

Accessory Publication

Table S1. List of the annotations for the 40 differentially expressed genes from the susceptible library

Using the Z test we were able to identify 239 tags that were preferentially expressed in the library made from the susceptible individuals. This table is a list of the 40 differentially expressed tags that we were able to annotate in the library made from the susceptible individuals. The information given includes the tag sequence, the respective tag count in each library, the putative identification and the functional category (S - susceptible and R - resistant library)

Tag	S	R	Putative identification	Category
AGATGTATGG	4*	0	gi 25355558 gamma-glutamyl hydrolase 8e-90	1
GCCACCGCAC	13**	0	gi 25989650 photosystem II 10 kDa protein 3e-22	1
TAATTTCAAT	28**	12	gi 22255887 rubisco activase alpha 2e-18	1
TGATTGTGAT	50**	22	gi 57898928 N-rich protein 2e-55	2
TGTGTGTTTG	190**	164	gi 81075517 fruit-ripening protein-like 2e-44	2
GTAACTTTGG	19**	6	gi 75222628 translationally-controlled tumor protein 4e-30	2
GTCTGAAGGA	14**	3	gi 115187479 translationally controlled tumor protein 2e-68	2
TTATTTTGAA	10*	2	gi 29367519 receptor-like protein kinase-like 1e-43	2
AGTGTATTGC	6*	0	gi 88193285 osmotin-like 5e-14	2
ATGGCCAAGT	13*	4	gi 50299509 calmodulin cam-205 2e-46	2
TCATTCTTCA	14*	6	gi 92895945 universal stress protein 7e-36	2
TATTTTCCTT	6*	1	gi 8489786 dehydration-induced protein 5e-33	2
TCTGATATTT	6*	1	gi 15810219 putative lactoylglutathione lyase 6e-26	2
AATAAAGTAT	11*	4	gi 11131026 ADP-ribosylation factor 2e-40	3
TAATTTGAAA	12*	5	gi 14423860 profilin-3 1e-52	4
CTAGGAGGGA	7*	1	gi 92878290 ribosomal protein L19e 9e-87	4
GTTTTAGAA	30*	18	gi 13430182 ribosomal protein L17 4e-30	4
TGAGAGTCCA	10*	2	gi 21593177 26S proteasome subunit 4 8e-34	5
ATGAACAAGT	7**	0	gi 4678279 carboxyl terminal protease-like protein 3e-05	5
GAACGCTATC	117**	92	gi 14422331 cysteine protease 4e-08	5
CAATCTTAAA	5*	0	gi 18398633 protein binding/ubiquitin-protein 7e-66	5
GAAGAACTGA	4*	0	gi 71040675 ubiquitin-conjugating enzyme 1 7e-49	5
GTGATGGTAT	39**	22	gi 50660327 chloroplast chaperonin 21 2e-05	5
ACTTATGATG	10*	3	gi 21592325 bHLH transcription factor 4e-38	5
TGACTGGAAA	4*	0	gi 28629811 transcription factor Myb1 2e-20	5
GCCGTTCTTA	115**	66	gi 94420039 hypothetical protein 2e-20	6
GGCAGGCAAG	38**	21	gi 92884108 hypothetical protein 4e-19	6
AGGACTTGTG	5*	0	gi 90657614 hypothetical protein 1e-07	6
TTATTTCTGT	5*	0	gi 15230905 unknown protein 3e-14	6
GACAAGGGGT	37**	10	No significant similarity found	6
GATGATGAGA	10**	1	No significant similarity found	6
TTCTTGTTTT	5*	0	No significant similarity found	6
TTATGGTTTC	14**	4	No significant similarity found	6
TTGGGTTTGG	20*	9	No significant similarity found	6
GGATAACATC	85*	73	No significant similarity found	6
AAATCTTGAT	4*	0	No significant similarity found	6
ACGGAGCTTT	4*	0	No significant similarity found	6
GTAGTTCTAT	23**	10	No significant similarity found	6
TTGATAATTT	4*	0	No significant similarity found	6
ATATTCCTGA	19*	11	No significant similarity found	6

* $P \leq 0.05$, ** $P \leq 0.01$.

Table S2. List of the annotations for the 70 differentially expressed genes from the resistant library

Using the Z test we were able to identify 232 tags that were preferentially expressed in the library made from the resistant individuals. This table is a list of the 70 differentially expressed tags that we were able to annotate in the library made from the resistant individuals. The information given includes the tag sequence, the respective tag count in each library, the putative identification and the functional category (S - susceptible and R - resistant library)

