DNA Profiling of Selected Inbred Maize Germplasms Using SSR Markers Related to Canopy Architecture and Photosynthetic Traits

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Abstract

Inbred maize (*Zea maize* L.) lines play a crucial role in the production of novel hybrid maize varieties. However, the dispersion of alleles related canopy architecture and photosynthetic traits due to the inbred depression process is poorly understood. This research aims to examine the genetic diversity of four maize inbred accessions: *SEU2-S1, SEU2-S2, SEU10-S3, SEU16-S3*, and compare them with the elite cultivar, *cv. Bhadra*. Standard protocols were employed to extract genomic DNA from immature maize seedling leaves. PCR was then performed using the following SSR markers: *phi065, phi116, umc1066, umc1222, umc1231, umc1545*, and *bnlg155*. The data were analyzed using GenAlex and DARwin software. Based on the results obtained, 35 alleles were amplified, with the highest observed (6.0) and effective (5.556) alleles found in the *phi116* marker. This marker also showed the highest gene diversity and PIC values (0.820 and 0.794, respectively), while the lowest values were recorded in *umc1545* (0.640 and 0.563, respectively). Among all the SSR primers used, *phi065, umc1231, umc1066*, and *bnlg155* resulted in expected heterozygosity values of 0.8, 0.78, 0.8, and 0.76, respectively. Accordingly, the most genetic diversity parameters were found to be linked with the leaf area index and cob traits, while chlorophyll content and quantum yield efficiency were moderately diverse among maize accessions. Moreover, the cluster analysis identified two major genetic groups with a mean similarity of 0.764. These results elucidate the importance of genetic diversity when working with inbred lines in maize.

Keywords: Cluster analysis, Genetic diversity, Maize accessions, Maize breeding, Polymorphic Information Content, SSR markers