DNA fingerprinting, fixation-index (Fst), and admixture mapping of selected Bambara groundnut (Vigna subterranea [L.] Verdc.) accessions using ISSR markers system

ABSTRACT

As a new crop in Malaysia, forty-four Bambara groundnut (Vigna subterranea L. verdc.) genotypes were sampled from eleven distinct populations of different origins to explore the genetic structure, genetic inconsistency, and fixation index. The Bambara groundnut, an African underutilized legume, has the capacity to boost food and nutrition security while simultaneously addressing environmental sustainability, food availability, and economic inequalities. A set of 32 ISSRs were screened out of 96 primers based on very sharp, clear, and reproducible bands which detected a total of 510 loci with an average of 97.64% polymorphism. The average calculated value of $PIC = 0.243$, $RP = 5.30$, $H = 0.285$, and $MI = 0.675$ representing the efficiency of primer set for genetic differentiation among the genotypes. The ISSR primers revealed the number of alleles ($Na = 1.97$), the effective number of alleles ($Ne = 1.38$), Nei's genetic diversity ($h = 0.248$), and a moderate level of gene flow ($Nm = 2.26$) across the genotypes studied. The estimated Shannon's information index ($I = 0.395$) indicates a high level of genetic variation exists among the accessions. Based on Nei's genetic dissimilarity a UPMGA phylogenetic tree was constructed and grouped the entire genotypes into 3 major clusters and 6 subclusters. PCA analysis revealed that first principal component extracted maximum variation ($PC1 = 13.92\%$) than second principal component ($PC2 = 12.59\%$). Bayesian model-based STRUCTURE analysis assembled the genotypes into 3 (best $\Delta K = 3$) genetic groups. The fixation-index (Fst) analysis narrated a very great genetic diversity ($Fst = 0.19$ to 0.40) exists within the accessions of these 3 clusters. This investigation specifies the effectiveness of the ISSR primers system for the molecular portrayal of V. subterranea genotypes that could be used for genetic diversity valuation, detection, and tagging of potential genotypes with quick, precise, and authentic measures for this crop improvement through effective breeding schemes.