

DATING THE PRIMATE TREE: NEW INSIGHTS ON PRIMATE ORIGINS FROM COMPLETE MITOCHONDRIAL GENOMES.

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The origins and the divergence times of the most basal lineages within primates have been difficult to resolve, due to incomplete sampling of early fossil taxa and to the relatively short window of time in which major lineages diverged from each other. The main source of contention is related to the discordance between molecular and fossil estimates: while there are no crown primate fossils older than 55Ma, many molecule-based estimates extended the origins of crown primates over 80Ma. Here we present a phylogenetic analysis of 49 complete mitochondrial genomes representing all primate families and including 36 species within mammals. Phylogenetic analyses were conducted on different data sets (including protein-coding genes, tRNAs and rRNAs). An exploratory approach to calibrating evolutionary rates using two alternative Bayesian dating methods (BEAST and MultiDivTime) has been employed to account for calibration uncertainty. In contrast with previous mitogenomic studies, our results support primate monophyly and the position of tarsiers as sister group of Anthroproidea, with the exclusion of flying lemurs. Using recommended fossil calibration points throughout and outside of primates, we recalculated evolutionary timescales for primates. Our dating results support a long fuse model of evolution for primates, with an origin in the Late Cretaceous (68-71Ma), and the radiation of all major lineages just after the K/T boundary, in the early Tertiary (61-65Ma). We conclude that though a difference between the fossil record and molecular estimates still exists, the approach presented here may help to resolve this discordance for divergence date estimates in primate evolution.

Keywords: phylogenetics, molecular clock, mitogenomics, molecular dating