

GENOME WATCH

Microbiota shuns the modern world

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This month's Genome Watch highlights the variation in gut microbiota across different human communities and explores how this is associated with lifestyle and diet.

The human gut is a reservoir that contains trillions of bacteria and hundreds of species. The composition of the gastrointestinal microbiota is associated with many aspects of human health. Since the inception of the Human Microbiome Project (HMP)¹, the characterization of these bacterial communities has been undertaken in numerous diverse human populations. The first 16S ribosomal RNA amplicon-based study of the gastrointestinal microbiome of hunter-gatherer populations revealed distinct differences in the composition of the microbiota when compared with industrialized populations. In this study by Schnorr *et al.*², the microbiota composition of 27 Hadza hunter-gatherers in Tanzania was compared with two rural groups, comprising 22 farmers from Malawi and 11 Mossi children from Burkina Faso, and three industrialized cohorts. Consistent with the environment and lifestyle having an important role, the composition of the microbiota in individuals from the Hadza community was found to be more similar to the microbiota composition in individuals from rural communities than that in individuals from industrialized communities. In contrast to the microbiota from individuals living in rural and industrial communities, the microbiota of the hunter-gatherers was enriched in *Treponema* spp., unclassified Bacteroidetes and Ruminococcaceae, whereas *Bifidobacterium* (Actinobacteria) was absent.

These previous studies predominantly focused on single samples, however, recently, Smits *et al.*³ performed temporal sampling across 350 faecal samples from 188 Hadza individuals for almost 20 months. Detailed characterization of the

gastrointestinal microbiota revealed changes in the microbiota composition that were consistent with seasonal dietary variation. In the wet season, the diet of Hadza individuals is dominated by plant-based food sources, whereas in the dry season, diet is dominated by animal-based food sources. The longitudinal sampling also showed that the dry season-associated microbiota composition reoccurred and remained indistinguishable in the subsequent dry season. Both taxonomic diversity and functional diversity was found to increase in the dry season-associated microbiota compared with the wet season-associated microbiota. Interestingly, an association of *Prevotella copri*, *Faecalibacterium prausnitzii* and *Treponema* spp. with the wet season diet resembles the composition associated with a modern plant-based diet, however, *Bifidobacterium*, which was undetected in the Hadza community, is frequently detected in microbiota associated with both plant-based and animal-based diets in industrialized communities. Whereas previous studies suggest the potential role of lifestyle in driving microbiota composition, this study suggests that diet also has an important role.

The taxonomic composition of the gastrointestinal microbiota may change through environmental exposure; however, redundant functions between species may enable the functional capacity to remain constant. Using shotgun metagenomic sequencing and

metabolomics on 36 selected samples, Smits *et al.*³ examined the changes in the functional capacity associated with change in microbiota composition. Interestingly, carbohydrate-active enzymes that metabolize plant carbohydrates were enriched in the Hadza community microbiomes

unlike the HMP samples from an industrialized cohort. It has been previously suggested, based on experiments in mice, that a low-fibre diet is the major cause of reduced bacterial diversity in the microbiota of industrialized populations⁴. Similarly, antibiotic resistance genes were more diverse in the HMP cohort than in the Hadza population samples, supporting the hypothesis that the use of antimicrobials has influenced the composition of the gastrointestinal microbiota in industrialized populations.

Studies that compare microbiota communities across diverse individuals with vastly different diets and lifestyles provide important insights into the role of diet and environment in shaping these ecosystems. Additional detailed research across a range of individuals and communities from traditional hunter-gatherer societies, farming communities and individuals from urban environments will allow us to further our understanding of bacterial diversity and functions in the human gastrointestinal microbiota. This research will be essential in understanding human gut microbiota dynamics and for monitoring the future loss in this ecosystem that is associated with human lifestyle.

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Competing interests statement
The author declares no competing interests.

