

Genetic characterization of prairie grass (*Bromus catharticus* Vahl.) natural populations

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Introduction Prairie grass, *Bromus catharticus* Vahl., is a winter annual or biennial grass, native of South America which is widely distributed in the Pampeana area of Argentina and also cultivated in temperate regions of the world. Morphophysiological traits are currently used to assess the variability from natural populations and cultivars of this species. Molecular markers, which are not influenced by the environment, allow a more accurate assessment of genetic variability. Previous results from our group (Puecher *et al.*, 2001a) showed a narrow genetic basis for the prairie grass cultivars used in Argentina. On the other hand, we also observed that natural populations of this species collected in the typical area where prairie grass is cultivated in Argentina, showed a RAPD variability pattern similar to that previously observed for cultivars (Puecher *et al.*, 2001b). The objective of this work was to establish, using RAPDs, the genetic relationships among prairie grass natural populations including accessions from the margins of the cultivation area of this species in Argentina.

Materials and methods Twelve Argentinean *B. catharticus* natural populations collected from different geographical provenances were analyzed. Cultivars: Martín Fierro (*Bromus catharticus*), Zamba (*Bromus stamineus*), Pampera (*Bromus auleticus*) and Ona (*Bromus inermis*) were also included as controls. Genomic DNA was isolated of bulked samples derived from 10 plants per population using the protocol described by Puecher *et al.* (2001) and was further used as template in PCR with 8 selected primers (Operon) to produce RAPDs. Each band was scored as present or absent and low intensity bands were not considered. Genetic distances among populations were estimated using the Jaccard coefficient and UPGMA was used for cluster analysis and dendrogram plotting. All calculations were performed using the NTSYS-pc version 2.02g.

Results A total of 104 amplification products were scored from selected primers in the accessions and the control cultivars. The number of bands per primer showed a variation from 8 to 19. Considering the whole number of bands, 90% of them were polymorphic in at least one of the accessions. Cluster analysis clearly distinguished the different *Bromus* species (Figure 1). The genetic relationships among the controls were similar to those observed in our previous studies confirming the reproducibility of this method. The natural populations and the cv Martín Fierro of *B. catharticus* were grouped in five clusters with a genetic similarity coefficient ranging from 0.5 to 0.8. Two of these groups, one containing a single population and the other one four populations, were clearly separate from the other groups, indicating that these accessions were genetically distinct from others in this study. This difference was coincident with significant differences in morphological characters (flag leaf width, growing habit, vegetative tillering).

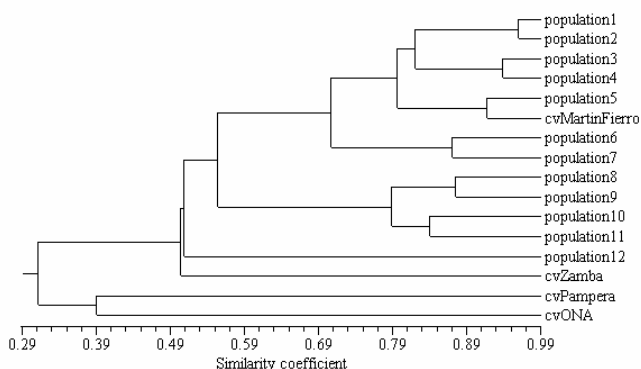


Figure 1 Dendrogram for *Bromus* accession and cultivars, resulting from a UPGMA cluster analysis based on Jaccard similarity coefficient using RAPD markers

Conclusions The results of the present study demonstrate that the inclusion of accessions collected at the marginal area of prairie grass cultivation in Argentina, contributed to broaden the genetic variability available for the breeding of this Argentinean native species.

References

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