Evaluation of genetic variation and relationships among tropical sweet corn inbred lines using agronomic traits

ABSTRACT

Genetic variability and relationship of 13 tropical sweet corn inbred lines derived from different source populations were investigated using agronomic traits during three consecutive years. Non-significant effects of years and years-by-lines indicated the stability of performance of the inbred lines per se over years. Contrastively, the effects of inbred lines were significant for all traits measured, indicating great genetic variability in their performance. Among the inbred lines, TSN-S8, TSK-S8, BAK-S8, MAN-S8, MMIN-S8 and TSG-S8 were found to be high yielding, with high husked fresh ear yield, dehusked fresh ear yield and number of ears per hectare, while DFS-S8 and TFZ-S8 were found to be superior for ear characteristics including husked ear length, dehusked ear length, number of kernel rows per ear and TSS. The high heritability estimates obtained from husked and dehusked fresh ear yields in this study indicate that the inbred lines have become homozygous at almost all the loci after eight generations of selfing. Husked fresh ear yield was phenotypically and genetically correlated with dehusked fresh ear yield, number of ears per hectare, husked and dehusked ear weights, dehusked ear length, husked and dehusked ear diameter, number of kernels per row and number of kernel rows per ear, indicating direct positive contribution of these traits to husked fresh ear yield. Visualizing the relationship among the inbred lines using singular value decomposition biplot analysis revealed that the inbred lines could be assigned into three distinct groups. This indicates a strong indication of the potential of the inbred lines for their utilisation towards production of new hybrid varieties by crossing the inbred lines from different groups. It can be concluded that the inbred lines studied varied substantially in many aspects, and these differences could be exploited for specific purposes in breeding programs.

Keyword: Sweet corn (Zea mays L saccharata); Inbred line; Genetic variation; Agronomic traits