Conservation genetics in Amentotaxus formosana

Ya-Zhu Ko¹, Mei-Hui Chen², Tzen-Yuh Chiang³, Yu-Chung Chiang¹*
1 Department of Biological Science, National Sun Yat-Sen University, Kaohsiung 804, Taiwan
2 Conservation Division, Forestry Bureau, Council of Agriculture, Executive Yuan, Taipei 100, Taiwan.
3 Department of Life Sciences, National Cheng Kung University, Tainan 701, Taiwan
E-mail: yuchung@mail.nsysu.edu.tw*

Amentotaxus formosana is an endemic insular species with its only populations in southern Taiwan. This species is categorized as an endangered species enlisted in the “A Preliminary Red List of Taiwanese Vascular Plants” according to the IUCN Red List Categories and Criteria Version 3.1 and announced as natural monument by the Council of Agriculture based on “Cultural Heritage Preservation Act” in Taiwan. In the inventory study, only thousands individuals remained within 100 square kilometers region and asexual reproduction by sprouting in the field. Therefore, the conservation strategies for A. formosana should be including the in situ protection and managements and ex situ conservation strategies such as clonal orchard. In this study, we evaluate the population genetics and identify distinct genetic units using simple sequence repeat (SSR) technology and Bayesian assignment analysis. The low values of observed heterozygosity (Ho) and expected heterozygosity (He) indicated decline of population heterozygosity and significant deviation from Hardy-Weinberg equilibrium. Low differentiation between Dawu Taiwan Amentotaxus Nature Reserve (DAWU), Mt. Dalili (DL), and Chachayalaishan Major Wildlife Habitat (CHCH) populations reflected continuous population in past and recently habitat defragmentation. In addition, populations of the DAWU, DL, and CHCH display high inbreeding coefficient, lowest effective population size, and large effective ancestral population size reflect the recent bottleneck or fragmentation causing population decline. Cryptic structure and distinct genetic units are identified by assignment test based by MCMC and Bayesian analysis. Our results display the population genetic structure of A. formosana and provide conservation strategies in considering the geographic distribution and distinct the genetics units.