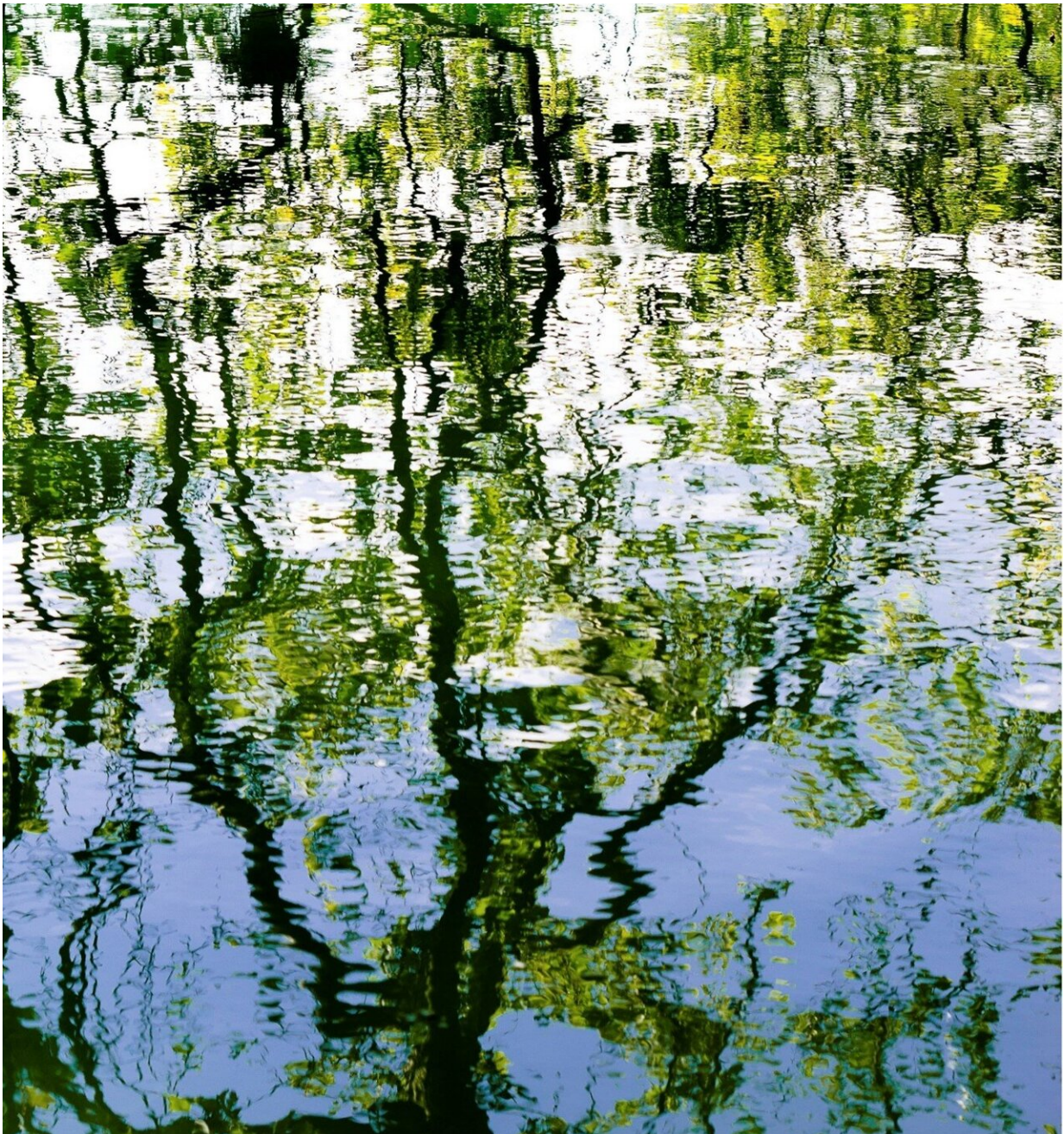


Rooted tree key to understanding bacterial evolution, new study suggests

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Gene transfers (movement of genes between bacterial lineages) have hampered traditional efforts to study bacterial evolution in deep time. Coleman et al. used a new method that combines the vertical and horizontal components of bacterial evolution to draw inferences about the the nature of the earliest Bacteria and the deepest divides in the bacterial tree. Credit: Gergely J. Szöllősi

The findings, published in the journal *Science* today, demonstrate how integrating vertical descent and horizontal gene transfer can be used to infer the root of the bacterial tree and the nature of the last bacterial common ancestor.

Bacteria comprise a very diverse domain of single-celled organisms that can be found almost everywhere on Earth. All Bacteria are related and derive from a common ancestral Bacterial cell. Until now, the shape of the bacterial tree of life and the placement of its root has been contested, but is necessary to shed light on the early [evolution](#) of life on our planet.

Just as in plants and animals, the genomes of Bacteria are home to many different [genes](#). However, Bacterial genes are not only inherited vertically from mother to daughter, but are also frequently exchanged horizontally between potentially distant family members. Amongst its many functions, horizontal gene sharing drives the rapid spread of antibiotic resistance amongst pathogenic Bacteria.

The combination of vertical and horizontal ancestry complicates how we think about evolutionary relationships among Bacteria, with the former best represented as a tree and the latter as a network. The team used phylogenetic methods that simultaneously consider the vertical and horizontal transmission of genes and found that, on average, genes travel

vertically two-thirds of the time, suggesting that a tree provides a meaningful framework for interpreting bacterial evolution.

Co-author Phil Hugenholtz, at the University of Queensland, Australia, noted: "For years, vertical and horizontal evolution have been seen as adversaries with researchers often falling into the tree or network camp. Here we show that they can be investigated together to address some of the most vexing questions in early evolution."

"Overlaying the horizontal movement of genes onto the vertical "species" tree allowed us to identify the most likely root of the tree and the gene content of the last bacterial common ancestor (LBCA)." explains co-author Gergely Szöllősi, at Eötvös Loránd University, Hungary.

The analysis predicts a root between two major clades, the Terrabacteria (mostly Bacteria with single-membranes such as Bacillus) and the Gracilicutes (mostly Bacteria with a double-membrane such as E. coli). This contrasts with recent proposals placing the Candidate Phyla Radiation (CPR) at the base of the tree. CPR are unusual ultrasmall Bacteria reliant on other host cells for survival.

"Our analyses suggested that the CPR are members of the Terrabacteria and sister to the free-living Chloroflexota meaning that the host dependency of CPR Bacteria is a derived rather than ancestral characteristic" said co-author Anja Spang, at The Royal Netherlands Institute for Sea Research (NIOZ) in the Netherlands.

The authors predict that LBCA was more complex than previously thought, having a double-membraned cell that was able to swim, sense its environment, and defend itself against viruses.

Dr. Williams explained: "Bacteria can have one or two cell membranes,

and one of the big questions in early evolution is how these two kinds of cells are related to each other. Our analysis suggests that the common ancestor of all living Bacteria already had two membranes, so the question now is how apparently simpler single-membrane cells evolved from double-membraned [cells](#), and how many times this has occurred during evolution. We believe that our approach to integrating vertical and horizontal gene transmission holds promise for answering this and many other open questions in evolutionary biology."

More information: "A rooted phylogeny resolves early bacterial evolution" *Science* (2021). [science.sciencemag.org/cgi/doi ... 1126/science.abe0511](https://science.sciencemag.org/cgi/doi/10.1126/science.abe0511)

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