

**Title**

**Integrative network analyses of wilt transcriptome in chickpea reveal genotype dependent regulatory hubs in immunity and susceptibility**

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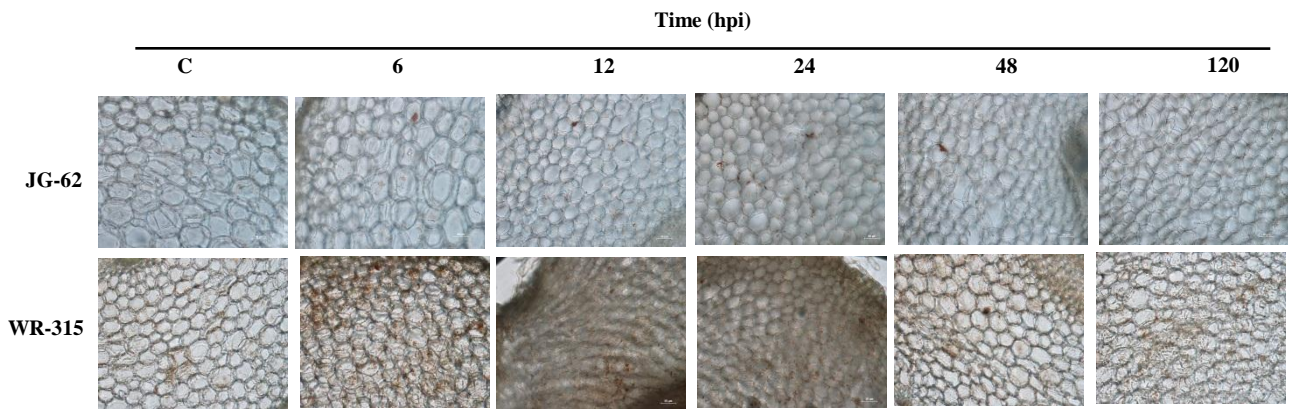
