



Characterization of chloroplast DNA microsatellites from *Saccharum* spp and related species

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ABSTRACT. Microsatellites, or simple sequence repeats (SSRs), and their flanking regions in chloroplast genomes (plastomes) of some species of the family Poaceae were analyzed *in silico* to look for DNA sequence variations. Comparison of the complete chloroplast DNA sequences (cpDNAs) of sugarcane (*Saccharum hybrid* cv. SP-80-3280 and *S. officinarum* cv. NCo310) and related species, *Agrostis stolonifera*, *Brachypodium distachyon*, *Hordeum vulgare* subsp *vulgare*, *Lolium perenne*, *Oryza nivara*, *O. sativa* subsp *indica*, *O. sativa* subsp *japonica*, *Sorghum bicolor*, *Triticum aestivum*, *Zea mays*, and *Z. mays* cv. B73, allowed us to examine the organization of chloroplast SSRs (cpSSRs) in genic and intergenic regions. We identified 204 cpSSRs in the sugarcane cpDNA; 22.5% were in genic regions. The *ndh*, *rps*, *trn*, and *rpl* gene clusters of the chloroplasts had the most repeats. Mononucleotide repeats were the most abundant cpSSRs in these species; however, di-, tri-, tetra-, penta-, and hexanucleotide repeats were also identified. Many base substitutions and deletions/insertions were identified in the cpSSR loci and their flanking regions. Multiple alignments of all cpSSR sequences of Poaceae species made identification of nucleotide

variability possible; repeat motifs are not uniformly distributed across the Poaceae plastomes, but are mostly confined to intergenic regions. Phylogeny was determined by maximum parsimony and neighbor-joining inference methods. The cpSSRs of these species were found to be polymorphic. It appears that individual cpSSRs in the Poaceae are stable, at least over short periods of evolutionary time. We conclude that the plastome database can be exploited for phylogenetic analysis and biotechnological development.

Key words: cpSSR; Plastome; Nucleotide polymorphism; Phylogeny; Molecular markers