

Comparative transcriptome analysis between a resistant and a susceptible wild tomato accession in response to *Phytophthora parasitica*

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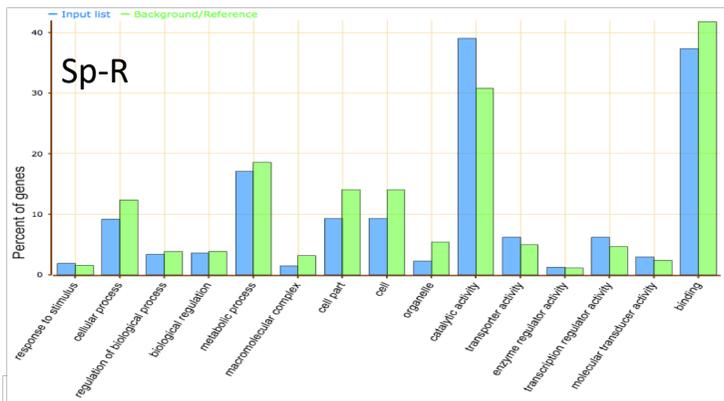
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Corresponding Author:

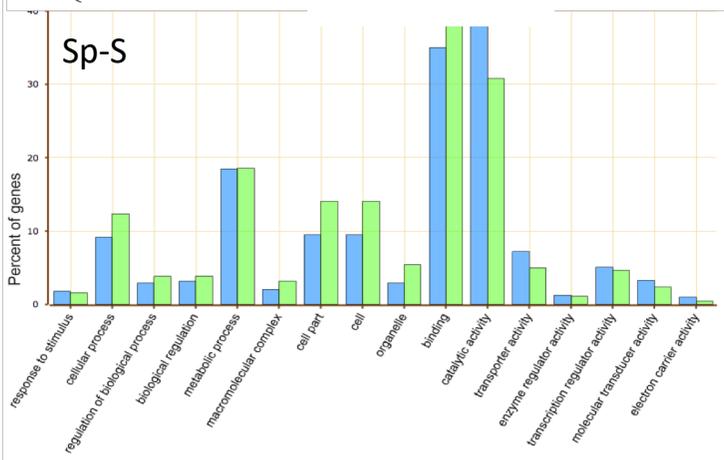
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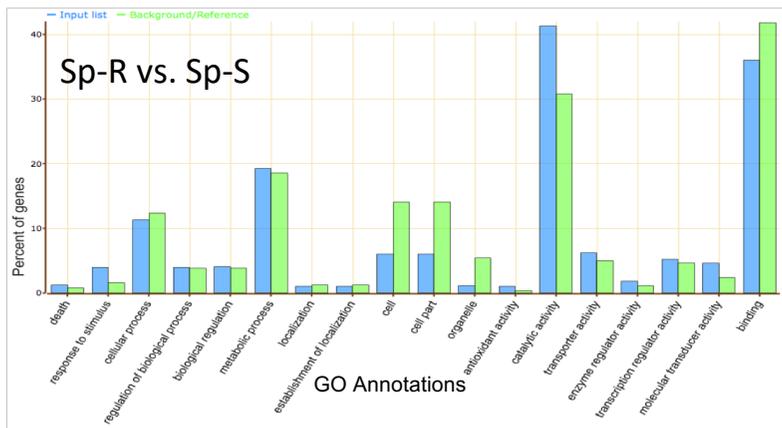
A