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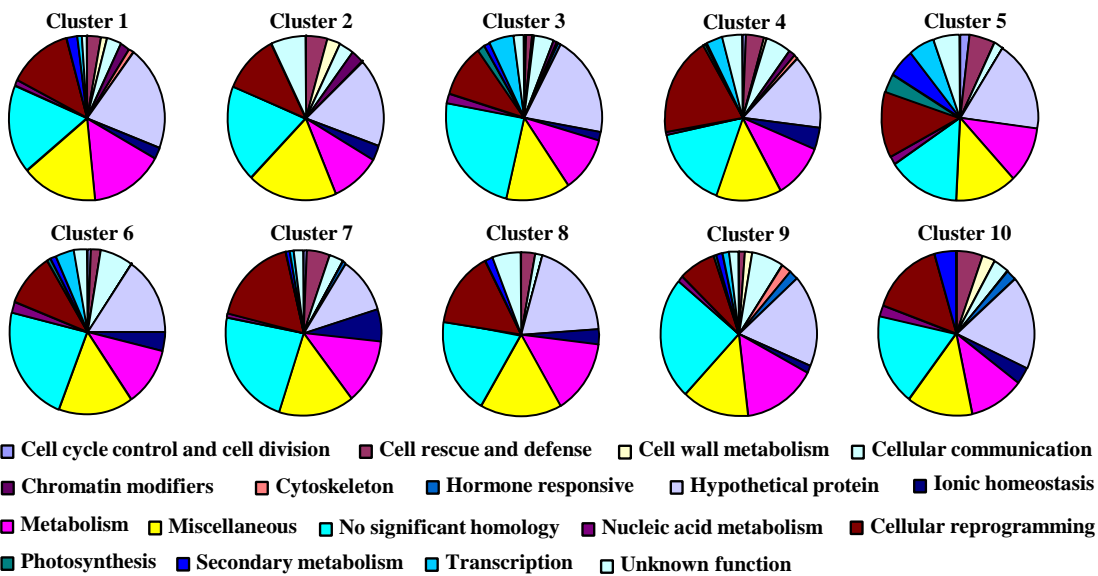
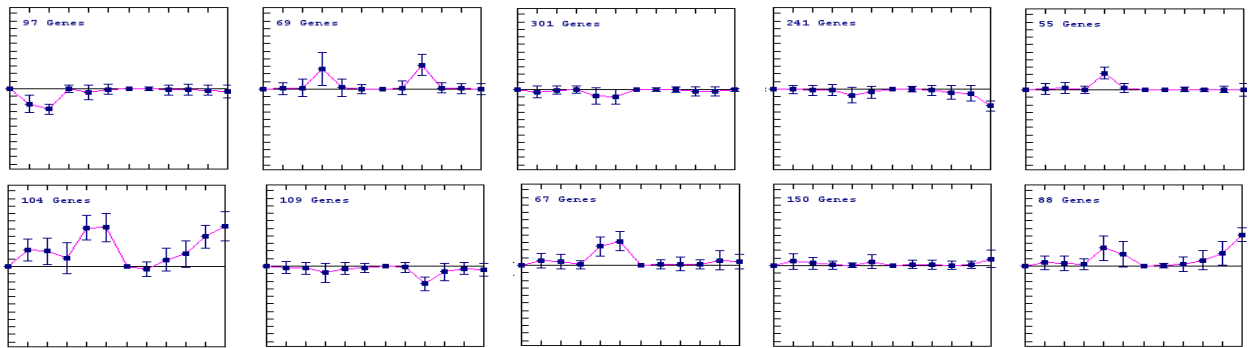
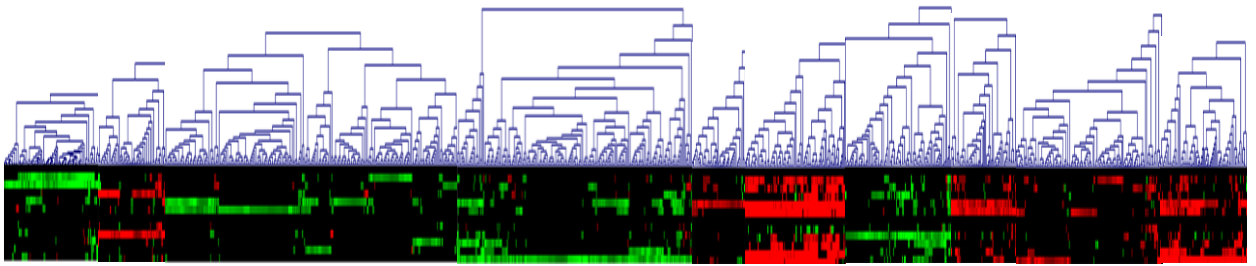
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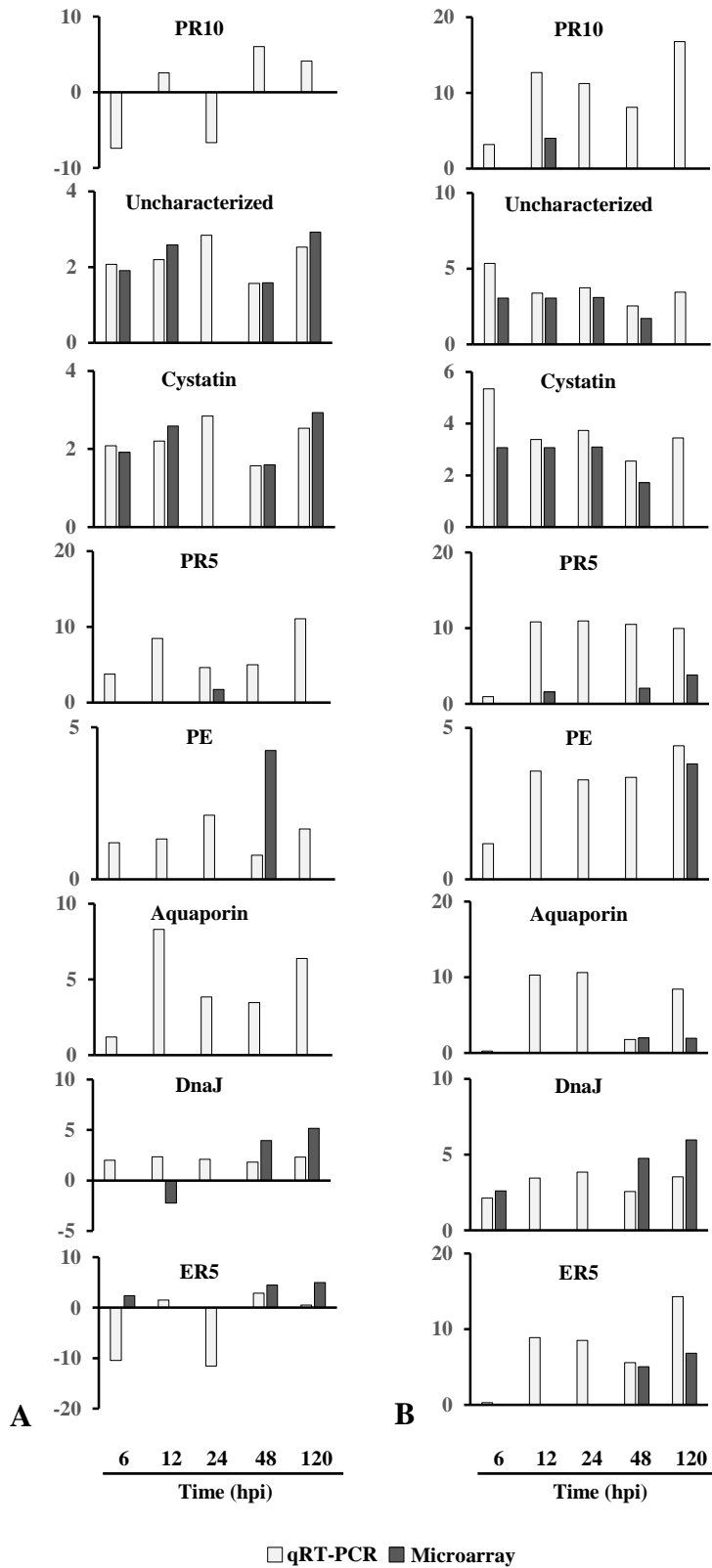
