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Entitled

MICROARRAY ANALYSIS IDENTIFIES POTENTIAL GENES ASSOCIATED WITH BOTRYTIS CINEREA AND HORMONAL STRESSES

by

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Abstract

Biotic and abiotic stresses critically influence plant survival and growth; survival depends on the ability to correctly sense and react to their environment. Certain environmental stresses must be overcome through careful manipulation of internal hormone levels, and of the resulting signaling cascades. Hormone signaling networks and the crosstalk among each respective hormone signaling pathway are principle for response mediation via transcriptional reprogramming or altered signaling pathways. The long-term objective is to determine how plants sense biotic stresses, and how hormone signaling networks control and direct plant responses to the fungal pathogen *Botrytis cinerea*. This research aims to identify commonly regulated genes in *Arabidopsis thaliana* that respond to both *B. cinerea* and four selected hormones to ultimately improve the understanding of biotic stress responses and resistances in plants. The specific aims were to: (1) identify regulated genes in response to *B. cinerea* infection, salicylic acid (SA), jasmonic acid (JA), ethylene (ET), and abscisic acid (ABA); and (2) determine common up- and down-regulated genes in response to *B. cinerea* infection and the phytohormones in Arabidopsis. These goals were accomplished by analyzing publicly available microarray data of Arabidopsis differentially-expressed genes (DEGs) in response to *B. cinerea*, SA, methyl jasmonate (MeJA), 1-aminocyclopropane-1-carboxylic acid (ACC; the ET natural precursor), and ABA. This analysis of microarray data revealed 6.9% of genes were up-regulated and 5.3% of genes were down-regulated at 18 hours post-infection with *B. cinerea*. Between 6.1-7.2% of genes were induced upon individual treatments of SA, MeJA, ACC, or ABA, with 9% and 1.2% of genes identified as commonly up-regulated and down-regulated genes, respectively, for all hormone treatments and *B. cinerea* together. Of these DEGs, most belong to biologically functional binding proteins (*i.e.*, transcription factors) or proteins related to cellular transport. Arabidopsis expression profiling of defense regulated genes in response to *B. cinerea* and hormone stresses aims to improve the understanding of how plants cope with biotic stresses on the transcriptional level and will help identify potential up- and down-regulated genes involved in Arabidopsis defense against this pathogen. This study could lead to the introduction of novel defense genes into crops, or to utilize genes already present in the organism to subtly modify the hormonal signaling cascade in reaction to *B. cinerea* improving these crop's resistance to *B. cinerea* infections. Changes in hormone regulation through natively expressed genes following exposure to *B. cinerea* would allow a marketable and responsible solution to improving crop resistances to *B. cinerea* without the need to introduce foreign genes into crops.

Keywords: Arabidopsis, Botrytis cinerea, abscisic acid, jasmonic acid, ethylene, salicylic acid, hormone signaling pathway.