

Abundant Bacterial Species in YOUR Beyond Bacteria Sample

All four Beyond Bacteria participants had very different microbiome profiles when looking at the top ten genera detected in each participant. The microbiome composition of each participant provided intriguing bits

of food for thought. Disclaimer: science is not at the stage to confidently assess human health status based on the microbiome, and the American Gut is not a medical diagnostic. The microbiome could also follow the old adage that too much of a good thing is a bad thing, and not enough studies have been done to determine whether certain abundance thresholds of "good" bacteria become harmful. Only time and well-designed, peer-reviewed research will tell us how useful microbiome composition can be as a proxy for predicting human health status.



You can find the specific top taxa in your sample [here](#).

A large proportion (44%) of your gut microbiome (000009544) was composed of two *Roseburia* species, *R. intestinalis* and *R. inulinivorans*. As described in the top taxon [document](#), both of these bacterial species ferment plant polysaccharides to produce butyrate, an anti-inflammatory molecule associated with GI tract health. Additionally, *R. inulinivorans* produces propionate, which decreases lipogenesis. A third butyrate producer, *F. prausnitzii*, was also detected in your gut (8.14% abundance). Therefore, you appear to be harboring a microbiome with a large potential to promote your health by reducing inflammation and fat formation. You eat more than 30 types of plants as part of your regular diet, which could contribute to the large abundance of plant polysaccharide fermenters present in your gut. You also exercise daily and occasionally take supplements with Vitamin D, indicating that in general, you are health conscious; nevertheless, you have a BMI that classifies you in the overweight category (however, BMI measurements must be carefully interpreted, as in many cases, muscular people fit into the overweight category simply because muscle weighs more than fat). Interestingly, you did take antibiotics within the year prior to collection of your sample. Antibiotics have been shown to reduce microbiome diversity and have even been associated with recurrent GI tract infections in some people; nevertheless, you appear to be generally healthy physiologically and microbiologically.

Notable Metabolic Pathways in YOUR Beyond Bacteria Sample

The most abundant pathways were similar across the four individuals, despite taxonomic differences. This is not unprecedented; the Human Microbiome Project also large variations in taxonomy, while pathway abundance remained relatively stable ([ref](#)). Unsurprisingly, we find common housekeeping genes, like DNA biosynthesis and carbon metabolism, across all four samples. We also find less common pathways. Again, we

must issue a disclaimer: metagenomics is still in its infancy. Few samples have been analyzed in this way. Therefore, making health inferences based on metagenomic findings would be very premature at this time.

You can find the specific top pathways in your sample [here](#).

Your metagenome (000009455) showed a decreased capacity for the biosynthesis of lipopolysaccharide (LPS). LPS, also known as endotoxin, is a main component in bacterial cell walls. Endotoxin leads to a pro-inflammatory immune response ([ref](#)). Lower gene counts for endotoxin may mean less inflammation. However, your microbiome also had a lower capacity for glycosaminoglycan breakdown. Glycosaminoglycans are large, branched sugars found on the surface of host cells. In their native form, glycosaminoglycans can promote infection. Bacterial breakdown of glycosaminoglycans can promote an immune response, leading to faster clearance ([ref](#)).