

MITOGENOME ANNOUNCEMENT

**Complete mitochondrial genome of the agarophyte red alga
Gelidium vagum (Gelidiales)**Eun Chan Yang^{1*}, Kyeong Mi Kim^{2*}, Ga Hun Boo^{3*}, Jung-Hyun Lee¹, Sung Min Boo³, and Hwan Su Yoon²¹Marine Biotechnology Research Center, Korea Institute of Ocean Science & Technology, Ansan, Republic of Korea, ²Department of Biological Sciences, Sungkyunkwan University, Suwon, Republic of Korea, and ³Department of Biology, Chungnam National University, Daejeon, Republic of Korea**Abstract**

We describe the first complete mitochondrial genome of *Gelidium vagum* (Gelidiales) (24,901 bp, 30.4% GC content), an agar-producing red alga. The circular mitochondrial genome contains 43 genes, including 23 protein-coding, 18 tRNA and 2 rRNA genes. All the protein-coding genes have a typical ATG start codon. No introns were found. Two genes, *secY* and *rps12*, were overlapped by 41 bp.

Keywords

Complete mitochondrial genome, Florideophyceae, Gelidiales, *Gelidium vagum*, rhodophyta

History

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As a well-known agar-producing red alga with wide distribution, *Gelidium* (Gelidiales) is an important resource economically (Guiry & Guiry, 2013; Jeon et al., 2005; Kim et al., 2011; Millar & Freshwater, 2005). It has been used as a source of food and medicine, fertilizer, fodder for animals, and agar production. Recently, it has been used for alternative algal paper pulp and bioethanol production in Korea (Park et al., 2012; Seo et al., 2010). In spite of the economic and ecological importance of the members of the Gelidiales, no gelidialean genomes have been reported yet.

Gelidium vagum is common in Korea and Japan, and it has been introduced to North America and Europe (Mineur et al., 2012). In this study, we sequenced and characterized the complete mitochondrial genome of *G. vagum* (GenBank accession number KC875854) using next-generation genome sequencing methods (Ion Torrent PGM, Life Technologies, San Francisco, CA). The sample (vouch specimen ID: CNU032319) was collected from Manripo, Taean, Korea (36° 47' 05"N 126° 07' 49"E) and deposited in the Herbarium of the Chungnam National University (CNUK). This is the first complete mitogenome from the order

Gelidiales. The total length of mitogenome is 24,901 bp, which shows 36.6% A, 14.8% C, 15.6% G and 32.9% T with 69.5% AT content. Table 1 provides detailed information about the mitogenome. The *G. vagum* mitogenome contains 43 genes, including 23 protein-coding, 2 ribosomal RNA (rRNA) for large and small subunits, and 18 transfer RNA (tRNA) genes. Most of the protein-coding genes (18 out of 23 genes) encode respiratory proteins such as ATP synthase, cytochrome oxidase, and NADH dehydrogenase. All protein-coding genes start with an ATG codon, and stop with TAA codon, except *nad2*, *nad4L* and *sdh2*, which are terminated with TAG stop codon. The *rps12* and *secY* genes overlap by 41 bp. The 18 tRNAs range from 72 to 86 bp in length, and can be folded into the typical cloverleaf secondary structures.

The gene arrangement pattern of *G. vagum* is very similar with those of other florideophycean red algal species, such as *Chondrus crispus* (NC_001677), *Gracilaria andersonii* (HQ586060), and *Gr. oryzoides* (HQ586059), and *Plocamium pulvinata* (HQ586061) (Hancock et al., 2010; Leblanc et al., 1995). Regarding the base composition, the *G. vagum* mitogenome has relatively higher GC content (30.5%) than those of other florideophycean species; *C. crispus* (27.9%), *Gr. andersonii* (28%), *Gr. oryzoides* (28.1%), and *P. pulvinata* (23.9%).

