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EXPRESSION PROFILING AND MUTANT ANALYSIS REVEALS COMPLEX REGULATORY NETWORKS INVOLVED IN ARABIDOPSIS RESPONSE TO BIOTIC, ABIOTIC AND HORMONAL STRESSES

by

Arjun Sham Valiyaveettil Shamgopal

Faculty Advisor

Prof. Synan F. AbuQamar, Department of Biology
College of Science

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Abstract

Biotic and abiotic stress factors consistently threat during different stages of the plant's life cycle. A complex network of signaling molecules is required to overcome stresses, which is linked to general physiological and molecular processes. *Botrytis cinerea* is a necrotrophic fungal pathogen that causes grey mold disease on many crops. Apart from *B. cinerea*, several biotic, abiotic and hormonal stresses have detrimental effects on plant growth and productivity. The aim of this study is to identify common genetic components during stress response and to find out the role of differentially expressed genes in *Arabidopsis*-*B. cinerea* pathosystem. The transcriptomic data were analyzed to identify the overlapping stress-regulated genes in response to *B. cinerea* and other biotic, abiotic and hormonal stresses. Among the 1554 *B. cinerea* up-regulated genes, 24%, 1.4% and 14% were commonly induced by biotic, abiotic and hormonal treatments respectively. Similarly, about 18%, 2.5% and 22% of *B. cinerea* down-regulated genes were commonly repressed by these stress groups. *WRKY33* transcription factor was previously reported for its resistance to *B. cinerea*. In this study, *Arabidopsis WRKY33* over-expression and mutant lines were compared for their response to *B. cinerea* infection. The *wrky33* mutant plants showed altered susceptibility, whereas the 35S:*WRKY33* overexpression plants showed resistance to *B. cinerea*. The expression profile of 12-oxo-phytodienoic acid and phytoprostane A1-treated *Arabidopsis* plants in response to *B. cinerea* showed that cyclopentenones can also modulate *WRKY33* regulation upon inoculation with *B. cinerea*. These results support the role of electrophilic oxylipins in mediating plant responses to *B. cinerea* infection through the TGA transcription factor. Results obtained from the metatranscriptomic and *in silico* gene analyses revealed the involvement of *RAP2.4* (related to *AP2.4*) in plant immunity. *Arabidopsis rap2.4* T-DNA insertion mutant lines exhibited increased resistance to *B. cinerea*. This is the first report to uncover the role of *RAP2.4* in plant defense against *B. cinerea*. This will pave the way to producing crops with less use of chemical pesticides and will provide a basis for breeding programs to increase tolerance and improve yield performance in crops.

Keywords: *Arabidopsis*, *Botrytis cinerea*, expression profiling, microarray, plant defense response, transcriptome.