B

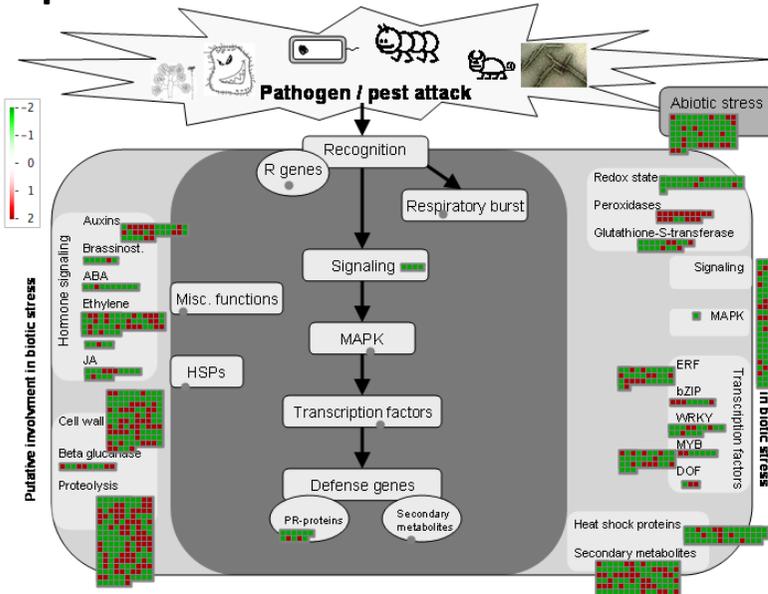


C



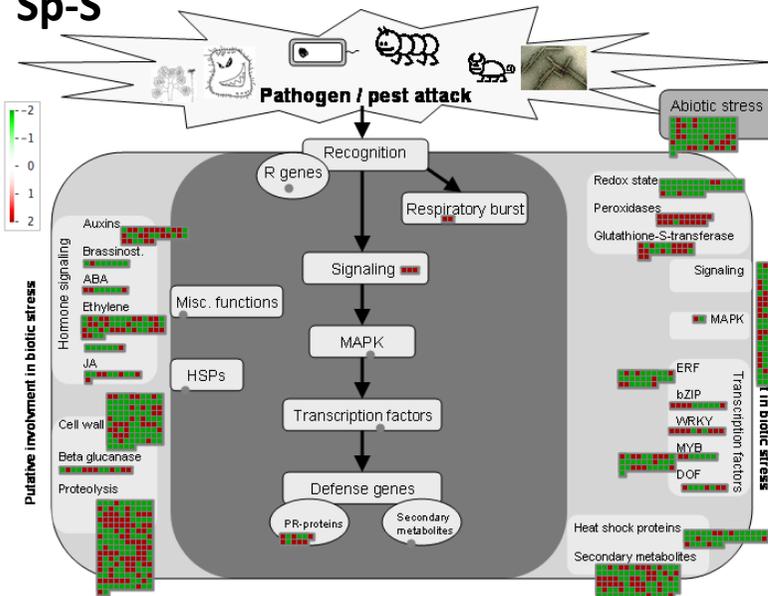
Supplementary Figure 1. Overview of GO annotations assignment of DEGs by SEA tool of AgriGO. Percent distribution of DEGs across enriched GO terms for cellular component, molecular function and biological processes for all DEGs found in *P. parasitica* treated vs. control samples of Sp-R genotype at both 24 and 48hpi (A) for Sp-S genotype (B) DEGs identified by Sp-R treated vs. Sp-S treated samples at both time points (C). Green bars represents reference background (*S. lycopersicum* ITAG 2.4) used to calculate enrichment and blue bar represent input DEGs.

Sp-R



Biotic Stress.png
 mapping: Syc_ITAG2.3.m02
 mapped: 3278 of 3208 data points
 visible: 982 data points
 data: R_mapman.txt

