Complete plastid genome of *Kappaphycus alvarezii*: insights of large-scale rearrangements among Florideophyceae plastid genomes

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Abstract	Kappaphycus alvarezii is a large commercial tropical marine red alga. In this study we used next- generation sequencing to determine the complete plastid genome of K. alvarezii. The plastid genome mapped a 178,205-bp circular DNA molecule with a GC content of 29.6%, without any inverted repeat region, and encoded a standard set of 202 protein-coding genes, including 4 open reading frames, 30 transfer RNA genes, 3 ribosomal RNA genes, and 1 transfer-messenger RNA gene. Only one group II intron interrupting the trnMe gene was detected. Comparative analysis of the seven plastid genomes from three orders including Gigartinales, Gracilariales, and Peyssonneliales revealed that the genomes were more conserved except five remarkable gene rearrangements. However, an approximately 12.5-kb gene fragment from the psaM to ycf21 gene in K. alvarezii plastid genome was completely reversed compared to that in published plastid genomes from the Florideophyceae. To our knowledge, the gene rearrangement was identified for the first time in the plastid genomes of red algal species. In addition, phylogenetic analysis of 49 Florideophyceae species based on 144 shared protein-coding genes suggested that different species from the same class clustered together according to their sources: three species of Gigartinales formed one group as the subbranch of Florideophyceae, but K. alvarezii was the most closely related to Riquetophycus sp. from the Peyssonneliales.
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