

Genetic diversity, gene flow and conservation of *Picea jezoensis* under dramatically changing climate

Motoshi Tomita*

Species have been expanded and contracted its range along with climate changes. The population on the retreating edge of distribution would experience fragmentation, isolation and severe genetic bottleneck^{*1}, then extinct finally. *Picea jezoensis* and varieties distribute widely to boreal region of east Asia, including Hokkaido, far east Russia, Sakhalin, Kamchatka, north east China and Korean peninsula (Fig. 1). In South Korea, however, *P. jezoensis* is limited to a few high elevation refugia^{*2}, such as Mt. Chiri. Therefore, the risk of further reduction or extinction due to future climate change is now concern. On the other hand, in Hokkaido, although *P. jezoensis* is the representative tree species of mixed-coniferous forest, its distribution and biomass are now going decreased because of past extensive logging and the difficulty of regeneration. Also we need to concern on conservation and successive use of *P. jezoensis* of Hokkaido. Here I discuss



Fig. 1 Distribution of *Picea jezoensis* and varieties (var. *hondoensis* in Honshu island of Japan, var. *komarovii* in China and Korean peninsula). Data on North Korea and China were not shown.

about population genetic approaches for the assessment of population integrity and conservation from the local to global scale.

Recent studies of genetic diversity and molecular phylogeny of *P. jezoensis* around East Sea / the Sea of Japan revealed low genetic diversity of the isolated population of Korea (Mt. Chiri) which suggests the existence of genetic bottleneck (Aizawa et al., 2005). Meanwhile, genetic diversity was moderate to high at populations of Hokkaido. But if the story of further reduction of population would come true, owing to both anthropogenic and climatic impact, genetic diversity might be decreased together. We need to monitor genetic diversity and population state throughout the changing environment to prevent local extinction in east Asia.

Whereas, studies on mating system or gene flow of *P. jezoensis* were quite rare. Genus *Picea* is predominantly outcrossing; strong inbreeding depression^{*3} may act as barrier against mating among relatives. But once a population was fragmented and isolated, several researches suggested slightly high inbreeding occurred, in spite of inbreeding depression. It might not only lead to loss of genetic diversity, but also lower stand integrity by inbreeding depression. Information about mating system and gene flow, mainly via pollen, is important for assessment of population integrity and planning conservation strategies. Beside monitoring genetic diversity, we also need to investigate whether and how much inbreeding occurred in the population, and how much the effective pollination distance, mating area and gene flow were.

I study mating system and pollen dynamics of *P. jezoensis* for undergraduate thesis project. The first goal of the research is to know fundamental mating system parameter such as selfing ratio and effective pollination area in the natural stand of Hokkaido, and to develop research framework for further studies. In the future, I hope to extend this project to inter-population comparison of mating system, like managed-natural, continuous-fragmented or dense-sparse. Joint research project for genetic diversity and regeneration of *Picea jezoensis* is now started between Korea and Japan. This action will be a pioneer of inter-population study for genetic diversity conservation.

Reference

Aizawa, M., H. Yoshimaru, H. Saito, T. Katsuki, T. Kawahara, K. Kitamura, and M. Kaji. 2005. Genetic diversity and historical distribution change of varieties of *Picea jezoensis*. Abstract of 116th Conference of Japanese Forest Society. In Japanese.

* Laboratory of Silviculture, Department of Forest Science, Hokkaido University, N9W9 Kita-ku, Sapporo, Hokkaido, 060-8589, Japan
Email: motoshi@sea.plala.or.jp
Tel/Fax: +81-11-706-3346

*1 Loss of genetic diversity due to reduction of effective population size.

*2 Small and limited population which might have survived during climate change.

*3 Lower survival of progeny derived from inbreeding, may caused by abnormal gene namely lethal recessive allele