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Molecular Phylogenetics and Evolution xxx (2005) xxx–xxx

MOLECULAR
PHYLOGENETICS
AND
EVOLUTIONwww.elsevier.com/locate/ympev

Reply to Letter to the Editor

Response to Ulfur Arnason: where's the beef?

Arnason in response to “Phylogeny of mysticete whales based on mitochondrial and nuclear data” (Rychel et al., 2004) rightly points to previous studies, both nuclear (Adegoke et al., 1993; Arnason et al., 1992) and mitochondrial (Arnason et al., 1993; Arnason and Gullberg, 1994, 1996) that have investigated the phylogenetic relationships among mysticete whales. Indeed, all of these studies show the position of Eschrichtiidae (gray whales) to be non-basal. Importantly, however, none of these prior studies were able to show with a convincing level of support exactly where Eschrichtiidae belongs, and none of these studies were able to definitively place the other monotypic whale family Neobalaenidae. The omission of citation of the two earlier satellite DNA studies is an oversight. However, as in later studies, neither of these satellite DNA studies provided strong support for the definitive placement of Eschrichtiidae and Neobalaenidae, other than strongly supporting them in a clade that contains all mysticetes to the exclusion of balaenids. Also, this does not change the fact that between 1994 and 2004 the subject of mysticete whale phylogeny had been largely ignored, with most studies focused on higher-level cetacean phylogenetics. We are interested in the evolution of mysticete whales and this requires that we reconstruct a robust phylogeny that places all species, including those of the problematic monotypic Eschrichtiidae and Neobalaenidae, in the phylogeny with a greater level of confidence than has been attained in the handful of previous studies (most of which did not include all mysticete species).

Our mention of some studies (i.e., Gatesy, 1997; Shimamura et al., 1997), but not others (e.g., Irwin and Arnason, 1994; Ursing and Arnason, 1998), on the relationship between Hippopotamidae and Cetacea was intended only to emphasize that recent work on whale phylogenetics had been focused on this higher-level question (i.e., the origin of whales), showing further that completely resolving mysticete phylogenetic relationships has not been emphasized.

Arnason criticizes our study by stating that we did not comment on “some striking discrepancies” between

the phylogenies resulting from analyses of the combined data (Fig. 1; mtDNA relationships identical) and the α -lactalbumin data (Fig. 2). However, Arnason did not explicitly state what these “striking discrepancies” are that we should have commented on. Yes, there are differences between the combined/mtDNA and nuclear phylogenies. The results of our reciprocal SH-tests indicated that there was significant incongruence between the combined/mtDNA and nuclear DNA phylogenies. The nature of such topology tests only tells us that significant incongruence exists, but not what specific alternate relationships are causing the significant incongruence. Examination of the estimated clade support values (i.e., bootstraps and posterior probabilities) revealed that all but one of the handful of differences between the two phylogenies were only weakly supported incongruencies (i.e., could not rule out the possibility that the differences were only the result of random error within one or both analyses). Thus, we felt it was not necessary (nor warranted) to direct attention to these few weakly supported incongruent relationships. However, we did explicitly comment on the single instance of strongly supported incongruence between the two phylogenies (i.e., likely the main contributors to the significant results in the SH-tests) and this strong incongruence is restricted to alternate placements of the fin whale and humpback within the Balaenopteridae/Eschrichtiidae clade. Whatever other “striking discrepancies” Arnason perceives must be based only on comparison of the topologies alone, without any explicit testing of alternate topologies.

With regard to our speculation on the position of *Balaenoptera omurai* we did not intend to imply that Wada et al. (2003) did not support their claim with morphological and molecular data. We do find problems with their methods. First, using only a mitochondrial dataset (control region) does not rule out the possibility that this new species is a hybrid. Furthermore, their study left out several mysticete species, including the balaenopterid humpback whale (*Megaptera novaeangliae*), the eschrichtiid gray whale (*Eschrichtius robustus*), the balaenids bowhead (*Balaena mysticetus*) and Southern right whale (*Eubalaena australis*), and neobalaenid pygmy right whale (*Neo-*

balaena marginata). Reliable and consistent systematic conclusions should be based on taxon and character inclusivity rather than subsampling of taxa and characters which has in the past mislead phylogenetic results, including those among cetaceans (O'Leary et al., 2004).

Finally, we acknowledge the importance of including citations of relevant previous work on mysticete phylogenetics but we argue that weakly supported phylogenetic results and methodological inconsistencies among previously reported studies have caused far more serious problems in our attempts to resolve the phylogenetic relationships among mysticetes.

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