DIFFERENTIAL GENE EXPRESSION FOR ELUCIDATING *Paspalum regnellii* RESISTANCE AGAINST SPITTLEBUGS (*Mahanarva spectabilis*)

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Abstract - Spittlebugs from Mahanarva genus are pests that cause significant losses in livestock, hindering the production of grasses in Brazil. The most suitable solution for this insect control is the development of resistant cultivars due to the potential genetic conservation of resistance mechanisms. Despite the lack of information at genomic level, a field experiment at Embrapa Southeast Livestock (São Carlos - SP) identified resistance to *Mahanarva spectabilis* in some *Paspalum regnellii* genotypes. In this context, the main objective of the project is to analyze the root transcriptome of two *P. regnellii* genotypes with different levels of susceptibility to *M. spectabilis* spittlebug nymphs infestation. Root samples were collected from BGP248 and BGP344 genotypes in triplicate for three conditions: (T0) before infestation, (T1) after nymphs hatch in the roots (48h after T0), and (T2) after initiating death from some nymphs (72h after T0), totalizing eighteen plants. We performed the total RNA extraction, cDNA libraries preparation and sequencing on the Illumina HiSeq 2500 platform (paired-end 2x100pb). We analyzed data quality using FastQC and trimmed the reads with Trimmomatic and SortMeRNA. We assembled the transcripts with the *de novo* method in Trinity software and checked the quality with BUSCO and Bowtie2, then performed a differential gene expression (DGE) analysis using the edgeR package. We enriched the terms in Gene Ontology (GO) with biological processes and metabolic pathways in KEGG analysis. The assembly resulted in 575,219 contigs without redundancy, with a N50 contig size of 788bp. Reads were 80.89% aligned with Bowtie2 and BUSCO found 90.4% of the transcripts in plant orthologous. After filtering, we continued with 21,508 genes and 3,231 were considered significant differentially expressed genes (DEGs), 1,530 upregulated and 1,701 downregulated. A total of 162 GOs terms of biological process were enriched and some closely related to spittlebugs resistance in the resistant genotype can be emphasized, like response to herbivores (GO:0080027). KEGG enriched 19 pathways and 7 of them are exclusive for one genotype, highlighting two related to resistance (purine and glutathione metabolism). The understanding at the genetic and metabolic level of *Paspalum* resistance mechanisms can provide development for species and targets for editing tools.

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