

NEWS:

Metagenomics and proteomics to study the skin microbiome

The recent evolutions of metagenomics allowed to comprehend the gut microbiota diversity and to highlight the importance of species balance. Major similarities with skin microbiome are already described (Grice and all. Nat Rev Microbiol 2011 April ; 9(4) : 244-253).

Gut microbiota metaproteomics also moved forward with untargeted LC-MS/MS coming and genomics for database. The advantage is always to highlight the structures and active functions directly in the microorganisms by differential effects (Erickson and all. Plos One 2012 November ; 7(11) e49138). The method is available, but nothing has been published yet on untargeted skin proteomics.

Our experience, based on our EUROSTARS program Nosofight, allowed us to develop workflows based on 16s DNA and ITS sequencing and highres proteomics. It allows to comprehend only the microbiota (starting at 10^7 cells) or the microbiota and host with earlier fractioning depending on the interest with microorganisms - host interactions.

With MS Phylogene, you can also characterize the effects of your products on skin microbiota

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™ data processing: The efficient tools for microbiota analysis

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