GENETIC VARIATION AND STRUCTURE OF NATURAL POPULATIONS IN *ABIES HOLOPYLLA* MAXIM. EPLOYING ISSR MARKERS

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Introduction

Fir (*Abies*) genus in Korea has Needle Fir (*Abies holopylla* Maxim.), Korea Fir(*Abies koreana* E.H. Wilson) and East Siberian Fir [*Abies nephrolepis* (Trautv.) Maxim.]. Needle Fir widely distributed in the mountains such as Mt. Seorak, Mt. Odae and Mt. Taebaek. Indigenous species are distributed on altitude of 200 ~ 1,400 meters above sea level. The purpose of this study was to provide the genetic data for *in-situ* and *ex-situ* conservation.

Materials and Methods

Young leaf samples were collected from 20 individual samples of six natural populations, *Abies holopylla*, in South Korea. The selection of individual samples was made in such way that they are apart at least 30 meters away from other individule sample in order not to select a related tree. After screening for total 46 UBC primers, 6 primers were analyzed to estimate the genetic variation, genetic structure and relationships based on observed allele by PCR analysis.
To estimate the distribution of I-SSR variants among the categories of presence or absence within population, the Shannon's index (Shannon 1948) was calculated using the POP-GENE 1.31 program (Yeh et al. 1999). Level of genetic differentiation among populations was estimated by AMOVA on the basis of genetic distance using Arlequin 2.0 program (Scheider et al. 2000). Genetic relationships among populations were reconstructed by UPGMA on the basis of pair-wise Manhattan distance (Wright 1978) between populations, which was computed by RAPDDIST v. 1.0. Statistical test for the topology of each node was performed with 100 bootstrapped samples prepared by RAPDDIST v. 1.0 (Wright 1978)

Results and Discussion

From these results, we found that relationship among populations by analyzing genetic variation and genetic structure of six populations using ISSR (Inter Simple Sequence Repeat) primers. Genetic diversity was the highest in population of Mt. Odae (*S.I* = 0.469), while population of Mt. Heungjeong (*S.I.* = 0.403) was the lowest (Table 1). These degrees of genetic diversity were higher than other deciduous trees such as *Oplopanax elatus*, its degree of genetic diversity was 0.187 (Lee et al., 2002) in Korea and *Kirengeshoma palmate*, its degree of genetic diversity was 0.259 (Zhang et. al. 2006) in China. This is because endangered plant species have low genetic diversity due to the genetic drift and gene flow (Karron 1991).

Table 1. Genetic diversity in 6 populations of of *A. holopylla* in South Korea.

Population	N	*S.I.*[*]
Mt. Seorak	20	0.419
Mt. Odea	20	0.469
Mt. Heungjeong	20	0.403
Mt. Undal	20	0.405
Mt. Unmoon	20	0.433
Mt. Jiri	20	0.445
Mean	**20**	**0.429**

[*] *S.I.*: Shannon's information index

Genetic diversity of an average 0.429 of the species level showed similar level, when compared with the studied species up to now and the others species similar to ecologic and life historic characteristics. The results by AMOVA (Analysis of Molecular Variance) on six populations of *A. holopylla* showed that 5.61% of total genetic variation was caused by the difference among populations and 94.39% of the others were caused by between the individuals within populations.

It is more effective and economical to conserve species by selecting many individuals within a population rather than selecting many populations for *ex-situ* conservation. You also can conserve species intensively by selecting a few populations rather than selecting many populations for *in-situ* conservation.

Table 2. Analysis of molecular variance within/among populations.

Source of variation	d.f.	Percentage of variation (%)
Among populations	5	5.61
Within populations	114	94.39
Total	**120**	**100**

