Transcriptome profiling of eight *Zea mays* lines identifies genes responsible for the resistance to *Fusarium verticillioide*s.

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The current study characterized the plant response to Fusarium seedling rot disease in maize using gene expression profiling of eight divergent maize MAGIC founder lines with contrasting levels of resistance. The cultivation of maize (*Zea mays* L.), one of the most important crops worldwide for food, feed, biofuels, and industrial applications, faces significant constrains due to *Fusarium verticillioides*, a fungus responsible for severe diseases including seedling blights, stalk rot, and ear rot. Its impact is worsened by the fact that chemical and agronomic measures used to control the infection are often inefficient. Hence, genetic resistance is considered the most reliable resource to reduce the damages. Young seedlings of eight divergent maize lines, founders of the MAGIC population, were artificially inoculated with a *F. verticillioides* strain. Phenotypic analysis and transcriptome sequencing of both control and treated samples identified several hundred differentially expressed genes enriched in metabolic processes associated with terpene synthesis. A Weighted Gene Co-expression Network Analysis (WGCNA) further refined the pool of genes with potential implications in disease response and found a limited set of hub genes, encoding bZIP and MYB transcription factors, or involved in carbohydrate metabolism, solute transport processes, calcium signaling, and lipid pathways. Additional gene resources were provided combining transcriptomic data with previous QTL mapping, thereby shedding light on the molecular mechanisms in the maize-*F. verticillioides* interaction.
The transcriptome profiling of eight divergent maize MAGIC founder lines with contrasting levels of *Fusarium verticillioides* resistance combined with phenotypic analysis, clarifies the molecular mechanisms underlying the maize-*F. verticillioides* interaction.