

TRANSCRIPTIONAL ANALYSIS OF EIGHT MAGIC MAIZE PARENTAL LINES INFECTED WITH *FUSARIUM VERTICILLIOIDES*

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Maize (*Zea mays* L.) is the second major cereal crop in the world, with significant economic importance as food, feed, and biofuel source. Maize production is constrained by several diseases caused by *Fusarium*, a manifold and widespread fungus. *Fusarium verticillioides* causes severe diseases for maize including seedling blights, stalk rot, and ear rot. Currently, genetic resistance is considered as the most reliable to reduce damages caused by *F. verticillioides*. This study aims at elucidating the genetic and molecular basis of resistance to *F. verticillioides* in maize. Young seedlings of eight MAGIC Maize parental lines were artificially inoculated with a *F. verticillioides* strain using the rolled towel assay method, and RNA was extracted after 72 hours from control and treated samples and underwent paired-end sequenced with Illumina technology. After quality checking and reference mapping of the reads obtained, we identified early transcriptional changes and differentially expressed genes (DEGs). The comparison between control and treated samples within each parental line showed 125 DEGs in the most resistant line and 125 DEGs in the most susceptible line (H99 and Mo17, respectively). A cross-comparison between differential expression of two most resistant and two most susceptible lines was conducted to gain further insights into the regulatory network underpinning the response to *F. verticillioides* infection. A Gene Ontology Enrichment analysis was performed on DEGs of each parental line to show their differential regulation after fusarium infection. Approximately 42 DEGs were associated with pathogenesis-related proteins being involved in several pathways related to defense response after pathogen infection. The results identify a limited set of these DEGs that might play important roles in maize resistance to *F. verticillioides* providing new insights into the molecular resistance mechanisms against the pathogen.