



Supplemental files 1:Figure S1

Subcellular localization of GFP alone or GhENODL1-GFP fusion on onion epidermis transiently transformed by Particle bombardment. The green fluorescence were monitored using a confocal laser scanning microscope. Bars = 200 μ m.

ATIG45063.1 VGDS DG. WTAKD. HLYYHWTEDEKE. I HVGDSL I FEYDH. NLNDVTQVS GGLEYEF DSS FPKAVYNT. GHDVTFTEPCSYFYI TS NH. TQTS GQRIGVFVV
 AT3G53330.1 VGGS RG. WS. GKTNS WAERKE. FHVGDSL I FQYHQ. NVNDVTQLS DALKYES NSS S PKAVYNT. GHDVTF LSS MKS HVRS LHHH. EARPVNGHDLAI T
 AT4G01380.1 PSL S. TI ETWFSI KLV. FHVGDSL I FEHNH. NLNDVTQVS GALEYEF DSS S PKAVYNT. GHDI S. VCGS.
 AtPLC1 VGDS. GI WTFN. AVGWPKGKH. FRAGDVL VFNYP. RNHN VVKVD. SGS YNN KTP TGA KPYTS. GKDR I TLS K. QGNFFI CNFP. NHCES. DVI AVT
 AtSC1 VGNT. KGWTM I G. G. DYEAWASSRV. FQVGD L V FAYNK. DYHDVTEVT. HNDFEM EESS KPLRRYKT. GS DSI S LTKPGLQHFI CGVP. GHCKK. GOKLQI H
 AtSC2 VGDS. DGWTI AS. V. NYETWASTI T. FQVGD L V FAYNK. DYHDVTEVT. HNDFEM EESS KPLRRYKT. GS DI VI LTKPGLQHFI CGFP. GHCDV. GOKLQI H
 AtSC3 VGDD. TEWTRPMDP. EFTYT WATGKT. FRVGDELEFDFAA. GRHDVAVVS. EAAFE N EKEKPI SHMTVP. PVKI MLNTTGPQYFI CTVG. DHC RF. GOKLSI T
 AtSC4 VGDS. AGWTI ANV. DYKL VASTKT. FHI GDTVLFEYNP. QFN VNVRYT. HPVYRS CNTS KPI STFTT. GNDSI TLTNHGHFFHF CGVP. GHCLA. GOKLDLH
 AtUC1 VN. WSLGT. DYTPLT TGT. FSVGDTI VFNYG. AGHTVDEVS. ENDYKS I TLGNSI TS DSS. GTTI I ALTTTGPYFI CGI P. GHCAA. GOKLAVT
 AtUC2 VE. WSLGK. DYSSLATGKS. FAVGDTI VFNYG. AGHTVDEVS. ES DYKS I TLGNAI SS DSS. GTTS I ALKTPGPHYFI CGI P. GHCTG. GOKLSVI
 AtUC3 I GGP. SGWTVG. ASLRTWAAGQT. FAVGDN L VFSYPA. AFHDVVEVT. KPEFDS QAVKPI TFAN. GNSLVPLTTPGKRYFI CGMP. GHCS Q. GOKLEVN
 AtUC4 I E. WTTGV. DYS GWATGKT. FRVGDI LEFKYK. SSHTVDVVD. KAGYDG DAS S TENHS D. GDTKI DLKT VGI NYFI CSTP. GHCR TNGG KLAVN
 AtUC5 I GGS. QGWEQS. VDFDS VSS DQS. FKVGDQI VFKYS. ELIS VVELGS ETAYKS I DLGTS VNS LSS. GNDVVKLS KTGT RYFA CGTV. GHCEQ. GOKI KVN
 AtUC6 VGDN. DGWTI GV. EYTS WVS EKT. FRVGDTLEFKYK. PSIS VAVVN. KADYDG ETS RPTQS FSD. GDTKI DLT KVGA I HFL CLTP. GHCS L. GOKLAVQ
 AtUC7 VGDI. SGWTS NL. DYT VWTGKT. FRVGDTLEFVYG. LSIS VSVVD. KAGYDN DSS GATQNFAD. GDTKI DLT VGT M HFL CPTF. GHCKN. GOKLAVP
 AtUC8 VGDS. SGWDI SS. DLES WTS GKR. FSPGDVL M FQYS. STIS VYEVA. KDNYQN NTTDAI RTFTN. GNTTVALS KPGNRFV CGNR. LHCF A. GOKRLVN
 AtENODL1 VGGN. GAWVTNP. QENYNTWAERNR. FQVNDLSYFYKAK. GS DSVQVN. KADFDG NVRNPI KNFEN. GESVVT LDRS GAFYFI SGNQ. DHCKK. GOKLI VV
 AtENODL2 VGGS. GAWVTNP. PENYES VSGKNR. FLVHDTL FSYKAK. GADS VLEV N. KADYDA NTKNPI KRVD. GDS EI S LDRYGP FYFI SGNE. DNCKK. GOKLNVV
 AtENODL3 VGKK. DGWVTP. SEDYS HVS HRNR. FQVNDTLHFYKAK. GKDS VLEV T. EQEYNT NTTHPLTS LSD. GDS LFLLS HS GS YFYFI SGNS. QNCLK. GOKLAVK
