

The first report of the parasitic red alga *Gracilaria babae* (Rhodophyta: Gracilariaceae) from Singapore

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Abstract. The presence of a red alga *Gracilaria babae* growing on its congener *G. salicornia* in Singapore is reported for the first time. The parasitic *G. babae* is distinguished by having pigmented pustules without rhizoids penetrating into host tissue. The tissues between the parasite and the host appeared continuous. The Singaporean *G. babae* has tetrasporangia and deep spermatangial conceptacles formed at the periphery of the pustule. Based on the sequences of molecular markers belonging to different genomic compartments (nuclear ITS and LSU, mitochondrial *cox1* and plastid *rbcL*), there was no genetic variation in the Singaporean *G. babae* collected from several different habitats.

Key words. *Gracilaria babae*, red algal parasite, ITS, LSU, *cox1*, *rbcL*.

INTRODUCTION

Yamamoto established the genus *Congracilaria* in 1986 to accommodate *C. babae* parasitic on *Gracilaria salicornia* (Dawson, 1954). This red algal parasite is characterised by the absence of rhizoids penetrating into the host tissues, by having a colouration similar to that of its host, the presence of bisporangia, and in possessing deep spermatangial conceptacles of *verrucosa* type. Yamamoto (1991) subsequently reported the presence of *C. babae* in the Philippines based on his observation of bisporangia in the Philippine specimens. Despite being slightly larger in pustule size, the Philippine specimens were similar to the type specimens in terms of external morphology, cellular structures and reproductive organs. The occurrence of similar red algal parasites with some anatomical variations had been reported in other Southeast Asian countries including Malaysia (Yamamoto & Phang, 1997), Indonesia (Gerung et al., 1999), and Thailand (Terada et al., 1999). Until recently, there was no further investigation carried out to clarify the taxonomic conundrum of these parasitic taxa since their original taxonomic descriptions.

The application of molecular data has addressed a number of phylogenetic issues when morphological and anatomical observations alone are insufficient to delineate species boundaries (Tan et al., 2013; Poong et al., 2013), especially in resolving the relationships between the red algal parasites and their hosts (Zucarello et al., 2004; Kurihara et al., 2010;

Ng et al., 2013, 2014). Considering the unique biology of the red algal parasites (Goff & Coleman, 1987, 1995), molecular characterisation of the parasites is more reliable with a multi-loci approach using markers from different genomic compartments (Kurihara et al., 2010; Ng et al., 2013, 2014). Using molecular tools, Ng et al. (2013) identified the Malaysian parasitic red alga on *G. salicornia* as *C. babae* despite the anatomical variations observed. In a subsequent study, Ng et al. (2014) transferred *C. babae* to the genus *Gracilaria* as the parasite was placed in the *Gracilaria* sensu stricto clade in the molecular phylogenies based on the plastid, mitochondrial and nuclear markers.

Gracilaria salicornia has been recorded in the Singapore waters (Lee et al., 2009), but the occurrence of parasitic red algae on *G. salicornia* remains undocumented in Singapore. The presence of this parasite is anticipated, since the distribution of its host species is within the range where a similar parasite has been previously reported (Yamamoto & Phang, 1997; Terada et al., 1999). This paper provides the first formal record of *G. babae* from Singapore. The Singaporean samples collected from Ubin Island were compared against our previous collections of *G. babae* from Japan (Okinawa) and southeast Johor, Malaysia (Che Kamat Island and Ramunia Bay). We aimed to characterise the Singaporean *G. babae* growing on *G. salicornia* with the DNA sequences of nuclear ITS and LSU, mitochondrial *cox1* and plastid *rbcL*. Morphological and anatomical features of the Singaporean parasite are also described. The utility of haplotype network analyses in inferring the relationships between the red algal parasite and its host, as well as that among the parasite individuals was demonstrated in this study. The haplotype networks were congruent with the phylogenies of *G. babae* and *G. salicornia* inferred from the sequences of the ITS, LSU, *cox1* and *rbcL* from a previous study by Ng et al. (2013), in which ITS proved useful in discriminating the parasites from its host.

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