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Analysis of Genetic Variability among Subpopulations in Northern Taiwan of *Arundinaria usawai* Hayata

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ABSTRACT

Arundinaria usawai, Taiwan arrow bamboo, is dominated in open area of Yang-Ming Shan National Park in northern Taiwan. Samples collected from 9 subpopulations were estimated for their genetic variability by isozyme analysis. Thirteen enzymes with 18 polymorphic loci were surveyed. The results indicated high genetic diversity among subpopulations of *A. usawai*. There was nearly half of polymorphic loci in surveyed enzymes ($P = 50.5\%$), the numbers of allele per locus ($A = 0.167$) and the expected heterozygosity ($H_E = 0.221$) were also high. The data implied that highly genetic variability within single population was caused not only by accumulation of variation in cloneme, but also by the sexual reproduction and asexual propagation. Highly structured population in Yang-Ming Shan may due to the Wahlund effect and rhizomatous propagation. The lose of locus PER and SKD-1 in Chin-Kua-Shih-II may refer to the genetic drift in this isolated subpopulation.

Key words: *Arundinaria usawai*, genetic variability, isozyme, geneflow, genetic drift