 AtENODL4 VGGK. DGWVLT. SEDYS HVS HRNR. FQVNDTLFVYK. GKDS VLEV S. EKEYNT NTTHPLTS LSD. GDS LFLLS RS DP FFFVS GS. GS CLK. GOKLAVT
 AtENODL5 VGGENGW I VPKS KTLGDAFNQWAS DNR. FKVGDTLRFKYK. KDS VLVVS. EEEYKK KATKPLQLYSNN. EDTVFK LDRP GLFYFI SGVS. GHCEK. GOKM I VK
 AtENODL6 AGGENGW I PQSSNQSDI FNQWAS KNR. FKVGDTLRFKYK. KDS VLVVT. EDEYKK QTTKPELYS NH. DDTVFK LDRP GLFYFI SGVS. GHCEQ. GOKM I K
 AtENODL7 VGDEF GMRVPLQND. SAVYS HWASS NR. FHI GDSLS FYVD. KDS VMEVD. KWGYH GDS DPI TAFDN. GNS TFDLDRP GLFYFI SGSN. GHCTS. GOKLI VE
 AtENODL8 VG. DLDAWGI PI D. AKVYS KMPKS HS. FKI GDS LFLFYPP. SEDS LI QVT. PSNFKS NTKDPI LYND. GNS LFLNTQNGTLYFIS ANP. GHCTK. YOKLLVS
 AtENODL9 VGGK. TGWVTPS G. SQVYS QWAEQS R. FQI GDS LFLFYQS. NQDS VLQVT. RDAYDS NTDS PTKAFAD. GKTS VTLNHS GPYFYFI SGNK. DNCKK. NEKL VVI
 AtENODL10 VGGKS NTWKAPES R. DETLNQWAS GRTR. FKI GDS LFLVYKNA. ENDS VLQVR. QTDYER DRS EPI RGYKD. GHNTI ELKRS GPYFYFI SGEE. GHCR. GEKL RVV
 AtENODL11 VGGS LDWVKPES P. NLSLNHWAS VR. FQVGDALLFKYDS. KI DS VLQVT. KENYEK NTQKPLEEHKD. GYTTVK L DVS GPYFYFI SGAPS. GNAK. GEKVTVV
 AtENODL12 VGGS VGS WKVPDS P. NNTLNHWAE NN R. FKVGDFI VWKYDN. KVDS VLQVT. KEDYES NTANPLKQYND. GNTKVALDKS GPYFYFI SGAP. GNAK. GEKI TLV
 AtENODL13 VGGKTSS WKI PSSP. SES LNKWAS LR. FRVGDTLVWYDE. EKDS VLQVT. KDAYI NNTTNPAA NYSN. GDTKVKLERS GPYFYFI SGSK. SNQVE. GEKLH I V
 AtENODL14 VGGKS GDWKI PPSS. SYS FTEWAQKAR. FKVGDFI VFRYES. GKDS VLEV T. KEAYNS NTNNPLANYTD. GETKVKLDRS GPYFYFI SGAN. GHCEK. GOKLSLV
 AtENODL15 VGGKS GDWKI PPSS. SFS FNEWAQKAR. FKVGDFI VFKEYA. GKDS VLQVT. REAYEK NTTS PKAS YTD. GNTKVKLDAQGPYFYFI SGTE. GHCKK. GOKLRLV
 AtENODL16 VGDN. KFWNPNI. NYTI WAQDKH. FYLDWLYFYVYER. NQY NVI EVN. ETNYI S CNPNPI ANWS RGA. GRDLVHLNVTRHYLLI SNG. GCY G. GOKLAVL
 AtENODL17 VGDN. KFWNPNI. NYTI WAQDKH. FYLDWLYFYVYER. NQY NVI EVN. ETNYI S CNPNPI ANWS RGA. GRDI VTLNQTKHYLLDGGK. GCY G. GOKLSVK
 AtENODL18 VGESTGWFDI QERP. SANYQWADS KS. FSLGDFLI FNTD. SNIS VVQTYDFKTYKD. DYDNNE NNDTTEWS AANPS ATS PVPVSI SVPLVKEGS NYFFS GNYDGEQCK. FGQHFMI NV
 AtENODL19 VGDK. KFWNPNI. NYTLWAQGKH. FYVGDWLYFYVYR. DQNI LEVN. KADYEK I SNRPI RNWTRGA. GRDI VPLYETRRYLLDGRG. GCY G. GOKLDVL
 AtENODL20 GGGR. YTWS DV. NFS DWANHOR. FYS GDWLYFGFNR. TRNI LQVN. KSS YEQ VDNVYI FNI TR. G. GRDV FQLLEPKPYFYFI CGRG. YCLK. GOKLAI T
 AtENODL21 LN. WVP PANS. SES FNDWAS NKR. FQVGDI I QFKYK. KDS VMQVT. KES YKQ NSS HPRFYSNT. GKTRFMDHS VPYFYFI SGTS. GHCEK. GOKM I VE
 AtENODL22 VGGD. DGWDVPVP. MDTWARGKT. FYAGDI LEFKYDY. QRFNLI VVN. RTGYET EAVNGAI EYSS. GDDKI QLN. YGNYFI GTYTP. EDCIT. GLKVAI K
 Ghir_D06G001340.1 VGGS. ENWRYG. YNYTEWAANTAPFYHDTLVFKYENSTPIS VYLLPNLWS YSTDFS KAKLLANPTQVKG. DGFEFVLNQWRVYFASGEA. NDCKEG. GOKM I V

