

## MITOGENOME ANNOUNCEMENT

**Complete mitochondrial genome of the marine red alga *Grateloupia angusta* (Halymeniales)**Su Yeon Kim<sup>1</sup>, Eun Chan Yang<sup>2</sup>, Sung Min Boo<sup>1</sup>, and Hwan Su Yoon<sup>3</sup><sup>1</sup>Department of Biology, Chungnam National University, Daejeon, Republic of Korea, <sup>2</sup>Marine Biotechnology Research Center, Korea Institute of Ocean Science & Technology, Ansan, Republic of Korea, and <sup>3</sup>Department of Biological Sciences, Sungkyunkwan University, Suwon, Republic of Korea**Abstract**

The first complete mitochondrial genome (27,943 bp) of the halymenialean red alga, *Grateloupia angusta*, was sequenced. The circular mitogenome contains 47 genes, including 26 protein-coding, 19 tRNA and 2 rRNA genes. The *rps3* and *rpl16* genes are overlapped by 7 bp. The majority of protein-coding genes (17 of 26 genes) use typical ATG start codon, however, 9 genes use alternative start codons such as ATT, AAT, TTA and TTG. The *G. angusta* mitogenome shows a significant difference to that of *Chondrus crispus* (Gigartinales) in gene synteny and tRNA compositions.

**Keywords**

Complete mitochondrial genome, Florideophyceae, *Grateloupia angusta*, Halymeniales, Rhodophyta

**History**

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The marine red algal genus *Grateloupia* is the most speciose genus (91 species) in the red algal Halymeniales that is widely distributed in cold-temperate to tropical waters (Lee et al., 2009; Mateo-Cid et al., 2005). Recently, *Grateloupia* has become the focus of research because several species have been introduced from East Asia to Australasia, Europe and North America (García-Jiménez et al., 2008; Gavio & Fredericq, 2002; Miller et al., 2011; Verlaque et al., 2005). *Grateloupia angusta* is one of common subtidal species in Korea and Japan, and it is the unique host species for *Kintokiocolax aggregato-cerantha*, a parasitic red alga. For the identification, monitoring and management of red algal species, mitochondrial genes have been usefully employed (Kim et al., 2011; Le Gall & Saunders, 2010). The mitochondrial genome data will be broadly used in population genetics and biogeographic studies (Kim et al., 2012).

We sequenced and characterized the complete mitochondrial genome of *G. angusta* (GenBank accession number KC875853) using a next-generation genome sequencing method (Ion Torrent PGM, Life Technologies, San Francisco, CA), the first species from the Halymeniales to be investigated. The mitogenome of *G. angusta* shows a total 27,943 bp of circular genome with 30.2%

GC content with a typical florideophycean red algal gene synteny (i.e. *Chondrus crispus*, NC\_001677, Leblanc et al., 1995). The *G. angusta* mitogenome contains 47 genes as shown in Figure 1, including 2 ribosomal RNAs for large and small subunits (rRNA), 19 transfer RNAs (tRNA) and 26 protein-coding genes. The protein-coding genes consist of 18 respiratory protein-coding, 5 ribosomal protein-coding, 1 translocase protein-coding (*secY*), 1 intronic reading frame (*orf-Gang5*) and 1 hypothetical protein-coding gene (*orf-Gang35*) that similar to the unique *orf172* in *C. crispus*. Majority of the protein-coding genes (17 out of 26 genes) start with an ATG codon, however, 9 genes start with alternative codons (i.e. ATT for *atp6*, *orf-Gang5*, *rps11* and *secY*; TTA for *rpl16*, *sdh2* and *yfm39*; TTG for *cox2* and *sdh3*). The *cox1* and *trnI* genes are interrupted by group II introns. The *rpl16* and *rps3* are overlapped each other by 7 bp. The 19 tRNAs range from 71 to 86 bp in length, and can fold into the typical cloverleaf secondary structures.

The mitogenome of *G. angusta* (Halymeniales) is distinguished from that of *C. crispus* (Gigartinales) in gene contents and synteny. In total length, *G. angusta* is larger by 2111 bp than that of *C. crispus* (25,836 bp), because *G. angusta* contains a large group II intron (2333 bp) in *cox1*. Three hypothetical protein-coding genes of *C. crispus* mitogenome (*orf74*, *orf94* and *orf105*) are not found in *G. angusta*. In tRNA contents, *G. angusta* contains a unique *trnU* (Selenocystein), but lacks *trnH*, *trnW* and *trnY* genes. In gene synteny, two arrangements of transfer RNA genes in *G. angusta* (*trnG-sdh2* and *trnA-trnN*) are different from the homologous positions of *C. crispus* (*trnG-trnH1-trhH2-sdh2* and *trnA-trnR-trnY-trnN*). These differences could play important roles in mitogenome evolution in florideophycean red algae.

