

Count your blessings: Quantitative microbiome profiling

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A broad range of metabolic and inflammatory diseases is associated with alterations in gut microbiota composition and metabolic potential. Until now, sequencing-based gut microbiota research has described such dysbiotic states in terms of proportional shifts in microbiome composition. However, when it comes to the gut bacterial content and how it relates to health, it's not only percentages that matter, but also numbers. That is according to the latest research by Jeroen Raes (VIB-KU Leuven) and his team, published today in *Nature*.

In their manuscript titled "Quantitative microbiome profiling links gut community variation to microbial load," the VIB-KU Leuven scientists demonstrate a novel methodology that allows both fast and accurate determination of the bacterial load in a fecal sample.

Prof. Jeroen Raes (VIB-KU Leuven): "The method we developed is based on parallelization of microbiome sequencing and flow cytometry enumeration of microbial cells in fecal material. The combination of these two workflows enables us to generate true quantitative microbiome profiles expressed as numbers of cells per gram, rather than percentages."

According to the VIB-KU Leuven researchers, Quantitative Microbiome Profiling can really make a difference.

Prof. Jeroen Raes (VIB-KU Leuven): "Until now, proportional approaches have been the standard in microbiome research. However,

without quantitative data, percentages cannot tell you whether a particular bacterium is actually becoming more abundant under specific conditions. A proportional increase could just as well imply that this species of interest is just maintaining its initial levels, while all other taxa are declining. This makes it very difficult to link microbiome data to quantitative health parameters and infer [disease](#) mechanisms. With Quantitative Microbiome Profiling, we are one step closer to solving this issue."

In 2012, Jeroen Raes and his team launched the Flemish Gut Flora Project, one of the first population-level microbiome monitoring efforts worldwide. VIB-VUB-KU Leuven scientists collected over 3000 fecal samples from healthy volunteers. This collection allowed them to assess microbiome variation in a non-diseased population. The results of the Flemish Gut Flora Project proved to be essential for the interpretation of the lab's quantitative [microbiome](#) findings.

Prof. Jeroen Raes (VIB-KU Leuven): "Using the Flemish Gut Flora Project database, we were able to identify a new microbiota community type based on quantitative findings. This enterotype is characterized by a low microbial load. It harbors lower abundances of taxa that might play a role in maintaining a healthy gut ecosystem. While we do observe this enterotype to be present in a minority of healthy volunteers, it is by far the most prevalent microbiota configuration among Crohn's Disease patients."

Prof. Séverine Vermeire, gastroenterologist at UZ Leuven/KU Leuven: "Using Quantitative Microbiome Profiling, we observed that feces from Crohn's Disease patients harbor up to 50 times less bacteria than those of healthy volunteers. This striking decrease in bacterial abundance appears to be a key element of dysbiosis in Crohn's Disease. Next steps will be to find out whether having a low cell count enterotype increases your risk of developing Crohn's Disease—and if so, what can be done to prevent

it."

More information: Quantitative microbiome profiling links gut community variation to microbial load, *Nature* (2017).

[nature.com/articles/doi:10.1038/nature24460](https://doi.org/10.1038/nature24460)

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