I

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II

III

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IV

Supplemental files 2:Figure S2

Multiple Alignment of the Amino Acid Sequences of the PCNL Domains of the *A. thaliana* Phytocyanin Family and target gene *GhENODL1*(Ghir_D06G001340.1).The Cys residues involved in the disulfide linkage are indicated in red and the amino acid residues (His, Cys, His and Gln/Met) involved in Cu binding are indicated in I II III IV respectively.

Supplemental files 3: Table S1

PCs Identified in *G. hirsutum* Genomes

Name	Gene ID	Length (aa)	MW (kDa)	Isoelectric Point	Charge
GhPC1	Ghir_D06G011310	107	11.763	10.232	7
GhPC2	Ghir_A06G007340	127	13.789	5.518	-2
GhPC3	Ghir_D11G003980	127	14.585	6.33	-0.5
GhPC4	Ghir_D05G005610	128	14.513	10.255	13
GhPC5	Ghir_A11G004040	137	15.901	7.546	3
GhPC6	Ghir_D06G001340	139	15.707	7.403	1
GhPC7	Ghir_A06G001480	139	15.717	7.243	0.5
GhPC8	Ghir_A05G010410	154	17.903	9.444	6.5
GhPC9	Ghir_A05G006200	159	17.165	9.592	6.5
GhPC10	Ghir_D07G003740	161	17.383	9.387	5
GhPC11	Ghir_A05G013540	167	18.494	6.778	1
GhPC12	Ghir_A13G003590	167	18.904	10.573	19
GhPC13	Ghir_D11G007700	167	18.685	9.529	7
GhPC14	Ghir_D04G004910	170	19.555	6.783	0.5
GhPC15	Ghir_A05G038140	171	19.764	6.941	1
GhPC16	Ghir_A05G012210	172	18.63	8.313	3.5
GhPC17	Ghir_D05G011920	173	18.682	8.313	3.5
GhPC18	Ghir_A11G007760	175	19.405	9.265	6
GhPC19	Ghir_D11G007710	175	19.359	9.299	6
GhPC20	Ghir_D05G006280	176	18.939	10.309	11.5
GhPC21	Ghir_A07G003720	178	19.011	9.605	6
GhPC22	Ghir_D05G013280	180	19.862	6.618	0.5
GhPC23	Ghir_A13G003640	184	21.078	9.286	8
GhPC24	Ghir_A05G005530	185	20.409	10.016	10.5
GhPC25	Ghir_D13G025800	188	21.473	9.039	7
GhPC26	Ghir_A13G013740	194	21.579	6.673	0.5
GhPC27	Ghir_D13G014420	194	21.634	6.344	-0.5
GhPC28	Ghir_A02G010500	196	21.218	6.739	0.5
GhPC29	Ghir_D03G009570	196	21.18	8.19	3.5
GhPC30	Ghir_A13G014720	217	23.245	4.915	-3.5
GhPC31	Ghir_D13G015400	217	23.329	4.637	-5.5
GhPC32	Ghir_D07G015760	229	24.983	6.657	0.5
GhPC33	Ghir_A07G015510	231	24.864	4.829	-4.5
