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Genetic structure and AFLP variation of six native *Festuca hallii* (Vasey Piper) populations in the Northern Great Plains of Canada

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Key words: genetic structure, AFLP, *Festuca hallii*, native

Introduction *Festuca hallii* (Vasey) Piper is a dominant native grass species in the Fescue Prairie of Northern Great Plains that has undergone dramatic range reduction in the past century. However, little is known about the genetic diversity and structure of this species. Also, little effort has been made to assess the effectiveness of sampling in capturing genetic diversity in native plant species. The objective of this study was to assess the comparative genetic diversity of plains rough fescue using AFLP markers.

Materials and methods Six *F. hallii* populations were collected from Prince Albert National Park, Batoche National Historical Site, Riding Mountain National Park, Macrorie, Kernen Research Farm and Turtleford. Three AFLP primer pairs were employed to screen 529 samples representing about 30 samples each of reproductive tiller, vegetative tiller and seed collected from each population. The gel images were scored as 1 (present) or 0 (absent). The scored bands were analyzed for the level of polymorphism by counting the total number of bands and the number of polymorphic bands, and calculating the proportion of polymorphic bands. The within-population variation was calculated with respect to population as the average number of pairwise differences within a population using AMOVA (Excoffier et al. 2005). Mantel test and PCO analysis were conducted using GenAlEx 6.

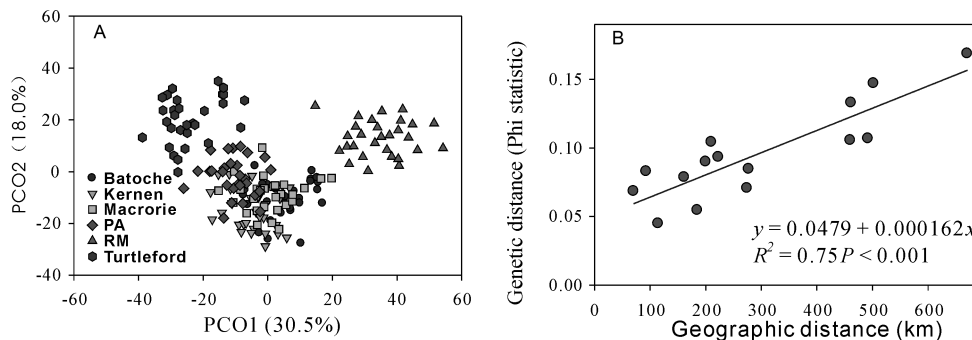


Figure 1 Principal coordinate analysis of 529 individual plants (A) and the relationships between geographic and genetic distance (Phi statistic) (B) from six *Festuca hallii* population as reflected in the samples of reproductive tiller.

Results A total of 330 polymorphic AFLP bands were scored for each sample and their occurrence frequencies ranged from 0.01 to 0.99 and averaged around 0.47. Comparisons of the three sample types in each population revealed more polymorphic bands in the seed samples than the tiller samples, while the mean band frequencies were similar. AMOVA revealed more than 90% of the total AFLP variation resided within natural populations (reproductive and vegetative tillers) and within seed samples. Only 0.2% AFLP difference was revealed among the three sample types. The tiller samples revealed not only the larger among-population variation than the seed samples, but also the significant associations of AFLP variation with population geographic distances.

Conclusions A large number of polymorphic DNA fragments detected by three AFLP primer pairs show the utility of AFLP in assessments of genetic variability in *F. hallii*. Different sampling methods captured different population structures. This finding along with those of Fu et al. (2004) suggests that different sampling methods may differ in the effectiveness of capturing genetic variation. Results from this study are significant for germplasm sampling for ex situ conservation, are useful for the germplasm development for pasture seeding, and should facilitate the management of fragmented fescue populations.

Reference

Excoffier, L., Laval, G., and Schneider, S. (2005). Arlequin ver. 3.0: An integrated software package for population genetics data analysis. *Evol. Bioinformatics Online*, 1, 47-50.