

The complete mitochondrial genome of the economic red alga, *Gracilaria chilensis*

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<b>Abstract</b>	<p><i>Gracilaria chilensis</i> is an economically important marine alga. In this study, we obtained complete mitogenome of <i>G. chilensis</i> by high-throughput sequencing, which was mapped as a circular molecule of 26,897 bp with 27.56% GC content and was identified 53 genes, including 25 protein-coding genes, 2 rRNA genes, 26 tRNA genes, and 1 group II intron inserted into the trnI gene. In addition, a 162-bp stable stem loop was found in intergenic regions, which was most likely associated with DNA transcription and replication. The Bayesian phylogenetic tree of Gracilariaceae revealed that <i>G. chilensis</i> and <i>G. salicornia</i> and <i>G. changii</i> shared a closer relationship than <i>G. vermiculophylla</i> in the genus <i>Gracilaria</i>.</p>
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