



A genetic diversity assessment of *Halymenia malaysiana* (Halymeniaceae, Rhodophyta) from Malaysia and the Philippines based on COI-5P and *rbcl* sequences

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Abstract

Little is known about the genetic diversity and phylogeographic structure of seaweeds in Southeast Asia particularly for *Halymenia* species. Herein, molecular analyses based on DNA sequences of the COI-5P and *rbcl* were performed to assess the genetic structure within the foliose *Halymenia* species *H. malaysiana* in Malaysia and the Philippines. A total of ten COI-5P haplotypes and eight *rbcl* haplotypes were recognized from 42 specimens of *H. malaysiana* examined in this study. The genetic diversities of *H. malaysiana* were relatively higher based on the COI-5P sequences compared with the *rbcl* sequences. The results showed that populations from Peninsular Malaysia (East, South, and West coast) were genetically homogenous and exhibited low level of genetic divergence from populations from East Malaysia. In contrast, populations from the Philippines were distinct from Malaysian populations. Site-specific distribution was also evident in the Philippine populations of *H. malaysiana*.

Keywords COI-5P · *Halymenia malaysiana* · Rhodophyta · Genetic variation · Phylogeography · *rbcl* · Red algae

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Introduction

Southeast Asia, of which Malaysia and the Philippines are part, is a world-renowned biodiversity hotspot (Briggs 2005; Hughes 2017). Owing to its high species richness and complex geological history, it encompasses plenty of interesting study sites for genetic diversity studies. Malaysia consists of Peninsular Malaysia (part of the mainland Southeast Asia) and East Malaysia (northern part of Borneo Island), which are separated by the southern part of South China Sea, but connected during the Last Glacial Maximum (23,000–19,000 years ago) when the Sunda Shelf was exposed (Wurster et al. 2010). The surface current circulation in the South China Sea is affected by monsoon seasons and may promoted genetic connectivity between populations (Wyrski 1961). The isolation of northern South China Sea as refugium during the late Pleistocene and postglacial recolonization of the southern South China Sea may have impaired the genetic connectivity in the region and caused subsequent diversification within Malaysian populations (Chan et al. 2013). Likewise, the Philippines, consisting of more than 7000 islands, has caught much attention as an area of exceptional endemism that is in critical need of conservation (Heaney et al.