**Final report for Northwest Potato Research Consortium**

**TITLE:** **Development of Genomic Resources for**

**Management of Verticillium wilt of Potato**

**PERSONNEL:**

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**REPORTING PERIOD**: Year Initiated: 2020; Terminating Year: 2021.

**ACCOMPLISHMENTS:**

The goal of this project was to generate genomic resources for potato, brown mustard, and *Verticillium dahliae*. More specifically, the objective of this project was to validate a subset of differentially expressed genes (DEGs) in potato, brown mustard and *Verticillium dahliae* during infection. Potato and brown mustard plants were grown in a greenhouse. A third of the plants were inoculated with a strain of *V. dahliae* that is aggressive towards potato (called Vd-653), another third were inoculated with a strain virulent towards mint (called Vd-111), and the last third were mock-inoculated with sterilized water. All plants were harvested 10 days after inoculation and RNA was isolated. A quantitative real time-PCR (qRT-PCR) method was used to validate DEGs that were first detected with RNA-sequencing (RNA-seq). DEGs were selected for validation if they exhibited the highest fold change values from the RNA-seq study or were assigned putative roles in pathogenicity, virulence or defense. A total of 26 DEGs were validated, including 12, 10, and 4 from potato, brown mustard, and *V. dahliae*, respectively. The direction of DEGs were similar between both RNA-seq and qRT-PCR data sets. Moreover, the correlation coefficient (R) between fold changes obtained from RNA-seq and qRT-PCR methods were 0.91, 0.97, and 0.85 forpotato, brown mustard, and *V. dahliae,* respectively. For potato defense response genes like *PR04, PRR1*, *WRK40*, *TIF5A* and few with unknown biological functions were validated. For *V. dahliae*, genes with putative virulence functions like peptidase, hydrolase, and oxidoreductase were validated. This study confirms the transcriptional changes in potato, brown mustard, and *V. dahliae* during infection. Results from this study will (i) contribute towards disease resistance breeding in potato, (ii) increase our understanding of non-host resistance, and (iii) help identify host and pathogen genes that are required for symptomatic and asymptomatic interactions.

**PROCEDURE:**

**Sample collection:**

Potato cv. Russet Burbank, and brown mustard cv. ISCI 99, were planted in 3.5” pots filled with Turface® (Profile Products LLC, Buffalo Grove, IL) in the greenhouse. Plants were fertigated with 20-10-20 NPK. After emergence, plants were drenched with two strains of *V. dahliae*, Vd-653 and Vd-111 (Fig. 1A-D). Vd-653 is virulent towards potato while Vd-111 is primarily virulent towards mint (Dung et al. 2013). Both strains can colonize brown mustard but do not incite symptoms (Wheeler and Johnson, 2016). After inoculation, ten replicates of each treatment were arranged in a randomized complete block design. Ten days after inoculation, plants were destructively sampled, and flash-frozen in liquid nitrogen. The collected plant samples were stored at -80°C for ten days and lyophilized for 48 hours.

**RNA Extraction and cDNA synthesis:**

Total RNA was extracted from all collected samples following the method described by Kumar et al. 2007 with some modification. To avoid genomic DNA contamination, total RNA was digested with Ambion DNAse I (RNase-free) (Invitrogen). Quantification of total RNA was completed with a QUBIT fluorometer (Life Technologies), and integrity was assessed by gel electrophoresis. The quantities of total RNA in the samples ranged from 72 to 2000 ng/µl. RNA samples free from genomic DNA and with two clear bands representing 28S and 18S ribosomal RNA were used for the cDNA synthesis and qRT-PCR validation (Fig. 1E). cDNA was synthesized from 1 µg of total RNA in 20µl reaction volume using qScriptTM cDNA SuperMIX (QuantaBio) following the manufacturer’s instructions. The cDNA was diluted to 1:5 in DNAase and RNAase free sterile water for potato and mustard gene validation and 1:3 for V. dahliae gene validation. cDNA was stored at -20°C prior to validation.

