

**Optimization and characterization of novel EST-SSR markers for
cassava (*Manihot esculenta*).**

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ABSTRACT

Microsatellites, or simple sequence repeats (SSRs) are very useful molecular markers for a number of plant species. They are commonly used in cultivar identification, plant variety protection, as anchor markers in genetic mapping, and in marker-assisted breeding. Their utility is due to their abundance, hyper variability, and suitability for high-throughput analysis. Early development of SSRs was hampered by the high cost of library screening and clone sequencing. Currently, large public SSR datasets exist for many crop species, but the numbers of publicly available, mapped SSRs for cassava are relatively low. A database mining approach to identify SSR-containing expressed sequence tags (EST) in the IITA/Craig Venter Institute database was utilized. The overall aim of this study was to optimize and characterize in terms of polymorphism new EST-SSR primers that may be useful for diversity assessments and genetic linkage mapping in cassava. Seventy primer pairs were synthesized and used to amplify SSRs from diverse cassava DNA genotypes. This study identified 33 (63%) useful SSRs markers which were polymorphic in a set of 24 cassava genotypes from South America and Africa together with four parents of a mapping population from drought tolerant and four parents of a cassava brown streak disease (CBSD) mapping population. The polymorphic information content (PIC) values ranges were from 0.0 to 0.7381 and average allele frequency of 2.5. The high proportion of (63%) polymorphic EST-SSRs obtained in this work validates the use of transcribed sequences as a source of markers. These markers will be useful for genetic mapping, diversity assessments and genomic research.