

Patterns of macroevolution among Primates inferred from a supermatrix of mitochondrial and nuclear DNA

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Abstract

Here, we present a new primate phylogeny inferred from molecular supermatrix analyses of size 42 kb containing 70% of missing data, and representing 75% of primate species diversity. The supermatrix was analysed using a gene-partitioned maximum likelihood approach to obtain an exhaustive molecular phylogenetic framework. All clades recovered from recent molecular works were upheld in our analyses demonstrating that the presence of missing data did not bias our supermatrix inference. The resulting phylogenetic tree was subsequently dated with a molecular dating method to provide a timescale for speciation events. Results obtained from our relaxed molecular clock analyses concurred with previous works based on the same fossil constraints. The resulting dated tree allowed to infer of macroevolutionary processes among the primates. Shifts in diversification rate and speciation rates were determined using the SymmeTREE method and a birthdeath process. No significant asymmetry was detected for the primate clade, but significant shifts in diversification rate were

identified for seven clades: Anthroidea, Lemuriformes, Lemuridae, Galagidae, *Callithrix* genus, the Cercopithecoidea and Asian *Macaca*. Comparisons with previous primate supertree results reveal that (i) there was a diversification event at the root of the Lemuriformes, (ii) a higher diversification rate is detected for Cercopithecoidea and Anthroidea and (iii) a shift in diversification is always recovered for *Macaca* genus. Macroevolutionary inferences and primate divergence dates show that major primate diversification events occurred after the Paleogene, suggesting the extinction of ancient primate lineages.

Keywords: Supermatrix; Primate; Phylogeny; Molecular dating; Macroevolution; Diversification