

## **Pinpointing the Root of Extant Eukaryotic Diversity**

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Determining the root of the eukaryotic tree is of crucial importance to determine the sequence of events at the earliest stages of eukaryotic evolution. Recent studies of mitochondrion-derived genes have suggested that the root may fall between unikonts and bikonts, whereas a gene family evolutionary analysis indicated that the root may fall between excavates and other supergroups. However, deep level analyses like these are plagued with artefacts and the historical signal versus systematic error in rooted phylogenomic analyses of eukaryotes have not been comprehensively examined.

We have addressed this question by carefully selecting and analyzing two classes of eukaryotic genes that can be outgroup rooted: genes whose closest orthologs are from the Archaea; and genes of potential mitochondrial origin, where alpha-proteobacterial homologues can be used as the outgroup.

Orthologs from a large sample (~170) of eukaryotes from all supergroups, including many novel deep-branching ‘orphan’ lineages, were assembled for each gene. Sophisticated phylogenetic methods, exploratory data analysis and ‘robustness’ procedures were used to determine support for alternative eukaryotic root positions.