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MICROBIOLOGY

Modern Hunter-Gatherers Have Thriving Gut Microbiome, Compared with Californians

A Western lifestyle seems to diminish the diversity of gut microbes

By Gemma Conroy, Nature magazine on June 26, 2023

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The Hadza people of Tanzania are among the last hunter-gatherer societies in Africa. Credit: Boyd Norton/Alamy Stock Photo

The human gut is teeming with trillions of microbes, but most studies of this vast community have focused on people living in urban regions. Now, a team of researchers has sequenced gut microbiomes from Hadza people — members of a hunter-gatherer

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The Hadza had an average of 730 species of gut microbe per person. The average Californian gut microbiome contained just 277 species, and the Nepali microbiomes fell in between. People with a farming-based lifestyle had an average of 436 microbe species, whereas those who live by foraging had an average of 317.

The team also found species in the Hadza microbiomes that were not present in the Californian samples, such as the corkscrew-shaped bacterium *Treponema succinifaciens*. Only some of the Nepali microbiomes contained this microbe, suggesting that the bacterium is dying out as societies become more industrialized.

REDRESSING THE BALANCE

Previous research has found that human gut microbiomes vary across regions and lifestyles, but there is a lack of data from non-industrialized populations, says study co-author Justin Sonnenburg, a microbiologist at Stanford University in California. “Part of the sequencing effort was to help fill that gap and provide more data for regions of the world that are under-represented,” he says.

Although it is well known that the microbiomes of people living non-industrial lifestyles are more diverse than those of people in industrialized societies, the findings show that the difference is more pronounced than previously thought, says study co-author Matthew Carter, also a microbiologist at Stanford.

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The researchers sequenced microbiomes from fecal samples collected from 167 Hadza people — including infants and mothers — between 2013 and 2014. For comparison, the team also generated sequences from stool samples collected from four groups of people in Nepal in 2016, and samples from Californian participants in a 2021 study² that explored how diet affects the microbiome.

DIVERSITY DWINDLES

From these samples, Sonnenburg and his team sequenced more than 90,000 genomes from microbes found in the human gut, including bacteria, viruses that infect bacteria, and single-celled organisms from groups called archaea and eukaryotes. Some 44% of these microbial genomes had not yet been recorded in large catalogues such as the Unified Human Gastrointestinal Genome database. Among the genome sequences recovered from the Hadza samples, more than 1,000 were from bacterial or archaeal species that are new to science.

Furthermore, gut-microbe species commonly found in industrialized populations often contained genes associated with responding to oxidative damage. The team suspects chronic inflammation in the gut could trigger such damage, creating a selective pressure for those genes, says study co-author Matthew Olm, a microbiologist at Stanford. “If you have a state of chronic inflammation, it would make sense that your gut microbiome has to adapt,” he says. These genes were not detected in the Hadza

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more complete picture of the human gut microbiome and how it differs across lifestyles and regions. This could help researchers to track which species are disappearing in industrialized populations and how that affects human health, says Forster. “We have an opportunity to understand the full complement of microbes we carry,” he says. “It’s effectively avoiding an extinction event by understanding them now, before they’re lost.”

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