

Parallel adaptations to high temperatures in the Archaean eon

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Fossils of organisms dating from the origin and diversification of cellular life are scant and difficult to interpret, for this reason alternative means to investigate the ecology of the last universal common ancestor (LUCA) and of the ancestors of the three domains of life are of great scientific value. It was recently recognized that the effects of temperature on ancestral organisms left 'genetic footprints' that could be uncovered in extant genomes. Accordingly, analyses of resurrected proteins predicted that the bacterial ancestor was thermophilic and that Bacteria subsequently adapted to lower temperatures. As the archaeal ancestor is also thought to have been thermophilic, the LUCA was parsimoniously inferred as thermophilic too. However, an analysis of ribosomal RNAs supported the hypothesis of a non-hyperthermophilic LUCA. Here we show that both rRNA and protein sequences analysed with advanced, realistic models of molecular evolution provide independent support for two environmental-temperature-related phases during the evolutionary history of the tree of life. In the first period, thermotolerance increased from a mesophilic LUCA to thermophilic ancestors of Bacteria and of Archaea-Eukaryota; in the second period, it decreased. Therefore, the two lineages descending from the LUCA and leading to the ancestors of Bacteria and Archaea-Eukaryota convergently adapted to high temperatures, possibly in response to a climate change of the early Earth, and/or aided by the transition from an RNA genome in the LUCA to organisms with more thermostable DNA genomes. This analysis unifies apparently contradictory results into a coherent depiction of the evolution of an ecological trait over the entire tree of life.

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