

Supplementary Tables and Figures

Manuscript title: The transcriptional response to yellow and wilt disease, caused by race 6 of *Fusarium oxysporum* f. sp. *ciceris* in two contrasting chickpea cultivars

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Table S1 Primers for qRT-PCR. Gene identifiers, annotation NCBI, primer sequences, amplicon size and chromosome position. Primer PCR efficiency and PCR product T_m data represent mean values. PCR efficiencies (E) calculated according to the equation $(1 + E) = 10^{\text{slope}}$.

ID Gene	Annotation	Primer Sequence (5'-3')	PCR product size (bp)	Chr position	PCR E	PCR product T _m (°C)
LOC101498889	carbonic anhydrase 1	F-CTTTGTCCTCTGCCAAAACCTC R-GAAAACCGGCTTGTCTTGAATC	140	Ca2: 2190241..2 193896	2.2	60
LOC101507324	putative protein TPRXL	F-GAACTTTAGGCAGCAACTCCT R-CAAGCTATTGTCCCCTAGCA	83	Ca6: 50702624.. 50703264	1.87	60
LOC101495793	MATH and LRR domain-containing protein PFE0570w	F-CCAGAAGCAATTCAAGGACTC R-CACCTTCTCTTCTACGATGAC	105	Ca5: 30905134.. 30907624	2.04	60
LOC101497118	transcription factor MYB41	F-ACGTCACCTTCACCTTCTAG R-GTCATAAGTGTATCTCTCACCT	96	Ca1: 16391425.. 16394227	1.94	60
LOC101510034	basic 7S globulin-like	F-GGCAACTCCTCCCATATCCAT R-GGGTGCAATGAAGAACAGTAGG	140	Ca4: 2179311..2 181111	1.95	60
LOC101513347	spermidine hydroxycinnamoyl transferase-like	F-CTTGTTGTGGCGATTTGTTTG R-CCCTTTAACCACCTAACATTGC	122	Ca3: 26823706.. 26825488	1.88	60
LOC101489892	expansin-like B1	F-CTCATTAAGCCTTCTCTTGAGC R-GGTACACAGGCGAGGTAAGAA	175	Ca8: 2678285..2 680891	2.02	60
LOC101491624	linoleate 9S-lipoxygenase-like	F-CCTTCTCCTGCTATGTATGGTC R-GCTCCATCACAATACAAGGTACA	113	Ca7: 32157827.. 32162937	1.93	60
LOC101501931	heat shock cognate 70 kDa protein 2	F-GGCTGGAAAAGGTGAAGGTC R-GTAGTTCTGTTCCCTTGGTCG	120	Ca6: 26638762.. 26641344	2.03	60
LOC101495891	1-aminocyclopropane-1-carboxylate oxidase	F-GAGCAAGCAACCTGCAATAAAC R-CTGGGAAGTTCTCCATATCTCT	101	Ca5: 41656988.. 41659172	1.92	60
LOC101513977	serine/threonine-protein kinase-like	F-AGCTGTAGACCTTTATCCTATCC R-CATCACATGACATAGTTGCAGG	121	Ca1: 47140415.. 47152696	1.93	60
LOC101493121	protein ENHANCED PSEUDOMONAS SUSCEPTIBILITY 1	F-CAACAAGTAGTGTGAGTGAAACC R-CGACACCCAAATCCAATCCAC	114	Ca6: 48162598.. 48164521	1.99	60

Table S2 List of important DEGs based on their responses to Fusarium wilt (Foc6) disease in both Ana (resistance) and Hashem (susceptible) chickpea cultivars.

