

EVALUATION OF GENETIC DIVERSITY AMONG MAIZE GENOTYPES USING SSR MARKERS

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Maize has become a significant crop all over the world owing to its potential for fulfilling food demand of people. Present study was carried out to evaluate genetic variations among maize genotypes through SSR markers. For genetic diversity analysis 15 genotypes of maize collected from different research institutes of Punjab Pakistan. Several growth and quality parameters were also examined such as fresh root weight, fresh shoot weight, dry shoot weight, dry root weight, crude protein, crude fat, ash content, acid detergent fiber and neutral detergent fiber. On the basis of reproducibility and high PIC value, 22 SSR primers were selected for DNA finger printing of all collected genotypes. Binary method was used for band scoring. The polymorphism information content (PIC) value of primers was calculated to estimate extent of genetic differences. It was calculated that polymorphism information content ranged from 0.1 to 0.8. Only three markers umc1122, umc1568 and umc1988 provided highly polymorphic values which were 0.8, 0.5 and 0.6 respectively. Unweighted Paired Group Method using Arithmetic Averages (UPGMA) cluster analysis has grouped the genotypes into three major clusters. Cluster analysis revealed that maximum genetic distance was found 3.16 between Sgd 2002 and Golden, while minimum genetic distance was observed 1.414 between Fsd maize and Neelam. The identified clusters may find useful to plan crossing program in maize breeding. This study concluded SSR as a good source for genetic characterization. It was cleared from phylogenetic analysis that genetic diversity among above mentioned genotypes was limited since all these genotypes were collected from nearby areas in province of Punjab and there were no exotic genotype. On the other hand, data recorded for growth and quality parameters subjected to statistical analysis and results showed all maize genotypes had considerable genetic differences for all growth and quality traits and maximum genetic variability was examined for fresh shoot weight, fresh root weight, dry shoot weight, dry root weight, crude protein, crude fat, acid detergent fiber (ADF), neutral detergent fiber (NDF) and ash content in Sgd 2002 (13.5g), Agaiti 72 (18g), Fsd maize 2018 (6.8g), Agaiti 72 (8.7g), EY 1098 (5.1g), YHM (1.9g), Pearl maize (30g), Agaiti 2002 (49g) and MS 2010 (30g) respectively. These findings of genetic diversity analysis among maize genotypes with the help of SSR markers as well as on basis of growth and quality traits may be consider for further evaluation and selection as parents in breeding programmes.

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