

Genetic diversity of *Saccharum officinarum* accessions in Pakistan as revealed by random amplified polymorphic DNA

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ABSTRACT. Genetic diversity of 20 sugarcane accessions in Pakistan was studied using 21 random amplified polymorphic DNA markers. The mean genetic distance between the cultivars was 39.03%, demonstrating that a large part of the genome is similar among the accessions. This probably arises from a lack of parental diversity, with few clones, which are themselves related, contributing to the parentage of these varieties. Among the varieties, none was found to be totally distinct and divergent from the others. We conclude that the current Pakistan commercial varieties have a limited genetic base and that there is a need to diversify commercial sugarcane lines in Pakistan by introducing new germplasm sources.

Key words: Sugarcane; Random amplified polymorphic DNA; Genetic diversity; Polymerase chain reaction