

Mito-communication

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Cetacean mitogenomics

Cetacean phylogenies have been ambiguous as a result of incomplete taxonomic sampling, limited datasets such as single mitochondrial DNA loci, and sub-optimal analyses leading to unreliable molecular clocks. Examples of these analyses include various phylogenetic optimality criteria (maximum parsimony, maximum likelihood, distance) with independent evolutionary rates for all lineages, and even phenetic approaches such as Unweighted Pair Group Method with Arithmetic Mean (UPGMA) with all lineages evolving at the same rate.

The first issue has been tackled by an increase in species coverage, which has helped resolve ambiguities resulting from biases in taxon sampling. However, low morphological variation and homologous character evolution often mask underlying genetic divergence, confounding studies of cetacean evolution.

The second issue has begun to be addressed with the incorporation of mitogenomic phylogenies of most extant cetaceans excepting the Delphinidae family. Arnason et al. (2004) used the mitogenomes of 16 cetacean species to resolve the question of monophyly of the Odontoceti and Mysticeti suborders, the polyphyly of extant river dolphins, and the sister relationship between the Pontoporiidae–Iniidae clade and Delphinidae. Yan et al. (2005) and Turvey et al. (2007) revised this phylogeny, including the mitogenome of the now extinct *Lipotes vexillifer* river dolphin. Yan et al. shed light on the river dolphin phylogenetic

relationships, further supporting their polyphyletic nature. The newly sequenced *Lipotes* mitogenome places this taxon as sister to the Pontoporiidae + Iniidae complex (Figure 1, dotted branch), whereas Platanistidae remains sister to the grouping (Delphinidae, (Lipotidae, (Pontoporiidae, Iniidae))) (Figure 1, dotted branch).

Recent research by Xiong et al. (2009) makes use of the newer, more powerful Bayesian approaches to address the important analytical shortcomings of most cetacean phylogenies. The authors evaluated cetacean mitogenome relationships employing a partitioned Bayesian framework, and a “relaxed molecular clock” that allows for not only locus-specific substitution models and rates, but also for variation in the evolutionary rate among lineages. In their study, Xiong et al. sequenced seven new dolphin mitogenomes, suggesting that Platanistidae would be basal to the Ziphiidae family (Figure 1, solid branch) and that Lipotidae would be part of a trichotomy with Delphinidae and the (Pontoporiidae, Iniidae) complex (Figure 1, solid branch). This new analytical approach improved our current understanding of the relationships of the major cetacean families, supporting the hypothesis that the delphinid genera *Tursiops* and *Stenella* are polyphyletic (data not shown). The more robust relaxed molecular clock approach used in this analysis serves to help explain the typical ambiguity of the river dolphin complex in their deep and rapid divergence.

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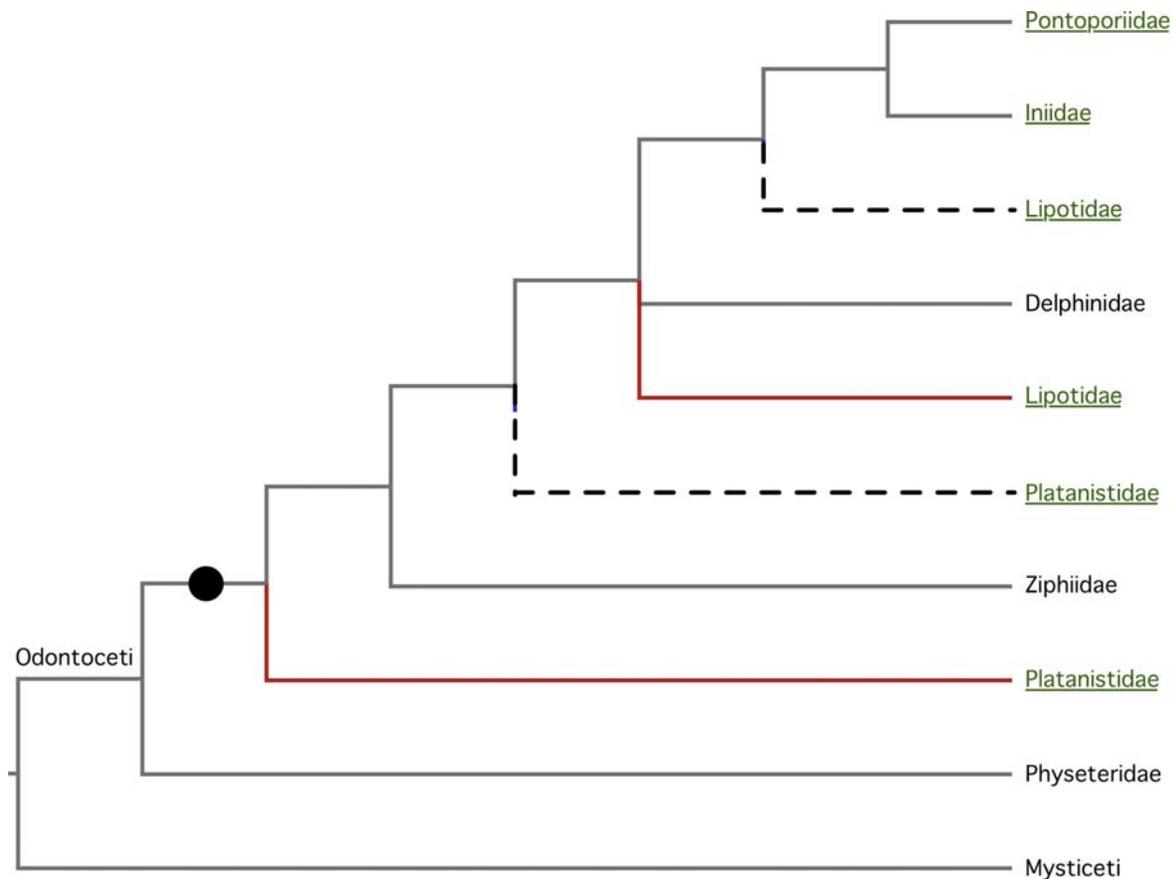


Figure 1. Schematic phylogenetic tree depicting the different hypotheses discussed. Underlined family names correspond to river dolphins. Blue and red branches represent alternative positions in the tree, as postulated by Yan et al. (2005) and Xiong et al. (2009), respectively. The black solid circle marks the point of rapid cetacean radiation, discussed in detail in Xiong et al. (2009).

Efforts like those carried out by Xiong et al. have proven key in enhancing our understanding of phylogenetic relationships among cetaceans as well as the evolutionary processes behind them, and will undoubtedly influence the way we examine other complex phylogenetic issues in the future.

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