Comparative Transcriptomes Analysis Reveals Candidate Genes Associated with Powdery Mildew Resistance in Cultivated Strawberry

Ronald Tapia and Seonghee Lee*

Gulf Coast Research and Education Center, University of Florida, IFAS, Wimauma, FL

Abstract

Powdery mildew (PM) caused by *Podosphaera aphanis* is one of the major fungal diseases in cultivated strawberry. The development of cultivars resistant to the PM pathogen is a long-term goal of the University of Florida strawberry breeding program. However, the genetics underlying the resistance trait are largely unknown. This study aimed to discover genes associated with PM resistance using transcriptome profiling of selected UF strawberry accessions with varying responses to PM infection. A total of 16 RNA-seq libraries were generated from two resistant ('13.55-195' and '14.34-33') and two susceptible ('Sensation®Florida127' and '12.55-220') accessions at 0 and 24 hours post infection (hpi). RNA-seq analysis showed that the number of differentially expressed genes (DEGs) were significantly higher in susceptible genotypes than resistant genotypes at 24 hpi. In total, 6679 and 7420 DEGs were detected in '13.55-195' and '14.34-33' while 8965 and 8358 DEGs were detected in 'Sensation®Florida127' and '12.55-220', respectively. Among all the DEGs, 31 genes are specifically expressed in both resistant genotypes. These include MYB transcription factor, ABC transporter, hypersensitive-induced response, and photosynthesis-associated genes that could be essential for pathogen-triggered immunity. We also detected 48 DEGs specifically expressed in both susceptible genotypes and identified few candidate susceptibility genes that include *Mildew Resistance Locus O (MLO)* gene members known to play key role during PM infection. Selected candidate genes from RNA-seq were validated using qRT-PCR. Overall, our study provides a valuable information to elucidate the defense mechanism of strawberry during *P. aphanis* infection.

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*Corresponding author. Email: Seonghee105@ufl.edu