



TRANSCRIPTOME ANALYSIS OF *PASPALUM NOTATUM* AND *PASPALUM VAGINATUM* UNDER WATER DEFICIT CONDITION

Joyce Etsuko Arakaki^{1*}; Wilson Malagó Junior²; Mauricio de Alvarenga Mudadu³; Patricia Menezes Santos²; Alessandra Pereira Fávero²; Ricardo Caneiro Borra¹; Bianca Baccili Zanotto Vigna².

¹Programa de Pós-Graduação em Genética Evolutiva e Biologia Molecular, Universidade Federal de São Carlos, São Carlos, São Paulo, Brazil. ²Embrapa Pecuária Sudeste, São Carlos, São Paulo, Brazil. ³Embrapa Informática Agropecuária, Campinas, São Paulo, Brazil.

*joyce.e.arakaki@gmail.com

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Drought is one of the abiotic stresses that most affect plant growth and productivity. Grasses of the genus *Paspalum* are successfully used as turf and forage in Australia, Argentina, Brazil and United States. *Paspalum notatum* has good forage quality, and *P. vaginatum*, high tolerance to salinity. In addition, their potential to tolerate drought has been described previously, making them interesting for transcriptome studies under water deficit. The objective of this work was to analyze the gene expression profiles of both species in response to drought. The accessions *P. vaginatum* BGP 114 and *P. notatum* BGP 216 were chosen according to their characteristics, importance and ability to tolerate drought. The drought experiment was carried out in a greenhouse at Embrapa Pecuária Sudeste (Nov/2016) and cultivated in triplicates. Leaf samples of each biological replicate were collected under two conditions, with no water deficit (28% of relative soil moisture) and under water deficit (4% of relative soil moisture), in which *P. vaginatum* achieved this percentage after eight days with no irrigation and *P. notatum*, after five days. Their RNAs were extracted and sent for sequencing using Next Generation Sequencing (NGS) technology on Illumina HiSeq 2500 equipment. The paired-end (2x100 bp) cDNA libraries (~80M reads/library) of leaves from each genotype, three from the control group and three from the water deficit, passed through FastQC quality control and Trinity software performed the *de novo* assemblies of the transcriptomes. The assemblies were evaluated using contig N50 and ExN50 values. Also, Bowtie2 software estimated the percentage of mapped reads and BUSCO3 evaluated the completeness of transcriptomes against embryophyta dataset. RSEM software estimated the abundance of transcripts using Transcripts per Million Transcripts - TPM. EdgeR package considered differentially expressed genes (DEGs) those with FDR <0.05 and log₂Fold-Change ≥ 2. Trinotate software suite was used for functional annotation of transcriptomes followed by functional enrichment analysis with Goseq package. The GO terms were summarized and clustered according to their p- values using REVIGO platform. Both libraries and assemblies achieved satisfactory quality results. RSEM estimated 31.835 genes for *P. vaginatum* and 38.002 for *P. notatum*. For *P. vaginatum*, 3280 DEGs (10.3%) and 658 enriched GO terms were identified while for *P. notatum*, 1978 DEGs (5.2%) and 720 enriched GO terms. Results from both species showed genes related in responses to water deficit such as LEAs, aquaporins, auxin related proteins, accumulation of carbohydrates, heat shock proteins and responses to ROS.

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