Gene	Description	ID Genes	Fold Change (Log2): Ana&Hashem	Subcellular Location	Function	Reference
CaNLR-RPM1	disease resistance protein RPM1 (Pseudomonas syringae pv. maculicola 1)	LOC101504665	A: 1.3 H: -	Cytoplasm	Sensing	Martin et al. 2003; Baggs et al. 2017; Yuan et al. 2019
CaLYK5-RLK	receptor-like kinase	LOC101494861	A: 1.8 H: -	Membrane & Nucleus	Sensing	Tang et al. 2017; Yadav et al. 2023; Cao et al. 2014
CaPR5-RLK		LOC101493461	A: 1.3 H: -			
CaLRR-RLK		LOC101489235	A: 2.3 H: -			
CaLRR-RLK		LOC101513977	A: 2 H: 1.6			
CaRLP-EIX2		LOC101498360	A: 1.7 H: -			
CaPP7	serine/threonine-protein phosphatase 7 long form homolog	LOC105852653	A: 10 H: -	Nucleus	Signaling	Luan 1998
CaHSC70	heat shock cognate 70 kDa protein 2	LOC101501931	A: 2.3 H: 1.9	Endoplasmic reticulum	Signaling	Wang et al. 2020; Garg et al. 2023; Stanley et al. 2005; Xing et al. 2016
CaEPS1	enhanced Pseudomonas susceptibility 1	LOC101493121	A: 1.8 H: -	Cytoplasm	Signaling	Khan et al. 2022
CaPR-1	pathogenesis-related protein 1-like	LOC101503659	A: 1.5 H: -	Membrane & Vacuole	Signaling	Patil et al. 2021
CaPR-4	thaumatin-like pathogenesis-related protein 4-like	LOC101511048	A: 5.7 H: 4.1	Membrane & Vacuole	Signaling	Patil et al. 2021
CaSTY13	serine/threonine-protein kinase STY13-like	LOC101511109	A: 10 H: -	Nucleus & Membrane	Signaling	Gupta et al. 2017; Garg et al. 2023; Kim et al. 2011
CaSTY-OXI1	serine/threonine-protein kinase OXI1-like (OXI1: Oxidative Signal-Inducible1)	LOC101501979	A: 3.1 H: 1.4	Nucleus & Membrane	Signaling	Gupta et al. 2017; Garg et al. 2023; Kim et al. 2011
CaTLP1b	Thaumatococcus-like protein 1b	LOC101495985	A: 5.6 H: 4.3	Cytoplasm	Signaling	Petre et al. 2011; Yadav et al., 2023
CansLTP-like	non-specific lipid-transfer protein 1-like	LOC101503860	A: 5.5 H: 2.3	Cell wall	Signaling	Petre et al. 2011; Yadav et al., 2023
CaMYB41	transcription factor MYB41	LOC101497118	A: 4.7 H: -	Nucleus	Transcription regulation	Kosma et al. 2014; Li et al. 2015
CaMYB108	transcription factor MYB108	LOC101490747 LOC101492267	A: 3 H: - A: 2.6 H: -	Nucleus	Transcription regulation	Mengiste et al. 2003; Zhang et al. 2012
CaMYB-related	probable transcription factor At5g61620	LOC101507725	A: 10 H: -	Nucleus	Transcription regulation	Mengiste et al. 2003; Li et al. 2015
CaGLK	uncharacterized LOC101491042	LOC101491042	A: 10 H: -	Nucleus	Transcription regulation	Riechmann et al. 2000; Han et al. 2016
CaERF9 CaERF113 CaERF113-like	ethylene-responsive transcription factor	LOC101502158 LOC101515629 LOC101513362	A: 1.3 H: - A: 1.3 H: - A: 2.1 H: -	Nucleus	Transcription regulation	Sakuma et al. 2002; Dong et al. 2020; Yadav et al. 2023

