

TRANSCRIPTIONAL ANALYSIS OF EIGHT MAGIC MAIZE PARENTAL LINES INFECTED WITH FUSARIUM VERTICILLIODES

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Rolled Towel Assay, Fusarium seedling rot, RNA-seq, differentially expressed genes, MAGIC maize population

Maize (*Zea mays* L.) is among the most important crops worldwide for food, feed, biofuels, and industrial applications. Its cultivation faces significant constraints due to *Fusarium* species that affect the quality and quantity of maize products. Among these, *Fusarium verticillioides* is responsible for severe diseases including seedling blights, stalk rot, and ear rot. The impact of the fungus is worsened by the fact that chemical and agronomic measures used to control *Fusarium* infection are often inefficient. Hence, genetic resistance is considered the most reliable resource to reduce damages caused by *F. verticillioides*. This study aims to elucidate the genetic basis of resistance to this fungus in maize. Young seedlings of eight divergent maize lines, founder of the MAGIC population, were artificially inoculated with a *F. verticillioides* strain using the rolled towel assay method. Total RNA was extracted from both control and treated samples after 72 hours of artificial inoculation and underwent paired-end sequenced with Illumina technology. Here we report the use this large transcriptomic dataset to identify the early transcriptional changes and the differentially expressed genes (DEGs) involved in fungal infection. The analysis identified several hundred DEGs, whose functions were explored through Gene Ontology enrichment analysis. A co-expression network analysis

further refined the set of genes with potential implications in disease response. The results identify a limited set of genes that might play an important roles in maize resistance to *F. verticillioides* providing new insights into the molecular resistance mechanisms against the pathogen.