Development of AFLP markers and genotyping of elite maize inbred lines

(Received: 10.11.2003; Accepted: 1.1.2004)

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ABSTRACT

The AFLP technology was used to develop AFLP markers characterizing 10 maize inbred lines and generating unique fingerprint for each inbred line. Selective amplification of the genomic DNA from the ten inbred lines, using eighteen primer combinations, revealed a total number of 1143 amplicons. The number of polymorphic amplicons across the 10 inbred lines was 902, representing a level of polymorphism of 78.9%. Genetic distances between lines were calculated from AFLP data using the Dice coefficient. UPGMA analysis and dendrogram clustered the ten inbred lines into two main clusters, each composed of different groups revealing relationships which were basically consistent with the pedigree of the inbred lines. Moreover, unique AFLP markers characterizing each of the ten inbred lines were identified. The total number of unique markers was 122 positive markers and 73 negative markers. The number of unique markers per genotype ranged from 4 to 45. Inbred line Sd 7 was characterized by the highest number of unique markers (39 positive and 6 negative markers). While, line A188 revealed the lowest number of unique markers (4 markers). The results assess the potentiality of the AFLP technology for characterizing at the molecular level and for generating unique fingerprint for each inbred line. This could have great impact in plant improving programs, particularly, of important crops such as maize.

Keywords: *Molecular markers, AFLP, maize, fingerprinting, genotyping, structural genomics and genetic similarity.*

INTRODUCTION

The emerging technologies have revolutionized plant genetics and breeding in the last few decades. Plant genomic research has produced molecular tools for scientist to improve breeding efficiency and accuracy. One of these important tools is the development of molecular markers. The usefulness of DNA markers for germplasm characterization and estimation of genetic relationships has been well demonstrated for different crops (Ahmed, 1999; Cao *et al.*, 1999; Moeller and Schaal, 1999; Hussein *et al.*, 2000, 2002 a & b and 2003, Adawy *et al.*, 2002, Fernandez *et al.*, 2002; Coulibaly *et al.*, 2002 and El-Khishin *et al.*, 2003).

In addition, the use of DNA markers for marker assisted selection brings extraordinary promise for streamlining many crop improvement efforts (Tanksley *et al.*, 1988 and Ribant and Hoisington, 1998).

Moreover, DNA markers proved to be useful in predicting genotypes that may be used in new crosses, particularly in certain crops such as maize where the challenge to maize breeders is to identify inbred lines that