

論文の内容の要旨

生圏システム 専攻

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論文題目 Study on the factors affecting genetic diversity of *Fraxinus mandshurica*,
an ecologically and economically important tree species in Northeast China
(中国東北部の生態的経済的重要樹種ヤチダモの遺伝的多様性に影
響する諸要因に関する研究)

Fraxinus mandshurica is a key species in the succession of climax community in cool-temperate forests and an important timber tree in Northeast China (NEC). The natural forest resource of *F. mandshurica* is increasingly threatened, due to over exploitation and widespread deforestation during the past century. Thus, it was designated as an endangered tree species in need of national priority protection in China. However, the levels of genetic diversity and population genetic structure of *F. mandshurica* in NEC remain unknown.

The thesis attempted to understand the magnitudes of genetic diversity of *F. mandshurica* using nuclear microsatellites. It focused on clarifying the factors affecting the structure of genetic distribution at various spatial and temporal scales in NEC, the species' central range.

The thesis was divided into five chapters. Chapter 1 and 2 were the general introduction and review, respectively. In chapter 3, the wide-scale genetic variation and phylogeographical structure of *F. mandshurica* adult populations in NEC were primarily investigated. At a comparable level, a phylogeographical evaluation of the variety in Japan (var. *japonica*) was also conducted. Chapter 4

was concerned on understanding the impacts of landscape heterogeneities, recent regeneration processes and silvicultural practices on genetic diversity of *F. mandshurica* in two typical landscapes in NEC. Ultimately, the genetic information overall the thesis would be useful of proposal for management and conservation of *F. mandshurica* in NEC, which was thoroughly demonstrated in the general discussion of chapter 5.

Chapter 1 generally introduced the status of forest resources in NEC, importance of genetic information in forest management and ecology, biology and silviculture of the study species. Then, chapter 2 presented a retrospect of the previous work of population genetic studies of forest tree species using molecular markers, focusing on the factors affecting the patterns of population genetic structure of forest trees. Population genetic knowledge of related *Fraxinus* species in Europe and tree species in NEC was also summarized in this review chapter.

In chapter 3, a wide-scale phylogeographical investigation indicates the possibility of *F. mandshurica* maintaining a high level of genetic diversity within extant adult populations across NEC. The intra-population genetic diversity (both allelic richness and expected heterozygosity) were significantly negatively correlated to latitude. These results were possibly associated with the systematically northward shifts of forest biomes in eastern China during the mid-Holocene. Conversely, a low level of genetic differentiation and a lack of modern genetic structure were detected among these populations across NEC (with the exception of Jianxin). These results might be elucidated by the abundant (historical) gene flow and the presence of a wide refuge rather than multiple small refugia in NEC during the last glacial maximum. In contrast, the most northerly population in NEC (Jianxin) was significantly diverged from the continuous gene pool in NEC and exhibited the lowest allelic diversity. It proposes that Jianxin population requires priority conservation efforts to prevent it from being extirpated from its native habitat, such as the establishment of a distinct management unit and in the combination of *in situ* and *ex situ* conservation strategies.

In this chapter, the phylogeographical structure of *F. mandshurica* var. *japonica* was also investigated on a wide-scale in Japan – one of the species' traditionally marginal ranges. Contrasting patterns of genetic variation and population structure were identified between northern (Hokkaido

and Shimokita) and southern (Honshu) populations in Japan. Based on the common usage of microsatellites, similar sampling scheme and balanced analysis algorithm however, populations in NEC showed significantly lower levels of allelic richness and expected heterozygosity than those in populations of var. *japonica* in Japan. These results seemed to disagree with the classical central-peripheral hypothesis that genetic diversity within peripheral populations is normally reduced as compared to more central populations. Bayesian clustering algorithm further identified all individuals into the NEC cluster and Japan cluster. This suggests that long-term interglacial isolation might have led to aggravation of population differentiation and speciation of intraspecific species (var. *japonica*). The opposite patterns of genetic variation and phylogeography of *F. mandshurica* between NEC and Japan allowed the development of effective conservation strategies for this species.

In chapter 4, spatial analysis of molecular variance and principal coordinate analysis consistently revealed that *F. mandshurica* exhibited landscape genetic structure across a riparian–mountain system, despite the overall low level of genetic differentiation between populations. This is probably due to the different effects of landscape heterogeneities (riparian corridors and mountain obstacles) on seed dispersal. Conversely, there was no spatial genetic structure among populations within the riparian system, suggesting that the Hydrochory corridors might enhance genetic connectivity among riparian populations. A significant accumulation of genetic diversity within downstream populations was not detected, probably because gene flow in *F. mandshurica* is prevailed by the primary, bidirectional wind-dispersal.

In a severe anthropogenic landscape, similar magnitudes of intra-population genetic diversity of *F. mandshurica* were detected in the recently colonized populations (seedlings and juveniles) naturally regenerated in the *L. gmelinii* plantation forests or open farmlands, when they were compared to adjacent adult populations. Spatial autocorrelation analysis failed to detect a significant fine-scale spatial genetic structure in any of the recent generations or natural populations. On the contrary, two seedling cohorts in the adult forests exhibited significantly positive fine-scale spatial genetic structure over short distances and also demonstrated a significant trend of lower allelic richness but higher inbreeding coefficient than those in the adult forests. These results suggest that the seedling

cohorts were probably half-siblings and largely originated from a few related parents within their respective adult forests. In addition, this study also suggests that the negative impacts of recent anthropogenic practices (selective thinning and artificial regeneration) on the genetic diversity and/or fine-scale spatial genetic structure of *F. mandshurica* are negligible.

In the light of the overall genetic information of *F. mandshurica*, the fundamental proposal on conservation and management practices for this species in NEC was ultimately formulated in chapter 5. In general, the present neutral genetic resources of *F. mandshurica* in NEC may not be seriously threatened; thus it does not necessitate specific conservation programmes for solely safeguarding intra-population genetic diversity. The properly applied silvicultural treatments and recent regeneration processes on *F. mandshurica* may not lead to genetic degradation in the future generations. However, it requires effective efforts to maintain or enhance genetic connectivity among present populations on landscapes and among future generations at the whole scale of NEC.