

Study shows strong influence of external environment on fungal communities in the primate gut

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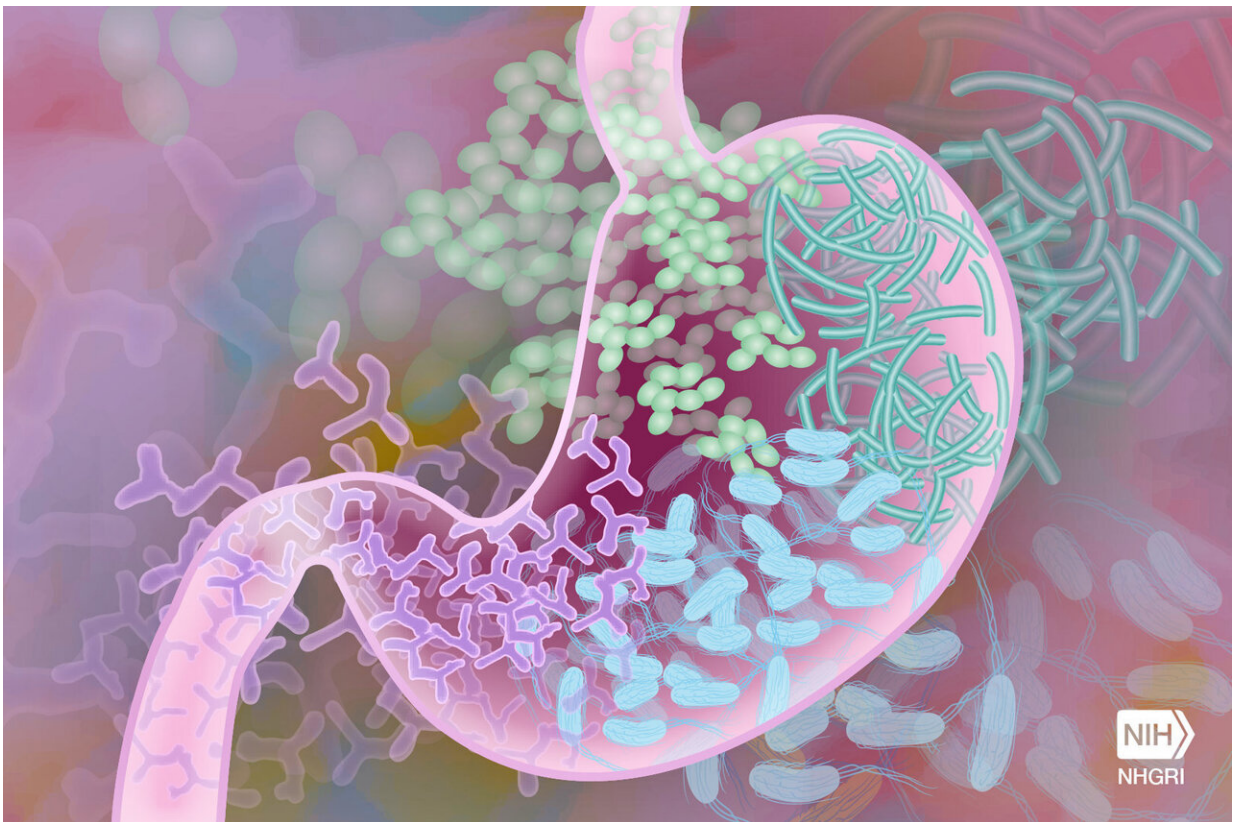


Illustration of bacteria in the human gut. Credit: Darryl Leja, National Human Genome Research Institute, National Institutes of Health

Researchers are starting to understand the importance of gut fungi in

mammals and the ways different environmental factors can shape these fungal communities, which play a crucial role in regulating immune responses.

In a new study in *npj Biofilms and Microbiomes*, researchers from the University of Minnesota and Czech Academy of Sciences presented an overview of gut fungal community composition and fungal-bacterial interactions in different nonhuman primates (captive and wild), and [human populations](#) with a diverse set of food acquisition practices (traditional agriculturalists, [hunter-gatherers](#) and the western human population).

The research team was led by computational biologist Ashok Kumar Sharma, a postdoctoral researcher formerly with the U of M, now with Cedars-Sinai. The scientists sequenced ITS2 and 16S rRNA gene markers in fecal samples of four nonhuman primate species and three different human groups to profile fungal and bacterial community composition.

"Understanding how the fungal community adapts and interacts with bacterial communities in response to different factors such as diet and lifestyle would provide a basic framework to explore their potential roles in [human health](#) and diseases," said Sharma.

Similarities between captive apes and humans following industrialized lifestyles indicate a potential influence of diet and lifestyle factors over genetics in shaping gut fungal community composition and fungal-bacterial interactions. Higher similarities in the fungal composition between humans consuming non-industrialized diets and wild apes further support these observations.

Overall, results suggest the influence of ecological, behavioral and individual factors in shaping the primate's gut mycobiome, the

communities of fungi colonizing the gastrointestinal tract of primates.

The researchers found:

- There was a strong influence of host-ecological factors, including dietary lifestyle in shaping the fungal community composition in the primate's gut. This is in contrast with the gut bacterial fraction, which seems to be more influenced by the host genetics.
- Ecological differences between and within primate populations not only impact the [fungal communities](#) but also how fungi and bacteria co-inhabit the gut.
- Fungal and bacterial taxa with similar functional potential may interact to accomplish common metabolic roles, such as degradation of a wide range of carbohydrates.

"These data indicate the [external environment](#) may have a very strong influence on populating communities of fungi in the primate gut; whether those fungi are largely transient (short lived) or long-term colonizers remains unknown. But perhaps a more interesting question should focus on whether the lack of fungal diversity in western/industrialized human populations affects health," said Andres Gomez, PhD, an assistant professor in the Department of Animal Science.

"As the environmental factors probably play a more important role than host genetics in shaping the mycobiome, we could consider that mycobiome can be a better indicator of a healthy and stable ecosystem in which the primates live," said Klara Judita Petrzelkova, PhD, a researcher at the Institute of Vertebrate Biology of the Czech Academy of Sciences.

In the future, measuring the contribution of specific food sources to

determine mechanisms of fungal assembly in the gastrointestinal tract would be a significant step moving forward.

More information: Ashok K. Sharma et al, The primate gut mycobiome-bacteriome interface is impacted by environmental and subsistence factors, *npj Biofilms and Microbiomes* (2022). [DOI: 10.1038/s41522-022-00274-3](https://doi.org/10.1038/s41522-022-00274-3)

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