



# Genetic diversity of wild soybean populations in Dongying, China, by simple sequence repeat analysis

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**ABSTRACT.** Annual wild soybean (*Glycine soja* Sieb. et Zucc.), the ancestor of cultivated soybean (*G. max*), is believed to be a potential gene source for further improvement of soybean to cope with environmental stress. In this study, 10 simple sequence repeat (SSR) markers were used to evaluate the genetic diversity and population genetic structure in five wild soybean populations using 195 accessions collected from Dongying, China. Ten SSR markers yielded 90 bands, with an average of nine bands per marker. The percentage of polymorphic loci (P) was 97.78%, the distribution of expected heterozygosity ( $H_e$ ) was 0.1994-0.4460 with an average of 0.3262, and the distribution from Shannon's information index ( $I$ ) was 0.3595-0.6506 with an average of 0.5386. The results showed that wild soybean had a high degree of genetic diversity at the species level. Nei's differentiation coefficient ( $F_{ST}$ ) was 0.1533, and gene flow ( $N_m$ ) was 1.3805, which indicated that genetic variation mainly existed within populations and that there was a certain level of gene exchange between populations. Some genetic differentiation occurred among populations, although this was not significant. Cluster

analysis indicated that there was no significant correlation between the genetic structure of wild soybean populations and their geographic distribution, and the clustering results may be relatively consistent with the habitats of the accessions. In the present study, the genetic diversity of wild soybeans showed a broad genetic base and enables suggestions for the conservation of this plant to be made.

**Key words:** Wild soybean; Simple sequence repeat; Genetic diversity; Conservation