GhPC34	Ghir_D05G007560	234	25.916	4.128	-14.5
GhPC35	Ghir_D05G037420	242	26.017	5.545	-3
GhPC36	Ghir_A04G002000	243	26.253	5.2	-4
GhPC37	Ghir_A03G017320	268	29.84	6.492	0

GhPC38	Ghir_D02G018560	269	30.009	7.361	2.5
GhPC39	Ghir_A13G015310	338	35.113	9.043	12.5
GhPC40	Ghir_D13G016040	338	35.2	9.043	12.5
GhPC41	Ghir_A04G003340	832	88.307	7.018	17.5
GhPC42	Ghir_D04G015900	115	12.455	7.439	1.5
GhPC43	Ghir_A06G003430	127	13.698	4.426	-4
GhPC44	Ghir_D06G003450	141	15.577	4.684	-3
GhPC45	Ghir_A09G026390	158	17.061	6.488	0
GhPC46	Ghir_A05G017860	161	17.24	4.607	-4.5
GhPC47	Ghir_A04G011560	165	17.192	8.226	4.5
GhPC48	Ghir_A07G024480	167	18.025	7.383	1.5
GhPC49	Ghir_D07G024530	167	17.953	7.383	1.5
GhPC50	Ghir_D05G017860	171	18.184	4.938	-4
GhPC51	Ghir_D05G027080	171	17.992	6.214	-0.5
GhPC52	Ghir_A05G027060	172	18.222	7.857	2.5
GhPC53	Ghir_A06G003420	175	18.017	4.992	-2.5
GhPC54	Ghir_D06G003440	175	17.999	4.992	-2.5
GhPC55	Ghir_A08G006290	177	17.806	4.305	-4
GhPC56	Ghir_D08G006420	177	17.782	4.305	-4
GhPC57	Ghir_A06G016540	179	19.466	4.763	-4.5
GhPC58	Ghir_D03G011670	184	19.68	6.233	-0.5
GhPC59	Ghir_D06G017430	184	20.136	4.48	-7
GhPC60	Ghir_A03G007100	187	19.968	6.228	-0.5
GhPC61	Ghir_D05G022710	188	19.292	6.746	0.5
GhPC62	Ghir_A05G022790	192	19.586	6.738	0.5
GhPC63	Ghir_A12G014590	204	20.971	4.303	-7
GhPC64	Ghir_D12G014730	209	21.427	4.181	-8
GhPC65	Ghir_A13G005810	216	22.805	4.161	-8
GhPC66	Ghir_D13G006500	258	27.022	3.894	-15
GhPC67	Ghir_A02G007150	82	8.94	9.856	7
GhPC68	Ghir_D05G024440	94	9.932	9	4
GhPC69	Ghir_A09G009400	98	10.681	4.162	-6.5
GhPC70	Ghir_A09G009410	109	11.846	6	-1
GhPC71	Ghir_D09G009120	109	11.863	5	-2
GhPC72	Ghir_D09G009110	119	13.016	5	-5
GhPC73	Ghir_D01G018560	123	13.098	10.446	14.5
GhPC74	Ghir_A01G017010	123	13.257	10.679	16.5
GhPC75	Ghir_D04G018430	126	13.281	10	12
GhPC76	Ghir_A04G013970	127	13.255	10.02	10.5
GhPC77	Ghir_A05G024630	127	13.346	9.605	8
GhPC78	Ghir_D02G007560	339	36.175	9.082	12
GhPC79	Ghir_A08G007230	157	17.562	9	8
GhPC80	Ghir_A11G025230	161	17.416	9	5
GhPC81	Ghir_A11G025240	162	17.378	8	3

