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ASSESSING THE GENETIC AND MOLECULAR BASIS OF RESISTANCE TO *FUSARIUM VERTICILLIOIDES* IN MAIZE

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Maize (*Zea mays* L.) is a major cereal crop, the second most cultivated crop in the world. Maize is used for human consumption, livestock feed, and biofuel. In addition to its economic importance, maize has been a widely used model species for genetics and plant biology. Among the limitations to maize production and seed quality, the several diseases caused by Fusarium are severe and largely diffused. Maize research has been oriented towards distinguishing the levels of resistance to ear rot caused by *Fusarium verticillioides*, however, it has not yet been possible to clarify the model of genetic action of the resistance that could guide the selection of resistant genotypes. The Multi-parent Advance Generation Intercross (MAGIC) maize population was previously used to identify quantitative trait loci (QTL) for Fusarium seedling rot resistance using the rolled towel assay (RTA) that allows fast and reliable phenotyping at early developmental stages. Production of transcriptomic data specific to the infection phase may increase the precision by which candidate genes are identified. RNA-Seq approach was used to compare the genome-wide gene expression patterns in maize scutella and early germinating shoots in the eight MAGIC maize founder lines in mock and *F. verticilloides* treated seeds. The RTAs were performed at 48, 72, 96, 120, 168 hours post inoculation (hpi) under two conditions control and treated to identify the appropriate time point for the investigation of MAGIC maize founder lines transcriptome profiles. Twenty seeds were used for each RTA in both treatments, in the treated, the seeds were inoculated with 100 µl of a 3.5 x 106 ml-1 spore suspension of *F. verticillioides* ITEM10027 (MPVP 294). Real-time PCR was applied on plant and pathogen specific genes to identify the best time point for RNA extraction, which turned out to be 72 hpi. RNA was extracted from the scutella and early germinating shoots and a total of 48 cDNA libraries (8 genotypes x 2 conditions x 3 biological replicates) have been produced and subjected to sequencing. Transcriptomic data on the parental lines will be projected onto recombinant inbred lines reconstructed genomes and used to narrow down QTL intervals to their genetic determinants. The defense-related transcriptional changes will shed light on and related them to the specific genomic regions identified by QTL mapping.