

**WHAT CAN PHYLOGENETIC STUDIES TELL US ABOUT EARLY PRIMATE EVOLUTION?**

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With the growth of molecular technology, the use of morphological data in phylogenies has slipped from favor. However, analyzed in combination with molecular data, well-chosen morphological characters can act to strengthen the historical signal in molecular data, particularly at depths where the molecular signal becomes ambiguous. We present the results of a Bayesian analysis of 3543 mtDNA bp and 42 multistate morphological characters to investigate inconsistencies in strepsirhine phylogenetic models. Our analysis provides a well-supported tree, with most branches having 90-100% support. It also gives four Malagasy strepsirhine families, not five. Our use of morphological characters allows us to trace the evolution of key adaptive character suites during the radiation of this group, with a view to reconstructing their ancestral states. Body size, hind limb proportions and locomotor adaptations, basicranial flexion, dietary adaptation, and activity rhythm all show reiterative evolution in several strepsirhine lineages, complicating ancestral reconstructions. We present a reconstruction of the clade ancestor using phylogenetically independent contrasts, which contradicts the common perceptions of the model strepsirhine ancestor.

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