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Understanding complex microbiomes with metaproteomics

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Microbial ecosystems play a major role for elemental cycling in nature and for the benefit of plants and animals. Their immense diversity and huge complexity are challenging the scientific method. How microorganisms interact with each other, with their neighbors and hosts, and with their environment remains a difficult question to resolve. Metaproteomics aims to identify the taxa present in a given microbiota, and more importantly, to characterize the preeminent protein players and main metabolic pathways of these taxa to better understand the functioning of the microbial ecosystem. Currently, this approach is gaining momentum because it is highly complementary to 16S/18S rRNA metabarcoding and metagenomics. The recently developed concept of “phylopeptidomics” allows more precise quantification of the protein biomass of the identified taxa [1], highlighting a new dimension from microbiome data, and improves the proteotyping of environmental taxa [2,3].

The latest generation of high-resolution tandem mass spectrometers can record information on thousands of peptides within minutes. This huge amount of data opens up new horizons for metaproteomics but requires optimization of searches in better quality databases [4]. Several examples will be discussed to illustrate the potential of current technology and the importance of the bioinformatics pipeline, such as the alliance of proteogenomics and metaproteomics which allows an in-depth characterization of microbiomes from non-sequenced animals used as sentinels of our environment [5].

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