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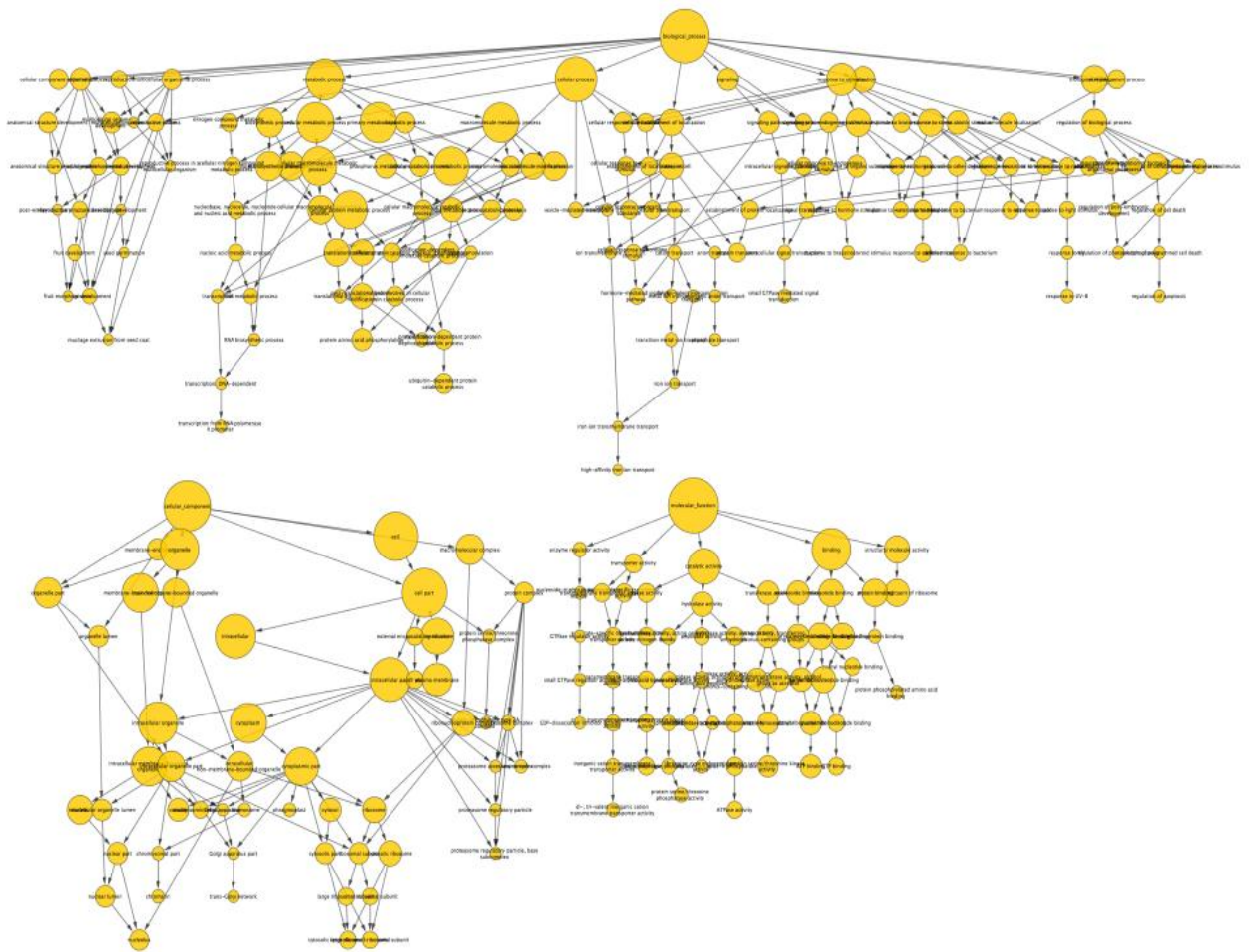
**Supplementary Figure S1. ROS production and progression of *F. oxysporum* in the roots of JG-62 and WR-315 plants. *F. oxysporum*-infected roots of JG-62 and WR-315 stained with DAB.**



