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

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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, refinining 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