstructions. The difference between these phylogenetic reconstructions was only found in the relationships among species within Delphinidae. The

ML and BI analyses of total sites recovered identical topologies, as shown in Fig. 1A, which suggests that *G. griseus*, *S. chinensis*, and *T. aduncus* are the most basal clades and that there is a sister relationship between *Stenella coeruleoalba* and *Delphinus capensis*, *Tursiops truncatus* and *Stenella attenuata*. However, the combined analyses of the BI method and the RY strategy strongly support a sister relationship between *S. chinensis* and *T. aduncus* (Fig. 1B). The MP tree did not reveal the phylogenetic relationship of Delphinidae, which showed a polytomy (rather than sequential bifurcations) consisting of *S. coeruleoalba*, *T. aduncus*, *D. capensis*, and *T. truncatus* + *S. attenuata* (Fig. 1C) with a comparatively low BS value (60%).

Because all the differences and competing topologies were recovered for the family Delphinidae, we analyzed rate constancy among lineages in this family using Tajima's relative rate test. When the concatenated sequences were considered, it was shown that *T. truncatus* evolved at a faster rate than other species (Table S1 in SI file 1). However, removing *T. truncatus* did not change the topology shown in Fig. 1 (see Fig. S1 in SI file 1). We further analyzed the data set with the SF method, which was designed to reduce the effect of LBA and increase the phylogenetic signal-to-noise ratio (Delsuc et al., 2005). The six most trimmed alignments (S0–S5) containing increasing fractions of fast-evolving positions

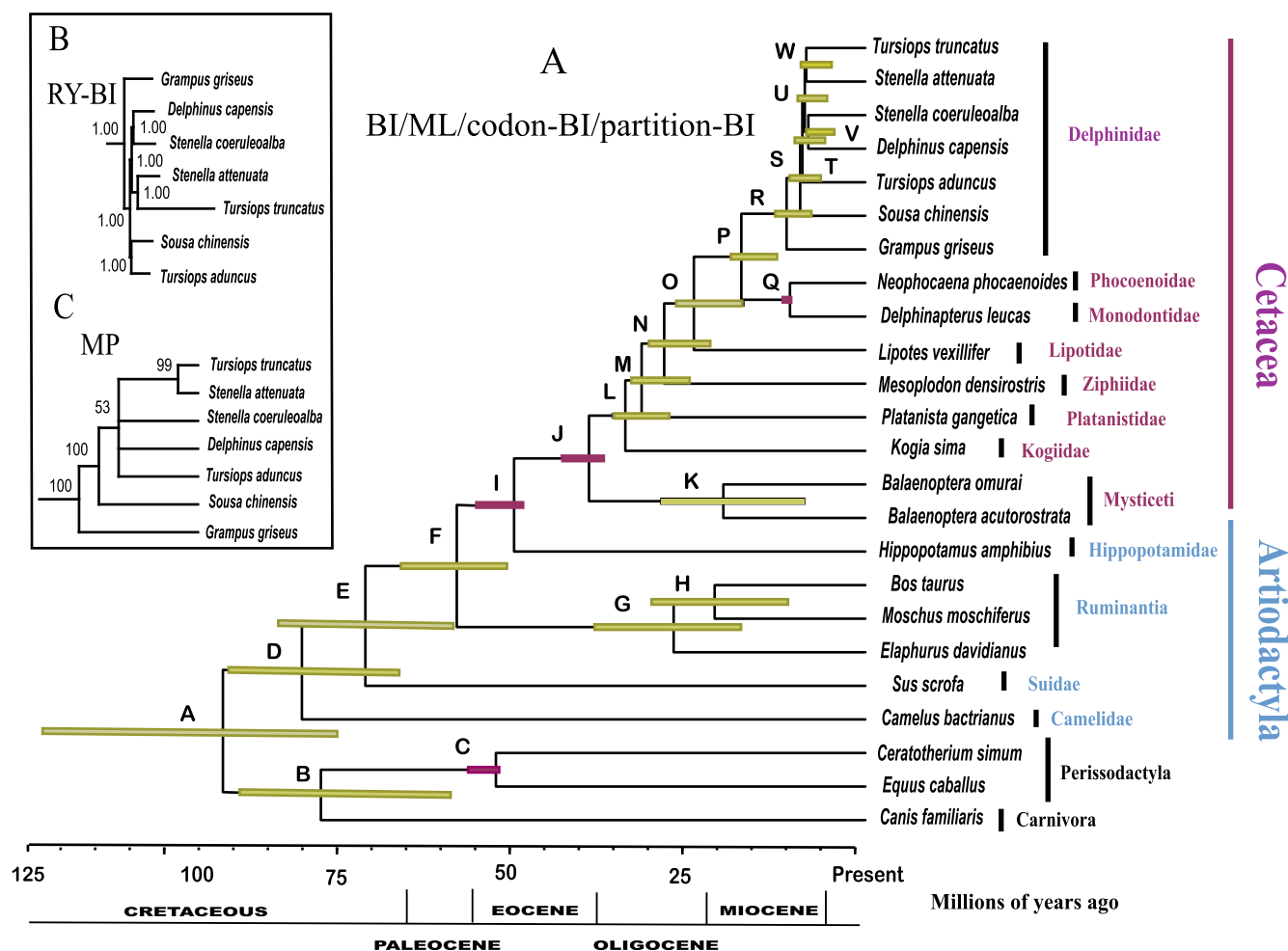


Fig. 1. Phylogenetic relationships of 21 Cetartiodactyla and three outgroup species. These trees were inferred from 110 nucleus-encoded proteins using BI, ML (A), and MP (C) methods. phylogenetic analysis was also performed using BI method combining with partitional model analyses or combining with RY-coding strategy (B). The only difference between these phylogenetic results is the relationships within Delphinidae. Support values obtained with 1000 bootstrap replicates on the concatenated data with RAxML and Bayesian posterior probability with MrBayes were shown in Table 3. Red boxes indicate nodes for which a prior calibration constraint distribution was used and orange boxes indicate divergence dates estimated for that node and the bounds of the boxes delimit the 95% highest posterior density (HPD) for the clade age.