

# Complete mitochondrial genome of *Gracilaria changii* (Rhodophyta: Gracilariaceae)

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**Abstract** *Gracilaria changii* is an agarophyte that has been used for agar extraction and as salads. Currently, there are only three complete mitochondrial genomes of *Gracilaria* species available in GenBank. We report here the complete mitogenome of *G. changii* from Peninsular Malaysia using next-generation sequencing. It had a total length of 25,729 bp, comprising 50 genes (25 protein-coding genes – PCGs, 2 rRNA genes, and 23 tRNA genes). The gene synteny of *G. changii* was similar to *G. salicornia* from Peninsular Malaysia with three additional tRNA genes (*trnY*, *trnR*, *trnS1*) in comparison to *G. salicornia* from Hawaii. *G. changii* had similar start codons (ATG) for all the PCGs, but three (*rps3*, *rpl20*, and *secY*) had incomplete T-stop codons. Genomic data of *G. changii* is useful to build a more complete dataset for phylogenetic analyses in Gracilariaceae.

**Keywords** *Gracilaria changii* · Mitochondrial genome · Rhodophyta

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## Introduction

*Gracilaria changii* (B. M. Xia & I. A. Abbott) I. A. Abbott, J. Zhang & B. M. Xia (Abbott et al. 1991) is a marine species occurring in Southeast Asia (Myanmar, Malaysia, Thailand, Vietnam and Philippines) and southern China (Guiry and Guiry 2016). In Malaysia, *G. changii* and other *Gracilaria* species (e.g., *G. tenuistipitata* C.F.Chang & B.M.Xia) are consumed as salads as well as used for agar extraction (Phang 2006). The mass spectrometry standardized methanolic extract of *G. changii* possesses anti-inflammatory, gastroprotective, and anti-ulcerogenic properties (Shu et al. 2013).

The genetic diversity in *G. changii* from the west coast of Peninsular Malaysia is represented by six mitochondrial haplotypes as determined by *cox1* gene (Yow et al. 2011). Microsatellite markers from expressed sequence tags (ESTs) of seaweeds have been used to differentiate *G. changii* from various localities and two other *Gracilaria* species (Song et al. 2013). Surprisingly, most phylogenetic studies have not included *G. changii* for comparison (Yang et al. 2012; Lyra et al. 2015; Song et al. 2015).

The genus *Gracilaria* is represented by 186 species that are currently accepted taxonomically (Guiry and Guiry 2016). Despite this rich species diversity, to date, there are documented complete mitochondrial genome (mitogenome) for only three species (*G. chilensis* C.J. Bird, McLachlan & E.C. Oliveira (NC\_026831), *G. salicornia* (C. Agardh) E.Y. Dawson (NC\_023784 and KT373903), and *G. vermiculophylla* (Ohmi) Papenfuss (NC\_027064)) in the NCBI GenBank. We report here for the first time the complete mitogenome of *G. changii* determined by NextSeq next-generation sequencing.