

Genetic variation of two mangrove species in *Kandelia* (Rhizophoraceae) in Vietnam and surrounding area revealed by microsatellite markers

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Abstract: Genetic variation of the mangrove genus *Kandelia* (Rhizophoraceae) in the South China Sea region, in four populations in Vietnam and in one population each in Iriomote, Japan, and Bako, Borneo, was evaluated using microsatellite markers. A total of 54 alleles in the six populations were detected by using four microsatellite loci. The two northern Vietnamese populations (Don Rui and Xuan Thuy) showed a high allelic diversity (40 alleles in total) and a high level of gene diversity ($H_E = 0.773$ on average). In contrast, the two southern Vietnamese populations (Can Gio and Ngoc Hien) showed low allelic diversity (11 alleles in total) and a low level of gene diversity ($H_E = 0.244$ on average). There was only one allele common to the two regions. The Iriomote population was genetically related to the northern Vietnamese populations, while the Bako population was related to the southern populations. The findings and the morphological observations indicate that these two genetically differentiated vicariant lineages represent two different species groups, *Kandelia obovata* Sheue, Liu, and Yong for northern Vietnam and Japan and *Kandelia candel* (L.) Druce for southern Vietnam and Borneo. The difference in the amount of genetic variation shows that these two species experienced a different adaptive process during the past glacial ages.

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