

HIGH-THROUGHPUT FUNCTIONAL METAGENOMICS FOR THE DISCOVERY OF GLYCAN METABOLIZING PATHWAYS

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Key Words: Metagenomics, CAZymes, glycans, human gut

Glycans are widely distributed in nature. Produced by almost all organisms, they are involved in numerous cellular processes, such as energy supply and storage, cell structuration, protein maturation and signalling, and cell recognition. Glycans are thus key elements mediating the interactions between mammals, plants, bacteria, fungi and even viruses. They also represent a reliable source of carbon for microbes, which have developed complex strategies to face their structural diversity and to harvest them. However between 70 and 99% of these microorganisms are still uncultured, while they represent a goldmine for the discovery of new enzymes. In order to boost their identification and characterization, a functional metagenomic approach was developed, based on the design of various high-throughput, robust and sensitive screening strategies. The functional potential of Gbp of metagenomic DNA from various origins was explored, revealing dozens of novel enzyme families and functions.

Integration of biochemical, structural, meta-omic and omic data allowed us to decipher, from the molecular to the ecosystemic scale, novel mechanisms of plant, microbial and mammal glycan metabolization. These new metabolic pathways involve batteries of glycoside-hydrolases, glycoside-phosphorylases and sugar transporters. These fascinating proteins appear as new targets to control host-microbe interactions. They also constitute very efficient biotechnological tools for biorefineries and synthetic biology.