**Gene selection and primer design:**

A total of 36 DEGs comparisons from RNA-seq results were selected for validation. For potato and brown mustard genes, three pairwise comparisons were made: Vd-653 vs control, Vd-111 vs control and Vd-111 vs Vd-653. Likewise, all possible treatment combinations of the potato and mustards were used for the *V. dahliae* gene. DEGs were selected for each host if they exhibited the highest fold change values or represented putative pathogenicity or virulence-related genes. Primers spanning exon-exon junction (if applicable) were designed for each gene using NCBI Primer-BLAST (https://www.ncbi.nlm.nih.gov/tools/primer-blast). Primer sequences and amplicon lengths are presented in Table 1. Primers with 19-23 bp size, 40-60% GC content, amplicon size of 70-180 bp with no self-annealing and primer dimer formation were used.

**Quantitative real-time PCR:**

qRT-PCR was performed in a QuantStudioTM Real-Time PCR System (Applied Biosystems) using SYBRTM Select Master Mix (2X) (Applied Biosystems) in 10µl reaction volume. The reaction mixture consisted of 5µl SYBR Select Master Mix(2X), 0.5µl of each forward and reverse primers (10µM), 1µl diluted cDNA and 3µl sterile water. The cycling conditions for qRT-PCR were 95°C for 10 minutes, followed by 40 cycles of 95°C for 15s and 60°C for 1 min. Melting curve analysis was performed from 60°C to 95°C with fluorescence reading acquired at 0.5°C increments per cycle to confirm the presence of a single amplified product. Three biological and technical replications were used for all genes. Negative controls consisted of samples without cDNA. Primer efficiency and Ct values were calculated using LinRegPCR software (Ruijter et al. 2009). The Ct value for each biological replicate was calculated by taking the average Ct values of three technical replicates. The log2 fold change value was derived using the delta-delta Ct method for each comparison (Livak and Schmittgen 2001). Normalization of the DEGs for potato was completed with house-keeping gene, elongation factor 1-α (EF1α), and with actin gene (ACT*)* for brown mustard and V. *dahliae* (Table 1). To confirm the direction of fold change values. qRT-PCR data were compared with fold changes obtained from RNA-sequencing. Correlation coefficients were calculated between fold change obtained from these two methods for each host.

**RESULTS/DISCUSSION:**

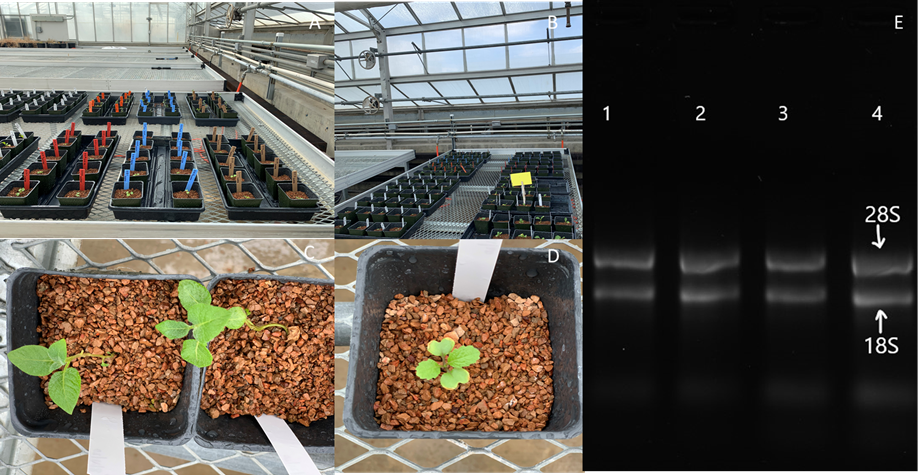
This study validated the differentially expressed genes from previous RNA-seq results utilizing qRT-PCR. A total of 26 out of 36 (13/18) comparisons of DEGs, including 12 for potato, 10 for brown mustard and 4 for *V. dahliae* were validated. These comparisons include expression changes of 9, 5, and 4 genes for potato, brown mustard, and *V. dahliae*, respectively. The direction (up or down-regulation) of fold changes were same in both qRT-PCR and RNA-seq data (Figure 2). The correlation coefficient of gene expression changes (log2fold change) between qRT-PCR and RNA seq were 0.91, 0.85, and 0.97 for potato, brown mustard, and *V. dahliae* respectively (Figure 3).