<i>CaZAT11-like</i>	zinc finger protein ZAT11-like	LOC101498044 LOC101492538	A: 10 H: - A:1.5 H: -	Nucleus	Transcription regulation	Gechev et al. 2005; Qureshi et al. 2013
<i>CaNAC6</i>	NAC domain-containing protein	LOC101514169	A: 2.2 H: -	Nucleus	Transcription regulation	Jensen et al. 2007; Nakashima et al. 2007; Chen et al. 2013
<i>CaPGI2-like</i>	polygalacturonase inhibitor 2-like	LOC105852278	A: 3.9 H: -	Cell wall & Cytoplasm	Cell wall	De Lorenzo and Ferrari 2002; Martin et al. 2003; Yadav et al. 2023;
<i>CaPE2</i>	pectinesterase 2-like	LOC101508209	A: 4.3 H: 2.3	Cell wall	Cell wall	Shu et al. 2021
<i>CaPME7</i>	probable pectinesterase/pectinesterase inhibitor 7	LOC101489717	A: 3.5 H: 2.5	Cell wall	Cell wall	Shu et al. 2021
<i>CaEXLB1</i> <i>CaEXLB1</i> <i>CaEXLA2</i>	expansin-like B1 expansin-like B1 expansin-like A2	LOC101489892 LOC101507544 LOC101514490	A: 3.6 H: - A: 3.8 H: 2.1 A: 2 H: 1.2	Cell wall	Cell wall integrity	Abuqamar et al. 2013; Chen et al. 2016; Muthusamy et al. 2022; Guo et al. 2024;
<i>CaCSLD</i>	cellulose synthase	LOC101509896 LOC101488214 LOC101499287	A: 1.2 H: - A: 1.8 H: - A: -2 H: -	Membrane & Chloroplast	Cell wall integrity	Malinovsky et al. 2014; Gupta et al. 2017
<i>CaCYP73A100-like</i>	cytochrome P450 CYP73A100-like	LOC101503511	A: 3.9 H: -	Endoplasmic reticulum & Membrane	Cell wall integrity	Pandian et al. 2020; Yadav et al. 2023; Gan et al. 2024
<i>CaXTH23</i>	probable xyloglucan endotransglucosylase/hydrolase protein 23	LOC101489989 LOC101490102	A: 4.6 H: - A: 2.9 H: -	Cell wall & Cytoplasm	Cell wall	Shu et al. 2021
<i>CaNR/NADH</i>	nitrate reductase [NADH]-like	LOC101498580	A: -1.7 H: -	Peroxisome	Transport-related genes	Gupta et al. 2017
<i>CaCa²⁺-ATPase</i>	calcium-transporting ATPase, endoplasmic reticulum-type	LOC101512366	A: 1.5 H: -	Endoplasmic reticulum	Transport-related genes	Upasani et al. 2017; Yadav et al. 2023
<i>CaSWEET13-like</i>	bidirectional sugar transporter SWEET13-like	LOC101491054	A: -1.8 H: -	Membrane	Transport-related genes	Liu et al. 2022; Yadav et al. 2023
<i>CaSWEET17</i>	bidirectional sugar transporter SWEET17	LOC101509872	A: -2.6 H: -1.3	Membrane	Transport-related genes	Liu et al. 2022; Yadav et al. 2023
<i>CaSWEET1</i>	bidirectional sugar transporter SWEET1	LOC101498274	A: -2.1 H: -1.9	Membrane	Transport-related genes	Liu et al. 2022; Yadav et al. 2023
<i>CaCAT5</i>	cationic amino acid transporter 5	LOC101509123	A: 1.5 H: -	Membrane	Transport-related genes	Yang et al. 2014
<i>CaNRAMP5</i>	metal transporter Nramp5-like (Nramp: natural resistance-associated macrophage proteins)	LOC101489317	A: -3.5 H: -	Membrane	Transport-related genes	Noor et al. 2023
<i>CaSULTR_{3.5}</i>	probable sulfate transporter 3.5	LOC101512274	A: 3.4 H: 2.5	Membrane	Transport-related genes	Leggett and Epstein 1956; Zhou et al. 2017

<i>CaDTX27</i>	protein DETOXIFICATION 27-like	LOC101503133	A: 2.5 H: -	Membrane	Transport- related genes	Nawrath et al. 2002; Tiwari et al. 2014; Caballo et al. 2019
<i>CaUFGT3</i>	putative UDP-glucose flavonoid 3-O- glucosyltransferase 3	UGT71S3	A: 3.3 H: -	Membrane & Nucleus	Metabolism	Morkunas and Ratajczak 2014; Gupta et al. 2017
<i>CaUGT</i>	putative UDP-glucose glucosyltransferase	UGT84F2	A: 1.4 H: -	Membrane & Nucleus	Metabolism	Morkunas and Ratajczak 2014; Gupta et al. 2017
<i>BF-CWI</i>	beta-fructofuranosidase, cell wall isozyme-like	LOC101513089	A: 4.2 H: 3	Cell wall	Metabolism	Proels and Hückelhoven 2014
<i>CaGSTs</i>	probable glutathione S- transferase	LOC101494465 LOC101506971	A: 3.4 H: 1.4 A: 1.8 H: -	Cytoplasm	Metabolism	Marrs 1996; Taxak et al. 2017; Gupta et al. 2013, 2017
<i>CaASI</i>	alpha-amylase/subtilisin inhibitor-like	LOC101508812	A: 2 H: -	Vacuole	Metabolism	Yamasaki et al. 2006; Yu et al. 2017
<i>CaCA1</i>	carbonic anhydrase 1	LOC101498889	A: 10 H: -	Chloroplast	Metabolism	Dreher and Callis 2007; Guangsheng et al. 2012; Taxak et al. 2017
<i>CaSHT-like</i>	spermidine hydroxycinnamoyl transferase-like	LOC101513347	A: 3.4 H: 2.5	Cytoplasm	Metabolism	Galston et al. 1985; Perrin et al. 2021
<i>CaSAG39- like</i>	senescence-specific cysteine protease SAG39-like	LOC101497435	A: 2.9 H: -	Membrane & Vacuole	Plant- pathogen interaction	Channale et al. 2021
<i>CaBg7S-like</i>	basic 7S globulin-like	LOC101509822	A: 4.4 H: -	Membrane	Plant- pathogen interaction	Hirano 2021
<i>CaMDCP</i>	MATH (Meprin And TRAF Homology) and LRR domain-containing protein PFE0570w	LOC101495793	A: -2.4 H: -	Nucleus	Plant- pathogen interaction	Kushwaha et al. 2016



