

Supertree: Toward a comprehensive phylogeny for brown seaweeds (Phaeophyceae, Ochrophyta)

Van der Aa Pierrot¹, Vieira Christophe¹, Guiry Michael², Verbruggen Heroen³ and De Clerck Olivier¹

¹ Universiteit Gent: Onderzoeksgroep Fycologie (UGent), Campus De Sterre, S8, Krijgslaan 281, 9000 Gent, Belgium

E-mail: pvderaa@vub.be

² National University of Ireland, AlgaeBase, Room 301, Ryan Institute, National University of Ireland, University Road, Galway, H91 TK33, Ireland

³ School of Botany, University of Melbourne, Botany building (122), Professors Walk, Ground floor, room 104, Victoria, 3010, Australia

Large and comprehensive phylogenetic trees are desirable for studying macroevolutionary processes. The brown seaweeds or Phaeophyceae comprise of over 2000 species (Guiry and Guiry, 2018). Over the past few years, molecular-assisted taxonomic studies have significantly contributed to our knowledge of the biodiversity within several phaeophycean groups. Phylogenetic efforts have nonetheless been directed towards lower taxonomic ranks, notable genera or family at best. Silberfeld et al. (2011, 2014) provided the first phylogenetic tree for the Phaeophyceae including representatives of most orders, refining our understanding of ordinal-level phylogenetic relationships. A comprehensive phylogeny of the Phaeophyceae, encompassing all presently known species, is nevertheless still lacking. This project aims to provide the first all-inclusive tree of life of the brown seaweeds, by applying a supertree approach. This will be done by compiling sequences of all species of brown seaweeds for twelve well represented nuclear, mitochondrial and chloroplast markers from online nucleotide databases. Phylogenies at the ordinal-level will be first constructed using a maximum likelihood and Bayesian analyses, and latter grafted to an updated backbone phylogeny.

Keywords: Phaeophyceae; Phylogeny; Supertree; Brown seaweeds