

Quantitative microbiome profiling in health and disease

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Alterations in the gut microbiota have been linked to various pathologies, ranging from inflammatory bowel disease and diabetes to cancer. Although large numbers of clinical studies aiming at microbiome-based disease markers are currently being performed, our basic knowledge about the normal variability of the human intestinal microbiota and its determining factors remains limited.

Here, I will discuss our findings studying a large-scale study (Flemish Gut Flora Project; n=3400) of the gut microbiome variation in a geographically confined region (Flanders, Belgium), in which analysis of microbiome variability in health identified the primary parameters associated to microbiome composition. In this presentation, I will discuss our experiences in large-scale microbiome monitoring, show how the development of dedicated computational approaches can assist in microbiome analysis and interpretation, and which confounders are essential for inclusion in microbiome disease research.

In addition I will show how Quantitative Microbiome Profiling (QMP; Vandeputte et al. Nature 2017), which combines microbiomics with flow cytometry-based cell counts, is profoundly changing our view on gut microbiota variation and allowed the identification of an inflammation-associated, cross-disease enterotype.

Short Professional Biography:

Postdoc: Department of Plant Systems Biology, VIB, Ghent, Belgium

Postdoc: EMBL, Heidelberg, Germany

Scientist at EMBL, Heidelberg, Germany

Professor (10% ZAP; Oddyseus fellowship), group leader at VIB-VUB, Brussels, Belgium (2009-2015)

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Vice director, Center for Microbiology, VIB, Belgium (since 2020)



























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Studies:

PhD: Ghent University, Ghent, Belgium

Research interests

The Raes Lab combines large-scale, next-generation sequencing with novel computational approaches to investigate the functioning and variability of the healthy human microbiome at the systems level and study its alteration in disease. They focus on the development of computational methods for the analysis of (next-generation) sequence data and the investigation of community properties from metagenomics, metatranscriptomics and meta-metabolomics data, which are applied in a wide range of environments (gut, ocean, etc.).























