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Metaproteomics for deciphering biomass contributions and functions of complex aquatic microbiota

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Metaproteomics aims at comprehensively identifying the preeminent metabolic pathways for gaining insight into the functions of microbiota. This large scale molecular phenotypic analysis is highly complementary to 16S rRNA metabarcoding and metagenomics. We have developed a new method for exploiting metaproteomic datasets and defining the biomass contribution of the organisms present in the sample. The phylopeptidomics concept is based on a signature describing the number of peptide sequences shared with all other organisms calculated by mathematical modeling and phylogenetic relationships. Its efficiency was exemplified with artificial mixtures, as well as with more complex microbiota models. This methodology was applied on aquatic microbiota such as those discovered within the water used to cool a nuclear reactor core. We highlighted in a nuclear reactor at shutdown the predominance of two phyla: Proteobacteria with the genus *Methylobacterium* (50% of the signal) and Actinobacteria with two genera *Asanoa* (25%) and *Streptomyces* (25%). This approach proved to be highly complementary to the metabarcoding analysis of the same samples. We also successfully applied the method to biofilms sampled from the walls of a pool used to store radioactive sources. These examples applied to aquatic microbial communities pave the way to new discoveries regarding novel microorganisms of biotechnological interest.