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Molecular Characterization Of Soybean (Glycine Max (L.) Merril) Genotypes Using Ssr Markers

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Six SSR primers were used to amplify genomic DNA from 10 soybean genotypes, after which the level of diversity among the genotypes were elucidated based on marker polymorphism. Seventeen alleles with a mean value of 2.8 alleles per locus were detected. The polymorphic information content (PIC) among genotypes ranged between 0.16 to 0.60 with an average PIC of 0.45 and a gene diversity of 0.51. A phylogenetic tree was produced from the allelic diversity data, which clustered the genotypes into two groups. The major cluster was divided into two subgroups, each consisting of 3 genotypes, while the minor cluster was divided into three sub-groups. Findings on the single sequence repeat (SSR) primers used in the study indicated high levels of polymorphism, which is an important attribute for ascertaining genetic diversity. The utility of the SSR marker system and reliability of DNA characterization are both useful tools for assessing soybean genetic diversity.

Biography

Kehinde D. Tolorunse currently works at the Department of Crop Production, Federal University of Technology Minna, Nigeria. Kehinde does research in Agronomy, Horticulture and Agricultural Plant Breeding. Their most recent publication is 'Yield stability studies of soybean (Glycine max (L.) Merrill) under rhizobia inoculation in the savanna region of Nigeria

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