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RESEARCH ARTICLE

## Genetic and morphological analyses of Gracilaria firma and G. changii (Gracilariaceae, Rhodophyta), the commercially important agarophytes in western Pacific

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## Abstract

Many studies classifying Gracilaria species for the exploitation of agarophytes and the development of the agar industry were conducted before the prevalence of molecular tools, resulting in the description of many species based solely on their morphology. Gracilaria firma and G. changii are among the commercially important agarophytes from the western Pacific; both feature branches with basal constrictions that taper toward acute apices. In this study, we contrasted the morpho-anatomical circumscriptions of the two traditionally described species with molecular data from samples that included representatives of G. changii collected from its type locality. Concerted molecular analyses using the rbcL and cox1 gene sequences, coupled with morphological observations of the collections from the western Pacific, revealed no inherent differences to support the treatment of the two entities as distinct taxa. We propose merging G. changii (a later synonym) into G. firma and recognize G. firma based on thallus branches with abrupt basal constrictions that gradually taper toward acute (or sometimes broken) apices, cystocarps consisting of small gonimoblast cells and inconspicuous multinucleate tubular nutritive cells issuing from gonimoblasts extending into the inner pericarp at the cystocarp floor, as well as deep spermatangial conceptacles of the verrucosatype. The validation of specimens under different names as a single genetic species is useful to allow communication and knowledge transfer among groups from different fields. This study also revealed considerably low number of haplotypes and nucleotide diversity with apparent phylogeographic patterns for G. firma in the region. Populations from the Philippines and Taiwan were divergent from each other as well as from the populations from Malaysia, Thailand, Singapore and Vietnam. Establishment of baseline data on the genetic diversity of this commercially important agarophyte is relevant in the context of cultivation, as limited genetic diversity may jeopardize the potential for its genetic improvement over time.