Two genes of potato, *PRS2\_SOLTU* and *IER1\_SOLLC* and four genes of brown mustard, *UVB31\_ARATH*, *LUC7L3*, Cluster-15354.91015, and Cluster-15354.125147 did not show a similar expression pattern as RNA-seq (data not shown). Different sensitivity of two methods, use of different template RNA for quantification and inconsistent expression of transcripts in some treatments could be potential reasons for such differences in results (Wang et al. 2016). For brown mustard genes, *UVB31\_ARATH* and Cluster-15354.125147, there was either no amplification or very poor amplification in certain treatments. This inconsistency in amplification can be explained by no gene expression in those treatments throughout all biological replications in RNA-seq count data.

Validated genes include those with functional role in defense response in hosts and pathogenicity in *V. dahliae*. The Pathogenicity related (PR) like genes *PR04\_SOLLC*, *PRR1\_TOBAC* which have a role in plant defense (Vleeshouwers et al. 2000) were significantly upregulated (adjusted *P* value < 0.05) when challenged with Vd-653 isolate compared to control and Vd-111 isolate in potato. Similarly, transcription factor, *WRK40\_ARATH*, which play an important role in the signal transduction in plant upon pathogen recognition was also differentially expressed in potato (Eulgem and Somssich 2007). Jasmonic acid (JA) regulation gene, *TIF5A* was upregulated in Vd-111 compared to Vd-653 infected potato plants. JA regulates the host defense against necrotrophic pathogen like *V. dahliae* (Scholz et al. 2018). Similarly, oxidoreductase and *lipoxygenase* (*LOX12*) gene was also confirmed to be upregulated in response to Vd-111 infection. In addition, genes involved in oxidoreductase, DNA binding, catalytic, and transferase activities were validated using the qRT-PCR method in potato. In *V. dahliae*, genes with putative role in virulence such as peptidase, hydrolase, oxidoreductase, and catalytic activity were also validated. The heptaketide hydrolase, *AYGI*, differentially expressed in this study was shown to play a role in melanin biosynthesis (Fujii et al. 2004). *AYGI* was also differentially expressed in *V. dahliae in vitro* studies(Duressa et al. 2013). In brown mustard, DEGs involved in nuclear mRNA export, ATP binding, kinase, DNA binding transcription factor, RNA binding were validated.

Previously, our RNA-seq study also identified at least 7, 9, and 7 DEGs in potato, brown mustard and *V. dahliae* respectively with no known biological function and their role in defense or pathogenicity. The qRT-PCR study confirmed those few uncharacterized genes as well. The further investigation and functional analysis of these genes would help to decipher the host-pathogen interaction and could be used as novel targets for Verticillium wilt management.

This qRT-PCR study confirms the transcriptional changes in potato, brown mustard and *V. dahliae* in response to *V. dahliae* infection. The study provides the bigger picture of changes in hosts at the molecular level upon *V. dahliae* infection and could be used as a basis to solve complex puzzle of host and *V. dahliae* interaction. Also, validated defense response genes in the host could be used as an important genomic resource in disease resistance breeding program.



**Figure 1:** A, B) Greenhouse experiment, C) Potato plantlets, D) Mustard plants, and E) Total RNA integrity test on 1% agarose gel. Lane 1,2,3 and 4 indicates RNA samples with two 28S and 18S ribosomal RNA.

