

Conférence



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Amphithéâtre Hydro-Québec, salle 1210 Pavillon Marchand - IBIS

Functional characterization of microbial communities

Microbes typically live in close association with one another in mixed communities. These communities maintain high levels of complex interactions exchanging nutrients, vitamins and other chemicals. The microbes in these mixed communities therefore function very differently from microbes isolated in pure cultures in the laboratory, producing phenotypes that can't be replicated in one individual cell type. Thus, microbial communities and their interactions must be studied as a whole to fully understand their properties and dynamic relationships.

These complex interactions add to the difficult task of deciphering metagenomic (mixed community DNA) sequencing data. Large numbers of genes have no known function, or function that is very poorly defined. Our research centre has been exploring enzymes from metagenomes, and microbial community dynamics in defined mixed microbial consortia used to treat wastes. The design of enzyme or culture assay conditions relevant to the microbial community or application under study is critical. Using native PAGE protein separation coupled to functional screening and proteomics, and from activity assays in mixed cultures, we have stumbled upon new co-factors that modulate vital activity in certain microbial consortia. The examples of how prenylated FMN and certain corrinoid cofactors modulate biotransformation reactions will be described.