Microbes for macroalgae and plant biorefining

Magda Dudek*, Jessica Adams, Sharon Huws, Matt Hegarty, Martin Swain and Joe Gallagher**
IBERS, Aberystwyth University, Plas Gogerddan, Aberystwyth SY23 3EB;*mad27@aber.ac.uk; +44 (0) 1970 823 123; **jbg@aber.ac.uk; +44 (0) 1970 823 147

Introduction

Macroalgae are considered as third generation biofuel feedstock and have recently received a lot of attention as one of the most promising non-food sources of biomass derived renewable energy. Due to their high biomass output consisting of readily degradable carbohydrates, macroalgae can be converted not only into biofuels but also into broad range of platform chemicals. Sustainable use of macroalgae cultivated in immense resources of available sea water can create a promising alternative to products derived from fossil fuel based refineries. However, to unlock potential of macroalgae as a new generation feedstock there is a need to develop an efficient conversion system that will facilitate macroalgae break down and conversion into desired products. This conversion can be achieved by applying unique properties of microbes that use complex macroalgae polysaccharides converting them to simple sugars that can be subsequently fermented to bioproducts (Fig. 1)

Main aims of the project

1. Screen for microbes/enzymes capable of hydrolysing macroalgal biomass and fermenting the component sugars to products of interest.
2. Characterise microbes/enzymes under a range of conditions including high salt concentrations to determine suitability for use in commercial applications.

Results

- A large number of microbes were isolated.
- Microbes were identified that produced enzymes capable of hydrolysing macroalgal polysaccharides.
- Genomic sequence analysis showed these microbes contained pathways for the production of a range of platform chemicals.
- A metagenomic library was constructed and is currently being screened.

Future plans

- Develop specific screening assays for environmental microbes’ enzymes degrading fucoidan and cellulose.
- Functional based and sequence based screening of metagenomic libraries/metagenomic DNA.
- Determine biocommodities produced by selected microbes.
- Assess selected microbes/enzymes to work under extreme conditions.

Methods

1. Culture dependent methods include isolation of microbes from three different sources: from macroalgae itself, from intestines of marine limpets parasitizing on macroalgae and from faecal contents of the North Ronaldsay Sheep that graze on macroalgae as part of their diet. Isolates were screened for enzymes degrading alginate, laminaran, fucoidan and cellulose. Selected microbes are subsequently screened for fermentation products of commercial importance and assessed to work in extreme conditions (Fig. 2)
2. Culture independent methods include isolation of metagenomic DNA from marine limpets intestines and construction of metagenomic libraries. The libraries/metagenomic DNA was subsequently screened for macroalgae polysaccharide degrading enzymes using functional based approaches as well as sequence based screening (Fig. 3)