Fig. S1 Ana cultivars were approximately 12 days after inoculation with FOC race 6.



Fig. S2 Hashem cultivars were approximately 12 days after inoculation with FOC race 6.

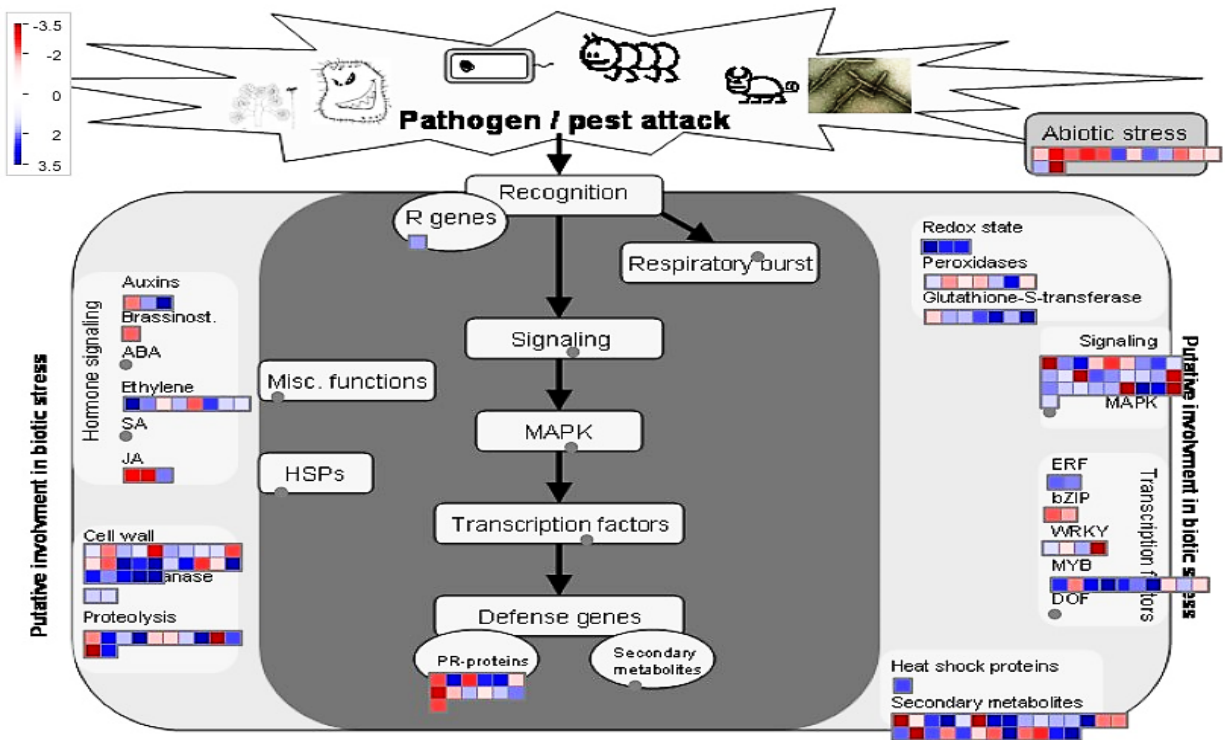


Fig. S4 MapMan presentation of DEGs in Ana chickpea cultivar under Fusarium wilt stress category. The color change from dark blue (+3.5 LogFC) to dark red (-3.5 LogFC) through white (0 LogFC) indicates the differential expression ranging from up-regulation and down-regulation genes.