From the UPGMA cluster analysis results, geographically close groups tended to be grouped into the same group (Figure 1), and showed positive correlation (r = 0.827, p <0.01) between geographic distance and genetic distance for populations (Figure 2).
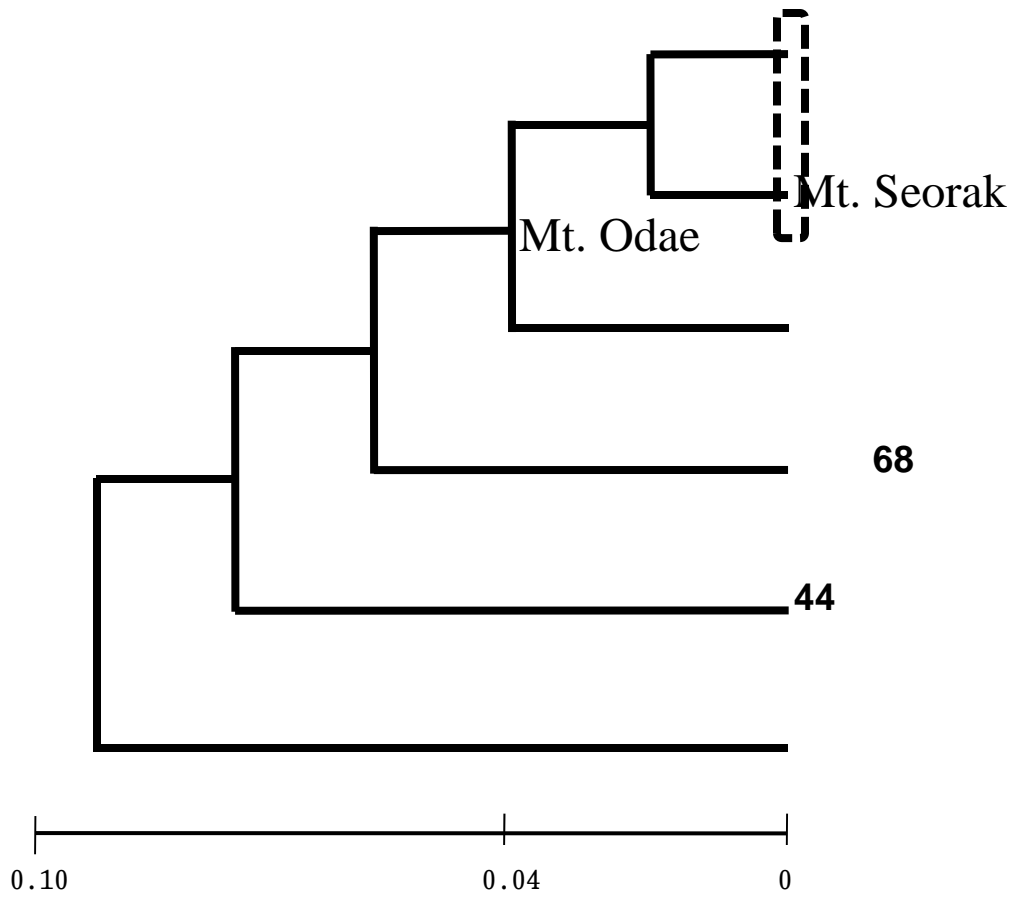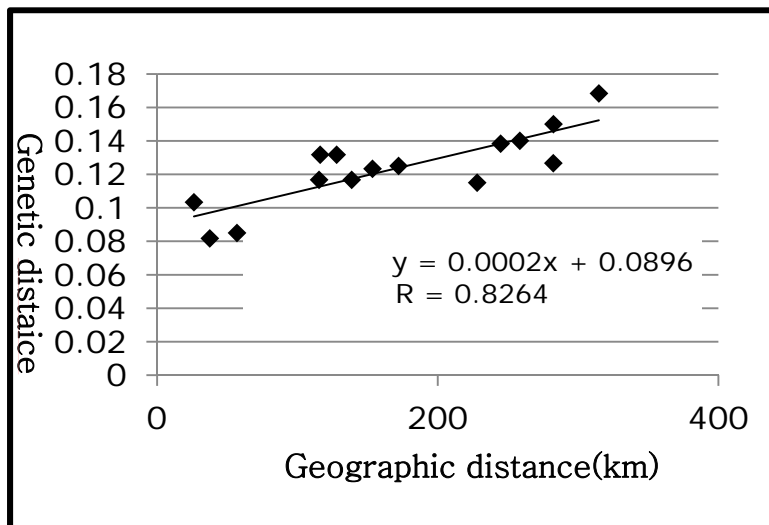
Figure 1. UPGMA dendrogram of *A. holopylla* populations.

Figure 2. The correlation between genetic distance and the geographic distance for *A. holopylla*.

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