PHYLOGENY OF THE CLADOPHOROPHYCEAE (CHLOROPHYTA) INFERRED FROM PARTIAL LSU RRNA GENE SEQUENCES: IS THE RECOGNITION OF A SEPARATE ORDER SIPHONOCLADALES JUSTIFIED?

Leliaert Frederik¹, Florence Rousseau², Bruno de Reviers² and Eric Coppejans¹

- Ghent University (RUG), Biology Department, Research Group Phycology Krijgslaan 281, S8, 9000 Ghent, Belgium e-mail: frederik.leliaert@rug.ac.be
- Département de Systématique, MNHN-UPMC-CNRS (FR 1541) Herbier Cryptogamique, Muséum National d'Histoire Naturelle 12, rue Buffon, F-75005 Paris, France

Phylogenetic relationships within the class Cladophorophyceae were investigated. For 36 species, representing 17 genera, the sequences of the 5'-end of the large subunit rRNA were aligned and analysed. *Ulva fasciata* and *Acrosiphonia spinescens* were used as outgroup taxa. The final alignment consisted of 644 positions containing 208 parsimony informative sites. The analysis showed three lineages within the Cladophorophyceae: *Cladophora horii* diverging first, followed by two main lineages. A first lineage includes *Cladophora* species and genera with a reduced thallus architecture. The second lineage comprises siphonocladalean taxa (excluding part of *Cladophoropsis* and including some *Cladophora* species). From this perspective the Siphonocladales form a monophyletic group, the Cladophorales remaining paraphyletic.