

Towards an understanding of the cytological diversity of green seaweeds (*Ulvophyceae*)

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In coastal environments green seaweeds (Ulvophyceae) are extremely successful from an evolutionary as well as an ecological perspective. The diversity of morphologies and cytologies they display is remarkable. Morphological types range from unicells and simple filaments to sheet-like and complex corticated thalli. Cytological layouts range from typical small cells containing a single nucleus to giant cells containing millions of nuclei. 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 seaweeds (*Acetabularia*, *Blastophysa*, *Bryopsis*, *Boodlea*, *Caulerpa*) and unicellular Ulvophyceae. Here, as a first step we evaluate the efficiency of *de novo* assembly of transcriptomes. Thereto, we use a reference dataset of *Chlamydomonas*, the closest relative to the Ulvophyceae for which a complete whole genome sequence is available. 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.

Keywords: Ulvophyceae; morphology; evolution; transcriptomics