TRANSCRIPTOME ANALYSIS OF PASPALUM VAGINATUM UNDER DROUGHT CONDITION

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 others5. 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.

RESULTS AND DISCUSSION

The results obtained from bioinformatics analyses to evaluate the quality of the de novo transcriptome assembly, the identification of DEGs between the plants with and without drought stress and 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 stresses2. The overexpression of LEA protein was extensively reported in plants in order to protect them from damage caused by stresses, especially drought3,4 and the same behaviour was found in P. vaginatum.

CONCLUSION

The analyses 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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