Abstract

Population genetics analysis is aprerequisite to understanding how and why genotypes and allele frequencies and change over time between and within populations.Consequently, it offers insight into the process of evolutionary change and makes it possible to map variants linked to traitsthat differ among populations.In the present study, Single Nucleotide Polymorphisms (SNPs) markers were utilized to study the genetic characterization of 17 provenances from the Coast region of Kenya.164 genotypes of Moringa oleifera were selected from 17populations and genome sequencing undertaken utilizing genotyping by sequencing (GBS). Identification of polymorphisms (SNP Calling) in the selected genotypes and population genetic studies were carried out.SNP calling was done by Illumina's SNP caller algorithmin the CASAVA software. 20,921 SNPs were called with an average call rateof 0.82. Average polymorphsm content (PIC) for the SNPs was 0.24 and reproducibility was 0.98.A phenetic tree was constructed using a neighbor-joining approach using DArT R. For the population genetics analysis, F statistic (Fst) utilising the functions StAMPP package in DArT R was performed whereby Gede and Samburu exhibited the least heterozygosity/correlation with a value of 0.0003 whereas Pwani University and Samburu had the highest correlation of genes at 0.37. Euclidean was used as a measure distance,and the average distance between the populations was 33.024. The molecular variance analysis (AMOVA) described a lower, 2.55%, variation within the population and 2.73% among the populations. The high similarity between the genotypes could be attributed to the Moringa plants in the various provenances having the same ancestry. This study may help identify links between gene allelic forms and phenotypes, allowing the alleles to be connected to desired characteristics such as rapid growth and high yield (functional analysis), because of the high frequency of SNPs and their role as a source of allele variations.