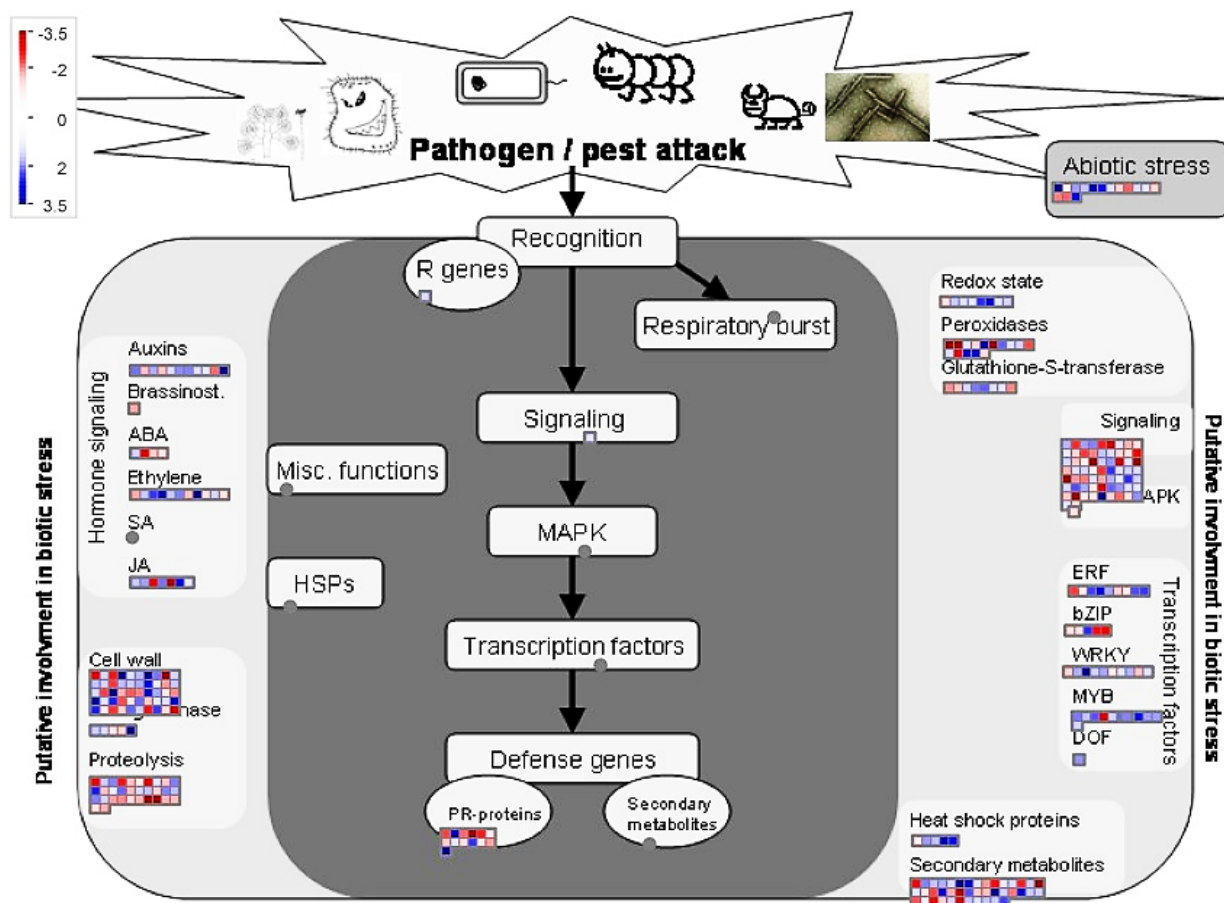


Fig. S5 MapMan presentation of DEGs in Hashem chickpea cultivar under Fusarium wilt stress category. The color change from dark blue (+3.5 LogFC) to dark red (-3.5 LogFC) through white (0 LogFC) indicates the differential expression ranging from up-regulation and down-regulation genes.