

Unraveling the nuclear and chloroplast genomes of an agar producing red macroalga, *Gracilaria changii* (Rhodophyta, Gracilariales)

ABSTRACT

Agar and agarose have wide applications in food and pharmaceutical industries. Knowledge on the genome of red seaweeds that produce them is still lacking. To fill the gap in genome analyses of these red algae, we have sequenced the nuclear and organellar genomes of an agarophyte, *Gracilaria changii*. The partial nuclear genome sequence of *G. changii* has a total length of 35.8 Mb with 10,912 predicted protein coding sequences. Only 39.4% predicted proteins were found to have significant matches to protein sequences in SwissProt. The chloroplast genome of *G. changii* is 183,855 bp with a total of 201 open reading frames (ORFs), 29 tRNAs and 3 rRNAs predicted. Five genes: *ssrA*, *leuC* and *leuD* CP76_p173 (*orf139*) and *pbsA* were absent in the chloroplast genome of *G. changii*. The genome information is valuable in accelerating functional studies of individual genes and resolving evolutionary relationship of red seaweeds.

Keyword: Agarophyte; *Gracilaria changii*; Nuclear genome; Plastid genome