

Wealth of unsuspected new microbes expands tree of life

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This is a new and expanded view of the tree of life, with clusters of bacteria (left), uncultivable bacteria called 'candidate phyla radiation' (center, purple) and, at lower right, the Archaea and eukaryotes (green), including humans. Credit: Zosia Rostomian, Lawrence Berkeley National Laboratory

The tree of life, which depicts how life has evolved and diversified on the planet, is getting a lot more complicated.

Researchers at the University of California, Berkeley, who have discovered more than 1,000 new types of [bacteria](#) and Archaea over the past 15 years lurking in Earth's nooks and crannies, have dramatically rejiggered the tree to account for these microscopic new [life](#) forms.

"The tree of life is one of the most important organizing principles in biology," said Jill Banfield, a UC Berkeley professor of earth and planetary science and environmental science, policy and management. "The new depiction will be of use not only to biologists who study microbial ecology, but also biochemists searching for novel genes and researchers studying evolution and earth history."

Much of this microbial diversity remained hidden until the genome revolution allowed researchers like Banfield to search directly for their genomes in the environment, rather than trying to culture them in a lab dish. Many of the microbes cannot be isolated and cultured because they cannot live on their own: they must beg, borrow or steal stuff from other animals or microbes, either as parasites, symbiotic [organisms](#) or scavengers.

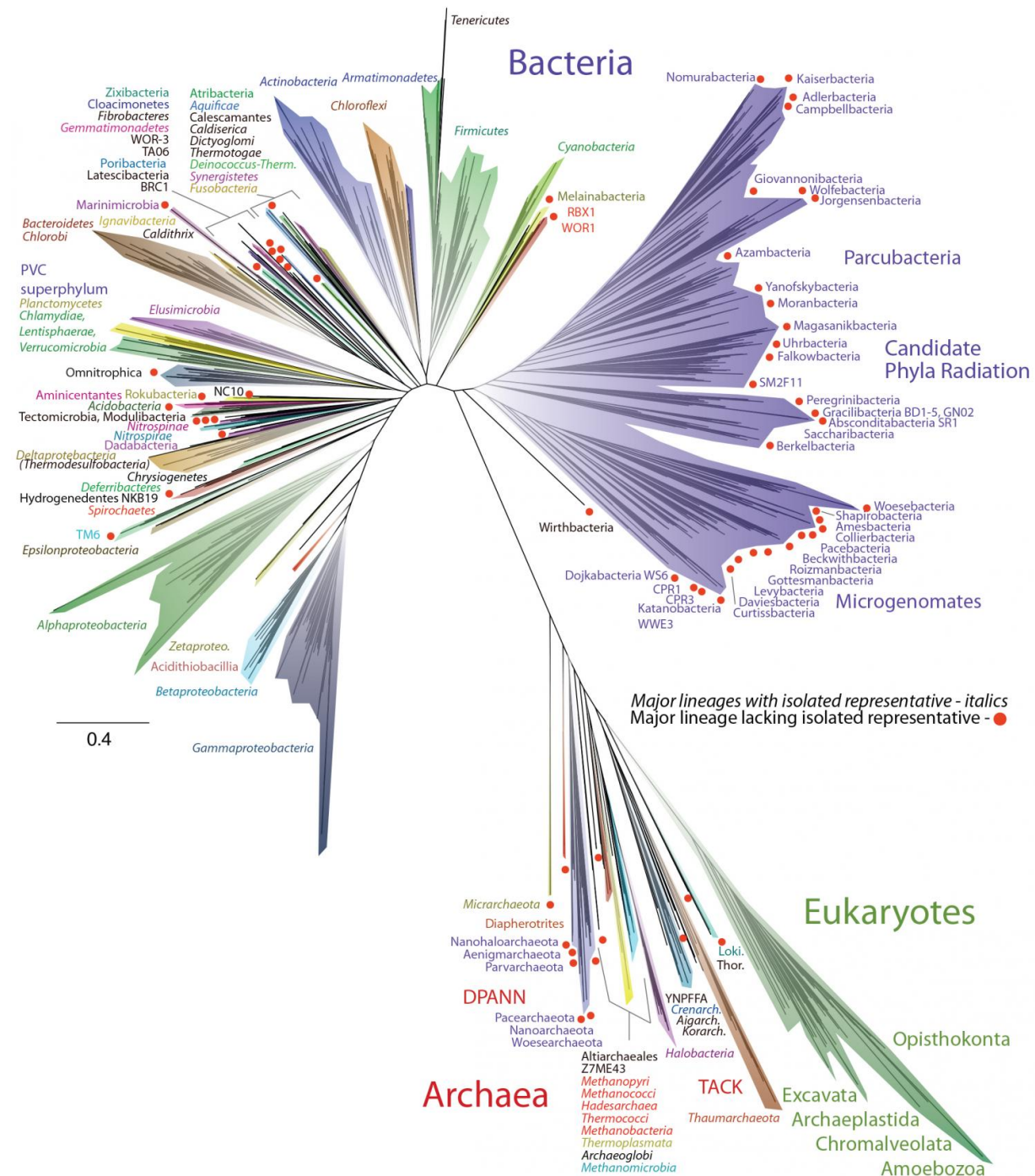
The new tree, to be published online April 11 in the new journal *Nature Microbiology*, reinforces once again that the life we see around us - plants, animals, humans and other so-called eukaryotes - represent a tiny percentage of the world's biodiversity.

