

Phylogeography of *Bruguiera gymnorrhiza*

J. Ono¹, K. Takayama², S.H. Meenakshisundaram³, W.K. Shan⁴, M.N.B. Saleh⁵, E.L. Webb⁴, T. Asakawa¹, B. Adjie⁶, E.R. Ardli⁷, M.K.K. Soe⁸, N.X. Tung⁹, N.B. Malekal¹⁰, Onrizal¹¹, O.B. Yllano¹², S. Sungkaew¹³, S.G. Salmo III¹⁴, Y. Watano¹, S. Baba¹⁵, Y. Tateishi¹⁶ & T. Kajita¹

¹Department of Biology, Graduate School of Science, Chiba University, 1-33 Yayoi, Inage, Chiba, 263-522, Japan. E-mail: tkaji@faculty.chiba-u.jp

²Institute of Botany, University of Vienna, Austria.

³Biotechnology Programme, M.S. Swaminathan Research Foundation.

⁴Department of Biological Science, National University of Singapore, Singapore.

⁵Faculty of Forestry, Putra Malaysia University, Malaysia.

⁶Bali Botanic Garden, Indonesian Institute of Sciences, Indonesia.

⁷Faculty of Biology, Jenderal Soedirman University, Indonesia.

⁸Department of Botany, University of Yangon, Union of Myanmar.

⁹Mangrove Ecosystem Research Centre, Hanoi National University of Education, Vietnam.

¹⁰Institute for Tropical Biology and Conservation, Universiti Malaysia Sabah, Malaysia.

¹¹Forestry Sciences Department, Universitas Sumatera Utara, Indonesia.

¹²Biology Department, College of Sciences and Technology, Adventist University of the Philippines.

¹³Faculty of Forestry, Kasetsart University, Thailand.

¹⁴Department of Environmental Science, School of Science and Engineering, Ateneo de Manila University, Philippines.

¹⁵Tropical Biosphere Research Center, The University of the Ryukyus, Japan.

¹⁶Faculty of Education, University of the Ryukyus, Japan.

Abstract

Bruguiera gymnorrhiza (L.) Lam. is one of the most widely distributed major mangrove species in the Indo-West Pacific (IWP). The vast distribution range of *B. gymnorrhiza* is attributed to its sea-drifting and dispersing propagules. Using both chloroplast and nuclear DNA markers, Minobe et al. (2009) suggested distinct genetic structure over Malay Peninsula. However, there was no clear structure within either the larger Pacific or the East Indian Oceanic regions. Moreover, the number of populations used in the study was very small despite the vast distribution range of the species, and the molecular markers was too short to detect fine scale genetic structures within each oceanic region. Furthermore, the phylogenetic relationship of *B. gymnorrhiza* with the putative sister species, *B. sexangula*, has not been clearly understood. To obtain comprehensive understanding on genetic structure of *B. gymnorrhiza*, we used samples collected from wide range of in IWP by our research network. We analyzed genetic structure using two cpDNA markers and 6 SSR markers. Our results revealed a clear genetic structure between the east and west side of Malay Peninsula, although there was a mixture of patterns observed in some populations. In Phuket, Thailand, for example, a simple mixture of two genotypes is suggested by both nuclear and cpDNA markers rather than admixture. This result raises a question about artificial transfer of plants with different genotype into this area. The NJ tree based on genetic distance (Da) showed that geographically close populations formed clusters. There was a significant correlation between genetic distance and geographic distance both in the Pacific and in the Indian Oceanic regions.

Keywords

Bruguiera sexangula, population structure