

phenotype. The complete phenotyping of the segregant population will allow to test functional links between parietal composition, cell morphology and turgor pressure, and to determine the nature of the mutation responsible for the [ecb] phenotype, the locus of which will be identified by an NGS-based positional cloning technique (Billoud et al., 2015).

### 16PO.3

#### A FORWARD GENETICS APPROACH IN *ULVA MUTABILIS* (CHLOROPHYTA) TO DECIPHER BACTERIA-INDUCED MORPHOGENESIS AND CROSS-KINGDOM INTERACTIONS

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Morphogenesis of the green macroalga *Ulva* is highly dependent on the appropriate microbiome in the surrounding environment. *U. mutabilis* (Føyn) loses its typical morphology and develops into callus-like colonies, when grown in the laboratory under axenic conditions. Interestingly, normal growth and morphogenesis can be completely recovered by the combination of two specific bacteria belonging of the strains *Roseobacter* and *Cytophaga* or by the application of partly purified morphogenetic compounds released by these bacteria (1, 2). The cross-kingdom cross talk of this unique tripartite community will be now investigated on its molecular genetics level including the generation of transgenic *Ulva*. An “*Ulva* genetic tool kit” containing a stable macroalgal transformation system was developed and paves thus the way to study the underlying regulatory mechanism of *Ulva*'s morphogenesis (W. Oertel, T. Wichard and A. Weissgerber, Journal of Phycology, in revision). Here, we used the codon adapted phleomycin resistant cassette for an insertional mutagenesis approach. Our screening for mutant phenotypes was based on the missing response to the bacterial morphogenetic compounds. A first collection of insertional mutants revealed morphotypes comprising atypical thallus formations and/or altered algal attraction patterns of the associated bacteria. We thus isolated preferentially those transformants that develop callus-like structures or incomplete morphotypes in the presence of the two essential bacteria, hypothesizing that the algal perception of bacterial morphogenetic compounds is impaired. Now, we aim to identify and functionally characterize the affected genes that are involved in signal transduction pathways mediating the bacteria-induced algal morphogenesis. This forward genetic approach will shed light on the molecular and cellular mechanisms in seaweed development.

References: (1) Spoerner et al. 2012, Journal of Phycology 48, 1433-1447; (2) Wichard et al., 2015, Frontiers in Plant Science 6:72.

### 16PO.4

#### TOWARDS AN UNDERSTANDING OF THE CYTOLOGICAL DIVERSITY OF GREEN SEAWEEDS (ULVOPHYCEAE)

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Although there is truth in the assertion that red algal-derived lineages dominate the oceans while green lineages dominate terrestrial environment, at least green seaweeds defy this sweeping statement. In coastal environments, green seaweeds (Ulvophyceae) proved extremely successful from an evolutionary as well as an ecological perspective. A rich fossil record testifies their presence since at least the Ordovician and even now green seaweeds are ubiquitous from polar to tropical regions. Perhaps more spectacular than the number of species they comprise, are the diversity of morphologies and cytologies they display. Morphological types range from unicells and simple multicellular filaments to sheet-like and complex corticated thalli. Cytological layouts range from typical small cells containing a single nucleus and chloroplast to giant cells containing millions of nuclei and chloroplasts. This cytomorphological differentiation most likely coincided with profound changes in their genomes, which reflects in the use of different translation factors, an altered genetic code as well as accelerated evolution of the ribosomal DNA. In order to understand how the evolution of these morphological and cytological types links to genomic changes we combine whole genome sequencing (*Ulva*) with transcriptomics of selected green seaweed (*Acetabularia*, *Blastophysis*, *Bryopsis*, *Boodlea*, *Caulerpa*) and unicellular ulvophytes. We analyze the generated data with state-of-the-art methods for comparative genomics and transcriptomics; moreover, we implement the data in the online infrastructure pico-PLAZA (<http://bioinformatics.psb.ugent.be/pico-plaza/>) that integrates information generated by green algal sequencing initiatives and advanced tools for data mining.