

# Study supports distant relationship between Archaea and Bacteria in tree of life

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Scientists have found further evidence to support the idea that the primary two domains of life, the Archaea and Bacteria, are separated by a long phylogenetic tree branch and therefore distantly related. The

findings are reported in a study published today in *eLife*.

The analysis, by researchers at the University of Bristol and internationally, adds to an ongoing debate about how much the archaeal domain diverges from the bacterial domain and shines a light on the limitations of conventional methods for estimating the evolutionary path of ancient organisms.

Together with Bacteria and Eukarya, the Archaea make up the three domains of the tree of life. Originally, it was thought that Archaea were a type of Bacteria, typified by their ability to live in extreme environments. But the use of molecular data to reconstruct phylogenetic trees and advances in [genetic sequencing](#) have transformed our understanding of the diversity of these organisms and their relationship with Bacteria and Eukarya.

In the tree of life, a long branch length between organisms corresponds to a greater degree of genetic change. Researchers studying the evolutionary history of the Archaea and Bacteria have estimated branch length by studying differences between a core set of essential genes encoding cellular machinery involved in producing proteins and processing genetic information. But recently, researchers used an expanded set of genetic markers from Bacteria and Archaea to estimate the genetic distance between the two domains and proposed a much shorter branch length—that is, that the two domains were more closely related.

"This [recent work](#) raised two important issues regarding estimates about the universal tree of life," explained first author Edmund Moody, a Ph.D. candidate at Bristol's School of Biological Sciences. "First, that estimates of the genetic distance between Archaea and Bacteria from the classic 'core genes' may not be representative of ancient genomes as a whole and, second, that there may be many more suitable genes to

investigate early evolutionary history than previously realized, which could improve the precision and accuracy of these estimates."

To investigate these issues, Mr Moody and colleagues examined the evolutionary history of the expanded 381 gene [marker](#) set, and re-evaluated marker gene sets used in previous analyses. They found several features of the expanded marker set, such as inter-domain gene transfers and paralogous genes—which are genes that have evolved by duplication and that code for proteins with similar but not identical functions. "Our data suggests that the inclusion of marker genes with such features could artificially shorten the branch that separates the archaeal and bacterial domains," said co-author Tara Mahendrarajah, a Ph.D. candidate at NIOZ, Netherlands.

Traditionally used gene marker sets include genes for many proteins that make up the ribosome—the cell's machinery for translating DNA. It had been suggested that if ribosome proteins experienced an accelerated period of evolution at any point, it might lead to an artifactually long phylogenetic tree branch. So, the team compared a set of ribosomal and non-ribosomal gene markers to produce an estimate of branch length and found it to be similar.

Co-senior author Anja Spang, Senior Scientist at NIOZ, said: "These results did not support the hypothesis that ribosomal proteins evolved any faster than non-ribosomal genes, and affirm that ribosomal proteins are useful markers for phylogeny. However, the analyses suggested that both the true Archaea-Bacteria [branch](#) length and diversity of Archaea may be underestimated even by the best current models."

"The debate around these issues really speaks to more general limitations of the current models: for example, it is clearly unsatisfactory to base our view of early evolution or genetic diversity on a small set of [genes](#)," added co-senior author Tom Williams, Associate Professor in Molecular

Evolution at Bristol's School of Biological Sciences. "Exploring the evolutionary signal in more of the genome than we have been able to previously is an important goal that previous studies have approached in different ways. Our work suggests that new methods, including more realistic models of gene duplication, transfer and loss, could help resolve some of the differing views by enabling genome-wide estimates of evolution while accounting for the varying evolutionary histories of individual gene families."

**More information:** Edmund RR Moody et al, An estimate of the deepest branches of the tree of life from ancient vertically-evolving genes, *eLife* (2022). [DOI: 10.7554/eLife.66695](https://doi.org/10.7554/eLife.66695)

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