

The complete plastid genomes of *Betaphycus gelatinus*, *Eucheuma denticulatum*, and *Kappaphycus striatus* (Solieriaceae: Rhodophyta) and their phylogenetic analysis

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<b>Title</b>	The complete plastid genomes of <i>Betaphycus gelatinus</i> , <i>Eucheuma denticulatum</i> , and <i>Kappaphycus striatus</i> (Solieriaceae: Rhodophyta) and their phylogenetic analysis
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<b>Abstract</b>	<p><i>Betaphycus</i>, <i>Eucheuma</i> and <i>Kappaphycus</i> (Gigartinales, Florideophyceae) are the most commercially important genera of the family Solieriaceae that produce carrageenan. Here, three complete plastid genomes of <i>Betaphycus gelatinus</i>, <i>Eucheuma denticulatum</i> and <i>Kappaphycus striatus</i> were fully sequenced using next-generation sequencing technology. Genome organizations and gene contents of the three plastid genomes were highly alike. They all had circular mapping organizations and the sizes were 178,394 bp (<i>B. gelatinus</i>), 177,003 bp (<i>E. denticulatum</i>), and 176,763 bp (<i>K. striatus</i>). They encoded almost the same set of plastid genes (238-240), including 202 to 204 protein-encoding genes, 30 transfer RNA genes (tRNAs), 3 ribosomal RNA genes (rRNAs), 2 misc_RNAs (<i>ffs</i>, <i>rnpB</i>), and 1 transfer-messenger RNA gene (<i>tmRNA</i>). One group II intron interrupting the <i>trnM</i> gene was identified in each of these three plastid genomes. Other three plastid genomes from species of the order Gigartinales including <i>Kappaphycus alvarezii</i>, <i>Chondrus crispus</i> and <i>Mastocarpus papillatus</i> have been reported. The plastid genome organization at the level of the order Gigartinales was highly conserved. Co-linear analysis among the six plastid genomes of the Gigartinales showed the considerable sequence synteny with the exception of one remarkable gene rearrangement. The approximately 12.5-kb gene fragment from <i>genepsaM</i> to <i>toycf21</i> in plastid genomes of the four species of the Solieriaceae was completely reversed compared to that of <i>M. papillatus</i> and <i>C. crispus</i>. It might be used as the potential phylogenetic markers uniting the species of the Solieriaceae. In addition, phylogenetic analysis based on 138 shared protein-encoding genes from 53 Florideophyceae plastid genomes indicated all species were clearly divided into five clades corresponding to their subclasses. The results suggested there was a non-monophyletic relationship of the order Gigartinales. Four species of the family Solieriaceae formed one clade and <i>E. denticulatum</i> was basal relative to the other three species. The novel plastid genomes expand the available plastid pool for red algae which would facilitate the phylogenetic study in algae.</p>
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