

Differential Regulation of Maize and Sorghum Orthologs in Response to the Fungal Pathogen *Setosphaeria turcica*

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Project Goals: The goals of this project are to understand the relationship between the sorghum and maize defense responses to a common pathogen, *S. turcica*, to identify candidate genes involved in the reaction to *S. turcica* in both maize and sorghum, and to examine the extent of conservation in gene expression in compatible and incompatible interactions between maize and sorghum.

Abstract: Host jumps are a threat to food security, and host resistance is critical for ensuring food security. *Setosphaeria turcica* infects both maize and sorghum and the isolates are host-specific, offering a unique system to examine compatible and incompatible interactions. We hypothesized that resistance mechanisms are conserved between hosts. We conducted transcriptional analysis of maize and sorghum in response to maize-specific and sorghum-specific *S. turcica* isolates and identified functionally related co-expressed modules. Maize had a larger transcriptional response than sorghum. *S. turcica* responsive genes were enriched in core orthologs in both crops, but only up to 16% of core orthologs showed conserved expression patterns. Most changes in gene expression for the core orthologs, including hub genes, were lineage-specific, suggesting that resistance in maize and sorghum evolved largely independently. We identified several defense-related shared differentially expressed orthologs with conserved expression patterns between the two crops, suggesting a role for parallel evolution of those genes in both crops. Many of the differentially expressed genes during the incompatible interaction were related to quantitative disease resistance. This work can inform how to engineer an incompatible interaction and offer insights into how different hosts with relatively recent divergence interact with a common pathogen.

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