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Study on genetic diversity of wild Lespedeza germplasm resources

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Key words : Lespedeza Michx ., genetic diversity , RAPD marker , protein marker , morphological marker

Introduction Lespedez a Michx . are perennial plants which belongs to Leguminosae, it has excellent characteristics (Clewell, 1964; Hoveland and Donnelly, 1985), but little is known about its genetic diversity. The aim of the study was to identify genetic differences between 20 wild germplasm materials of Lespedez a Michx . including 3 species and 1 variety, collected from Inner Mongolia, Shanxi, Hebei, Gansu and Ningxia provinces in China using three approaches: morphology marker; seed storage protein marker and DNA marker.

Materials and methods Using the same criterion, morphological data were collected for 19 quantitative characters and then the genetic diversity based on seed storage protein marker and DNA marker among 20 wild germplasm materials were tested by SDS-PAGE and RAPD. Statistical analysis was made by SPSS11.5, NTSYS-pc and Popgene Version 32.

Results and discussion The genetic diversity of Lespedeza Michx. is very abundant, the diversity of intra-population is higher than that of inter-population. We can conclude that variation between populations is the main reason that results in variation of Lespedeza Michx. Among 3 species and 1 variety, the genetic diversity of L. *potaninii* Vass. was the highest (Zhang 2003; Zhao 2006). The relationship among 3 species and 1 variety was estimated by the statistical analysis of the diversity parameters and cluster analysis. The results from three approaches showed that the relation between L. *hedysaroides* (Pall.) Kitag. var. subsericea (Kom.) Kitag. was closer; for L. *davurica* (Maxim.) Schindl. and L. *potaninii* Vass. was also closer, but L. *hedysaroides* (Pall.) Kitag. var. subserices (Pall.) Kitag. Cluster analysis was made with the un-weighted pair group method for arithmetic averages (UPGMA) using Euclid distance coefficients which based on 19 morphological characters, using the symmetric matrix of similarity coefficients based on seed storage protein patterns and RAPD marker. The three dendrograms indicated that the relationships among 20 wild germplasm materials were basically confirmed on the traditional taxonomy of the species and interspecies which material was collected.

Conclusions We conclude the following by using the three evaluation approaches : (1) there is a large amount of genetic diversity in *Lespedeza* Michx. germplasm resources, either within or between populations, although the variation between populations which was significantly higher than that within populations was the main cause that resulted in variation of *Lespedeza* Michx. germplasm resources. (2) The genetic diversity of *L. potaninii* Vass. was highest. (3) The relation between *L. hedysaroides* (Pall.) Kitag. and *L. hedysaroides* (Pall.) Kitag. var. subsericea (Kom.) Kitag. was closer; *L. davurica* (Maxim.) Schindl. and *L. potaninii* Vass. Was also closer, but *L. hedysaroides* (Pall.) Kitag. var. subsericea (Kom.) Kitag. var. subsericea (Kom.) Kitag. var. subsericea (Kom.) Kitag. was even closer than *L. hedysaroides* (Pall.) Kitag. and (4) Cluster analysis showed that the materials from the same species could cluster together, but a few could not do the same. Relationships of inter-species confirmed the traditional taxonomy of 3 species and 1 variety belonging to *Lespedeza* Michx.

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