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Molecular characterisation of *Solanum lycopersicum* L. accessions using simple sequence repeat (SSR) marker

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Abstract

Solanum lycopersicum L. (tomato) is one of the most economically important climate-resilient crops cultivated globally and critical for nutrition and income of smallholder farmers in the tropics. Previous studies reported morphological and molecular characteristics of tomato with limited information on characterisation using Simple Sequence Repeat (SSR) marker. This study was therefore carried out to evaluate the genetic diversity of tomato accessions using SSR primers for breeding of climate-adapted accessions. Eight tomato accessions were obtained from the National Centre for Genetic Resources and Biotechnology (NACGRAB), Ibadan, and Technoserve, Kano, while one local accession from Oojo served as a check (control). A screen house experiment was conducted using complete randomised design with three replicates. Genomic DNA was extracted from three-week-old leaf samples using the Dellaporta method. Four SSR primers (LEga003, LECaa001, LETaa001, and LEAAT005) were employed, and PCR amplification products were analysed using gel electrophoresis. Genetic diversity was evaluated using PowerMarker software version 3.25. The SSR primers amplified polymorphic bands ranging from 100 to 1000 base pairs. Primers LETaa001 and LECaa001 exhibited the highest Polymorphic Information Content (PIC) of 0.56 and 0.52, respectively, with corresponding gene diversities of 0.64 and 0.58. The mean PIC of the primers was 0.45, indicating moderate genetic diversity. Phylogenetic results revealed two major clusters, and the Oojo accession formed an outgroup, suggesting a distinct genetic lineage. The NGB00752 and Rukuta Jubia accessions showed close genetic relationships. Primers LETaa001 and LECaa001 were highly informative and are recommended for molecular breeding programmes in tomato. A phylogenetic dendrogram was constructed using the maximum likelihood method implemented in PowerMarker software. Genetic distance matrices were calculated based on the binary data, and the dendrogram was generated to visualise genetic relationships among the eight tomato accessions. Bootstrap analysis with 1000 replicates was performed to assess the robustness of the clustering pattern. Therefore, genetic diversity provides valuable insights for germplasm conservation, improvement, and breeding of climate-resilient tomato cultivars for tropical farming systems.

Keywords: Climate resilience, genetic diversity, molecular breeding, Nigeria

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