

Analysis of genetic diversity identified by amplified fragment length polymorphism marker in hybrid wheat

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ABSTRACT. Amplified fragment length polymorphism markers were used to assess genetic diversity in 10 male sterile wheat crop lines (hetero-cytoplasm with the same nucleus) in relation to a restorer wheat line. These male sterile lines were evaluated using 64 amplified fragment length polymorphism primer combinations, and 13 primers produced polymorphic bands, generating a total 682 fragments. Of the 682 fragments, 113 were polymorphic. The polymorphic information content and marker index values demonstrated the utility of the primer combinations used in the present study. Unweighted pair group method with arithmetic mean and principal coordinate analysis of the genotypic data revealed clustering of accessions based on genetic relationships, and accessions were separated into 2 groups with their restorer line.

Jaccard's similarity coefficient values suggested good variability among the male sterile lines, indicating their utility in breeding programs. The fallouts of analysis of molecular variance showed large within-group population variation, accounting for 77% of variation, while amonggroup comparison accounted for 23% of the total molecular variation, which was statistically significant. The molecular diversity observed in this study will be useful for selecting appropriate accessions for plant improvement and hybridization through molecular-breeding approaches and for developing suitable conservation strategies.

Key words: AFLP marker; Genetic diversity; Male sterile lines; *Triticum aestivum*