GhPC82	Ghir_D11G025370	162	17.566	8.052	2.5
GhPC83	Ghir_D11G025380	162	17.52	8.052	2.5
GhPC84	Ghir_A01G016200	164	18.134	5	-6
GhPC85	Ghir_A12G023640	166	17.721	7	2
GhPC86	Ghir_D12G023630	166	17.721	7.383	1.5
GhPC87	Ghir_A05G001590	167	17.827	5	-4
GhPC88	Ghir_D06G005780	167	17.876	5.07	-3
GhPC89	Ghir_D05G001780	169	17.973	4.392	-5.5
GhPC90	Ghir_A08G018330	170	18.606	7	2
GhPC91	Ghir_D06G009280	170	18.164	9.379	8
GhPC92	Ghir_D01G017730	172	18.94	5	-6
GhPC93	Ghir_D08G007280	176	19.406	8.097	5
GhPC94	Ghir_D05G001760	180	19.072	7.193	2.5
GhPC95	Ghir_D11G013060	187	19.621	8.63	6
GhPC96	Ghir_A09G022890	189	19.813	9	8
GhPC97	Ghir_D09G022120	189	19.853	9.166	8
GhPC98	Ghir_A05G013010	200	21.162	4	-6
GhPC99	Ghir_D05G012760	200	21.157	4.354	-5.5
GhPC100	Ghir_D13G022130	200	20.488	4.469	-4
GhPC101	Ghir_A08G007220	205	22.038	8	4
GhPC102	Ghir_A13G021270	208	21.375	5	-3
GhPC103	Ghir_A11G025250	214	23.121	7	1
GhPC104	Ghir_D11G025390	255	27.285	4.972	-2
GhPC105	Ghir_D11G025400	259	27.691	5.004	-2
GhPC106	Ghir_D13G022140	268	28.239	10.033	12
GhPC107	Ghir_A13G010380	299	31.515	8	3
GhPC108	Ghir_A13G021280	347	35.14	8	7
GhPC109	Ghir_A13G021260	429	45.418	5	-14
GhPC110	Ghir_D13G022120	556	60.623	4.82	-16.5
GhPC111	Ghir_A05G043430	111	12.338	6.925	1
GhPC112	Ghir_D05G024780	111	12.38	6.925	1
GhPC113	Ghir_D05G001770	169	18.56	4.873	-3.5

