## Comparative Transcriptomics and green seaweeds: a novel approach to unravel the remarkable morphology of Ulvophyceae

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Multicellularity and macroscopic growth have evolved independently several times during the evolution of the class of green algae Ulvophyceae. This class is indeed characterised by an extraordinary variety in body morphology, and it includes both unicellular and multicellular organisms, siphonous cell structure and multinucleate cells (Leliaert *et al.*, 2012). However, genetic features leading to this morphological diversification remain poorly understood. Within this project, we aim to generate transcriptomic data from taxonomically relevant selected species belonging to the Class Ulvophyceae. Comparative transcriptomics and genomics, in fact, offer a promising approach to unravel differences and similarities in genome composition and gene expression profiles between different species, providing useful insights on how evolution shaped genomes and on how this is reflected in different phenotypes and in different organisms.

Here I will present data on a most unusual chloroplast architecture in this group of marine seaweeds. The chloroplast genome typically has a circular genetic map encoding for 100–200 distinct genes (Bendich, 2007), however, in certain Families within the Ulvophyceae Class, the chloroplast genomes result fragmented in several plasmid–like molecules that resemble the peculiar minicircule–based chloroplast genome of some dinoflagellates species (Howe *et al.*, 2008). We sequenced the protein and DNA content from the chloroplast–enriched fraction of selected ulvophyceae and RNA–Seq analysis of retro–transcripts generated with both oligo–dT and with random oligonucleotides. Our findings indicate that sequences encoded by the plasmid–like molecules are highly divergent from the respective ortholog sequences present in "classical" chloroplast genomes.

## **Keywords**

Seaweeds; Ulvophyceae; morphology; unusual chloroplast genome; comparative genomics; comparative transcriptomics.

## References

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