

DATING PRIMATE ORIGINS: INTEGRATING GENETIC AND FOSSIL DATA

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This work estimates the origin of primates through an analysis of molecular and paleontological data. Paleontological and molecular approaches have yielded conflicting dates for the origin of “crown” primates. A “crown” group consists of an extant group of organisms and all of their ancestors, including their last common ancestor. Crown primates include the ancestors of all living primates. Most molecular clock studies suggest crown primates have their origins before the KT boundary, while a direct reading of paleontological data suggests a more recent origin. Although these are often portrayed as conflicting viewpoints, it is preferable to recognize the interdependence of molecular and morphological data in the estimation of divergence dates. Furthermore, paleontological sampling models can be consistent with a Cretaceous origin for crown primates. Using a set of novel models for fossil calibration, divergence dates throughout primates are estimated for a large dataset of nuclear and mitochondrial data, including the origin of primates. These calibration models include those that integrate complex probabilistic sampling regimes from paleontological sampling data, and ‘soft bounds,’ which allow estimates to extend beyond calibration bounds. Using different analyses, primate origins are examined from both a maximally and minimally precise perspective rooted in both molecular and fossil evidence. The precision of molecular divergence estimates has important ramifications for testing among different models of primate origins and offering statistical evaluation of the different evolutionary scenarios.

Keywords: molecular clock, divergence dating, Bayesian, DNA sequence