

Genetic structures of natural populations of three mangrove species, *Avicennia marina*, *Kandelia candel* and *Lumnitzera racemosa*, in Vietnam revealed by maturase sequences of plastid DNA

Kado T., Fujimoto A., Le H.G., Tuan M., Phan N.H., Harada K., Tachida H.

Department of Biology, Faculty of Sciences, Kyushu University, Fukuoka 810-8560, Japan; Faculty of Agriculture, Ehime University, 3-5-7 Tarumi, Matsuyama, Ehime 790-8566, Japan; Mangrove Ecosystem Research Division, Ctr. Nat. Rsrc. and Environ. Studs., Vietnam National University, Hanoi, Viet Nam

Abstract: Mangroves are constituent plants of tropical and subtropical intertidal forest communities. In order to assess their genetic variations and understand the contributing factors determining their genetic structures, we investigated sequence variation of the matK (maturase K) region of plastid DNA in three widely distributed species, *Avicennia marina*, *Kandelia candel* and *Lumnitzera racemosa*, taking samples from multiple populations in Vietnam and samples from Okinawa. These three species have different types of seeds/propagules with regard to vivipary, size and other characteristics and are expected to have different migratory potentials. Generally, variation within a population was low, probably reflecting unstable habitats of mangroves. In contrast, we found very different patterns of differentiation between populations of the three species. In *A. marina*, we recognized three groups of geographic lineages that were moderately separated while in *K. candel*, two distantly separate geographic lineages were found. No genetic variation was found in the total population of *L. racemosa* from Okinawa to southern Vietnam. We discuss possible factors, such as properties of propagules, zonation and natural disturbances, that may influence the genetic structures of mangrove species.

Author Keywords: Differentiation; DNA polymorphism; Migration; Plastid DNA; Vivipary

Index Keywords: *Avicennia marina*; Embryophyta; *Kandelia candel*; *Lumnitzera*; *Lumnitzera racemosa*; Rhizophoraceae

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Correspondence Address: Tachida, H.; Department of Biology, Faculty of Sciences, Kyushu University, Fukuoka 810-8560, Japan; email: htachscb@mbox.nc.kyushu-u.ac.jp

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Authors with affiliations:

- Kado, T., Department of Biology, Faculty of Sciences, Kyushu University, Fukuoka 810-8560, Japan
- Fujimoto, A., Department of Biology, Faculty of Sciences, Kyushu University, Fukuoka 810-8560, Japan
- Le, H.G., Faculty of Agriculture, Ehime University, 3-5-7 Tarumi, Matsuyama, Ehime 790-8566, Japan
- Tuan, M., Mangrove Ecosystem Research Division, Ctr. Nat. Rsrc. and Environ. Studs., Vietnam National University, Hanoi, Viet Nam
- Phan, N.H., Mangrove Ecosystem Research Division, Ctr. Nat. Rsrc. and Environ. Studs., Vietnam National University, Hanoi, Viet Nam
- Harada, K., Faculty of Agriculture, Ehime University, 3-5-7 Tarumi, Matsuyama, Ehime 790-8566, Japan
- Tachida, H., Department of Biology, Faculty of Sciences, Kyushu University, Fukuoka 810-8560, Japan

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