

Phylogeny of algal sequences encoding carbohydrate sulfotransferases, formylglycine-dependent sulfatases, and putative sulfatase modifying factors

ABSTRACT

Many algae are rich sources of sulfated polysaccharides with biological activities. The physicochemical/rheological properties and biological activities of sulfated polysaccharides are affected by the pattern and number of sulfate moieties. Sulfation of carbohydrates is catalyzed by carbohydrate sulfotransferases (CHSTs) while modification of sulfate moieties on sulfated polysaccharides was presumably catalyzed by sulfatases including formylglycine-dependent sulfatases (FGly-SULFs). Post-translationally modification of Cys to FGly in FGly-SULFs by sulfatase modifying factors (SUMFs) is necessary for the activity of this enzyme. The aims of this study are to mine for sequences encoding algal CHSTs, FGly-SULFs and putative SUMFs from the fully sequenced algal genomes and to infer their phylogenetic relationships to their well characterized counterparts from other organisms. Algal sequences encoding CHSTs, FGly-SULFs, SUMFs, and SUMF-like proteins were successfully identified from green and brown algae. However, red algal FGly-SULFs and SUMFs were not identified. In addition, a group of SUMF-like sequences with different gene structure and possibly different functions were identified for green, brown and red algae. The phylogeny of these putative genes contributes to the corpus of knowledge of an unexplored area. The analyses of these putative genes contribute toward future production of existing and new sulfated carbohydrate polymers through enzymatic synthesis and metabolic engineering.

Keyword: Algae; Carbohydrate sulfotransferases; Sulfatases; Phylogeny; Sulfatase modifying factors