

Evidence for a New Root of the Tree of Life

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A new root of the tree of life is providing evidence for a last common ancestor that is very different from the traditional one. This root provides a new perspective on the habitats of early life, including the evolution of methanogenesis, membranes, and thermophily; and the speciation of major prokaryotic taxa.

Using **indels**, insertions and deletions, within **paralogous genes** our laboratory has obtained evidence for a new root to the tree of life in a series of recent papers (Lake et al., 2007; Servin et al., 2008; Skophammer et al., 2006; Skophammer et al., 2007). Through the analysis of indels present in 17 genes and their paralogous **outgroups** involved in diverse functions, including protein synthesis, DNA synthesis, heat shock responses, and nucleotide and amino acid synthesis, the root has been localized to a eubacterial branch of the tree between the **clade** consisting of the **Actinobacteria** and the double membrane (Gram negative) prokaryotes and the clade consisting of the Archaea and the **Firmicutes**.

Since these results, summarized in the figure, exclude the root from the archaeal- firmicute-clade, methanogenesis is excluded as a primitive prokaryotic metabolism. Mapping the phylogenetic distributions of genes involved in **peptidoglycan**- and lipid-synthesis onto this rooted tree implies that the ether archaeal lipids are not primitive, and that the ancestral prokaryotic population consisted of organisms enclosed by a single, ester-linked lipid membrane, covered by a peptidoglycan layer. These results explain the similarities previously noted by others between the pathways of lipid synthesis in Bacteria and Archaea (Boucher et al., 2004). Our results also imply that the last common ancestor was not hyperthermophilic, although moderate thermophily cannot be excluded, consistent with the results of others (Galtier et al., 1999; Miller and Lazcano, 1995; Philippe and Forterre, 1999).

References:

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Definitions:

- Indel** – deletion or insertion of a single DNA base in a gene. Usually, it leads to a “frameshift” mutation in reading mRNA.
- paralogous genes** - if a gene in an organism is duplicated to occupy two different positions in the same genome, then the two copies are paralogous.
- Outgroup** – if three or more groups of organisms are compared, and all but one of them are more closely related to each other than any single one of them is to the last, the latter group is known as the **outgroup**. The evolutionary conclusion from this is that the outgroup branched from the parent group before the other two groups branched from each other.
- Clade** - a taxonomic group comprising a single common ancestor and all the descendants of that ancestor.
- Actinobacteria** - a group of Gram-positive bacteria with high G+C ratio.
- Firmicutes** - a division of bacteria, most of which have Gram-positive cell wall structure. It includes bacilli, clostridia and mollicutes.
- peptidoglycan** - a polymer consisting of sugars and amino acids that forms a mesh-like layer outside the plasma membrane of Bacteria.