

Basal Cryptophytes. They form a sister clade to photosynthetic cryptomonads. These two clades together (cryptomonads and basal cryptophytes) are a sister clade to the *Goniomonas* clade. *Goniomonas* is aplastidic, has never acquired a plastid, and is currently considered as an ancestor to plastidic cryptomonadales. Upon the discovery of basal cryptophytes, the question arose whether they constitute the most divergent plastid-containing cryptomonad clade, or a new heterotrophic group at the base of the cryptomonad tree. Here, we combined phylogenetic and environmental study to address this question. The maximum likelihood phylogeny of 18S rRNA nuclear genes confirmed placement of basal cryptophytes at the base of the cryptomonad tree. We designed a specific oligonucleotide probe, to detect members of this clade in environmental samples by Catalysed Reported Deposition-Fluorescence *in situ* Hybridization (CARD-FISH), and to observe their basic morphology. None of the cells hybridized with the new probe showed chlorophyll-a autofluorescence at 590 nm, meaning they were aplastidic. The phylogenetic analysis of 18S rRNA nucleomorph genes did not produce a sister clade to photosynthetic cryptomonads, suggesting that Basal Cryptophyceae had not acquired a plastid at all. Altogether, these results indicated that the last aplastidic ancestor of cryptomonads could have been a basal cryptophyte, and that the engulfment of a red algal symbiont might have been a more recent event than when assuming radiation of the plastidic cryptomonads directly from *Goniomonas*. If confirmed upon culturing and studying a species from basal cryptophytes, it will change the view of evolution of plastidic cryptophytes and nucleomorphs.

## 5OR.7

### WHOLE GENOME SEQUENCING OF THE ANTARCTIC GREEN ALGA *PRASIOLA CRISPA*

Marie Pažoutová<sup>1</sup> ([marie.pazoutova@gmail.com](mailto:marie.pazoutova@gmail.com)), Olivier De Clerck<sup>2</sup> ([olivier.declerck@ugent.be](mailto:olivier.declerck@ugent.be)), Andrea Del Cortona<sup>3</sup> ([andrea.delcortona@gmail.com](mailto:andrea.delcortona@gmail.com)), Nicolas Dauchot<sup>4</sup> ([nicolas.dauchot@unamur.be](mailto:nicolas.dauchot@unamur.be)), Jiří Košnar<sup>1</sup> ([JiriKosnar@seznam.cz](mailto:JiriKosnar@seznam.cz)), Akira F Peters<sup>5</sup> ([akirapeters@gmail.com](mailto:akirapeters@gmail.com)), Fabio Rindi<sup>6</sup> ([f.rindi@univpm.it](mailto:f.rindi@univpm.it)), Alison R Sherwood<sup>7</sup> ([asherwoo@hawaii.edu](mailto:asherwoo@hawaii.edu)), David R Smith<sup>8</sup> ([dsmitt242@uwyo.ca](mailto:dsmitt242@uwyo.ca)), Heroen Verbruggen<sup>9</sup> ([heroen.verbruggen@gmail.com](mailto:heroen.verbruggen@gmail.com)) and Stephane Rombauts<sup>10</sup> ([strom@psb.ugent.be](mailto:strom@psb.ugent.be))

<sup>1</sup>Department of Botany, University of South Bohemia, České Budějovice 37005, Czech Republic;

<sup>2</sup>Phycology Research Group, Biology Department, Ghent University, Gent B-9000, Belgium;

<sup>3</sup>Department of Plant Systems Biology, VIB/Ugent, Gent B-9052, Belgium; <sup>4</sup>Research Unit in Plant

Biology, University of Namur, Namur 5000, Belgium; <sup>5</sup>Bezhin Rosko, Santec 29250, France; <sup>6</sup>Dipartimento di Scienze della Vita e dell'Ambiente, Università Politecnica delle Marche, Ancona 60131, Italy; <sup>7</sup>Botany Department, University of Hawai'i at Mānoa, Honolulu HI 96822, United States; <sup>8</sup>Biology Department, University of Western Ontario, London N6A 5B7, Canada; <sup>9</sup>School of BioSciences, University of Melbourne, Melbourne 3010, Australia and <sup>10</sup>Department of Plant Systems Biology, VIB/Ugent, Gent B-9052, Belgium

The trebouxiophycean genus *Prasiola* is an excellent model for the study of ecological transitions, as it is one of the rare algal genera that includes marine, freshwater and terrestrial representatives. The generitype *Prasiola crispa*, an extremophile widely distributed in cold temperate and polar regions of both hemispheres, has strong potential to serve as a good model of the evolution of both green algae and the land plants. We are using next-generation sequencing data (Illumina technology) to obtain its complete genome sequence. Additionally, we are testing the Oxford Nanopore's MinION technology in order to complete the assembly with ultra-long reads. We are presenting the first results of our project: complete sequences of *P. crispa* organelles, the mitochondrion (100,036 nt) and the plastid genome (211,767 nt). Both have relatively low GC content (29.3% and 28.8%, respectively), as is usual among green algae. The gene content corresponds well with other sequenced trebouxiophyte organellar genomes, with the only peculiarity being the presence of the *rp10* gene in the mitochondrion. In the plastid DNA, we discovered highly reduced remnants of the ancestral plastid inverted repeats (IRs, 851 bp) that bear no genes. There are clusters of non-algal mobile elements and unidentified open reading frames in both genomes; these elements appear to be organelle-specific.

## 5OR.8

### TACKLING RAPID RADIATIONS WITH CHLOROPLAST PHYLOGENOMICS IN THE RHODOMELACEAE

Pilar Díaz-Tapia<sup>1</sup> ([pdiaz@udc.es](mailto:pdiaz@udc.es)), Christine A Maggs<sup>2</sup> ([cmaggs@bournemouth.ac.uk](mailto:cmaggs@bournemouth.ac.uk)), John A West<sup>3</sup> ([jwest@unimelb.edu.au](mailto:jwest@unimelb.edu.au)) and Heroen Verbruggen<sup>3</sup> ([heroen.verbruggen@unimelb.edu.au](mailto:heroen.verbruggen@unimelb.edu.au))

<sup>1</sup>BioCost Research Group, University of A Coruña, A Coruña 15071, Spain; <sup>2</sup>Faculty of Science and Technology, Bournemouth University, Bournemouth BH12 5BB, United Kingdom and <sup>3</sup>School of Botany, University of Melbourne, Melbourne 3010, Australia

The family Rhodomelaceae, with about 1000 species, is the most species-rich family of the red algae. Its