

Phylogenetic relationships among *Saccharum* clones in Pakistan revealed by RAPD markers

S. Nawaz¹, F.A. Khan¹, S. Tabasum², M. Zakria³, A. Saeed¹ and M.Z. Iqbal⁴

¹Department of Plant Breeding and Genetics, University of Agriculture, Faisalabad, Pakistan ²University College of Agriculture, Sargodha, Pakistan ³Department of Mathematics and Statistics, University of Agriculture, Faisalabad, Pakistan ⁴Ayub Agriculture Research Institute, Faisalabad, Pakistan

Corresponding author: A. Saeed E-mail: drasifpbg@gmail.com

Genet. Mol. Res. 9 (3): 1673-1682 (2010) Received May 5, 2010 Accepted June 14, 2010 Published August 24, 2010 DOI 10.4238/vol9-3gmr903

ABSTRACT. Forty sugarcane genotypes (clones), including elite lines, commercial cultivars of *Saccharum officinarum* and *S. barberi* clones, were fingerprinted with 30 RAPD markers, using a PCR-based marker assay. The genetic distance for RAPD data was determined according to Nei, and relationships between accessions were graphed in a dendrogram. Genetic distance values ranging from 16.2 to 86.3% were observed among the 40 sugarcane accessions. The lowest genetic distance was found between genotypes US-406 and US-186. These two genotypes differed from each other in only 25 bands with 15 different primers. Genotypes Col-54 and CP-72-2086 were the second most similar group, with a genetic distance of 19.46%. The most dissimilar of all the accessions were CP-77-400 and US-133, with a genetic distance of 86.3%. RAPD fingerprints help sugarcane breeders clarify the genetic pedigree of commercial sugarcane varieties and can be used to evaluate the efficiency of conventional breeding methods.

Key words: DNA marker; RAPD; Genetic distance; Sugarcane; Fingerprinting

Genetics and Molecular Research 9 (3): 1673-1682 (2010)