



Enhancer/Suppressor mutator (En/Spm)-like transposable elements of cassava (*Manihot esculenta*) are transcriptionally inactive

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ABSTRACT. Transposable elements contribute to the size, structure, variation, and diversity of the genome and have major effects on gene function. Sequencing projects have revealed the diversity of transposable elements in many organisms and have shown that they constitute a high percentage of the genome. PCR-based techniques using degenerate primers designed from conserved enzyme domains of transposable elements can provide quick and extensive surveys, making study of diversity and abundance and their applications possible in species where full genome sequence data are not yet available. We studied cassava (*Manihot esculenta*) *En/Spm*-like transposons (*Meens*) with regard to genomic distribution, sequence diversity and methylation status. Cassava transposase fragments characteristic of *En/Spm*-like transposons were isolated, cloned and characterized. Sequence analysis showed that cassava *En/Spm*-like elements are highly conserved, with overall identity in the range of 68-98%. Southern hybridization supports the presence of multiple copies of *En/Spm*-like transposons integrated in the genome of all cassava cultivars that we tested. Hybridization patterns of *HpaII*- and *MspI*-digested cassava genomic DNA revealed highly methylated sequences. There were no clear differences in hybridization

pattern between the cultivars. We did not detect RNA transcripts of *Meens* by Northern procedures. We examined the possibility of recent transposition activities of the cassava *En/Spm*-like elements.

Key words: Cassava; Transposable elements; Transposon; *En/Spm*