**Table 1:** List of primer sequence of differentially expressed genes (DEGs) used for the qRT-PCR validation

|  |  |  |  |
| --- | --- | --- | --- |
| Gene name | Forward sequence (5’ to 3’) | Reverse sequence (5’ to 3’) | Amplicon size (bp) |
| St\_*PR04\_SOLLC* | GCCGTGCAATTGTGGGTGTC | CGCACACTTTTCCACTAGCAC | 76 |
| St\_*ABAH1\_ARATH* | CCACTTCCTCCTGGTACTTTAGG | AACTTGTTTAGCTGCCTCTGG | 177 |
| St\_PGSC0003DMG400024310 | GAGAAGGAAGATTGGTGGGACA | CTACCCATCCCTCCTCCACA | 105 |
| St\_*LOX12\_SOLTU* | ATTAGCTCTGTTCAAGGTGATCC | TCTCCAAGTAGGCTGGATTGC | 70 |
| St\_*PRR1\_TOBAC* | TGTCTTTTGCCCTTGAAGGCT | GACAACGTCTCACCAGCTCT | 115 |
| St\_*CHSB\_SOLTU* | GAGCTCAAGGAGAAATTTAAGCG | ACAACAACTATGTCTTGCCTTGC | 149 |
| St\_*EDL3\_ARATH* | AATGGTCGGATCGGAGGAGA | TCGGATTACACCCGCAACAG | 70 |
| St\_*WRK40\_ARATH* | AGACAACCCATCTCCAAGAGC | TCGATTGGTCTTCCACGCTT | 95 |
| St\_*TIF5A\_ARATH* | ATGTCCGAGCCTTCATCACC | GGAGCAACTAGTGATGGTATGGT | 130 |
| St\_ *EF1α* | ATTGGAAACGGATATGCTCCA | TCCTTACCTGAACGCCTGTCA | 101 |
| Vd\_*AOX\_PODAS* | GCTGCGTGGAAGTTTGTGC | TTCTTGTCAACCTGCTGCTCA | 83 |
| Vd\_*YDDQ\_BACSU* | AAGATTGTGCTCGTCGGGTA | TCTCAGCCAGAGCAACCTTC | 163 |
| Vd\_mRNA\_1341 | GCTGTCCGCATCTGACTTGT | GGTGACGTTGAACTTTGCCA | 97 |
| Vd\_*AYG1\_ASPFU* | GATTCGGCTGACCCAGACAG | ACCTTGCCCATATCGAACCG | 89 |
| Vd\_*ACT* | GGCTTCCTCAAGGTCGGCTATG | GCTGCATGTCATCCCACTTCTTC |  |
| Bj\_Cluster-15354.86688 | ATTCACACTGCTCCACGCTA | GGCTGAAGGGTGAGAATGGG | 78 |
| Bj\_*NUP1\_ARATH* | CCATCCTTGCTTGGATTGCC | ATGCAGGAGGCTAAGGTTGG | 110 |
| Bj\_*PDRP2\_ARATH* | TATAAAGCAGGCAGCGAAGC | GAGAGCACTCCCCAACGAT | 105 |
| Bj\_*SCL1\_ARATH* | AACTGCTGAAAAGGATGACAAGT | TGCTCTTGCTGCTTTCCGTT | 84 |
| Bj\_Cluster-15354.44072 | TGCGTTCCTCAGAACCAGAG | AGCTTCTTCTCCACTGCTGAC | 106 |
| Bj\_Cluster-15354.125147 | GCGAGAGCAAGACACAAAAGG | TGTTTGCTGAGGGGAGTTCG | 77 |
| Bj\_*ACT-2* | TGGGTTTGCTGGTGACGAT | TGCCTAGGACGACCAACAATACT | 290 |

**Figure 2:** Validation of relative expression changes of selected DEGs of *S. tuberosum*, *V. dahliae*, and *B. juncea* with the qRT-PCR method. The fold change was calculated using method for qRT-PCR and DESeq2 for RNA-seq. The x-axis represents the name of the genes, and the y-axis represents Log2 fold change value for the given comparison (shown in legend).



**Figure 3:** Scatter plots showing the linear relationship between qRT-PCR and RNA-seq gene expression changes in *S. tuberosum*, *V. dahliae*, and *B. juncea*. R-value represents the correlation coefficient for the respective host.

***Publications*:**

Manuscript in preparation

***Presentations and Reports:***

None to date.

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