
Algal-bacterial interactions: a culture-dependent method to study acclimation of *Ectocarpus subulatus* to salinity

Hetty Kleinjan*¹, Simon Dittami¹, Christian Jeanthon², and Catherine Boyen¹

¹Laboratoire de Biologie Intégrative des Modèles Marins [Roscoff] (LBI2M) – CNRS : UMR8227, Université Pierre et Marie Curie [UPMC] - Paris VI – Station Biologique de Roscoff Place Georges Teissier 29680 Roscoff, France

²Adaptation et diversité en milieu marin [Roscoff] (ADMM) – CNRS : UMR7144, Université Pierre et Marie Curie [UPMC] - Paris VI – Station Biologique de Roscoff Place Georges Teissier 29680 Roscoff, France

Abstract

Macroalgae live in close association with microbes, e.g. symbiotic bacteria, and their interactions are important determinants for algal performance and physiology. Despite these clear observations, the role of algal-bacterial interactions in adaptation and acclimation processes often goes unnoticed. Here, we study the fresh water strain (FWS) of *Ectocarpus subulatus*, a small filamentous brown alga. This strain tolerates a broad range of salinities compared to other algae within the *Ectocarpales*, yet this ability greatly depends on its associated microbiome (Dittami et al. 2016).

We are interested to elucidate the mechanisms involved in the acclimation of the alga to changing salinities. One strategy is to assess metabolic interactions between partners grown individually and in co-cultures.

Upcoming functional studies require cultivable isolates. To isolate bacterial partners, direct-planting and dilution-to-extinction techniques were used with both chemically defined and undefined low-nutrient culture media. Ground algae, algal culture medium, and cell wall extracts were used as inocula. These experiments resulted in the isolation of 250 strains, covering 35 bacterial species, within 29 different genera phylogenetically dispersed into the *Betaproteobacteria* (50%, mostly *Limnobacter* sp.), *Alphaproteobacteria* (27%, eg. *Bosea* sp., *Hyphomonas* sp.), *Gammaproteobacteria* (10%, mostly *Halomonas* sp.), *Firmicutes* (5%, mostly *Bacillus* sp.), *Bacteroidetes* (5%, only *Imperialibacter* sp.), and *Actinobacteria* (3%). The next step will be the identification of bacterial strains and/or minimal model communities that allow the FWS to grow at low salinity. The resulting simplified microecosystem, the so-called 'holobiont', and its response to changing salinities, will then be investigated in more detail using transcriptomics and metabolomics.

Keywords: brown algae, ectocarpus, abiotic stress, holobiont, bacterial cultivation, metabolomics, transcriptomics, marine model

*Speaker