**Supplementary Figure S2. Clusterogram of DEGs.** DEGs were grouped into 10 clusters based on their expression pattern. The SOTA cluster tree is shown at the top, and the expression pattern in clusters are shown below. High (or low) abundance ranges from pale to saturated red (or green).



**Supplementary Figure S3.** Co-relation of gene expression levels by qRT-PCR and microarray experiments. (A) JG-62 and (B) WR-315. Log<sub>2</sub> qRT-PCR expression were compared with the differential expression from Log<sub>2</sub> microarray data.



**Supplementary Figure S4. Function and coexpression analysis.** BLAST2GO results were merged through BINGO plugin of Cytoscape. The complex network of 389 EST's was subjected to BINGO along with BLAST2GO mapping data in form of a BINGO annotation file. These groups were divided into four major categories each including a sub category best suiting its parent.

**Supplementary Table S1.** Sequence of oligonucleotide primers used for quantitative real time PCR.

<b>Name of primer</b>	<b>Sequence of primer</b>
PR10 - F	5'-TCCTTCACCATCCAGCATAACC-3'
PR10 - R	5'-TGACGGGCTCGAGAAAATACA-3'
ERF - F	5'-GGGCAGGTGTCGACTCTCAT-3'
ERF - R	5'-CGAGTCATGGTTGTTGATGGA-3'
Aquaporin - F	5'-TCATCGGCAGTGTTGGAGACT-3'
Aquaporin - R	5'-AACAGCGCTTTAAATCAGGAGAA-3'
PR5 - F	5'-CCGTGTTAGGAGCGGGATTT-3'
PR5 - R	5'-CATCCCCGCAGTTTTGTGT-3'
DnaJ - F	5'-GCTTCCAGTTTACTGTCACACATCTT-3'
DnaJ - R	5'-TTCCCCAGGGTTTGATTTGA-3'
Cys - F	5'-CTTGGTGGAGTTCGCGATGT-3'
Cys - R	5'-TAGCGGGCGAGACTATCGAT-3'
Uncharaterized- F	5'-CGGATGCATTTGAGAAAAACC-3'
Uncharaterized - R	5'-GGAAGAGCCTTATCCAGTGAAATC-3'
PE - F	5'-GCAGATTGCTCATCCCACAA-3'
PE - R	5'-TGTCTAGCATGATGGAGCAGTTTT-3'
FoGPD*_F	5'-AAGGGTGCTTCTTACGACCA-3'
FoGPD*_R	5'-ATCGGAGGAGACAACATCGT-3'
Ca18s_F#	5'-CTCGGCCCAACTCCGGTTCG-3'
Ca18s_R#	5'-CGCACGAAAACCGTCTCCGGT-3'

\* FoGPD represents *Fusarium oxysporum* glyceraldehyde3-phosphate dehydrogenase.

# 18S was used as an endogenous control.

## Supplementary Reference

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