

# New bacteria found in human gut

October 2 2013, by Krishna Ramanujan

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(Medical Xpress)—Call it kin to blue-green algae. Cornell and University of California, Berkeley, researchers have identified a new bacteria found in groundwater and in mammalian guts – including those in humans.

The newly discovered Melainabacteria may play a role in digesting fiber; it is more abundant in herbivorous mammals and in people with plant-rich diets. The microbes also appear to add value to diets by synthesizing vitamins B and K for their hosts, according to research published in the journal *eLife* (Oct. 1). The scientists have sequenced the new [bacteria](#)'s genome and they describe the microbe's appearance and function based on genetic clues.

The human immune system recognizes specific sequences in the flagella of commensal and symbiotic bacteria, including Melainabacteria, offering evidence that the bugs are common gut residents.

Melainabacteria are close relatives of billion-year-old Cyanobacteria – often called blue-green algae – ancient photosynthesizing microbes that helped raise atmospheric oxygen in prehistoric eras, and likely led to early plant cells.

Only about a quarter of all bacteria can be cultured in the lab, so researchers look for a signature gene sequence – called 16S rRNA – to identify new types of bacteria. The human gut contains between 10 trillion and 100 trillion bacterial cells, and most of those fall into five different phyla, or lineages.

"We started picking up sequences [for Melainabacteria], but when we put them in context with other bacteria, they were on the branch of Cyanobacteria," said Ruth Ley, assistant professor of microbiology and a senior author of the study. Sara Di Rienzi, a postdoctoral researcher in Ley's lab, is co-lead author.

Melainabacteria belong on a common lineage with Cyanobacteria, but they diverged and do not photosynthesize, Ley said.

When scientists used computer programs to analyze genetic sequences of gut samples, the computers classified Melainabacteria as Cyanobacteria. But then researchers began asking, why are they in the gut? Some researchers proposed they were remnants of food. Others found similar [sequences](#) in mud samples. None had been cultured in the laboratory, so their roles were unknown.

In the study, the researchers used a new technique for stitching bacterial genomes together from aquifer groundwater and human stool samples. "This new technology allows you to assemble genomes from complex bits that you previously couldn't have assembled," said Ley.

Di Rienzi and colleagues picked four samples, three human stools and one from an aquifer, where the new bacteria accounted for up to 4 percent of the community of microbes. Using the new technique, they pieced together eight genomes, one of them from the aquifer sample. The genomes also confirm that the gut and environmental Melainabacteria belong in separate subphyla.

The researchers also believe that Melainabacteria facilitate fermentation in the [gut](#), probably to break down plant fibers, which produces hydrogen gas as a byproduct. But when hydrogen accumulates, it stops the fermentation process. The new bug is likely to rely on a partner microbe that processes hydrogen, Ley said. And because of this reliance,

it cannot be obtained in "pure culture" in the laboratory, which is why so little was known about it.

The study offers an example of where new genomic technologies, human health and evolutionary microbiology all come together, Di Rienza said. "Melainabacteria is a poster child for the field" of microbiology, she added.

Itai Sharon, a postdoctoral researcher, is also a co-lead author of the study, and Jillian Banfield, a professor of geomicrobiology, is the paper's other corresponding author, both at the University of California, Berkeley.

**More information:** "The human gut and groundwater harbor non-photosynthetic bacteria belonging to a new candidate phylum sibling to Cyanobacteria," *eLife*, 2013.

Provided by Cornell University

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