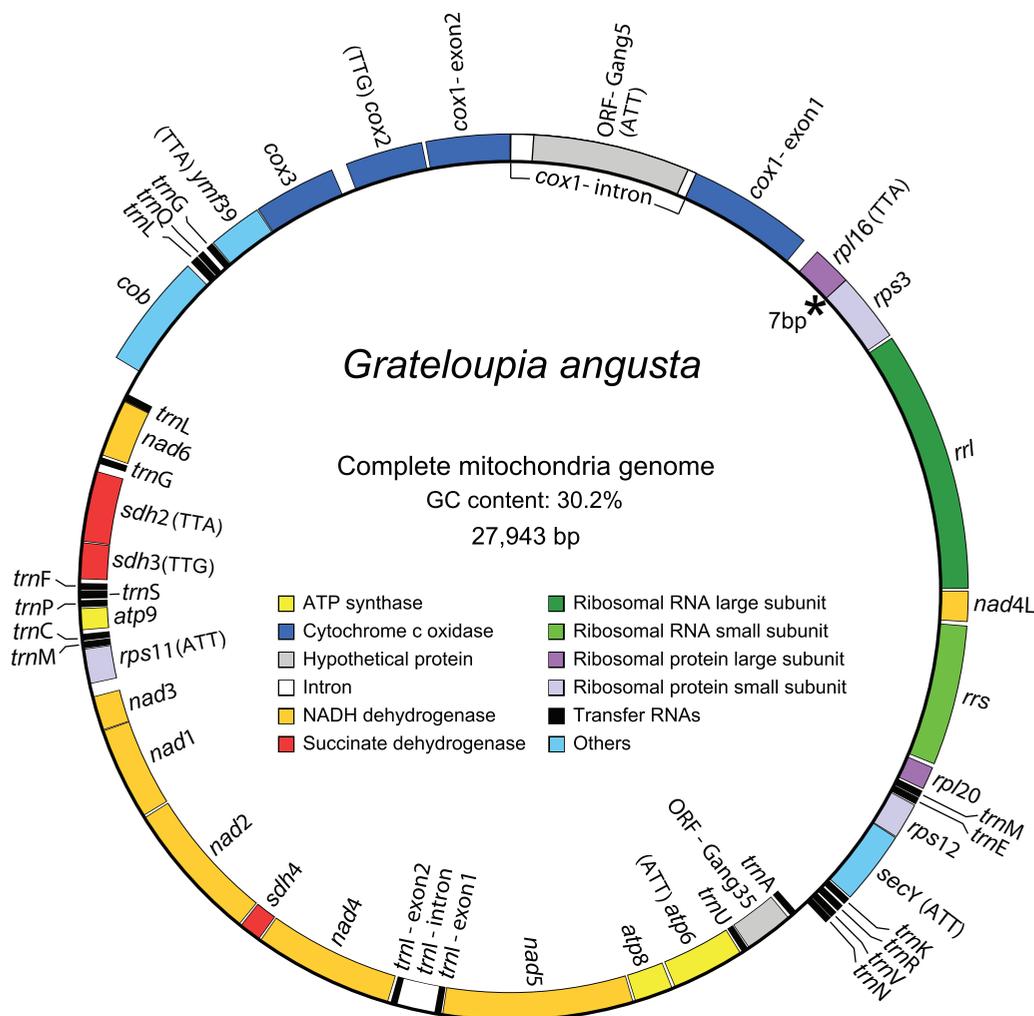


Figure 1. The circular-mapping mitochondria genome of *Grateloupia angusta*. The map was drawn by using OGDRAW (Bock et al., 2007). Features drawn on the inside and outside of the circle are transcriptionally clockwise and counter-clockwise strands, respectively. Genes belonging to different groups are color-coded. *cox1* interrupted by group II intron with reverse transcriptase homologous ORF and *trnI* interrupted by group II intron without ORF. The alternative start codons of 9 genes were given in parentheses. Asterisk indicates overlapping region between two genes.

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## Declaration of interest

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