

Rooting the eukaryotic radiation with new models of genome evolution.

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The deep relationships among the main lineages of eukaryotes, and in particular the root of the eukaryotic tree, remain debated. Two main rooting hypotheses are actively discussed. The first is the Unikont/Bikont hypothesis (UB), which places the root between the Unikonts, including Metazoa, Fungi, Amoebozoa and some related protist lineages, and the bikonts, i.e. all the other lineages, including the Archaeplastida and a large diversity of unicellular eukaryotes. The second hypothesis, Neozoan/Excavate (NE), proposes the root to be between the excavates, a very diverse group of protists, and all the other eukaryotes. Aside of these two main hypotheses, various positions have been proposed over the years and had not been dismissed, letting the early relationship among eukaryotes an open question. Each of these hypotheses has major implications for the nature of the last eukaryotic common ancestor (LECA), was it a complex organism with a rich gene content, or are the main feature of the different groups would have appeared along the evolution of each specific lineages? In order to solve this fundamental evolutionary question, we are exploring the use of concatenation, multispecies coalescent, and recently-developed approaches to gene tree-species tree reconciliation that allow species trees to be rooted without an outgroup. Our analyses make use of a broadly-sampled dataset of 98 complete genomes and largely-complete transcriptomes of Eukaryotes, including recently described or sequenced lineages such as the 'CRuMs' and *Ancoracysta twista*. We present ongoing work on the topology and root of the eukaryotic tree and the metabolic capabilities of the last eukaryotic common ancestor.