

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

Publons ID	32251024
Wos ID	WOS:000559876700001
Doi	10.1007/s10811-020-02120-5
Title	The complete plastid genomes of <i>Betaphycus gelatinus</i> , <i>Eucheuma denticulatum</i> , and <i>Kappaphycus striatus</i> (Solieriaceae: Rhodophyta) and their phylogenetic analysis
First Author	
Last Author	
Authors	Zhang, J; Liu, N; Meinita, MDN; Wang, XM; Tang, XM; Wang, GL; Jin, YM; Liu, T;
Publish Date	OCT 2020
Journal Name	JOURNAL OF APPLIED PHYCOLOGY
Citation	2
Abstract	<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 (ffs, rnpB), and 1 transfer-messenger RNA gene (tmRNA). One group II intron interrupting the trnM 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>genespsaM</i> to <i>ycf21</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>
Publish Type	Journal
Publish Year	2020
Page Begin	3521
Page End	3532
Issn	0921-8971
Eissn	1573-5176
Url	https://www.webofscience.com/wos/woscc/full-record/WOS:000559876700001
Author	Dr MARIA DYAH NUR MEINITA, S.Pi