## **NEWS:**

## Lactobacilli in situ: functional proteomics for uncovering the interactions between lactobacilli and environments, including human and animal sites.

Very few information is up to now available on the real working of Lactobacilli on skin, in the gut or even in a yogurt. Extensive genomic diversity analysis were conducted which could also provide information on available genes, but not on effective on going pathways.

The increasing number of sequenced genes of Lactobacilli strains and the evolution of high resolution LC-MS/MS proteomics now allows to make quantitative comparative proteomics for lactobacilli grown under different laboratory conditions, or in different environmental situations. Then together with bioinformatics tools to re-construct metabolic pathways, it is easy to open the way to metaproteomics approaches which allow uncovering the interactions between lactobacilli and environments, including human and animal intestine or other sites. (1)

(1) Functional proteomics within the genus Lactobacillus. De Angelis M and all 2016 <a href="https://www.ncbi.nlm.nih.gov/pubmed/27001126">https://www.ncbi.nlm.nih.gov/pubmed/27001126</a>

With Phylogene, you can also characterize and understand the Lactobacilli strains working.

High-resolution nano LC-MS/MS quantitative proteomics and CORAVALID™ / MicroXplore™ data processing: The efficient tool for discovery

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