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TRANSCRIPTOME PROFILING OF *Paspalum notatum* REVEALS CANDIDATE GENES ASSOCIATED TO POLYPLOIDY AND/OR APOMIXIS

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Apomixis is an asexual reproduction mode described in more than 400 angiosperm species, which plants are able to produce offsprings that are exact genetic replices of the female parent. It is frequently associated with polyploidy and might have arisen through the de-regulation of the sexual developmental pathway by a mechanism that could comprise both genetic and epigenetic components. As a reproductive strategy for cloning plants via seeds, it is a highly desirable trait in modern agriculture. *Paspalum notatum*, also known as “bahiagrass”, is a good model for studies of species that reproduce by apomixis, since the species is organized as an agamic complex, with sexual diploids and apomictic tetraploids. The objective of this study was to describe a transcriptome of *P. notatum* and identify genes that show altered expression profiles in response to changes in reproductive mode (sexual to apomictic) and/or ploidy. To accomplish this, we sequenced young leaves and flowers transcriptomes on an Illumina GAIIx platform from 2x sexual (2xSex), 4x sexual (4xSex) and 4x apomictic (4xApo) plants, with three biological replicates of each genotype. The filtered (phred score 30) short reads were submitted to *de novo* assembly through Trinity software. An annotation of the unigenes was carried out through the blastx against the main databases. The gene expression level was calculated by mapping in RSEM and the genes differentially expressed (DE) were identified by EBSeq, a R Package. We used FDR < 0.05 as the threshold to determine significant differences in gene expression. The *de novo* assembly resulted in 203,808 transcripts, with a N50 contig size of 1,599 bp, of which 114,306 unigenes. We obtained more than 70% of unigenes annotated. The analysis of differentially expressed resulted in 474 genes DE and common only between 2xSex vs 4xApo; when we compared the 2xSex vs 4xSex, we detected 10 genes common only in this comparison and DE, which can be related to ploidy; while the comparison of shared genes only between 4xApo vs 4xSex revealed 95 genes DE potential candidates for study of sexuality. Additionally, we identified exclusive genes for each biological group, with a total of 19,304 unique genes for apomictic tetraploids genotypes. These findings shed light on the genes related with reproductive mode and ploidy in *P. notatum*.

Keywords: RNASeq; bahiagrass; apomixis

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