

Appendix Known function genes induced by *Apolygus lucorum* in CCRI23 and CCRI41

Function	Varieties	Expression profiles	Accession No.	Gene annotation	E-value	Similarity
Transcription						
H109	CCRI23	upregulated	gi 87162496 gb ABD28291.1	catalytic region ribonuclease h	1.00E-57	73.25%
H130	CCRI23	upregulated	gi 110289286 gb AAP54315.2	retrotransposon ty1-copia subclass	1.00E-21	79.15%
H270	CCRI23	upregulated	gi 88595483 gb ABD43048.1	reverse transcriptase	1.00E-39	84.70%
H78	CCRI23	upregulated	gi 110289286 gb AAP54315.2	retrotransposon ty1-copia subclass	1.00E-64	72.30%
H89	CCRI23	upregulated	gi 224113759 ref XP_002332503.1	crs2-associated factor 1	1.00E-16	57.88%
H95	CCRI23	upregulated	gi 87162496 gb ABD28291.1	catalytic region ribonuclease h	1.00E-24	52.75%
H160	CCRI23	upregulated	gi 119368557 ref YP_913244.1	rf1 protein	1.00E-90	87.35%
Contig16	CCRI23	upregulated	gi 224131274 ref XP_002328498.1	tha4 protein	1.00E-45	66.30%
H148	CCRI23	upregulated	gi 87162496 gb ABD28291.1	protein binding	1.00E-44	84.10%
F31	CCRI23	downregulated	gi 255551787 ref XP_002516939.1	60s ribosomal protein	1E-27	97.15%
F16	CCRI23	downregulated	gi 145408590 ref YP_001152214.1	ORF124 [Pinus koraiensis]	1E-25	81.93%
F64	CCRI23	downregulated	gi 148807187 gb ABR13303.1	nucleolysin tia	1E-43	95.40%
F101	CCRI41	upregulated	gi 255541166 ref XP_002511647.1	DNA binding protein, putative [Ricinus	1.00E-24	52.00%

				communis]		
F203	CCRI41	upregulated	gi 1173209 sp P46293.1 RS16_GOSH 	40S ribosomal protein S16 RS16 protein, 40S subunit [Gossypium hirsutum]	5.00E-26	100.00%
F225	CCRI41	upregulated	gi 224060153 ref XP_002300063.1	predicted protein [Populus trichocarpa]	2.00E-31	75.00%
F227	CCRI41	upregulated	gi 255586077 ref XP_002533703.1	40S ribosomal protein S7, putative [Ricinus communis]	7.00E-31	95.00%
F248	CCRI41	upregulated	gi 91208941 ref YP_538976.1	ribosomal protein L2 [Gossypium hirsutum]	2.00E-64	100.00%
S_10	CCRI41	upregulated	gi 255557935 ref XP_002519996.1	60S ribosomal protein L13, putative [Ricinus communis]	1.00E-56	94.00%
S_15	CCRI41	upregulated	gi 3885515 gb AAC77928.1	similar to ribosomal protein S26 [Medicago sativa]	1.00E-07	62.00%
S_58	CCRI41	upregulated	gi 260766929 gb ACX50406.1	histone H4 [Eriobotrya japonica]	2.00E-38	100.00%
S_75	CCRI41	upregulated	gi 4589726 dbj BAA76883.1	DnaJ homolog protein [Salix gilgiana] DnaJ homolog protein [Salix gilgiana]	3.00E-73	66.00%
Signal transduction						
H67	CCRI23	upregulated	gi 224107351 ref XP_002314455.1	amp-activated protein gamma regulatory	1.00E-17	81.80%
S_36	CCRI41	upregulated	gi 133902306 gb ABO41836.1	alcohol dehydrogenase A [Gossypium arboreum]	2.00E-59	100.00%
S_45	CCRI41	upregulated	gi 224126465 ref XP_002329561.1	ADP-ribosylation factor GTPase-activating protein AGD8	2.00E-62	83.00%
S_72	CCRI41		gi 224134094 ref XP_002327754.1	calcium dependent protein kinase 18 [Populus	#####	86.00%

trichocarpa]

