

Genetic variability, heritability, and clustering pattern exploration of Bambara groundnut (*Vigna subterranea* L. Verdc) accessions for the perfection of yield and yield related traits

ABSTRACT

Bambara groundnut (*Vigna subterranea* L. Verdc.) is considered an emerging crop for the future and known as a crop for the new millennium. The core intention of this research work was to estimate the variation of landraces of Bambara groundnut considering their 14 qualitative and 27 numerical traits, to discover the best genotype fitted in Malaysia. The findings of the ANOVA observed a highly significant variation () for all the traits evaluated. There was a substantial variation (7.27 to 41.21%) coefficient value, and 14 out of the 27 numerical traits noted . Yield (kg/ha) disclosed positively strong to perfect high significant correlation (to 1.00;) with traits like fresh pod weight, dry pod weight, and dry seed weight. The topmost PCV and GCV values were estimated for biomass dry (41.09%) and fresh (40.53%) weight with high heritability (Hb) and genetic advance (GA) %, % and %, %, respectively. The topmost heritability was recorded for fresh pod weight (99.89%) followed by yield (99.75%) with genetic advance 67.95% and 62.03%, respectively. The traits with and suggested the least influenced by the environment as well as governed by the additive genes and direct selection for improvement of such traits can be beneficial. To estimate the genetic variability among accessions, the valuation of variance components, coefficients of variation, heritability, and genetic advance were calculated. To authenticate the genetic inequality, an unweighted pair group produced with arithmetic mean (UPGMA) and principal component analysis was executed based on their measurable traits that could be a steadfast method for judging the degree of diversity. Based on the UPGMA cluster analysis, constructed five distinct clusters and 44 accessions from clusters II and IV consider an elite type of genotypes that produce more than one ton yield per hectare land with desirable traits. This study exposed an extensive disparity among the landraces and the evidence on genetic relatives will be imperative in using the existing germplasm for Bambara groundnut varietal improvement. Moreover, this finding will be beneficial for breeders to choose the desirable numerical traits of *V. subterranea* in their future breeding program.