Estimating relative biomasses of organisms in microbiota using “phylopeptidomics”

Olivier Pible

François Allain

Virginie Jouffret

Karen Culotta

Guylaine Miotello

Jean Armengaud

Video Byte

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Abstract

Understanding how microbes relate in complicated ecosystems is important. Medicine, biotechnology, and environmental ecology depend on identifying the types and proportions of bacteria in a given sample. Metaproteomics has emerged as a powerful analytical tool for studying the protein content of complex microbial samples. Unfortunately, database limitations such as unequal coverage of life branches can influence protein inferences, leading to misidentification of species. Thus, for diverse samples, more robust methods are needed to fully understand the diversity of microorganisms present in biological samples. Now, researchers have developed a new method to identify the biomass contribution of an organism. The technique, called “phylopeptidomics,” uses mathematical models and phylogenetic relationships to evaluate the peptide signatures present in a sample. Phylopeptidomics uses peptides shared between taxa to improve discrimination and quantification of the taxa, allowing for a more precise understanding of the relative abundance of organisms. Although further study is needed, results using artificial mixtures of microbes suggest that phylopeptidomics will open new horizons for the study of microbiota dynamics, resulting in accurate label-free metaproteomics for a wide variety of applications.