Tag	S	R	Putative identification	Category
TGATGGGATA	2	10*	gi 30690243 ATP binding/nucleotide kinase/phosphotransferase 3e-22	1
AGACGGAATA	10	30*	gi 92873063 Adenosine kinase 7e-19	1
CTTTTGCCAA	0	5*	gi 21327029 glutamate decarboxylase 2e-32	1
AACCATTTTG	1	15**	gi 62321216 ketol-acid reductoisomerase 4e-58	1
TGTCCCGGCA	2	13*	gi 19352190 Acyl-CoA-binding protein 2e-33	1
TTGAGACTTG	1	10*	gi 3914361 phospholipase D alpha 1 3e-20	1
GTCTAGTTTT	47	117**	gi 5608497 galactinol synthase GolS-1 5e-65	1
CCTGACCCCG	13	35*	gi 5608497 galactinol synthase GolS-1 5e-65	1
TGACTAACCT	0	7*	gi 80973756 sucrose synthase 8e-54	1
TCGGTCTTAT	4	16*	gi 37729658 UDP-glucose pyrophosphorylase 9e-81	1
GTGAAGTCAG	1	8*	gi 6136119 UDP-glucose 6-dehydrogenase 1e-95	1
AATTTCCAG	1	88**	gi 10764491 allergenic isoflavone reductase 1e-14	1
TACAACCCCC	2	11*	gi 76559896 isoflavone reductase-like protein 9e-06	1
ATTTGCTGTT	0	11**	gi 21553614 blue copper protein, putative 9e-35	1
GTCATCTCAT	0	8*	gi 2493318 blue copper protein precursor 2e-39	1
TACGTTGTAA	0	5*	gi 16648905 NADH-cytochrome b5 reductase 2e-08	1
GTTATGAAGT	15	84**	gi 3694984 metallothionein-1-like protein 2e-28	2
CACATCCCTT	113	273**	gi 2497881 metallothionein-like protein 1 3e-22	2
CAATACTGAG	0	5*	gi 9755608 putative phytochelatin synthetase 4e-86	2
ATTCCTTGAC	0	10**	gi 9755608 putative phytochelatin synthetase 1e-33	2
TGCTGATCTT	6	26**	gi 90818816 catalase 3e-08	2
TGTGCTGTAG	0	13**	gi 3482933 similar to cdc2 protein kinases 5e-06	2
GAATATCCTG	3	14*	Gi 5869758 AT-LS1 product 6e-50	2
AGGTTTCTTG	0	7*	gi 152355 dopamine beta-monooxygenase 3e-53	2
AGATAAAAAA	0	5*	gi 15234016 phospholipase C 5e-52	2
AGGAGGTTCA	0	5*	gi 87240494 heat shock protein Hsp20 3e-59	2
CTTCCTAGTT	0	5*	gi 73919361 peptidyl-prolyl isomerase F 6e-31	2
TGTACATTCG	0	5*	gi 46805153 serine/threonine-protein kinase 5e-09	2
GGATGATCAG	0	5*	gi 89212808 aquaporin 1 9e-55	3
CGTAACCGCA	0	5*	gi 89475524 ADP-ribosylation factor-like protein 8e-26	3
GGGTTAACTG	7	23*	gi 7643794 ADP-ribosylation factor 1e-83	3
ATCTCTATTG	0	13**	gi 56481443 alpha tubulin 1 3e-81	4
AATCGCTATC	5	19*	gi 110742192 tubulin alpha-2/alpha-4 chain 2e-98	4
ACCAGGGCCG	0	8*	gi 47717929 fasciclin-like AGP 13 4e-26	4
GAATCAAAAT	0	8*	gi 67003907 cellulose synthase 1 2e-46	4
GTCTCCCACT	0	7*	gi 37051096 class1 chitinase 4e-45	4
GTTCCGCCGCT	0	9**	gi 78191442 S-adenosyl methionine synthase-like 7e-84	4
GTTTGCCGCT	0	8*	gi 50882499 S-adenosyl-L-methionine synthetase 1 1e-31	4
GTGATGCTGG	0	6*	gi 3024126 S-adenosylmethionine synthetase 2e-97	4
AACCTGAAAG	0	11**	gi 30688445 p-coumarate 3-hydroxylase 1e-30	4
AACCTAGAAA	3	15*	gi 3023419 caffeoyl-CoA O-methyltransferase 5e-140	4
GCCATCATAT	0	5*	gi 116486991 hydroxycinnamoyl transferase 5e-61	4
GTTCTTGAT	0	5*	gi 1169009 caffeic acid 3-O-methyltransferase 0.0	4
TCCAAAAAAA	1	8*	gi 6694693 dirigent protein 2e-30	4
CATCGTTTGG	5	17*	gi 33590374 40S ribosomal protein S25 3e-08	4
TACTGTTGTT	1	9*	gi 29468339 SGT1 5e-77	5
GCCAACCACT	0	5*	gi 117607067 ubiquitin extension protein 3e-69	5
TCTGTGTTGT	2	10*	gi 18423494 ubiquitin conjugating enzyme 4e-82	5
CTGCACCCAT	0	7*	gi 92890123 hypothetical protein 2e-31	6
GCGTTGCAAA	50	127**	No significant similarity found	6
GTAAAAAAA	2	18**	No significant similarity found	6
GTGTCTCCAG	1	15**	No significant similarity found	6
GAGTTGTCGT	4	19**	No significant similarity found	6
AGTAGTGCCA	2	13*	No significant similarity found	6
ATACACGCGA	0	7*	No significant similarity found	6
GAGGAGAGAG	0	7*	No significant similarity found	6

Table S2. (continued)

Tag	S	R	Putative identification	Category
TACCTCAGAC	0	7*	No significant similarity found	6
GTTTCTTGTA	0	6*	No significant similarity found	6
TGGAAGCGTA	0	6*	No significant similarity found	6
TTTTCCCCT	1	9*	No significant similarity found	6
ATGCAATACA	2	11*	No significant similarity found	6
TTGCTCGGAG	15	36*	No significant similarity found	6
GCGCAGACAC	0	5*	No significant similarity found	6
TTGAGGGCGA	0	5*	No significant similarity found	6
CATTCAGTCT	1	8*	No significant similarity found	6
CGAAAAAAAAA	1	8*	No significant similarity found	6
TTCCTCTTTT	1	8*	No significant similarity found	6
TGCTCTGCAG	9	24*	No significant similarity found	6
CCATTGCCGG	2	10*	No significant similarity found	6
TCTCAAAAAA	2	10*	No significant similarity found	6

* $P \leq 0.05$, ** $P \leq 0.01$.