

CONSTRUINDO SABERES, FORMANDO PESSOAS E TRANSFORMANDO A PRODUÇÃO ANIMAL

MINING OF SIMPLE SEQUENCE REPEATS IN THE GENOME OF *Urochloa mosambicensis*

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Urochloa mosambicensis (Hack.) Dandy, or commonly known as *capim corrente*, is a perennial forage plant species mainly used in tropical grazing systems. This livestock feed resource is recognized for its good forage quality and drought tolerance. Therefore, it has been suggested as a potential forage crop for small ruminant feeding in the Brazilian semiarid region. Yet, little attention has been given to its genetic basis. The characterization of the *U. mosambicensis* germplasm and working collections is of paramount importance in breeding programs, as this information is crucial in the selection of genotypes with desirable characteristics. The use of molecular markers can assist in genetic-breeding programs and help in the continuous release of new cultivars, as well as favour associations with agronomic characteristics. In turn, the identification of simple sequence repeats in the genome is an alternative step for the development of molecular markers. Here, we present the detection and abundance of simple sequence repeats (SSRs) in *Urochloa mosambicensis*. For this purpose, approximately 1 mg of plant tissue was extracted using the DNeasy Plant Mini Kit (Qiagen). A genomic library was constructed from 0.1 ng of genomic DNA, following the standard protocol of the Illumina Nextera DNA Kit. DNA sequencing was performed using the MiSeq sequencer (Illumina). A total of 149,259 contigs, from 57,170,592 reads, resulted from using the CLC Genomics Workbench 7.0.4 assembly program. The contigs had an average size of 411 bases. The Msaatcommander 0.8.2 software identified DNA sequence repeats with 1-6 block replicates in 5,535 contigs. Depending on the repeat units, average length of SSRs were 18 bp for mono-, 20 bp for di-, 17 for tri-, 17 bp for tetra-, 16 for penta- and 18 bp for hexa-nucleotide repeats. Average density of SSRs (bp/Mb of sequences mined) suggests that 7.74% of sequences contained SSRs. Mononucleotide repeats were most frequent repeat type (85.8%) followed by tri-nucleotide repeats (4.4%) and penta-nucleotides (3.9%). An attempt was made to design primer pairs for 100 identified SSRs and were subjected to *in silico* PCR analysis in the assembled genomic sequences. Results indicate that newly developed SSR markers would be used as potential SSR markers in *U. mosambicensis*.

Keywords: genomic analysis, ruminant feeding, molecular markers, forage, semiarid

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