GENETIC DIVERSITY AND CLONE STRUCTURE OF THE ENDANGERED SPECIES OF *THUJA KORAIENSIS*: CONSERVATION STRATEGY IN RESPONSE TO CLIMATE CHANGE

*Hye Jin Lee[1, 2], Hae In Kang[1], Kyung Nak Hong[2], **Ki-Won Kim**[1] and Kyu-Suk Kang[1]*
[1]Seoul National University, Seoul, Republic of Korea
[2]National Institute of Forest Science, Suwon, Republic of Korea

Comprehensive studies on the genetic diversity and structure of endangered species are urgently needed to promote effective conservation and management activities. Preserving the genetic diversity of endangered species can significantly affect their long-term survival and evolution in changing environments. Therefore, knowledge of the genetic diversity and population structure of endangered plant species is crucial for their conservation and management. *Thuja koraiensis* exhibits a very limited distribution with a few populations found on the Korean peninsula. It is the endangered tree species that can be found through alpine zones of Baekdudaegan Mountain Range from Baekdusan to Taebaeksan in the southernmost part of Gangwon province. Study on the life history of endangered species provides the basis necessary to investigate the reason for crisis faced and to establish the strategy of conservation. Unfortunately, limited information is available regarding the population genetics of this species.

Therefore, we conducted the germination test of seeds to understand the mechanism of reproductive propagation from three natural populations and the analysis of clone structure to characterize the genetic diversity of the species within a population of *T. koraiensis*. Microsatellite marker was used for analysis of the clonal structure and genetic variation. The microsatellite marker is the codominant marker showing high polymorphism and it has been widely used for population genetics and clonal structure analysis.

The cones were collected from Hwaaksan, Seoraksan and Hambaeksan populations in 2015, and the morphological characteristics of cone were measured. After cone drying, seeds were extracted and placed in chambers for germination tests. Additionally, some seeds from the Hambaeksan population were stored in a refrigerator until genomic DNA was extracted, and targeted to analyze clone structure and genetic variation. For clone structure analysis, a plot with 15 m x 15 m was set and seed samples were collected in Hambaeksan and the diameter at root collar was measured for all individuals in the plot.

The mean of cone length was highest in Hwaaksan (10.4 mm) and lowest in Hambaeksan (8.8 mm). The averages of 1,000 seed weight were 0.85 g (Hwaaksan) and 0.81 g (Seoraksan and Hambaeksan). The averages of germination percentage were 28.2% in Hambaeksa, 19.4% in Seoraksan and 12.2% in Hwaaksan. The germination speed was also peak in Hambaeksa and low in Hwaaksan. We developed 10 microsatellite markers and applied for clone structure analysis. A total of 152 trees were found in the plot and they were classified into four genotypes. The mean number of alleles was 6.3 and the mean number of effective alleles was 3.8 in the Hambaeksan population. The observed and expected heterozygosities were 0.629 and 0.642, which is an intermediate level compared to the other *Thuja* species distributed in North America.

The *T. koraiensis* is vulnerable to the drastic change of environment. Our results will assist with the design of conservation and management programs, such as *in situ* and *ex situ* conservation, seed collection for germplasm conservation and reintroduction.

Contact Information: Hae In Kang, Seoul National University, Gwanak-ro 1, Gwanak-gu, Seoul 08826, Republic of Korea, Phone: + 82-10-7380-2434, Email: emmahi@snu.ac.kr