**Resilience
related**

H252	CCRI23	upregulated	gi 34761728 gb AAQ82037.1	gag pol polyprotein	1.00E-20	58.70%
H310	CCRI23	upregulated	gi 270251062 emb CBI34436.1	multidrug resistance protein abc transporter family	1.00E-11	56.00%
H55	CCRI23	upregulated	gi 56744299 gb AAW28578.1	gag-pol polyprotein	1.00E-09	66.25%
H74	CCRI23	upregulated	gi 110742626 dbj BAE99225.1	ubiquitin ligase protein	1.00E-20	90.55%
H110	CCRI23	upregulated	gi 224060835 ref XP_002300276.1	myosin heavy chain-related	1.00E-10	65.54%
Contig2	CCRI23	downregulated	gi 211906498 gb ACJ11742.1	heat shock protein 70	1E-119	93.70%
F75	CCRI23	downregulated	gi 293332291 ref NP_001170482.1	ascorbate peroxidase	1E-17	95.00%
F63	CCRI23	downregulated	gi 192910730 gb ACF06473.1	light-inducible protein atls1	1E-27	93.95%
F218	CCRI41	upregulated	gi 73761689 gb AAZ83344.1	ACC oxidase 3 [Gossypium hirsutum]	4.00E-64	82.00%
F220	CCRI41	upregulated	gi 255555963 ref XP_002519016.1	Polyphenol oxidase, chloroplast precursor, putative [Ricinus communis]	9.00E-10	42.00%
F244	CCRI41	upregulated	gi 211906498 gb ACJ11742.1	heat shock protein 70 [Gossypium hirsutum]	7.00E-31	98.00%
S_17	CCRI41	upregulated	gi 270233745 emb CBI22354.1	Ubiquitin	1.00E-80	92.00%
S_55	CCRI41	upregulated	gi 211906476 gb ACJ11731.1	ascorbate peroxidase [Gossypium hirsutum]	#####	92.00%

S_80	CCRI41	upregulated	gi 186886510 gb ACC93637.1	chloroplast Cu/Zn superoxide dismutase [Gossypium hirsutum]	2.00E-37	100.00%
S_90	CCRI41	upregulated	gi 197209780 dbj BAG68929.1	cytochrome P450 88D6 [Glycyrrhiza uralensis]	2.00E-53	45.00%
F236	CCRI41	upregulated	gi 225463388 ref XP_002273366.1	cold acclimation protein cor413-tm1	2.00E-60	75.00%
S_14	CCRI41	upregulated	gi 62910995 gb AAAY21210.1	ultraviolet-b-repressible protein	3.00E-27	60.00%
F234	CCRI41	upregulated	gi 255574328 ref XP_002528078.1	Myosin heavy chain, putative [Ricinus communis]	7.00E-30	48.00%
S_92	CCRI41	upregulated	gi 192912974 gb ACF06595.1	translationally controlled tumor protein [Elaeis guineensis]	7.00E-74	84.00%
Respiratory chain						
Contig15	CCRI23	upregulated	gi 164685380 gb ABY66636.1	cytochrome oxidase subunit 1	1.00E-85	97.25%
S_64	CCRI41	upregulated	gi 224056767 ref XP_002299013.1	cox viia-like protein	2.00E-26	84.00%
Contig1	CCRI41	upregulated	gi 259156811 gb ACV96672.1	cytochrome c oxidase subunit 1 [Cucurbita pepo]	3.00E-68	96.00%
F233	CCRI41	upregulated				
Energy synthesis						
H156	CCRI23	upregulated	gi 50404475 gb AAT76902.1	asparagine synthase-related protein	1.00E-09	81.57%
H5	CCRI23	upregulated	gi 147777557 emb CAN69310.1	transferring glycosyl	1.00E-23	65.90%

Energy production

Contig3	CCRI23	downregulated	gi 57013900 ref YP_173374.1	uncharacterized mitochondrial protein g00030	1E-40	97.00%
F52	CCRI23	downregulated	gi 255541374 ref XP_002511751.1	atp binding	1E-41	89.65%
F230	CCRI41	upregulated	gi 224109616 ref XP_002315256.1	beta-ketoacyl-coa synthase family protein [Populus trichocarpa]	3.00E-48	73.00%
F245	CCRI41	upregulated	gi 14718252 gb AAK72864.1	ATP synthase beta subunit [Retanilla trinervia]	2.00E-75	99.00%
F249	CCRI41	upregulated	gi 224114948 ref XP_002316900.1	3-deoxy-manno-octulosonate cytidyltransferase	5.00E-61	91.00%
S_51	CCRI41	upregulated	gi 1352821 sp P31333.2 RBS_GOSHI	Ribulose biphosphate carboxylase small chain, chloroplastic;	1.00E-29	93.00%
S_77	CCRI41	upregulated	gi 270252578 emb CBI19189.1	Phospho-2-dehydro-3-deoxyheptonate aldolase 1, chloroplastic	#####	97.00%
S_7	CCRI41	upregulated	gi 171190268 gb ACB42440.1	aquaporin PIP2;3 [Gossypium hirsutum]	3.00E-93	99.00%
Contig3	CCRI41	upregulated	gi 1352821 sp P31333.2 RBS_GOSHI	Ribulose biphosphate carboxylase small chain, chloroplastic	8.00E-32	98.00%
Contig4	CCRI41	upregulated	gi 91208908 ref YP_538941.1	ATP synthase CF1 epsilon subunit [Gossypium hirsutum]	9.00E-56	90.00%
S_5	CCRI41	upregulated	gi 255555241 ref XP_002518657.1	progesterone 5-beta-reductase	1.00E-55	71.00%
Contig4	CCRI41	downregulated	gi 57013900 ref YP_173374.1	uncharacterized mitochondrial protein g00030	1.00E-40	94.50%
Contig1	CCRI41	downregulated	gi 7012724 gb AAF35186.1 AF19586 5_1	lipid transfer protein	1.00E-59	90.60%

