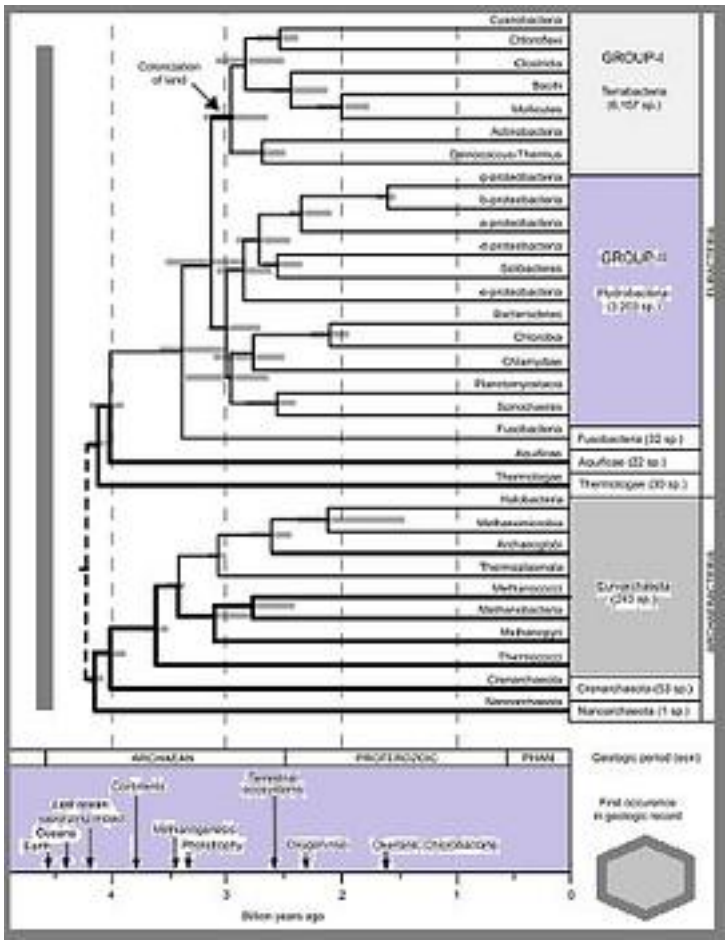
A Major Clade of Prokaryotes with Ancient Adaptations to Life on Land



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Evolutionary trees of prokaryotes usually define the known classes and phyla but less

often agree on the relationships among those groups. This has been attributed to the effects of horizontal gene transfer, biases in sequence change, and large evolutionary distances. Furthermore, higher level clades of prokaryote phyla rarely are supported by information from ecology and cell biology. Nonetheless, common patterns are beginning to emerge as larger numbers of species are analyzed with sophisticated methods. Here, we show how combined evidence from phylogenetic, cytological, and environmental data support the existence of an evolutionary group that appears to have had a common ancestor on land early in Earth's history and includes two-thirds of known prokaryote species. Members of this terrestrial clade (Terrabacteria), which includes Cyanobacteria, the gram-positive phyla (Actinobacteria and Firmicutes), and two phyla with cell walls that differ structurally from typical gram-positive and gram-negative phyla (Chloroflexi and Deinococcus–Thermus), possess important adaptations such as resistance to environmental hazards (e.g., desiccation, ultraviolet radiation, and high salinity) and oxygenic photosynthesis. Moreover, the unique properties of the cell wall in gram-positive taxa, which likely evolved in response to terrestrial conditions, have contributed toward pathogenicity in many species. These results now leave open the possibility that terrestrial adaptations may have played a larger role in prokaryote evolution than currently understood.

作者介绍:

目录:

标签

演化生物学

微生物学

古生物学

分子生物学

评论

* 31.8亿年: Terrabacteria-Hydrobacteria分裂; * 18亿年, Anoxic-Canifield:

GBS(FCB-Chlorobia), PBS(G-Proetobacteria, 北澳McArthur Basin);

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