We compared mitogenomes from agarophyte *G. vagum* (Gelidiales) and carraginiphyte *C. crispus* (Gigartinales), having close phylogenetic relationships (Le Gall & Saunders, 2007) with an available mitochondrial genome. It is apparent that *G. vagum* is 936 bp smaller than *C. crispus* (25,836 bp), mainly due to several missing genes in *G. vagum* [i.e., hypothetical protein-coding *orf172*, ribosomal protein-coding *rpl20*, *rnr5* rRNA, and 4 tRNAs (*trnG*, *trnH*, *trnR* and *trnY*)]. In contrast, three unique ORFs (*orf73*, *orf94*, and *orf105*) of *C. crispus* are not found in the *G. vagum* mitogenome. This result provides new insights into

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Table 1. Mitochondrial genome organization of *Gelidium vagum*.

Name	Strand	Start	End	Size	Start codon	End codon	Anticodon
<i>rnl</i>	+	21	2552	2532			
<i>rps3</i>	+	2569	3258	690	ATG	TAA	
<i>rpl16</i>	+	3260	3667	408	ATG	TAA	
<i>trnD</i>	+	3679	3750	72			GTC
<i>cox1</i>	+	3795	5393	1599	ATG	TAA	
<i>cox2</i>	+	5415	6182	768	ATA	TAA	
<i>cox3</i>	+	6345	7163	819	ATG	TAA	
<i>ymf39</i>	+	7166	7708	543	ATG	TAA	
<i>trnQ</i>	+	7789	7860	72			TTG
<i>trnL</i>	+	7874	7955	82			TAA
<i>cob</i>	+	7997	9148	1152	ATG	NAA	
<i>trnL</i>	–	9188	9271	84			TAG
<i>nad6</i>	–	9273	9881	609	ATG	TAA	
<i>trnG</i>	–	9899	9971	73			GCC
<i>sdh2</i>	–	10,047	10,796	750	ATG	TAG	
<i>sdh3</i>	–	10,798	11,187	390	ATG	TAA	
<i>trnF</i>	–	11,204	11,276	73			GAA
<i>trnS</i>	–	11,281	11,366	86			TGA
<i>trnP</i>	–	11,371	11,443	73			TGG
<i>atp9</i>	–	11,455	11,685	231	ATG	TAA	
<i>trnC</i>	–	11,728	11,800	73			GCA
<i>trnM</i>	–	11,803	11,877	75			CAT
<i>rps11</i>	–	11,880	12,239	360	ATG	TAA	
<i>nad3</i>	–	12,377	12,742	366	ATG	TAA	
<i>nad1</i>	–	12,755	13,738	984	ATG	TAA	
<i>nad2</i>	–	13,757	15,241	1485	ATG	TAG	
<i>sdhD</i>	–	15,254	15,496	243	ATG	TAA	
<i>nad4</i>	–	15,497	16,972	1476	ATG	TAA	
<i>nad5</i>	–	17,500	19,497	1998	ATG	TAA	
<i>atp8</i>	–	19,507	19,911	405	ATG	TAA	
<i>atp6</i>	–	19,913	20,674	762	ATG	TAA	
<i>trnU</i>	–	20,691	20,764	74			TCA
<i>trnA</i>	–	21,221	21,294	74			TGC
<i>trnN</i>	+	21,365	21,437	73			GTT
<i>trnV</i>	+	21,442	21,514	73			TAC
<i>trnR</i>	+	21,526	21,599	74			ACG
<i>trnK</i>	+	21,607	21,680	74			TTT
<i>secY</i>	+	21,708	22,496	789	ATG	TAA	
<i>rps12</i>	+	22,456	22,821	366	ATG	TAA	
<i>trnE</i>	+	22,832	22,904	73			TTC
<i>trnM</i>	+	22,906	22,977	72			CAT
<i>rrs</i>	+	23,195	24,567	1373			
<i>nad4L</i>	+	24,596	24,901	306	ATG	TAG	

the mitochondria genome evolution of the Florideophyceae with independent gene loss in two different orders.

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Declaration of interest

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