Genetic analysis and selection criteria in Bambara groundnut accessions based yield performance

ABSTRACT

The knowledge of genetic variability and breeding techniques is crucial in crop improvement programs. This information is especially important in underutilized crops such as Bambara groundnut, which have limited breeding systems and genetic diversity information. Hence, this study evaluated the genetic variability and established the relationship between the yield and its components in Bambara groundnut based on seed weight using multivariate analysis. A field trial was conducted in a randomized complete block design with three replications on 28 lines. Data were collected on 12 agro-morphological traits, and a statistical analysis was conducted using SAS version 9.4 software, while the variance component, genotypic and phenotypic coefficient variation, heritability, and genetic advance values were estimated. A cluster analysis was performed using NT-SYS software to estimate the genetic relations among the accessions. The results showed significant variability among the accessions based on the yield and yield component characteristics. The evaluated lines were grouped into seven primary clusters based on the assessed traits using the UPGMA dendrogram. Based on the overall results, G5LR1P3, G1LR1P3, G4LR1P1, G2SR1P1 and G3SR1P4 performed the best for the yield and yield components. These improved lines are recommended for large-scale evaluation and utilization in future breeding programs to develop high-yield Bambara groundnut varieties.

Keyword: Inheritance; Genetic analysis; Yield performance; Bambara groundnut