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Deciphering River Dolphin Evolution

In "river dolphins add branches to family tree" (News of the Week, 30 Mar., p. 2531), Dennis Normile discusses the molecular work of M. Nikaido and colleagues that indicates that river dolphins are old cetacean lineages that do not constitute a natural (that is, monophyletic) group (1). Nikaido *et al.* analyzed the insertion patterns for short interspersed elements (SINEs), which are transfer RNA-derived retroposons inserted throughout the genome, probably at random locations.

Although it was not mentioned by Normile, we published the same conclusions based on different molecular analyses more than 8 months earlier (2). Using phylogenetic analyses of nucleotide sequences from three mitochondrial and two nuclear genes (from 19 cetacean species, including all river dolphins), we demonstrated with statistical significance that extant river dolphins form a polyphyletic group. We suggested that they are relict species whose adaptation to riverine habitats incidentally ensured their survival against major environmental changes in the marine ecosystem or the emergence of Delphinidae (true dolphins). A few months later, Hamilton *et al.* (3) published an analysis of three fragments of the mitochondrial genome (from 29 cetacean species), confirming our results.

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References and Notes

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2. I. Cassens *et al.*, *Proc. Natl. Acad. Sci. U.S.A.* **97**, 11343 (2000).

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3. H. Hamilton, S. Caballero, A. G. Collins, R. L. Brownell, *Proc. R. Soc. London B Biol. Sci.* **268**, 549 (2001).

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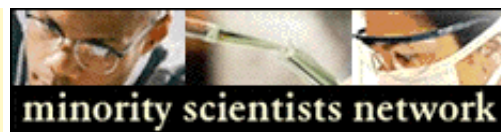
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