

Genetic diversity of some cowpea (*Vigna unguiculata* L. Walp) landraces from Nigeria based on microsatellite markers

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Cowpea (*Vigna unguiculata* L. Walp) ($2n=2x=22$) has a narrow genetic base but varies widely phenotypically. The narrow genetic base has resulted in cowpea low yield and high vulnerability to insect pest and diseases in Nigeria; hence is the need to assess the level of genetic diversity within and between cowpea landraces across the agro ecological zones of Nigeria and also assess the level of diversity within old and new accessions used in the study. Eighteen cowpea landraces across five agro ecological zones were used. Genomic DNA was extracted from leaves of five randomly sampled cowpea stands per landrace. This formed a total of ninety DNA samples across the landraces. Fifteen simple sequence repeat (SSR) primers were screened to obtain six polymorphic primers. Two to 4 alleles with mean allele frequency of 2.833 were detected across the loci. The mean polymorphic information content (PIC) of the markers and observed heterozygosity were 0.4331 and 0.2378 respectively. Cluster analysis based on Unweighted Pair Group Mathematic Arithmetic (UPGMA), Principal Coordinate Analysis (PCoA) and Analysis of molecular variance (AMOVA) gave consistent results of the genetic diversity. Genetic diversity within the landraces constituted 33.55% while between the landraces constituted 26.94%. Diversity arising from the spatial differentiation (39.51%) of the agro zones constituted the highest level of diversity. There was more diversity within the landraces from Sudan savannah, followed by Guinea Savannah and Derived Savannah. Landraces from Sahel Savannah and Humid Savannah had low diversity. The new accessions showed higher level of diversity than the old accessions.

Biography

Iseghohi Innocent O. is an Assistant Lecturer in the Department of Crop Science and Horticulture, Federal University Oye-Ekiti State, Nigeria. His research areas include diversity study of legumes, QTL analysis of drought resistance gene in rice and marker-assisted breeding for fruit quality traits in tomatoes. He has some publications in reputable Journals and conference proceedings.

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