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学位論文要旨
Dissertation Abstract

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学位論文題目： Title of Dissertation	Genetic diversity and structure in two endangered species, *Shorea albida* (Dipterocarpaceae) and *Quercus hondae* (Fagaceae) （絶滅危惧樹木であるフタバガキ科*Shorea albida*とブナ科*Quercus hondae*の遺伝的多様性と集団構造）

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The maintenance of biodiversity is an important issue for our society, and it is necessary to conserve as many existing species as possible to prevent further biodiversity loss. Populations in endangered species are small and often isolated each other. Such populations may have low genetic diversity and suffer from deleterious effects of inbreeding. If genetic diversity increases a chance for adaptation in changing environment, some extent of genetic diversity may guarantee the species viability. Therefore, in conservation, endangered species are intended to prevent the loss of genetic diversity, or even to increase it if necessary. Population genetics studies fundamentally the compound effects of population size, mutation, migration and natural selection on genetic diversity in natural populations. Knowledge about genetic diversity is also useful for other areas of biology, such as ecology, silviculture and conservation biology.

Forests are being contracting around the world despite their multifaceted role in the Earth’s climate and in our human lives. Considering the impact of species extinction by forest losses, it is important to prioritize the protection of endangered tree species. Population genetic studies of tree species provide the information that will be helpful for conservation projects for tree species, for example, the selection of protected forests and seed resources utilized for forest rehabilitation. However, the population genetic status, such as genetic diversity, genetic structure, and historical population demography, remains poorly studied in many endangered species. In this study, population genetic analysis was conducted for two endangered tree species of

Shorea albida and *Quercus hondae* to infer the population genetic status and the evolutionary history, and then concrete desirable conservation for each species was discussed.

Shorea albida, a species of Dipterocarpaceae, is endemic to northwestern Borneo, and often monodominant in peat swamps in this region. As well as most of the tropical forests in Southeast Asia, the peat swamps are also vulnerable to anthropogenic disturbances. Since natural regeneration of *S. albida* has been suggested to be fairly difficult, human interventions are necessary for the conservation and recovery of this species. Here the population genetic status was assessed for *S. albida* in Brunei using 18 microsatellite markers. The level of genetic diversity of *S. albida* was not lower compared to the other *Shorea* species. This is possibly due to the high stand density of *S. albida* in the peat swamp forests. Although genetic divergence among populations was generally low, two genetically distinct populations were found despite their geographic proximity. Based on the inferred divergence time between the genetic groups, it is suggested that the genetic structure is affected by the persistence of the past refugia rather than its limited gene flow between extant populations.

Quercus hondae, a species of Fagaceae, distributes in only Kyushu and Shikoku in Japan and is vulnerable due to conversion of forest into plantations and other development purposes. As this species only patchily distributed in several small forests, it is expected that the genetic diversity is lower than the widely distributed species. However, the population genetic status of this species has not yet been investigated to date. Genetic diversity was assessed for 12 populations of *Q. hondae* using 11 microsatellite loci and chloroplast DNA sequences and compared to widespread congeneric species, *Q. glauca*. In contrast to *Q. glauca*, low level of genetic diversity and high level of genetic differentiation among populations were found in *Q. hondae*. The results suggest less gene flow among populations and the greater effect of genetic drift in small populations of *Q. hondae*.

This study showed that patterns of genetic diversity and structure are different between two species, suggesting that desirable conservation strategies need to be considered for each species. Based on the results of this study, a suitable solution for *S. albida* is to maintain the current level of genetic diversity within populations, while for *Q. hondae* is to increase in genetic diversity for populations with low genetic diversity and to prioritize conservation of populations with high genetic diversity. On the other hand, presence of genetic structure, at least in part, in both species indicates that conservation of genetically different populations is recommended. This is because conserving genetically different populations and preventing anthropogenic movement among them are important for maintaining intraspecific genetic diversity in the species.