

NEWS:

Functional studies for microbiome-skin interactions

While recent advances in sequencing technologies have enabled a large number of studies to characterize the taxonomic composition of the skin microbiome at various body sites and under different physiological conditions, we have limited understanding of the microbiome composition and dynamics at the strain level, which is highly important to many microbe-related diseases. Functional studies of the skin microbial communities and the interactions among community members and with the host are essential for understanding. (1)

The reported discrepancy between expressed functions and functional potential suggests that caution should be used before drawing functional conclusions from metagenomic data, further supporting metaproteomics as a fundamental approach to characterize the human metabolic functions and activities. (2)

Metaproteomics is a promising approach to perform in-depth microbiome analysis as it simultaneously reveals both human and microbial changes. (3)

(1) Shaping of cutaneous function by encounters with commensals. Barnard and all 2017 <https://www.ncbi.nlm.nih.gov/pubmed/26988937>

(2) Potential and active functions in the gut microbiota of a healthy human cohort. Tanca and all. 2017 <https://www.ncbi.nlm.nih.gov/pubmed/28709472>

(3) Deep Metaproteomics Approach for the Study of Human Microbiomes. Zhang X and all. 2017 <https://www.ncbi.nlm.nih.gov/pubmed/28749657>

With Phylogene, you can also characterize and understand the microbiome effects.

***Bacterial 16s rDNA and fungal ITS sequencing with OTU-based estimation to investigate microbial communities diversity and determine taxonomic composition
High-resolution nano LC-MS/MS quantitative proteomics and CORAVALID™ / MicroXplore™ data processing: The efficient tool for discovery***

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