

Estimation of genetic diversity among sunflower genotypes through random amplified polymorphic DNA analysis

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ABSTRACT. The genetic diversity among eight sunflower lines was determined through the estimation of the random amplified polymorphic DNA method. One hundred and fifty-six DNA fragments were generated by 20 random primers, for an average of about 7.8 bands per primer. Of these amplified DNA fragments, 104 were polymorphic among the eight sunflower lines. Nei and Li's similarity matrix gave values from 51.59 to 77.78%, which indicated a broad genetic base. The maximum similarity, 77.78%, was observed between R-SIN-82 and RN-46. The lowest similarity, 51.59%, was observed between the exotic lines CM-612 and HA-27. After knowing the knowledge of genetic diversity based on these random amplified polymorphic DNA markers, highly diverse lines can be used for further breeding programs to develop an ideal local hybrid of sunflower.

Key words: Genetic diversity; Random amplified polymorphic DNA; Sunflower diversity; DNA markers