Supplemental files 3: Table S2

ENODLs Identified in *G. hirsutum* Genomes

Name	Accession ID	Length(aa)	singleIP	GPI	N-glyco	AG	Extensin
<i>GhENODL1</i>	Ghir_D06G011310	107	-	+	-	+	-
<i>GhENODL2</i>	Ghir_A06G007340	127	+	-	+	-	-
<i>GhENODL3</i>	Ghir_D11G003980	127	+	-	+	-	-
<i>GhENODL4</i>	Ghir_D05G005610	128	+	+	+	+	-
<i>GhENODL5</i>	Ghir_A11G004040	137	+	-	+	-	-
<i>GhENODL6</i>	Ghir_D06G001340	139	+	-	+	-	-
<i>GhENODL7</i>	Ghir_A06G001480	139	+	-	+	-	-
<i>GhENODL8</i>	Ghir_A05G010410	154	-	-	+	-	-
<i>GhENODL9</i>	Ghir_A05G006200	159	-	+	+	+	-
<i>GhENODL10</i>	Ghir_D07G003740	161	+	+	+	+	-
<i>GhENODL11</i>	Ghir_A05G013540	167	+	+	+	+	-
<i>GhENODL12</i>	Ghir_A13G003590	167	+	-	+	-	-
<i>GhENODL13</i>	Ghir_D11G007700	167	-	+	+	-	-
<i>GhENODL14</i>	Ghir_D04G004910	170	+	+	+	+	-
<i>GhENODL15</i>	Ghir_A05G038140	171	+	+	+	+	-
<i>GhENODL16</i>	Ghir_A05G012210	172	+	-	+	+	-
<i>GhENODL17</i>	Ghir_D05G011920	173	+	-	+	+	-
<i>GhENODL18</i>	Ghir_A11G007760	175	+	+	+	+	-
<i>GhENODL19</i>	Ghir_D11G007710	175	+	+	+	+	-
<i>GhENODL20</i>	Ghir_D05G006280	176	-	+	+	+	-
<i>GhENODL21</i>	Ghir_A07G003720	178	+	+	+	+	-
<i>GhENODL22</i>	Ghir_D05G013280	180	+	+	+	+	-
<i>GhENODL23</i>	Ghir_A13G003640	184	+	-	+	-	-
<i>GhENODL24</i>	Ghir_A05G005530	185	+	+	+	+	-
<i>GhENODL25</i>	Ghir_D13G025800	188	+	-	+	-	-
<i>GhENODL26</i>	Ghir_A13G013740	194	+	+	+	+	+
<i>GhENODL27</i>	Ghir_D13G014420	194	+	+	+	+	-
<i>GhENODL28</i>	Ghir_A02G010500	196	+	-	+	+	-
<i>GhENODL29</i>	Ghir_D03G009570	196	+	-	+	+	-
<i>GhENODL30</i>	Ghir_A13G014720	217	+	+	+	+	+
<i>GhENODL31</i>	Ghir_D13G015400	217	+	+	+	+	+
<i>GhENODL32</i>	Ghir_D07G015760	229	+	-	+	+	+
<i>GhENODL33</i>	Ghir_A07G015510	231	+	-	+	+	+
<i>GhENODL34</i>	Ghir_D05G007560	234	+	-	+	+	-
<i>GhENODL35</i>	Ghir_D05G037420	242	+	-	+	+	+
<i>GhENODL36</i>	Ghir_A04G002000	243	+	-	+	+	+
<i>GhENODL37</i>	Ghir_A03G017320	268	+	+	+	+	+

<i>GhENODL38</i>	Ghir_D02G018560	269	+	+	+	+	+
<i>GhENODL39</i>	Ghir_A13G015310	338	+	+	+	+	+
<i>GhENODL40</i>	Ghir_D13G016040	338	+	+	+	+	+
<i>GhENODL41</i>	Ghir_A04G003340	832	-	-	+	+	+

Supplemental files 3:Table S3

Genes ontology (GO) analysis involved in biological processes from differentially expressed genes by comparing *GhENODL1-4* transgenic line with WT.

Cate gory	GOID	Description	Gene Ratio	Bg Ratio	pvalue
BP	GO:0050832	defense response to fungus	134	298	4.55E-23
BP	GO:0006955	immune response	159	390	1.05E-21
BP	GO:0002376	immune system process	168	426	4.58E-21
BP	GO:0045087	innate immune response	154	382	1.70E-20
BP	GO:0009814	defense response, incompatible interaction	90	194	5.41E-17
BP	GO:0006979	response to oxidative stress	156	451	9.99E-14
BP	GO:0009627	systemic acquired resistance	41	79	2.22E-10
BP	GO:0009751	response to salicylic acid	82	219	1.09E-09
BP	GO:0000302	response to reactive oxygen species	70	179	2.10E-09
BP	GO:0031347	regulation of defense response	92	265	9.33E-09
BP	GO:0071555	cell wall organization	143	492	4.99E-07
BP	GO:0044550	secondary metabolite biosynthetic process	75	160	1.07E-14
BP	GO:0052542	defense response by callose deposition	16	23	3.36E-07
BP	GO:0070588	calcium ion transmembrane transport	30	65	1.51E-06

BP	GO:0009620	response to fungus	162	368	2.21E-26
BP	GO:0019761	glucosinolate biosynthetic process	31	53	7.03E-10
BP	GO:0009625	response to insect	21	30	3.84E-09
BP	GO:0009753	response to jasmonic acid	82	235	4.53E-08

Supplemental files 3: Table S4

Genes ontology (GO) analysis involved in biological processes from differential genes by comparing inoculated and non-inoculated *V. dahliae* in *GhENODL1-4* transgenic line.