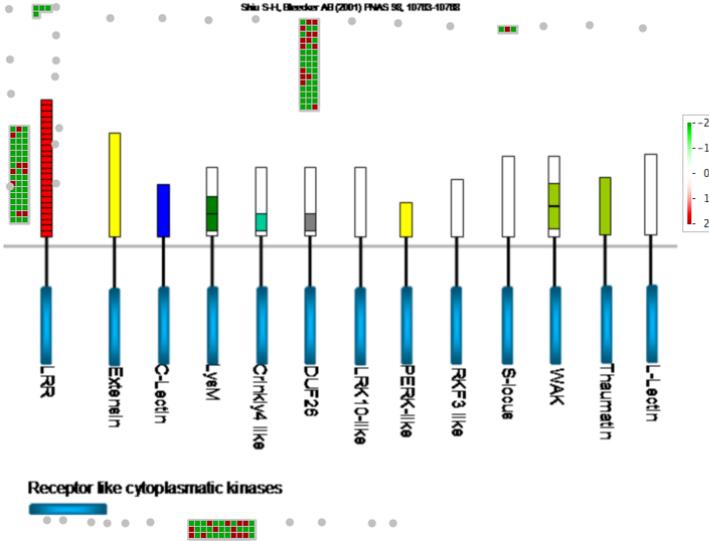
Sp-S



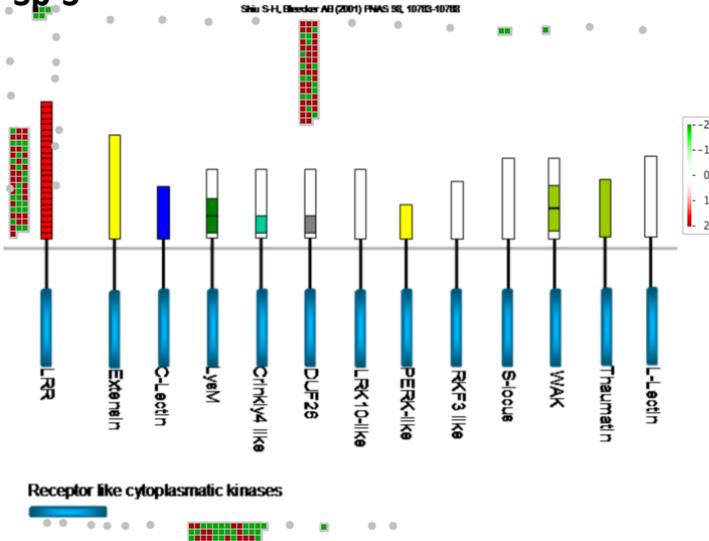
Biotic Stress.png
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 mapped: 3505 of 3425 data points
 visible: 970 data points
 data: S-maman.txt

Supplementary Figure 2: Visualization of differentially expressed genes in wild tomatoes in response to *P. parasitica* on biotic stress pathway , (A) Resistant accession (B) Susceptible accession. Color gradient represents log₂ fold ratios with red representing upregulation and blue representing downregulation in treatments over controls.

Sp-R



Sp-S



Supplementary Figure 3 : Differentially expressed genes of wild tomatoes in response to *P. parasitica*, encoding DUF26 type receptor like kinases (A) Resistant accession (B) Susceptible accession. Color gradient represents log₂ fold ratios with red representing upregulation and blue representing downregulation in treatments over controls.

Table S1. qRT-PCR primers for selected genes.

Transcript ID	Description	Primers
Solyc07g043420.2	2-oxoglutarate and Fe dependent oxygenase	GGAGGCAGGTTCTTTGACA
		ATGCATTGCGAATAGGCTGC
Solyc08g029000.2	lipoxygenase 1	AGCACACCCGATGAGTTTGA
		TGAAGAACTTGAGGTGTTGGGA
Solyc09g010630.2	heat shock protein 70	ATGGCTGGAAGGTTGAAGG
		ACGCTCAGAGTCGGTGAATC
Solyc11g069700.1	Elongation factor Tu family	TGTGCCGATTCTGGTTTCG
		ACGACCAACAGGAACAGTCC
Solyc04g080960.2	Papain family cysteine protease	GACTGGCGTGAAAAAGGAGC
		GGGTCACACTCATGGTCACA

Table S2: Number of DEGs found among all comparisons.

	Total DEGs	Up regulated DEGs	Down regulated DEGs	Specific DEGs
S-24hpi treated vs S-control	3079	1132	1947	775
S-48hpi treated vs S-control	1919	811	1108	152
R-24hpi treated vs R-control	2657	868	1789	519
R-48hpi treated vs R-control	1836	606	1230	293
	4598*			
R vs. S				
R-control vs S-control	322	155	167	178
R-24hpi treated vs S-24hpi treated	1158	287	871	589
R-48hpi treated vs S-48hpi treated	889	207	682	302
	1681*			