PATHOGEN-INDUCED CHANGES IN FLOWERING REGULATION GENES IN SUGARCANE SMUT DISEASE

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Abstract:
Sugarcane smut disease, caused by the fungus *Sporisorium scitamineum*, is one of the most relevant sources of yield losses. Its main symptom is the emergence of a structure called "whip" from the plant's apical meristem, which interferes with plant reproduction and houses the fungal teliospores. The so-called "smut" pathogens characteristically induce symptoms associated with the floral organs of their host plants, by directly affecting their reproduction, influencing the expression of genes related to meristematic functions in order to complete their biological cycle. In our analysis, we investigated the transcriptional profile of healthy and infected plants at the initial stages of disease development, at two days after inoculation. We focused on identifying genes involved with meristematic function and floral development modulated by the pathogen in resistant (SP80-3280) and susceptible plants (IAC66-6). We used Illumina total RNA sequencing data and analyzed read quality using FastQC v0.11.5. Next, we screened data using the bbmap suit along with SILVA NR database to filter out rRNAs contaminants and Cutadapt v1.18 to remove low-quality reads (Q < 20) and ambiguous bases (N). Reads were mapped against the reference genome of the fungus *S. scitamineum* (SSSC39) and subsequently on the reference data set of the R570 genotype with Hisat2 v.2.1.0. The read count table was obtained with the FeatureCounts v1.6.0 tool, and Differentially Expressed Genes (1 CPM in all three biological replicates of a given treatment, FDR < 0.05; LogFC >| 1|) were obtained using the EdgeR v3.30.3 package from Bioconductor R v.4.2.1. Homologues of sugarcane proteins encoded by flowering pathway genes were predicted by BLASTP2.2.26 (BLOSUM45, 1E-3 cutoff e-value) searches of corresponding encoding proteins of *Arabidopsis thaliana* genes available in the FLOR-ID database. The enrichment of GO terms was performed using topGo in Bioconductor R v.4.2.1 using Fisher test ($p<0.05$) and weight01 algorithm. We unveiled key flowering regulatory genes induced in the susceptible genotype, such as FT, SOC1, and AP1 homologs. In the resistant variety, we found other induced genes, such as HUA2 and UBC2 homologs, known to act by regulating the FLC gene, a flowering repressor. At the same time, we observed genes such as TEM2, ATH1, EMB14, ESD4, SFR6, and other genes from the circadian clock regulatory pathways being repressed, potentially acting in a negative regulation of flowering. Among the GO terms in both varieties, we found terms associated with the cellular replication processes, something expected due to modulation of meristematic functions by infection. In the resistant variety, the term GO:0050832 referring to "defense response to fungus," and GO:0006032 referring to "chitin catabolic process" in the susceptible variety, are indicative of the plant-pathogen interaction in the attempt at infection. Thus, we preliminarily verified that during *S. scitamineum* infection, there is modulation of pathways associated with flowering in sugarcane, which may differ between susceptible and resistant varieties. Previously, we identified a similar transcriptome profile for independent experiments. Additional experiments are necessary to understand in detail how this physiological manipulation occurs. The present study contributes to offering candidate genes for future functional analyses.
Palavras-chave: *Sporisorium scitamineum*; transcriptomics; susceptibility; floral development; meristematic function

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