Vendredi 4 décembre à 13h

Bâtiment Monod - salle V. Contesse - Mont-Saint-Aignan

Microorganisms and Biocatalysts with Potential for Macroalgal and Plant Biorefining

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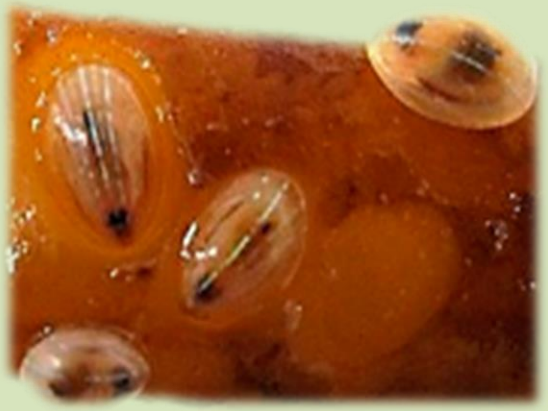

Macroalgae offer an attractive alternative to plant based feedstocks for the replacement of products currently produced by the petro-chemical industry. However, a suite of 'tools' are necessary to achieve this in an economically and environmentally sustainable way and is the focus of this thesis.

Microorganisms were isolated from faecal samples of North Ronaldsay sheep, gastrointestinal tract of marine limpet *Patella pellucida* and decaying brown algae. Isolates were screened for polysaccharide degrading activities and candidates displaying the best enzyme activities were subjected to a) further screening for polysaccharide hydrolysing enzymes, b) fermentation product formation and c) whole genome sequencing. A predicted laminarinase gene from LI 63 was expressed in *E. coli*, purified and characterised as an endo-1,3-β-glucanase.

Metagenomic DNA from microbial community extracted from the gastrointestinal tract of *P. pellucida* was used for construction of shotgun and fosmid metagenomic libraries. Employing bioinformatics, metagenomic shotgun reads were analysed for microbial biodiversity and polysaccharide degrading enzymes. Fosmid metagenomic libraries were functionally screened for specific enzyme activities.

This work identified microbial strains and biocatalysts for use in macroalgae and plant biorefining. Functional screening and draft genome analysis of 21 isolated strains delivered a unique library/collection of microorganisms and associated enzymes for macroalgae and plant degradation. Analysis of the diversity of potential laminarinase genes with molecular and biochemical studies on recombinant endo-1,3-β-glucanase from LI 63 constituted the first step towards understanding functionality of the laminarin degrading enzyme systems in these microorganisms.

Phylogenetic analysis of the shotgun libraries revealed 1) an abundance of industrially relevant bacterial phyla representing a resource for future enzyme mining, 2) a diversity of highly unique prokaryotic and eukaryotic sequences encoding predicted enzymes involved in depolymerisation of alginate, laminarin, cellulose and starch and 3) resources for further work on macroalgal and plant biorefining processes, to explore the economic viability of biorefining at industrial scales.

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