Cate gory	GO ID	Description	Gene Ratio	Bg Ratio	pvalue
BP	GO:0009620	response to fungus	134	360	2.54E-15
BP	GO:0006091	generation of precursor metabolites and energy	163	479	2.89E-14
BP	GO:0006979	response to oxidative stress	153	449	1.59E-13
BP	GO:0050832	defense response to fungus	106	290	7.64E-12
BP	GO:0009735	response to cytokinin	91	238	1.37E-11
BP	GO:0002376	immune system process	141	430	3.45E-11
BP	GO:0016052	carbohydrate catabolic process	95	258	5.78E-11
BP	GO:0009814	defense response, incompatible interaction	77	195	8.34E-11
BP	GO:0045087	innate immune response	126	386	5.28E-10
BP	GO:0006955	immune response	128	394	5.43E-10
BP	GO:0008652	cellular amino acid biosynthetic process	78	219	1.62E-08
BP	GO:0009751	response to salicylic acid	78	220	2.04E-08
BP	GO:0000302	response to reactive oxygen species	65	174	3.13E-08
BP	GO:0009069	serine family amino acid metabolic	33	72	3.70E-07

BP	GO:0009817	defense response to fungus, incompatible interaction	25	53	4.98E-06
BP	GO:0009414	response to water deprivation	136	373	1.05E-14
BP	GO:0006520	cellular amino acid metabolic process	154	457	3.70E-13
BP	GO:0006790	sulfur compound metabolic process	125	388	1.55E-09
BP	GO:0009627	systemic acquired resistance	31	79	3.99E-05
BP	GO:0016051	carbohydrate biosynthetic process	123	351	4.64E-12

Supplemental files 3: Table S5

Genes ontology (GO) analysis involved in biological processes from differential genes by comparing inoculated and non-inoculated *V. dahliae* in WT.

Cate gory	GOID	Description	Gene Ratio	Bg Ratio	pvalue
BP	GO:0009991	response to extracellular stimulus	38	258	5.04E-14
BP	GO:0031667	response to nutrient levels	34	221	3.07E-13
BP	GO:0042594	response to starvation	30	176	5.10E-13
BP	GO:0009267	cellular response to starvation	23	143	8.85E-10
BP	GO:0071456	cellular response to hypoxia	10	28	1.83E-08
BP	GO:0042737	drug catabolic process	26	210	2.17E-08
BP	GO:0016036	cellular response to phosphate starvation	14	69	8.91E-08
BP	GO:0098754	detoxification	25	213	1.16E-07
BP	GO:0009636	response to toxic substance	32	334	2.51E-07
BP	GO:0009409	response to cold	36	408	3.46E-07
BP	GO:0050832	defense response to fungus	28	309	4.18E-06
BP	GO:0009631	cold acclimation	10	51	8.65E-06
BP	GO:0009414	response to water deprivation	31	377	9.51E-06
BP	GO:0000272	polysaccharide catabolic process	18	158	1.03E-05
BP	GO:0046677	response to antibiotic	28	330	1.44E-05
BP	GO:0009415	response to water	31	385	1.44E-05

