

NEWS:



How to get a complete view on effects of a diet, a drug or an ingredient

In this study (1), two different diets are compared for their effects on gut microbial metabolism through stool samples analysis. A now classic workflow (2) of metaproteomics and bioinformatics has been applied as metaproteomic analysis of the bacterial proteomes in the microbial community provides a more direct measure of functional status associated with gut bacterial activity and metabolism by globally characterizing proteins and corresponding microbial species.

The study shows that the interrogation of the metaproteome at a **functional level** reflects metabolic shifts of mucin- and fiber-degrading enzymes in the microbial response to a dietary intervention.

As already well described for skin microbiota (3), unlike metagenomics (all of the genes and genomes in the microbial community), which measures the **functional potential** of the microbial community, metaproteomic signatures provide a **direct measure of the microbial activity** of the microbial community.

Clearly, the microbiota metabolism is not driven by a set of discrete linear pathways but a **web of interconnected reactions facilitated by a network of enzymes that connect multiple molecules across multiple pathways.**(4)

(1) Gut Microbial Protein Expression in Response to Dietary Patterns in a Controlled Feeding Study: A Metaproteomic Approach. Pan S and all. 2020 <https://www.mdpi.com/2076-2607/8/3/379/htm>

(2) Synbiotic-driven improvement of metabolic disturbances is associated with changes in the gut microbiome in diet-induced obese mice. Ke X and all. 2019 <https://www.ncbi.nlm.nih.gov/pubmed/30792016>

(3) A review of next generation sequencing technologies used in the evaluation of the skin microbiome: what a time to be alive. Sandhu SS and all.. 2019 <https://www.ncbi.nlm.nih.gov/pubmed/31450270>

(4) Metaproteomics reveals persistent and phylum-redundant metabolic functional stability in adult human gut microbiomes of Crohn's remission patients despite temporal variations in microbial taxa, genomes, and proteomes. Blakeley-Ruiz JA and all. 2019 <https://www.ncbi.nlm.nih.gov/pubmed/30744677>

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