

Genetic structure of Mongolian Wheatgrass (*Agropyron mongolicum* Keng) in Inner Mongolia of China

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Keywords: genetic diversity, RAPD

Introduction Mongolia wheatgrass (*Agropyron mongolicum*) is a cross-pollinated, long-lived, cool-season and drought-resistant perennial bunchgrass, which plays an important role in arid and semi-arid grasslands of Inner Mongolia. Collections of *A. mongolicum* from different areas of Inner Mongolia are valuable sources of useful genes for its breeding. The genetic diversity of 8 accessions of *A. mongolicum* were examined in this study. A dendrogram was constructed to obtain information on the relationship between cultivated and wild *A. mongolicum* genotypes, which is basic information to explore the possibility of its use in intra- and inter-specific breeding programs.

Materials and methods A total of 8 accessions (6 wild and 2 cultivated) of *A. mongolicum* were collected from 7 areas in arid and semi-arid grasslands of Inner Mongolia. Fifteen plants (spaced at least 10 m apart) were randomly sampled from each site. Seeds were collected from each plant and planted in a greenhouse. Leaves were collected from one seedling from each plant. The collected leaves were prepared to extract genomic DNA and RAPD markers that were used to detect the genetic diversity. Seventeen arbitrary primers were used and their markers were analysed by using SPSS 8.0 to generate Jaccard's similarity coefficient (S_{ja}), genetic distance ($D=1-S_{ja}$), and diversity coefficient (DC). UPGMA dendrogram was constructed using MEGA software.

Results The diversity coefficients (DC) ranged from 0.147 (Zhenlan) to 0.273 (Qingshuihe), with an average of 0.237 (Table 1) and the six wild populations showed a higher diversity than the cultivated populations. The diversity coefficient (DC) among the 8 populations was 0.222, among the six wild populations 0.250, while among the two cultivated varieties it was 0.181. This evidence was supported with a relatively small genetic distance between the two cultivated populations (average 0.290 among wild populations and 0.213 among cultivated populations). The UPGMA dendrogram showed that the eight populations could be divided into 3 groups, based on their geographic origin and on the soil type of their distribution areas.

Table 1 Diversity coefficients (DC) within populations

Site	Xiwu	Baiyinxi	Qingshuihe	Zhenlan	Yijihuole	Sunitezu	Var.1	Var.2	Average
DC	0.243	0.269	0.272	0.226	0.258	0.273	0.210	0.147	0.237

Conclusion The average diversity coefficient of 0.237 indicated considerable genetic diversity among populations of *A. mongolicum*. The open pollination and out-crossing system, as well as the strong gene flow led to a great diversity of *A. mongolicum* being retained in recessive genes in the heterozygotic state. As a geographically widely distributed species, *A. mongolicum* has a lot of ecotypes, each of them with their own physiological traits and adaptive capacity. It is noteworthy that there was a clear tendency for *A. mongolicum* that originated from the same location to be clustered together in the dendrogram.

References

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