

Comparative genomics and systematics of *Betaphycus*, *Eucheuma*, and *Kappaphycus* (Solieriaceae: Rhodophyta) based on mitochondrial genome

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<b>Abstract</b>	<p><i>Betaphycus</i> Doty, <i>Eucheuma</i> J. Agardh, and <i>Kappaphycus</i> Doty (Solieriaceae, Gigartinales) are the three most commercially important seaweed genera that produce carrageenan. In the present study we provide mitogenomes of <i>Betaphycus gelatinus</i>, <i>Eucheuma denticulatum</i> and <i>Kappaphycus alvarezii</i>. The mitogenomes of these three species contain a set of 50 genes, including 24 protein-coding genes, 2 rRNA genes, and 24 tRNA genes. The mitogenome length ranges from 25,198 bp (<i>Kappaphycus alvarezii</i>) to 25,327 bp (<i>Eucheuma denticulatum</i>). As compared with the previous published mitogenomes of Florideophyceae species, only the species in Gelidiaceae and Pterocladaceae have smaller mitochondrial genome size than these reported here. At the junction of two transcription units, we identified a stem-loop structure in six representative Gigartinales species, which is presumed to play an important role in the replication and transcription of mitochondrial genes. In Gigartinales the difference in gene order among the four Solieriaceae (<i>B. gelatinus</i>, <i>E. denticulatum</i>, <i>K. alvarezii</i>, <i>K. striatus</i>) and other two Gigartinales species (<i>Chondrus crispus</i> and <i>Mastocarpus papillatus</i>) can be explained by inversion of two tRNA genes. Collinearity analysis of the 12 mitochondrial genomes of Florideophyceae showed considerable sequence synteny across all the species compared, with the exception of a highly variable region between <i>atp6</i> and <i>rpl20</i> genes. Phylogenetic analyses based on 21 shared mitochondrial genes showed that the four Solieriaceae species form one clade (Solieriaceae clade). Within this clade, <i>B. gelatinae</i> is basal relative to the other three species. The genus <i>Kappaphycus</i> is more closely related to <i>Eucheuma</i> than <i>Betaphycus</i>.</p>
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