

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](#).

Your gut microbiome (000010538) was composed mainly of *Prevotella copri* (14.21%), *Eubacterium eligens* (13.35%), and *Faecalibacterium prausnitzii* (11.75%). *Akkermansia muciniphila* was also present, at an abundance of 9.16%. As discussed above, *P. copri* has been indicated in rheumatoid arthritis and potentially in GI tract inflammation, although the evidence remains preliminary in both cases, particularly in the case of GI tract inflammation. In contrast, both *E. eligens* and *F. prausnitzii* have been associated with GI tract health. Both are plant polysaccharide fermenters, with *E. eligens* appearing to be negatively correlated with obesity and *F. prausnitzii* acting as an anti-inflammatory in the gut. *A. muciniphila*, too, has been implicated multiple times in GI tract health. You appear to live a healthy lifestyle, exercising daily outdoors, drinking alcohol infrequently, and consuming a large variety of plants as part of your normal diet. Therefore, the presence of a potentially "harmful" bacterial species as the most abundant species in your gut is curious; nevertheless, you also harbor a large proportion of health-associated, plant polysaccharide-fermenting species.

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 sample (000010538) looks like the metagenome in most individuals in both the American Gut and HMP. However, your metagenome includes a degradation pathway for the aromatic amino acid, phenylalanine. Phenylalanine is an essential amino acid. Phenylalanine is also a metabolite of Aspartame, a common artificial sweetener. The two pathways for phenylalanine degradation take the planar ring structure, and break it down to carbon chains that can serve as precursors for other reactions.