Supplemental files 3: Table S6

Primers used in this study

Primer names	Sequence(5'to3')	Purpose
GhENODL1-V-F	GAATTCATGGCTTCAATTGGTTTC	VIGS vector
GhENODL1-V-R	CGGTACCTTAAAAACGTGGCC	VIGS vector
GhENODL1-F	CGATGGCTTCAATTGGTTTCA	cloning of GhENODL1
GhENODL1-R	TAAAAACGTGGCCAAGGGA	cloning of GhENODL1
GhENODL1-RT-F	CCTCTTGGTTGCTTTAGGTGCTT	qRT-PCR
GhENODL1-RT-R	CGCCCATTCGGTGTAATTGTAG	qRT-PCR
GhENODL1-G-F	GGGGACAAGTTTGTACAAAAAAGCAG GCTTCATGGCTTCAATTGGTTTCA	Gateway vector
GhENODL1-G-R	GGGGACCACTTTGTACAAGAAAGCTGG GTGAAAACGTGGCCAAGGGA	Gateway vector
AtEF-1 α -F	AACGGTGCCAGTGGGACG	qRT-PCR
AtEF-1 α -R	CCTTGACAGCAACATTCTTGACAT	qRT-PCR
AtEDS1-F1	CTGTGGAAATGGCTGTGAGGAGT	qRT-PCR
AtEDS1-R1	CGGCAAGTGCGTGACTGAAGATA	qRT-PCR
AtNDR1-F1	TCTTATGGCTTAGTCTCCGTGCG	qRT-PCR
AtNDR1-R1	CGAGGTGGACATCGTCGTAGTAG	qRT-PCR
AtPDF1.2-Q-F	CTTGTTCTCTTTGCTGCTTTC	qRT-PCR
AtPDF1.2-Q-R	CATGTTTGGCTCCTTCAAG	qRT-PCR
AtPR1-Q-F	GCTACGCAGAACAATAAG	qRT-PCR
AtPR1-Q-R	CCAGACAAGTCACCGCTACC	qRT-PCR
AtPR2-Q-F	GTCTCAAGGAAGGTTTCAG	qRT-PCR
AtPR2-Q-R	CGTTATCAACAGTGGACT	qRT-PCR
AtPR3-Q-F	CGGCGACCTCCTTCTTCCTC	qRT-PCR
AtPR3-Q-R	GAATGATGCCGCTTGTCCCTG	qRT-PCR
AtPR5F	ACTTCACTCTAAGGAACAAT	qRT-PCR
AtPR5R	GTTACACATCTACCGTTTC	qRT-PCR
AtRPP4F	ATATACATGTGAACGTTTCTG	qRT-PCR
AtRPP4R	CTATATCAACATCAGCATCATC	qRT-PCR
GhUBQ14-F	CAACGCTCCATCTTGTCCCTT	qRT-PCR
GhUBQ14-R	TGATCGTCTTTCCCGTAAGC	qRT-PCR
GhEDS1-F	GTGTTTACTGGACATTCATCTGG	qRT-PCR
GhEDS1-R	CTTGCTTCTTTGTCTACCGT	qRT-PCR
GhNDR1-F	CCCGTAACCAAGGAGGCTGT	qRT-PCR
GhNDR1-R	CTGCTAAGGGAAGGCAAGGATAG	qRT-PCR
GhNPR1-F	GTCTGGCTGATGTCAATCTGCG	qRT-PCR
GhNPR1-R	TCCTTCCCTTGCTCTGTCTTGG	qRT-PCR
GhPR1F	AAGAATGTGGGTTAGTGAGAGGGT	qRT-PCR
GhPR1R	ACCACTTGAGTATAATGCCCCG	qRT-PCR
GhPR2F	CCACCAGCAGCAGAAGTTATCG	qRT-PCR

GhPR2R	TTCAAGGTTTGCCTCGGAAGA	qRT-PCR
GhPR3F	ACTCCACAATCACCGAAGCCAT	qRT-PCR
GhPR3R	GCATTCCAACCCTTACCACATTC	qRT-PCR
GhPR4F	TTGCGGCAATGGCTTCAATC	qRT-PCR
GhPR4R	TGCTCTCACATTATTCGGCA	qRT-PCR
GhPR5F	GCCGTGATTCATACAGTTATCCTCA	qRT-PCR
GhPR5R	TTGGCTCTTACTTCCGACCATCT	qRT-PCR
GhPR6F	CTGGGTGTCCTGGGAAGAAC	qRT-PCR
GhPR6R	TTGTAGGGGGACGAACAACG	qRT-PCR
GhPR9F	CAACAGCGCCAACATACAGAG	qRT-PCR
GhPR9R	CAGCACAAGAGACAATGCCAG	qRT-PCR
GhPR16F	CCCAAAGCTTGCCAAAGCA	qRT-PCR
GhPR16R	GAACATTGGCTGGAGTGACC	qRT-PCR
ITS-F	CATCAGTCTCTCTGTTTATACCAACG	qRT-PCR
ITS-R	CGATGCGAGCTGTAATACTACGCAA	qRT-PCR