"Bacteria and Archaea from major lineages completely lacking isolated representatives comprise the majority of life's diversity," said Banfield, who also has an appointment at Lawrence Berkeley National Laboratory. "This is the first three-domain genome-based tree to incorporate these uncultivable organisms, and it reveals the vast scope of as yet little-

known lineages."

According to first author Laura Hug, a former UC Berkeley postdoctoral fellow who is now on the biology faculty at the University of Waterloo in Ontario, Canada, the more than 1,000 newly reported organisms appearing on the revised tree are from a range of environments, including a hot spring in Yellowstone National Park, a salt flat in Chile's Atacama desert, terrestrial and wetland sediments, a sparkling water geyser, meadow soil and the inside of a dolphin's mouth. All of these newly recognized organisms are known only from their genomes.

"What became really apparent on the tree is that so much of the diversity is coming from lineages for which we really only have genome sequences," she said. "We don't have laboratory access to them, we have only their blueprints and their metabolic potential from their genome sequences. This is telling, in terms of how we think about the diversity of life on Earth, and what we think we know about microbiology."



This is an expanded view of the tree of life, showing that bacteria make up two-thirds of all Earth's biodiversity, half of that from uncultivable bacteria called 'candidate phyla radiation.' The Archaea and eukaryotes, which includes humans, makes up another third. The red dots represent lineages that cannot, at present, be isolated and grown in the lab. Credit: Jill Banfield, UC Berkeley, and Laura

Hug, University of Waterloo.

One striking aspect of the new tree of life is that a group of bacteria described as the "candidate phyla radiation" forms a very major branch. Only recognized recently, and seemingly comprised only of bacteria with symbiotic lifestyles, the candidate phyla radiation now appears to contain around half of all bacterial evolutionary diversity.

While the relationship between Archaea and eukaryotes remains uncertain, it's clear that "this new rendering of the tree offers a new perspective on the history of life," Banfield said.

"This incredible diversity means that there are a mind-boggling number of organisms that we are just beginning to explore the inner workings of that could change our understanding of biology," said co-author Brett Baker, formerly of Banfield's UC Berkeley lab but now at the University of Texas, Austin, Marine Science Institute.

Tree depicts life we see today

Charles Darwin first sketched a tree of life in 1837 as he sought ways of showing how plants, animals and bacteria are related to one another. The idea took root in the 19th century, with the tips of the twigs representing life on Earth today, while the branches connecting them to the trunk implied evolutionary relationships among these creatures. A branch that divides into two twigs near the tips of the tree implies that these organisms have a recent common ancestor, while a forking branch close to the trunk implies an evolutionary split in the distant past.

Archaea were first added in 1977 after work showing that they are distinctly different from bacteria, though they are single-celled like

bacteria. A tree published in 1990 by microbiologist Carl Woese was "a transformative visualization of the tree," Banfield said. With its three domains, it remains the most recognizable today.

With the increasing ease of DNA sequencing in the 2000s, Banfield and others began sequencing whole communities of organisms at once and picking out the individual groups based on their genes alone. This metagenomic sequencing revealed whole new groups of bacteria and Archaea, many of them from extreme environments, such as the toxic puddles in abandoned mines, the dirt under toxic waste sites and the human gut. Some of these had been detected before, but nothing was known about them because they wouldn't survive when isolated in a lab dish.

For the new paper, Banfield and Hug teamed up with more than a dozen other researchers who have sequenced new microbial species, gathering 1,011 previously unpublished genomes to add to already known genome sequences of organisms representing the major families of life on Earth.

She and her team constructed a tree based on 16 separate genes that code for proteins in the cellular machine called a ribosome, which translates RNA into proteins. They included a total of 3,083 organisms, one from each genus for which fully or almost fully sequenced genomes were available.

The analysis, representing the total diversity among all sequenced genomes, produced a tree with branches dominated by bacteria, especially by uncultivated bacteria. A second view of the tree grouped organisms by their evolutionary distance from one another rather than current taxonomic definitions, making clear that about one-third of all biodiversity comes from bacteria, one-third from uncultivable bacteria and a bit less than one-third from Archaea and eukaryotes.

"The two main take-home points I see in this tree are the prominence of major lineages that have no cultivable representatives, and the great diversity in the bacterial domain, most importantly, the prominence of candidate phyla radiation," Banfield said. "The candidate phyla radiation has as much diversity within it as the rest of the bacteria combined."

More information: *Nature Microbiology*, [DOI: 10.1038/nmicrobiol.2016.48](https://doi.org/10.1038/nmicrobiol.2016.48)

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