Evolution of sterol biosynthesis from bacteria to eukaryotes

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Isoprenoids (or terpenoids) represent one of the largest groups of organic compounds in nature and are distributed universally in the three domains of life. Understanding the evolutionary history of isoprenoid biosynthesis in each domain of life is critical since isoprenoids are deeply interwoven in the architecture of life and thus would have had indispensable roles in the early evolution of life. Among isoprenoids, sterols are universally found in eukaryotic membranes used to regulate cell rigidity and fluidity, and are characteristic of the eukaryotic domain. However, sterols have recently been discovered in multiple bacterial phyla. The evolutionary relationship of bacterial sterols to eukaryotic ones could be a key to decipher the evolutionary trajectory towards eukaryogensis.

Our current study provides a comprehensive phylogenetic analysis of enzymes involved in the two major parts of isoprenoid biosynthesis: 1) from acetyl-CoA to isoprenyl diphosphate, and 2) from farnesyl diphosphate to sterol. In the first part, bacteria and eukaryotes are known to possess a distinct biosynthesis pathway, respectively. However, some bacteria do possess the eukaryotic-type pathway (mevalonate pathway). Among these bacteria, δ-proteobacteria are the only bacterial taxa that produce sterols similar to eukaryotes. Further, δ-proteobacteria always cluster next to the eukaryotic clade in the isoprenoid enzyme trees. Hence, δ-proteobacteria and eukaryotes are inferred to share a common ancestor for isoprenoid biosynthesis. Its implication for the emergence of the eukaryotic domain and for the interpretation of Precambrian biosignatures will be discussed.