



# Genetic diversity and the conservation priority of *Glycine soja* populations from Northern China

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**ABSTRACT.** Knowledge of the spatial patterns of genetic variation in wild populations has significant implications for *in situ* conservation and the determination of conservation order. To study the levels of genetic diversity, spatial genetic structures, and genetic distances in *Glycine soja*, 11 natural populations in northern China were analyzed by estimating genetic coefficients using inter-simple sequence repeat (ISSR) fingerprints via mixed sampling strategies. Sixteen ISSR primers generated 98 reproducible polymorphic amplification banding patterns of 172 scored, accounting for 56.98% of the polymorphisms among the populations. The dendrogram based on Nei's genetic distance showed that distinct genetic differentiation occurred in *G. soja*. The Unweighted Pair-Group Method with Arithmetic Mean cluster analysis indicated two broad groups, and one contained all of the populations except three from Chengde, which formed the smaller second group. The spatial genetic structure evident in the wild soybean populations may be attributed to restricted seed dispersal and the dominant breeding system of this species. The detection of genetic

structures in wild soybean populations could be a significant index for the effective conservation of many wild populations, and it could be exploited by soybean breeding programs to increase production.

**Key words:** Conservation strategy; Genetic structure; Wild soybean; Inter-simple sequence repeat