Unraveling the food web in your gut

June 13 2016

Despite recent progress, the organization and ecological properties of the intestinal microbial ecosystem remain under investigated. Using a manually curated metabolic module framework for (meta-)genomic data analysis, Sara Vieira-Silva, Gwen Falony and colleagues from the Jeroen Raes lab (VIB/KU Leuven) studied species-function relationships in gut microbial genomes and microbiomes. The team of the Flemish Gut Flora Project observed that half of the bacteria in the human gut were metabolic generalists, while others were specializing and feeding on specific substrates, such as carbohydrates, proteins, or lipids.

Jeroen Raes (VIB/KU Leuven): "We built a 'who does what' map of the gut microbiome. To do so, we linked the bacterial taxa to their functional potential. This is essential to begin to understand what happens with our food once digested. It allowed us to determine which food residues are fermented by what bacteria. By mapping the gut trophic chain, we found that the gut ecosystem has a lot of back-up mechanisms: when one bacterial genus disappears, another can take over its function in the fermentation cascade."

Correlation between diversity of gut bacteria and human health?

Last year, the Raes team was the first to question the prevailing assumption in gut microbiome research equaling high bacterial diversity in the colon ecosystem to host health. This assumption has been put forward based on frequent observations of reduced diversity associated with disease. Based on the results published now, the Raes team links high bacteria diversity not only to slow transit, but also to depletion of carbohydrates in the large intestine and increased fermentation of proteins. The latter suggests that the link between diversity and health is not as straightforward as previously assumed.

Jeroen Raes (VIB/KU Leuven): "We found that high biodiversity enterotypes (generally considered as healthy) also have a high capacity to produce potentially unhealthy compounds as a result of protein fermentation. High colon ecosystem biodiversity is maybe not the Holy Grail in the ongoing quest to improve gut health."

The Raes team also demonstrated that bacteria fermenting proteins are slower growers. This knowledge could be used to make sure they get outcompeted by feeding our colon ecosystem carbohydrates in the form of prebiotic substrates. Prebiotics will give a selective advantage to faster growing carbohydrate fermenters that do not produce undesired metabolites.

More information: Sara Vieira-Silva et al, Species–function relationships shape ecological properties of the human gut microbiome, *Nature Microbiology* (2016). DOI: 10.1038/nmicrobiol.2016.88

Provided by VIB (the Flanders Institute for Biotechnology)

Citation: Unraveling the food web in your gut (2016, June 13) retrieved 25 April 2024 from https://phys.org/news/2016-06-unraveling-food-web-gut.html