F75	CCRI41	downregulated	gi 255588941 ref XP_002534772.1	atpase subunit 9	1.00E-15	97.40%
F67	CCRI41	downregulated	gi 255550848 ref XP_002516472.1	vacuolar-processing enzyme	1.00E-79	87.70%
F78	CCRI41	downregulated	gi 270243350 emb CBI30290.1	plastid division protein	1.00E-51	85.50%
Photosynthesis						
F104	CCRI41	upregulated	gi 91208930 ref YP_538965.1	photosystem II protein H [Gossypium hirsutum]	1.00E-33	100.00%
F205	CCRI41	upregulated	gi 225462227 ref XP_002271791.1	Photosystem II 10 kDa polypeptide, chloroplastic	7.00E-31	82.00%
F214	CCRI41	upregulated	gi 226358409 gb ACO51067.1	chloroplast chlorophyll A-B binding protein [Gossypium hirsutum]	6.00E-75	99.00%
S_13	CCRI41	upregulated	gi 255567170 ref XP_002524566.1	chlorophyll A/B binding protein, putative [Ricinus communis]	3.00E-96	89.00%
S_46	CCRI41	upregulated	gi 255544369 ref XP_002513246.1	Cytochrome b6-f complex iron-sulfur subunit, chloroplast precursor	3.00E-62	95.00%
Contig6	CCRI41	upregulated	gi 290488476 gb ADD30622.1	photosystem II CP47 chlorophyll apoprotein [Lonocera japonica]	3.00E-65	100.00%
Contig8	CCRI41	upregulated	gi 290489412 gb ADD31090.1	cytochrome b6 protein [Euonymus americanus]	2.00E-85	94.00%
Contig3	CCRI41	downregulated	gi 53854435 gb AAU95599.1	photosystem ii cp43 chlorophyll apoprotein	1.00E-31	92.35%
F71	CCRI41	downregulated	gi 1345698 sp P27518.2 CB21_GOSH 	light-harvesting complex ii protein lhcb2	#####	97.80%
F77	CCRI41	downregulated	gi 91208930 ref YP_538965.1	photosystem ii phosphoprotein	1.00E-33	97.35%

Amino acids synthesis

F215	CCRI41	upregulated	gi 225424228 ref XP_002280671.1	hypothetical protein [Vitis vinifera]	4.00E-13	68.00%
S_63	CCRI41	upregulated	gi 224075958 ref XP_002304847.1	Pyruvate kinase, cytosolic isozyme	8.00E-46	83.00%
Contig2	CCRI41	upregulated	gi 57013942 ref YP_173415.1	Methionine aminopeptidase 1C, chloroplastic/mitochondrial	3.00E-34	96.00%
F231	CCRI41	upregulated	gi 255573020 ref XP_002527440.1	cys-containing conserved protein	6.00E-19	71.00%
S_86	CCRI41	upregulated	gi 225432654 ref XP_002278361.1	with no lysine kinase	8.00E-25	54.00%

Development related

F246	CCRI41	upregulated	gi 1170748 sp P46522.1 LEA5D_GOS HI	Late embryogenesis abundant protein Lea5-D late embryogenesis-abundant protein [Gossypium hirsutum]	1.00E-50	99.00%
Contig5	CCRI41	upregulated	gi 225462164 ref XP_002266780.1	similar to elongation factor 2 [Vitis vinifera]	9.00E-73	92.00%
F229	CCRI41	upregulated	gi 255585293 ref XP_002533345.1	Late embryogenesis abundant protein Lea14-A	4.00E-50	87.00%
F70	CCRI41	downregulated	gi 145334271 ref NP_001078516.1	histone h3	1.00E-24	99.80%

Cell wall synthesis

F247	CCRI41	upregulated	gi 183181280 gb ACC44799.1	polygalacturonase [Lygus hesperus]	6.00E-68	78.00%
S_39	CCRI41	upregulated	gi 54036488 sp Q6VAF5.1 TBB7_GOS HI	Beta-7-tubulin beta-tubulin 7 [Gossypium hirsutum]	7.00E-45	100.00%
S_6	CCRI41	upregulated	gi 4205741 gb AAD11255.1	class I chitinase [Gossypium hirsutum]	#####	91.00%

Protein inhibitor

S_40	CCRI41	upregulated	gi 55139090 gb AAV41233.1	21 kDa trypsin inhibitor [Theobroma bicolor]	6.00E-48	56.00%
F97	CCRI41	upregulated	gi 255542772 ref XP_002512449.1	auxin-repressed protein	7.00E-34	89.00%
