
Heterologous expression of the sorgoleone biosynthetic pathway and its effect on gene expression in *N. benthamiana*

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Abstract

Sorgoleone, a hydrophobic compound exuded from root hair cells of *Sorghum* spp., likely accounts for much of the allelopathic activity associated with members of this genus. The enzymes involved in the biosynthesis of this compound have recently been identified and functionally characterized. To further examine the mechanism of action of sorgoleone, a multi-gene DNA construct was prepared for the expression of genes required for sorgoleone biosynthesis *in planta*. The DNA construct was deployed in *Nicotiana benthamiana* leaf tissues via *Agrobacterium*-mediated transient expression, and successfully directed the *in planta* accumulation of sorgoleone, as detected by GC-MS. The transient production of sorgoleone observed in infiltrated leaves resulted in the rapid formation of necrotic lesions, indicating that the compound possesses significant phytotoxicity to these tissues. To investigate the molecular mechanism(s) underlying the phytotoxicity of sorgoleone to the host plant *N. benthamiana*, RNA-Seq was employed to profile gene expression changes in the host plant during sorgoleone-induced necrotic lesion formation. The results from these experiments concerning whole transcriptome responses to sorgoleone production *in planta* will be presented.

Keywords: Sorgoleone, biosynthetic pathway, phytotoxicity, RNA, Sequencing

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