

NEXT-GENERATION TRANSCRIPTOME OF LEAVES IN *Paspalum notatum*

de Oliveira F¹, Vigna BBZ², Fávero AP², de Souza AP^{1,3}

¹Center for Molecular Biology and Genetic Engineering (CBMEG), University of Campinas (UNICAMP), Campinas, SP, Brazil. ²Brazilian Agricultural Research Corporation (Embrapa) Southeast Livestock, São Carlos, SP, Brazil. ³Plant Biology Department, Biology Institute, UNICAMP, Campinas, SP, Brazil.

Paspalum notatum Flüggé (bahiagrass) is a rhizomatous species, being an important component of natural pastures in southern Brazil, Argentina and Paraguay. It is used as a model for studies of apomixis in grasses. It has genotypes with different ploidy levels and linked reproductive characteristics. Diploid plants ($2n=2x=20$) reproduce sexually, whereas polyploids ($3x$, $4x$, $5x$, $6x$) reproduce asexually by apomixis. The tetraploid cytotype ($4n=4x=40$) is the most common and widely distributed while the other polyploid cytotypes are rare or were experimentally obtained. The objective of the present work was to characterize the transcriptome of leaves of *P. notatum* from six genotypes differing in ploidy level and mode of reproduction. To accomplish this, we used young leaves from three biological replicates of each of the six genotypes, totaling 18 plants to be analyzed in the study. The experimental procedures started with total RNA extraction, cDNA libraries were constructed for the 18 samples, following the instructions from the Illumina TruSeq RNA Sample Preparation v2® kit. Then, cDNA molecules were anchored onto a polony array (flow cell) surface, which were then subjected to PCR amplification. Images were taken after each cycle for base calling and sequence generation, totaling 72 paired-end cycles. At each cycle, a nucleotide was incorporated in the sequence, with 72 base pairs (bp) length on an Illumina GAIIx platform. At the end of the sequencing were obtained 49.0 G data, of which 87% presented reads with high-quality bases (phred score 30). With the results obtained, it is evident the high quality of the sequences generated reinforcing the efficiency of the sequencing platform used. A *de novo* assembly and annotation of the transcriptome is ongoing. The information collected from this study are extremely important to the enrichment of public databases with sequences of *P. notatum*, promoting new discoveries and associations about the metabolism, will help us to characterize the transcriptome of bahiagrass leaves. Additionally, this study will support development of a large amount of the functional markers, which will be useful for the breeding program, including germplasm characterization, evolutionary and taxonomic studies and marker-assisted trait selection.

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Corresponding author: Fernanda A. de Oliveira, f.ancelmo.o@gmail.com