TRANSCRIPTOME ANALYSIS OF *PASPALUM VAGINATUM* UNDER DROUGHT CONDITION

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Paspalum vaginatum Swartz, also known as seashore paspalum, is a halophytic, diploid, self-incompatible, warm-season perennial grass, well adapted to coastal regions in tropical and subtropical environments, as Argentina, Brazil and United States. This grass tolerates several stresses as salinity, drought, low temperatures, among others. Due to its unique growth characteristics, it is a plant with great potential for studies of tolerance to drought and salinity. Transcriptome analysis can help to understand the mechanisms that make plants able to adapt to different environments. The objective of this study is to evaluate the gene expression profile of *P. vaginatum* Sw. in response to drought. The drought experiment was performed in a greenhouse at Embrapa Pecuária Sudeste (São Carlos, Brazil) where the accession *P. vaginatum* Sw. BGP 114 was cultivated in triplicates during Brazilian spring (Nov/2016). Leaf samples of each biological replicate were collected in two conditions, without water stress (28% soil water content) and after eight days under drought stress (4% of soil water content), and had their mRNA extracted. Samples were sequenced using Next Generation Sequencing (NGS) technology on Illumina HiSeq 2500 equipment and paired-end reads (2x100bp). The assessment of quality of the *de novo* transcriptome assembly, the differential gene expression analyzes and the functional annotations of the genes were performed following Trinity pipeline. The sequencing generated around 80 millions of reads per sample and more than 207 million bases were assembled from the *de novo* assembly, 135.997 transcripts were identified from 44.842 predicted genes and N50 stats of 2.259 with median contig length of 1.193 bp. Bowtie2 were used for alignment of reads to the Trinity assembly with great result of 91.39% mapped as proper pairs. Diamond Blast software resulted in 17.381 of 40.817 proteins which were covered by more than 90% of their protein lengths. This latter analysis, additionally to the others bioinformatics tools as FastQC, ExN50 stats and Transrate (score of 0.393), showed satisfactory results by inferring good quality of reads and assembly. BUSCO3 searched in embryophyta dataset from *OrthoDB v9* database returned a good result of 91.37% of transcriptome completeness. Differential gene expression analyzes using EdgeR software identified 3.280 differentially expressed genes (DEG) and Trinotate software suite were used for functional annotation of the transcriptome. Searches in UniProt databases and PubMed for the top ten annotated DEG showed relation to biological processes and molecular functions. The annotated genes *CCA1* and *LHY* were previously reported in *A. thaliana* and was suggested that they regulate the expression of genes (ex: *TOC1*) involved in drought, salt and heat responses such as stomata closure. *MGL3* gene was also annotated and encodes for LEA (Late Embryogenesis Abundant), which is already known in high activity under drought condition. The analyzes of physiological, genetic data and the regulation of genes will be essential for a better understanding of the mechanisms related to drought and development of new stress-tolerant cultivars.

PRESENTER BIO: Dr. Vigna is a Researcher at Embrapa and has more than 10 years of experience with genetic resources and molecular genetics breeding of various forage species (*Urochloa* spp., *Paspalum* spp., alfalfa).

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