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**Master Thesis Defense**

Entitled

*TRANSCRIPTIONAL PROFILING IDENTIFIES POTENTIAL GENES ASSOCIATED WITH MULTIPLE  
BIOTIC STRESSES IN ARABIDOPSIS*

by

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Abstract

Plants are exposed to many environmental stresses that affect their growth and development. These stresses include biotic stresses (organisms) and abiotic stresses (drought and salinity). Plants respond to these stresses by transcriptional reprogramming and different signaling pathways. *Arabidopsis thaliana* had shown great sensitivity to the biotic stress: *Botrytis cinerea*, *Alternaria brassicicola*, *Pseudomonas syringae* and the herbivore insect *Pieris rapae*. The overall goal is to identify common regulated genes that respond to all these biotic stresses to ultimately improve plant stress tolerance in *Arabidopsis*. The specific aims are to: (1) determine the regulated genes in response to an individual stress of *B. cinerea*, *A. brassicicola*, *P. rapa*, *P. syringae* and *P. rapa* infections, and (2) determine the common up- and down-regulated genes in response to combination of these biotic stresses in *Arabidopsis*. To achieve these objectives, a microarray-based analysis of *Arabidopsis* genes in pathogen (biotic) stress response pathways were evaluated for their regulation to disease and stress responses. The results of this study will help identifying the up- and down-regulated defense genes to these stresses and improving crop tolerance to these stresses. In addition, *Arabidopsis* expression profiling of defense regulated genes in response to these stresses will shed light on our understanding on how plants respond to multiple stresses under field conditions. Overall, this project enables us introducing defense genes that make the crops more resistance to different stresses, particularly *B. cinerea* and/or other biotic stresses.

**Keywords:** *Arabidopsis*, *Botrytis cinerea*, Biotic stresses, differentially expressed genes, Transcriptome.