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1: J Mol Evol 1997;44 Suppl 1:S98-116

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Phylogenetic reconstruction of the Felidae using 16S rRNA and NADH-5 mitochondrial genes.

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The Felidae family represents a challenge for molecular phylogenetic reconstruction because it consists of 38 living species that evolved from a relatively recent common ancestor (10-15 million years ago). We have determined mitochondrial DNA sequences from two genes that evolve at relatively rapid evolutionary rates, 16S rRNA (379 bp) and NADH dehydrogenase subunit 5 (NADH-5, 318 bp), from multiple individuals of 35 species. Based on separate and combined gene analyses using minimum evolution, maximum parsimony, and maximum likelihood phylogenetic methods, we recognized eight significant clusters or species clades that likely reflect separate monophyletic evolutionary radiations in the history of this family. The clusters include (1) ocelot lineage, (2) domestic cat lineage, (3) Panthera genus, (4) puma group, (5) Lynx genus, (6) Asian leopard cat group, (7) caracal group, and (8) bay cat group. The results confirm and extend previously hypothesized associations in most cases, but in others, e.g., the bay cat group, suggest novel phylogenetic relationships. The results are compared and evaluated with molecular, cytogenetic, and morphological data to derive a phylogenetic synthesis of field evolutionary history.

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