



Metaproteomics for deciphering biomass contributions and functions of complex aquatic microbiota

Jean Armengaud, Olivier Pible, Corinne Rivasseau

► To cite this version:

Jean Armengaud, Olivier Pible, Corinne Rivasseau. Metaproteomics for deciphering biomass contributions and functions of complex aquatic microbiota. Topical Day "Aquatic microbiota in or near nuclear facilities: insights, discoveries, solutions", SCK-CEN Academy, Sep 2019, Brussels, Belgium. hal-04476750

HAL Id: hal-04476750

<https://hal.inrae.fr/hal-04476750>

Submitted on 25 Feb 2024

HAL is a multi-disciplinary open access archive for the deposit and dissemination of scientific research documents, whether they are published or not. The documents may come from teaching and research institutions in France or abroad, or from public or private research centers.

L'archive ouverte pluridisciplinaire **HAL**, est destinée au dépôt et à la diffusion de documents scientifiques de niveau recherche, publiés ou non, émanant des établissements d'enseignement et de recherche français ou étrangers, des laboratoires publics ou privés.



Topical Day | Aquatic microbiota in or near nuclear facilities: insights, discoveries, solutions

September 12, 2019 | Bedford Hotel, Brussels, Belgium

Metaproteomics for deciphering biomass contributions and functions of complex aquatic microbiota

Jean Armengaud, Olivier Pible, Corinne Rivasseau, et al.

CEA-Marcoule, Laboratory “Innovative technologies for Detection and Diagnostics”,

BP 17171, F-30200 Bagnols-sur-Cèze, France.

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 phyloproteomics 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.