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## INTRODUCTION

*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<sup>1</sup>. Due to its unique growth characteristics, it is a plant with great potential for transcriptome studies under drought conditions. Transcriptome analysis can help to understand the mechanisms involved in plant adaptation to different conditions and environments.

## OBJECTIVE

The objective of this study is to evaluate the gene expression profile of *Paspalum vaginatum* in response to drought.

## MATERIAL AND METHODS

The diploid accession *P. vaginatum* BGP 114 (V D BdSv 10117) was selected for a drought stress experiment based on the climate characteristics of its site of collection, on the importance and ability of the species to tolerate drought. The drought experiment was performed in a greenhouse at Embrapa Southeast Livestock (São Carlos, Brazil) and the accessions were cultivated in triplicates during Brazilian spring (Oct-Nov/2016). Leaf samples of each biological replicate were collected in two conditions, without water deficit (28% of relative soil moisture) and under water deficit (4% of relative soil moisture), and had their mRNA extracted. Samples were sequenced using Next Generation Sequencing (NGS) technology on Illumina HiSeq 2500 equipment and paired-end reads (2x100bp). Bioinformatics tools were used to characterize the quality of the *de novo* transcriptome assembly, to analyze DGE between plants with and without drought stress followed by functional annotation of the genes (Figure 1).



Figure 1. Methodology used for *P. vaginatum* transcriptome analyses.

## RESULTS AND DISCUSSION

The results obtained from bioinformatics analyses to evaluate the quality of the *de novo* transcriptome assembly, the identification of DEGs between plants with and without drought stress and the functional annotation of the genes are shown in Figure 2.

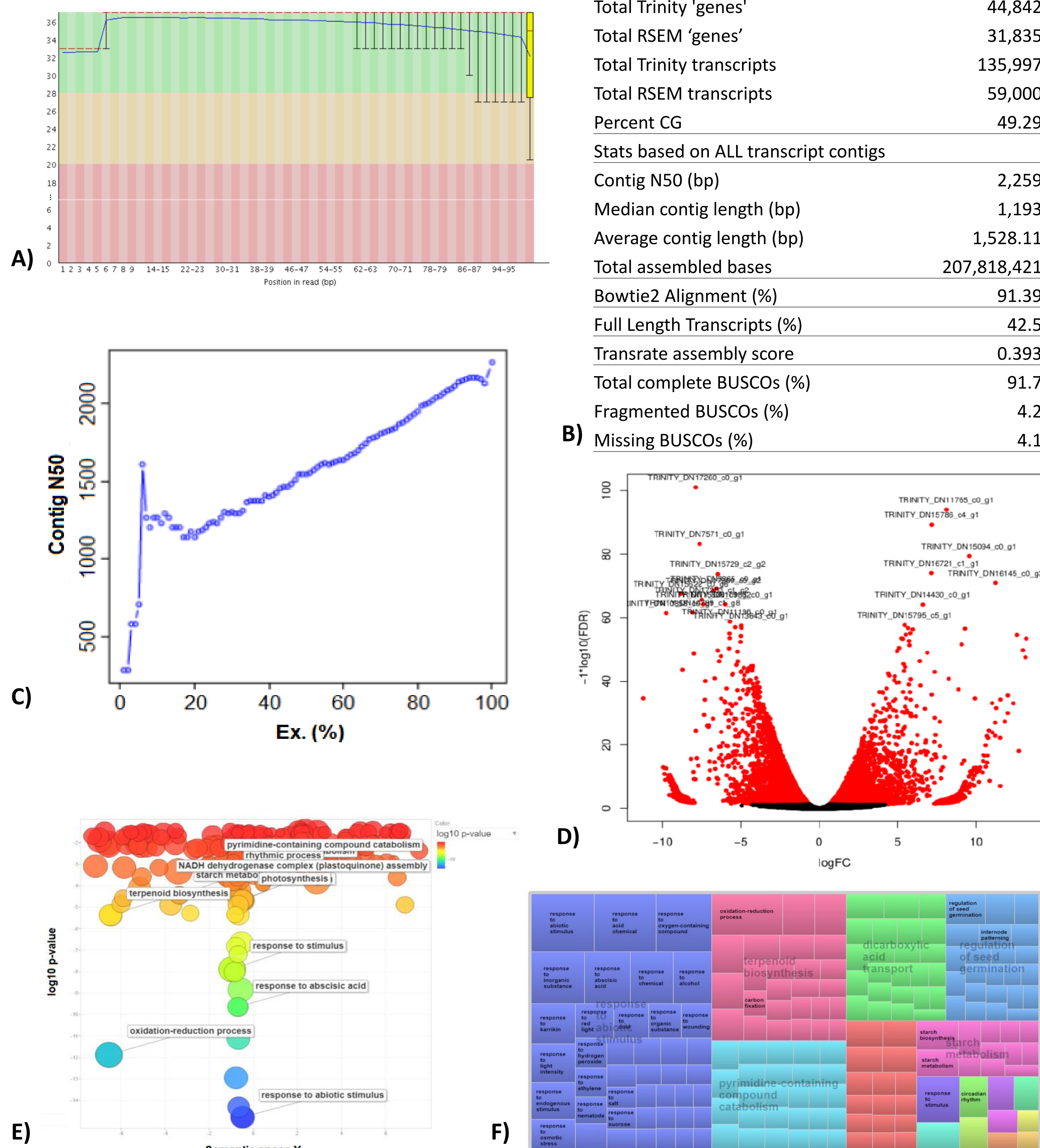


Figure 2. Results of *P. vaginatum* transcriptome analyses. The results from transcriptome analyses can be seen in: **A)** FastQC result: per base sequence quality, **B)** *De novo* assembly summary; **C)** ExN50 Stats; **D)** Volcano plot showing transcripts differentially expressed in red; **E)** Dispersion graphic showing the most represented GO terms and **F)** Tree map of the most represented GO terms.

The analyses of quality assessment of reads and *de novo* transcriptome assembly showed satisfactory results. The differential gene expression analyses identified 3280 differentially expressed genes (DEG) ( $p$ -value < 0.001 and Fold Change > 2). Many genes related to abiotic stresses were found among the most differentially expressed genes. *CCA1* gene was found down-regulated and was previously related to ROS control and regulation of phytohormones involved in responses to abiotic stresses<sup>2</sup>. The overexpression of LEA protein was extensively reported in plants in order to protect them from damage caused by stresses, especially drought<sup>3,4</sup> and the same behaviour was found in *P. vaginatum*.

## CONCLUSION

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.

## REFERENCES

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