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Random amplified polymorphic DNA analysis in section *Pnigma* of the genus *Bromus* L.

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Introduction The section *Pnigma* consists of about 60 species. It was shown that Eurasian species of the section with the same ploidy level have similar nuclear DNA contents (Tuna *et al.*, 2001). A linear correlation between nuclear DNA content and ploidy level was also found (Tuna *et al.*, 2001). Furthermore, karyotypes of Eurasian species are similar (Tuna *et al.*, 2004a) but differ from the North American species (Tuna *et al.*, 2004b). Yet, the genetic relationship among species within the section is poorly known (Armstrong, 1991). The objective of this study was to assess the phylogenetic relationships among species of section *Pnigma* by using the RAPD technique.

Materials and methods Thirty one *Bromus* accessions representing 7 species from the USDA Regional Plant Introduction Station, Pullman, WA and Plant Gene Resources of Canada, Saskatoon, Saskatchewan S7N 0X2 were used in the study. DNA was extracted following the protocol described by Doyle and Doyle (1987). Eighty ten-mer primers (Operon Technologies, Inc.) were screened for polymorphism. A cluster dendrogram was generated by the UPGMA clustering method using NTSYS-pc.

Results Thirteen primers used in the study generated 71 polymorphic RAPD markers. The size of the markers ranged from 491 bp to 3403bp. Four accessions (all diploids and *B.ciliatus*) could be distinguished from the other species by specific markers. Briefly, the dendrogram includes two main clusters (Fig 1). One cluster includes only decaploids except PI 325235 (*B. riparius*) while the other cluster includes tetraploids and octaploids. Accessions of *B. ciliatus* and all of the diploids appeared as distinct species in the dendrogram. Almost all accessions representing a species grouped most closely together.

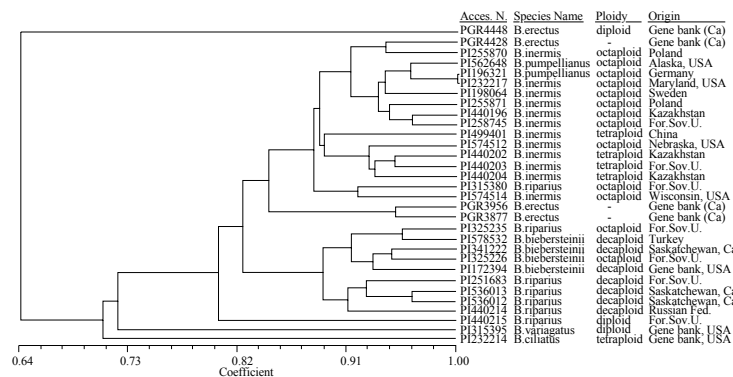


Figure 1 Dendrogram of 31 *Bromus* accessions constructed from RAPD-based genetic distance

Conclusion It appears that diploid species are more distinct than their related polyploids. The results of this study confirm the previous reports (Armstrong, 1991) suggesting that Eurasian polyploid species of section *Pnigma* are closely related and carry different number of copies of the same genomes.

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