

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](#).

Seven of the top ten species detected in your gut microbiome (000011924) were *Lactobacillus* species, and an additional two were *Bifidobacterium* species, both of which are generally typified as the probiotic strains. As discussed, many of these species have been tested for their probiotic potential in a number of contexts and have a wide range of purported effects, from a reduction in adiposity to a reduction in allergy related inflammation. The large proportion of *Lactobacillus spp.* in your gut is definitely curious, though the cause for this cannot be determined from the lifestyle information you provided. In general, you appear to live a healthy lifestyle, eating a variety of vegetables and exercising daily. Nevertheless, you are slightly underweight on the BMI scale. You did use antibiotics in the year prior to collecting your sample. An attempt to prevent or correct antibiotic-induced microbiome dysbiosis via the ingestion of probiotics could potentially explain the large amount of probiotic-like species in your gut, but without this specific information, this potential explanation remains conjecture.

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 (000011942) follows a general pattern of core pathways. Your sample lacks pathways associated with any type of aromatic degradation, including phenylalanine. Aromatics are rigid, stable carbon rings. Traditional physiology places aromatic degradation in the human liver, although some microbes include this capacity. The bacteria do not encode genes to break down glycosaminoglycan. 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](#)). Your metagenome also lacks some pathways involved in energy metabolism, including enzymes to convert between hydrogen sulfide (H₂S) and sulfate (SO₄²⁻). Hydrogen sulfide has a distinct rotten egg aroma and is commonly found in flatulence.