

## 学位論文要旨 Dissertation Abstract

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学位論文題目 : Phylogeographical study of the genus *Dryobalanops* Gaertn. f. (Dipterocarpaceae) based on nuclear microsatellite markers  
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The geographic area including the Malay Peninsula, Sumatra, Java and Borneo is called Sundaland and known to be a globally important hot spot of biodiversity. The lowland forests in this region are dominated by Dipterocarpaceae, but the area is considered to have been limited during the last glacial maximum (LGM). Population genetic analysis of dipterocarp species will help to elucidate the impact of the Pleistocene glaciations on distribution of the Sundaland tropical rainforests. In this study, extants and patterns of genetic variations of six species of the genus *Dryobalanops* (*D. aromatica*, *D. beccarii*, two subspecies of *D. oblongifolia*, *D. lanceolata*, *D. rappa* and *D. keithii*) in Dipterocarpaceae, were evaluated using microsatellite markers to (1) evaluate the abilities of these DNA markers for discriminating among the six *Dryobalanops* species and clarify the relationships among the species, and (2) reveal phylogeographic pattern and demographic history of two prominent species, *D. aromatica* and *D. beccarii*.

Firstly, seven microsatellite markers were used to analyze 46 natural populations of six extant *Dryobalanops* species ( $N = 700$  individuals). All seven microsatellite loci exhibited a large number of alleles per locus, suggesting that these loci will be of potential use in the studies of genetic diversity, population structure and species relationship of these *Dryobalanops* species. The mean gene diversities at the species level were ranged from 0.392 in *D. rappa* to 0.635 in *D. aromatica*. The genetic differentiation among populations ( $F_{ST}$ ) of respective species were ranged from 0.156 in *D. keithii* to 0.283 in *D. beccarii*, and all  $F_{ST}$  values were significantly greater than zero.

These results suggest that gene flow between populations has been limited and intensive genetic drift has occurred in all of the species. The species with narrower distribution, such as *D. keithii* and *D. rappa* tend to have lower levels of genetic diversity compared with widespread species *D. aromatica*. Although *D. aromatica* and *D. beccarii* resemble each other morphologically and are occasionally hard to identified in the field, the Bayesian model-based clustering method (the STRUCTURE analysis) could discriminate an individual effectively to the respective species from the others.

Secondly, the phylogeographic patterns of *D. aromatica* and *D. beccarii* were studied. Eight natural populations of *D. aromatica* ( $N = 200$ ) and sixteen natural populations of *D. beccarii* ( $N = 235$ ) were analyzed for this study. The species were clearly differentiated by the STRUCTURE analysis although hybridization probably occurred in the area where the two species coexist. *Dryobalanops aromatica* could be divided into two genetically distinct groups corresponding to Malay Peninsula-Sumatra and Borneo, while *D. beccarii* populations could be divided into four geographically distinct groups including western Sarawak, central inland Sarawak, central coastal Sarawak and Sabah. One population in the Malay Peninsula (Gunung Panti) was an admixture of these Bornean clusters, indicating occurrence of long distance migration. The analysis based on IM (Isolation with Migration) model estimated the time of divergence of the Malay Peninsula-Sumatra and Borneo populations of *D. aromatica* to be 7,300–3,600 years ago, i.e. after the last glacial maximum. This analysis also suggested that the ancestral population was twenty times larger than today's populations. This supports the idea that the present tropical rainforest is in a refugial state, and also suggests that the savanna corridor that is hypothesized to have covered the central part of the exposed Sundaland during the last glacial period, if it existed, was not contiguous but rather permeated by rainforests in some places.

This study demonstrates that each *Dryobalanops* species is genetically structured and that areas of high priority of conservation should make to ensure these genetically diverged lineages. The genetic structure data revealed in this study also can be used for silvicultural treatments in these highly potential species.