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A genetic diversity analysis of wild *Caragana korshinskii* based on allozyme and AFLP

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Key words: AFLP, allozyme, *Caragana korshinskii*, genetic diversity,

Introduction *Caragana korshinskii* Kom., a perennial sandy grassland and desert deciduous shrub species, is indigenous to and distributed in half-fixed and fixed sandy regions in the northwest of China and Mongolia. Recently, importance of the species is increasing for its high ecological and economical values. In addition, it has resource value as livestock fodder, green fertilizer, fuel, honey and wood based panel production as well. In order to have effective conservation strategies, the allozyme and AFLP technique were used (1) to determine genetic diversity; (2) to quantify genetic variation within and among populations.

Materials and methods Ten korshinsk peashrub populations were collected from China. Each population consisted of eight to ten seed samples, a total of 98 samples were used in the study. Allozyme analysis was followed by Wang (2005). AFLP analysis was performed according to Vos et al. (1995). The POPGENE software was used to analyze the genetic diversity. A dendrogram was constructed using the UPGMA of NTSYS 2.0.

Results and analysis

1. Genetic Diversity

At allozyme level, 61.8% and 72.7% of the percentage of polymorphic loci (P) was found at the populations and species level, respectively. The mean population gene diversity (H_e) ranged from 0.219 to 0.351, with a mean of 0.263 and 0.292 at the species level. At molecular level, the genetic diversity of the korshinsk peashrub was detected higher than allozyme loci not only at population level ($P=69.5\%$, $I=0.365$) but also at species level ($P=93.9\%$, $I=0.477$).

2. Population Structure and gene flow

The distribution of genetic diversity revealed a large proportion of gene differentiation (86%) based on the difference of individuals within populations, whereas only 14% among populations was based on their location sites revealed by allozyme marker. While the genetic differentiation among populations was higher for AFLP (22%) than allozyme loci. Based on G_{ST} values, the estimated number of migrants per generation (N_m) between populations revealed by allozyme and AFLP was 1.5 and 1.7, respectively.

Discussion Korshinsk peashrub is a long-lived, out-crossing, insect-pollinated species, and the combination of these life history traits enable the species to maintain a high level of genetic diversity (Hamrick and Godt 1989). The reproductive system is the most important factor in determining the genetic structure of plant populations. Nybom and Bartish (2000) compiled mean G_{ST} values of 0.59, 0.19 and 0.23 for selfing, mixed mating and outcrossing plant species, respectively. Compared with these values, the populations of korshinsk peashrub are close to that with an outcrossing breeding system. In addition, the high intrapopulation variability and genetic homogeneity across populations could also have arisen by high levels of gene flow. A migration rate of 0.5 was considered sufficient to overcome the diversifying effects of random drift (Ellstrand and Elam, 1993). In this study, the estimated gene flow of korshinsk peashrub ($N_m=1.70$) was higher than the average value reported for out-crossed animal-pollinated species ($N_m=1.154$) and higher than that of mixed-mating species ($N_m=0.727$) (Hamrick and Godt, 1989).

Reference

Ellstrand, N.C., and D.R. Elam. 1993. Population genetic consequences of small population size: implications for plant conservation. *Annu. Rev. Ecol. Syst.* 24: 217-242.