論文内容の要旨

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論文題目 Geographic variation and genetic structure of teak (*Tectona grandis*) in Myanmar revealed by cpSNP and nrSSR markers

(葉緑体 SNP と核 SSR マーカーで明らかにされたミャンマーにおけるチーク(*Tectona grandis*)の地理変 異と遺伝構造)

The tropical deciduous and semi ever-green tree species, teak, is one of the most economically important tree species. It naturally occurs in India, Myanmar, Thai and Laos. Genetic information of teak from its native regions has been investigated using molecular markers and they showed south India teak has the highest genetic diversity followed by teak from North India, Thai and Laos. About 60% of the total natural forest area occurs in Myanmar that is the largest area of natural teak forest. Few study for genetic diversity of Myanmar teak has been conducted but no comparison between Myanmar teak and from its indigenous countries has been reported. The same markers used in the previous study were applied for evaluating the level of genetic diversity of Myanmar teak has significantly lower genetic diversity than that of India teak, but significantly higher than that of Thai and Laos teak.

Natural teak forest in Myanmar drastically diminished due to over logging, illegal cutting and transforming landuse systems, therefore conservation of Myanmar teak is urgently needed to retain the natural

genetic resources of teak in the world. Furthermore, teak plantation was widely established at about 43 countries including its native countries, Myanmar. Knowledge of the genetic variation of extant populations over the entire range of their distribution is therefore essential for the conservation of genetic resources. Microsatellite markers (nrSSRs), which are highly polymorphic, are useful for elucidating the spatial genetic structure and the demographic patterns of variation which have resulted from migration and drift as well as through evolutionary history. Chloroplast markers are also useful for phylogeographic studies and gene conservation, because chloroplast genomes, which are haploid, are maternally inherited in angiosperms and hence transmitted by seeds. Nevertheless, no chloroplast markers for teak have been developed yet. Thus, cpSNP markers for teak have been developed to determine phylogeographic structure of Myanmar teak. After sequencing about one third of complete genome of teak about 43,734 bp, three cpSNP markers of teak were developed to study the geographic variation of teak in Myanmar.

Geographically genetic structure of Myanmar teak was examined using total 480 individuals of 20 natural populations from five regions representing almost natural teak forests in Myanmar and two types of molecular markers; three newly developed cpSNP markers and 10 nrSSR markers in chapter 4. The combined studied of cpSNP and nrSSR markers suggested there are at least four genetic resources of Myanmar teak. Randomized distribution of four haplotypes showed by cpSNP markers did not depicted clear geographic structure of Myanmar teak. On the other hand, four genetic clusters of 20 natural populations depicted by nrSSR markers suggested clear geographic genetic structure of Myanmar teak. The putative genetic boundaries of 20 populations suggested at least three zones such as planting or seed zones can be designated based on combined cpSNP and nrSSR data. Of 20 populations, four populations with their high contribution to total genetic diversity were found to be prioritized for conservation.

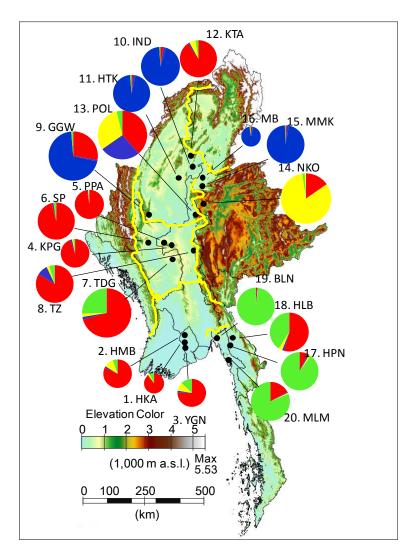


Fig 1. Genetic structure of Myanmar teak revealed nrSSR markers

Teak plantation in Myanmar has been started using local seeds since 1700 to replenish the degraded natural forests. A couple of years ago, private sectors were allowed to establish teak plantation at deforested area or some were around natural teak forests. No seed guideline of teak is formulated in Myanmar. Therefore, seeds from wherever available were used for teak plantation without considering their genetic component. Moreover, teak plantation established by private companies used alien teak from Indonesia, China and Costa Rica without information on genetic background. To prevent genetic disturbance for Myanmar natural teak, genetic component of recently established teak plantation by private sectors were investigated using 10 nrSSR markers and compared with that of natural teak and old teak plantation. Higher genetic diversity and less genetic differentiation among populations of recently established teak plantation supported the assumption of various seeds sources used for

those plantations. Alien teak showed low genetic diversity and significant level of genetically differentiated from Myanmar teak especially Indonesian teak.

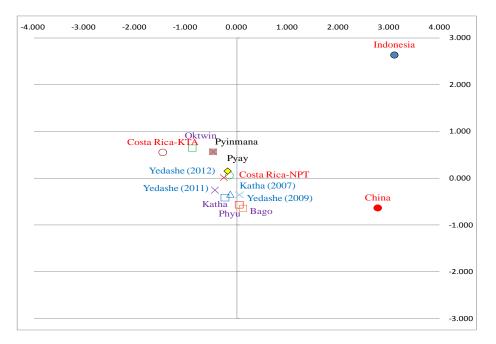


Fig 2. Scatter plot of population based principal coordinate analysis for alien teak and native teak

At last, gene conservation and afforestation strategy for Myanmar teak were discussed based on findings obtained in this study. Among four native countries of teak, Myanmar with the largest natural teak forests and high genetic diversity may be genetic core of teak in the world. The current four genetic resources of Myanmar teak should be retained not to be deteriorated by genetic erosion by designating the planting zones or seeds zone based on geographic genetic structure of Myanmar teak. Alien teak introduced to Myanmar for planting purpose should be restricted. Seeds from alien teak should be avoided for the establishment of next teak plantation in Myanmar because those seeds may be products of outbreeding between alien teak and Myanmar teak with high genetic divergence. Instead of using the alien teak, genetically improved planting materials, Myanmar teak should be focused on producing the planting materials through breeding and tree improvement programs. In doing so, retaining natural genetic resources of Myanmar and supplying the high demand of teak can be implemented. Genetic information of Myanmar teak observed in this study may take a part of role for the conservation of natural genetic resource of teak.