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FORUM

Comments on Allard and Carpenter (1996), or the "Aquatic Ape" Hypothesis Revisited

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The results of Allard and Carpenter's (*Cladistics* 12, 183–198, 1996) paper on weighting and congruence among mammalian mitochondrial genes are an artefact of errors in their data matrix; their "blue whale" ATPASE8 sequence is human, the actual blue whale sequence is assigned to the grey seal, and the "horse" sequence is that of the harbor seal. When these errors are corrected there is no evidence that the mitochondrial genes are incongruent. © 1999 The Willi Hennig Society

In a recent paper in this journal, Allard and Carpenter (1996) compared cladograms for 14 mammal species generated from 13 protein coding genes from the mitochondrial genome. Thier initial expectation, shared by other studies of congruence among mitochondrial DNA gene sequences (Cao *et al.*, 1994; Cummings *et al.*, 1995; Zardoya and Meyer, 1996), was that the different genes should support the same, or at least very similar, trees. Instead, they reported significant incongruence between trees from different genes. While most of the trees are similar, three trees (their D, E, and W) stand well apart from the rest (Fig. 1a). These trees were all generated from the ATPASE8 gene and have the striking feature of placing the blue whale within the primates as the sister taxon to humans (Fig. 1b)! This novel finding goes completely unremarked by the authors. In addition, the two seals are widely separated (one groups with the fin whale) despite their being sister taxa in every other tree. Inspection of the data file they assembled (which we downloaded from EMBL) shows that this result is not a printer's error in the figure but is due to errors in that data file—the "blue whale" ATPASE8 sequence is identical to the human sequence; the actual blue whale sequence is present—labeled as being from the grey seal—and the "horse" sequence is that of the harbor seal.

These errors clearly result from cut-and-paste errors in assembling the data file and would be little more than amusing (if not embarrassing) were it not for the fact that the authors' conclusion—that the mitochondrial genes are incongruent—is entirely dependent on their having the wrong ATPASE8 sequences for three taxa. We repeated the authors' test for incongruence among the 13 genes using the character partition test implemented in PAUP* (Swofford, in preparation). For

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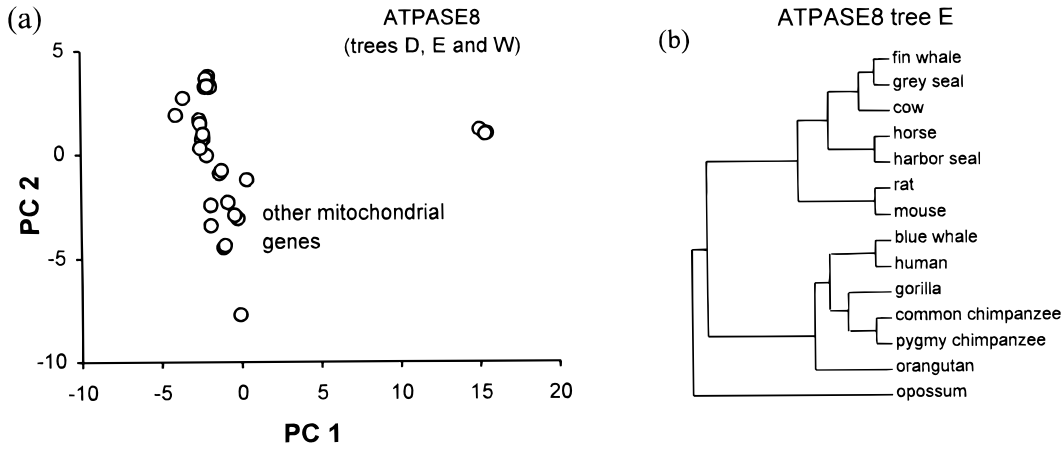

FIG. 1. (a) Principal coordinate ordination of the pairwise partition distances among the 29 trees computed from 13 mitochondrial DNA sequence shown in Allard and Carpenter's (1996) Fig. 2. The three trees obtained for ATPASE8 are very different from those for the other mitochondrial genes. (b) Allard and Carpenter's tree E for ATPASE8. Note the grouping of the human and blue whale sequences, the position of the fin whale, and the relative position of the two seal sequences.

each test we conducted 100 replications. When we use this test on Allard and Carpenter's original data file, the 13 genes are incongruent ($P = 0.01$). However, if we remove the partition corresponding to the ATPASE8 sequences and repeat the test on the 12 remaining genes, then there is no significant incongruence ($P = 0.41$). Repeating the test with the actual blue whale, grey seal, and horse ATPASE8 sequences, we also find no evidence for incongruence ($P = 0.37$). As might be expected from looking at the trees themselves (Fig. 1), this gene (or rather the incorrect sequences for this gene) is the sole reason Allard and Carpenter thought they had found evidence for incongruence.

We find it disconcerting that so blatant an error as accepting trees that group the blue whale with humans and not with its congener the fin whale went completely unnoticed in a paper on congruence, i.e., specifically concerned with the agreement among data sets and their trees. Perhaps this illustrates one potentially serious weakness of the "simultaneous analysis" approach the authors advocate. Had the authors paid more attention to the results of the analyses of the individual genes, they might have detected the typographical errors in their data file, upon which their entire analysis depends.

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