

Estimation of genetic distance between 10 maize accessions with varying response to different levels of soil moisture

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ABSTRACT. Ten maize accessions (NC-9, A50-2, M-14, B-42, NC-3, T-7, N-48-1, B-34, USSR, and WFTMS) were studied to estimate the genetic distance on molecular level by random amplified polymorphic DNA. These accessions were selected on the basis of their variable responses against different levels of moisture. Twenty-five primers were used to test genetic diversity, of which 14 were observed to be polymorphic. Ninety-three loci were amplified; among these, 77 showed polymorphism and the other 16 were monomorphic. Primers A-13 and C-02 gave the most polymorphic bands, while primers A-01 and C-06 gave the fewest polymorphic bands. The genetic similarities of the 10 maize accessions ranged from 82.8 to 54.8%. Accessions USSR and WFTMS showed greatest similarity, and accessions M-14 and B-42 were found more dissimilar than the other accessions. On the basis of cluster analysis, these 10 accessions were classified in two major groups, A and B, and then further divided into sub-groups. The cluster analysis showed that ac-

cessions in the same group as well as in the sub-groups were similar in their physical and morphological characters, since the characters are controlled genetically.

Key words: Random amplified polymorphic DNA; Maize; Genetic diversity; Germplasm conservation