NEWS:

Microbiotas functional metabolism is revealed with metaproteomics and data processing.

New recent publications on studies on gut and skin microbiotas show the variability at the genome, transcriptome and proteome level but a remarkable stability of metabolic shared functions which is shown with metaproteomics and data processing.

In the gut(2), almost all the functions observed are observed in multiple phyla, these functions are not specific to any one phylum, genus, or species.
There is a clear persistence of conserved metabolic functions across time and individuals.
The microbiome’s 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.**
Metaproteomics allows to perform in-depth microbiome analysis up to metabolism understanding in rat and swine. (3)(4)
And now, metaproteome analyses further revealed the **capabilities of dietary pre- and probiotics treatments in modulating metabolic pathways and functional activities of gut microbial ecosystem.** (5)
Functional studies of the skin microbiota at the metatranscriptomic and proteomic levels illustrate the interactions between the microbiota and the host skin(1).

(1)Shaping of cutaneous function by encounters with commensals. Barnard and all 2017 https://www.ncbi.nlm.nih.gov/pubmed/26988937
(2) 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
(3) Metaproteomics reveals potential mechanisms by which dietary resistant starch supplementation attenuates chronic kidney disease progression in rats. Zybailov BL and all. 2019 https://www.ncbi.nlm.nih.gov/pubmed/30699108
(4) Analysis of the Bacterial and Host Proteins along and across the Porcine Gastrointestinal Tract. Tröscher-Mußotter J. and all. 2019 https://www.ncbi.nlm.nih.gov/pubmed/30634649
(5) 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

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