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## **Unlocking the functions of the microbiota: the advantages of mass spectrometry**

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Microbial ecosystems play a major role in nature's basic cycles, plant development and animal health. How microorganisms interact with each other, with their hosts, and with their environment are fundamental questions. Omics methodologies open new perspectives due to their complementarity. The study of the proteins of these particularly complex samples by metaproteomics makes it possible to obtain four types of answers: 1) identification of the taxa present, 2) quantification of the biomass of these organisms, 3) identification of the proteins of these taxa and their functioning, and 4) global functional representation of the biological system. However, how to identify and quantify several hundred million chemical entities in a single sample, most of which are still unknown?

In order to better understand the functioning of microbiota, the question of biomass quantification is essential. The recently developed concept of "phylopeptidomics" allows a more accurate quantification of the protein biomass of identified taxa, highlighting a new dimension from the microbiome data, and improves the proteotyping of environmental taxa. Challenges in terms of mass spectrometry, interpretation and mining of results will be discussed. Screening large panels of microbial isolates or consortia for new compounds, new activities and new enzymes is an attractive playground.