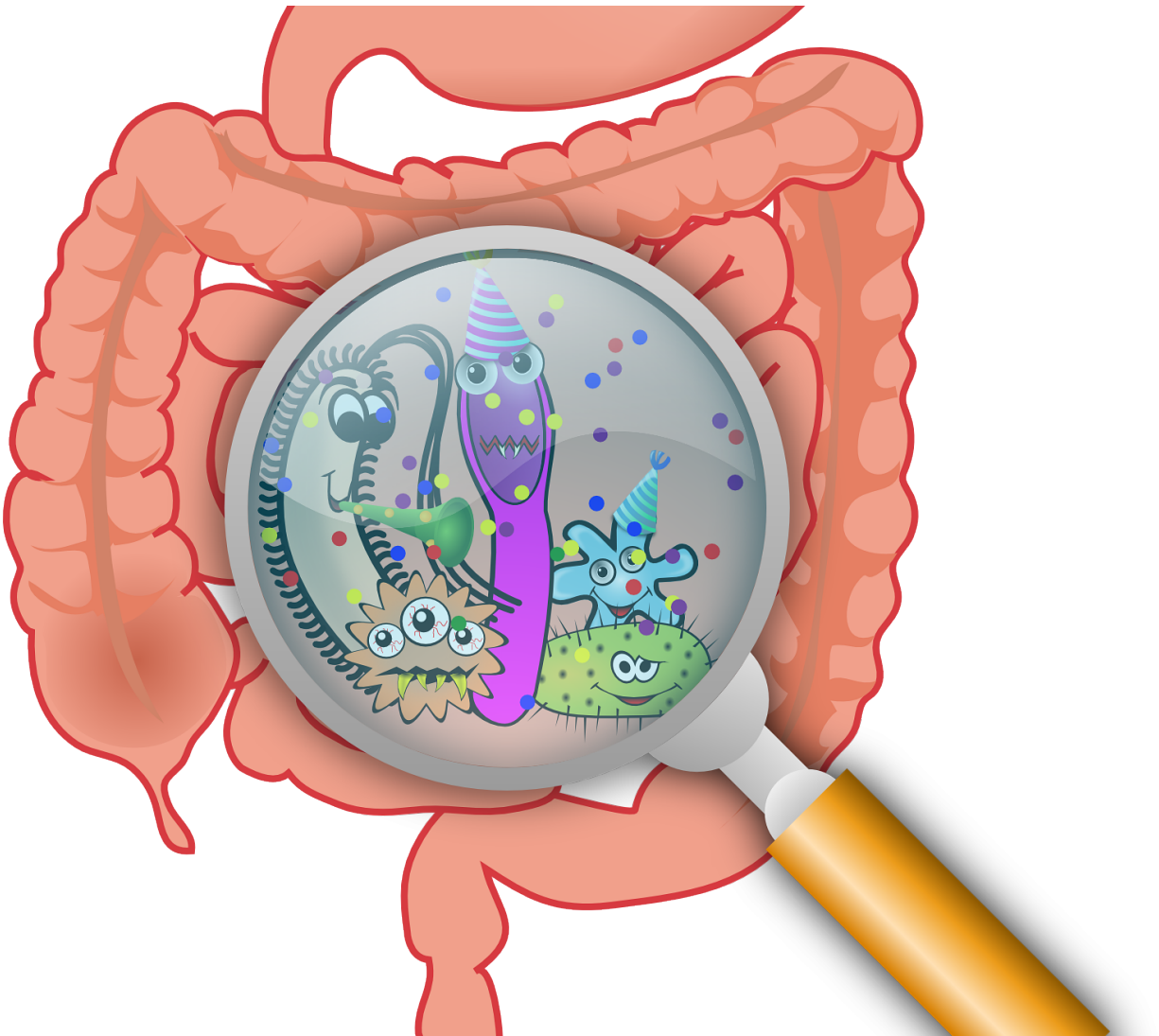


Gut microbes' role in mammals' evolution starts to become clearer

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An international collaboration led by Oregon State University scientists has made a key advance toward understanding which of the trillions of gut microbes may play important roles in how humans and other mammals evolve.

Researchers came up with a novel way of classifying the microbes—a taxonomy that groups them based on their ancestry and common distribution across mammals.

Findings were published this week in *mBio*.

Known as ClaaTU—short for cladal taxonomic units—the new algorithm and corresponding software sharpen and fine-tune the focus needed to clarify potential ecological or evolutionary mechanisms, said corresponding author Thomas Sharpton, a microbiology and statistics researcher in OSU's College of Science.

A clade is a group of organisms thought to have descended from a common ancestor.

"The gut microbiome matters to the health of mammals like humans and mice, so perhaps it also affects a mammal's ability to survive and reproduce in nature," said lead author Christopher Gaulke, a postdoctoral scholar in the College of Science. "If so, then the gut microbiome may influence how animals evolve such that individuals that carry the proper set of gut microbes are more likely to thrive."

Gaulke and Sharpton worked with collaborators in the OSU Department of Microbiology and College of Veterinary Medicine and at the University of Illinois and University of Quebec at Montreal to develop ClaaTU.

ClaaTU identifies microbial clades that manifest across multiple sets of

mammal communities more frequently than expected by chance. Those that do—the ones that are "conserved" in the mammalian microbiome—possibly played and continue to play important roles for their hosts.

"Identifying gut microbes that link to [mammalian evolution](#) is the first step toward evaluating this bold idea that gut microbes influence evolution," Sharpton said. "We were able to uncover an expansive array of such [microbes](#) by using our new approach to compare microbiomes across [mammalian species](#)."

Another find: Humans living "Western lifestyles—i.e., eating diets high in fat and low in fiber—tend strongly away from gut [microbiome](#) clade diversity when compared with non-Western humans and non-human primates. That suggests changes in lifestyle, environment and/or genetics that go along with Westernization are connected with the conservation of gut bacterial clades.

"It's an observation that elevates concern that industrialization may have impacted the [gut microbiome](#) that our human ancestors evolved to harbor," Sharpton said. "But future work will be needed to determine if the [gut microbes](#) identified in this study actually affect mammalian physiology in a way that could matter to their evolution."

More information: Christopher A. Gaulke et al, Ecophylogenetics Clarifies the Evolutionary Association between Mammals and Their Gut Microbiota, *mBio* (2018). [DOI: 10.1128/mBio.01348-18](https://doi.org/10.1128/mBio.01348-18)

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