

Supplemental material to the article by Chung, Kim and Sano "Control of seed and root development by WIPK-activated transcription factor, NtWIF in tobacco plants" Plant Biotechnology, 25: pp-pp, 2007.

Supplement Table 1. List of differentially expressed genes between NtWIF-overexpressing transgenic line, S7, and wild type tobacco plants.

Description	S7/WT (fold)	P value	Origin
Defense			
PMT	10.78	0.01033	<i>N. tabacum</i>
PR1b	8.00	0.00386	<i>N. tabacum</i>
cystathionine gamma-synthase isoform 1	5.45	0.00303	<i>S. tuberosum</i>
PR-Q	5.25	0.00002	<i>N. tabacum</i>
acidic chitinase III	5.23	0.00061	<i>N. tabacum</i>
CYP73A27	4.82	0.00364	<i>A. thaliana</i>
acidic beta-1,3-glucanase	4.76	0.00014	<i>N. tabacum</i>
ornithine decarboxylase	4.65	0.00798	<i>N. glutinosa</i>
cytochrome oxidase subunit 1	4.45	0.00159	<i>Sabal palmetto</i>
ACCS2	4.23	0.00130	<i>N. tabacum</i>
phenylalanine ammonia-lyase	4.19	0.00277	<i>N. tabacum</i>
putative Cytochrome P450 protein	4.17	0.00140	<i>S. melongena</i>
THT1(tyramine hydroxycinnamoyltransferase)	4.17	0.00373	<i>N. tabacum</i>
MRP4	4.15	0.00056	<i>A. thaliana</i>
osmotin-like protein	4.10	0.00491	<i>N. tabacum</i>
P450 hydroxylase	3.98	0.00106	<i>N. tabacum</i>
TAS14 (dehydrin)	3.97	0.00175	<i>N. tabacum</i>
IVR-like protein	3.94	0.00004	<i>N. tabacum</i>
HMGR1	3.92	0.00233	<i>N. tabacum</i>
acetyl-CoA synthetase	3.88	0.00885	<i>S. tuberosum</i>
glucosyltransferase	3.86	0.00042	<i>N. tabacum</i>
putative chloroplast terpene synthase	3.84	0.00323	<i>Quercus ilex</i>
endo-1,4-beta-glucanase	3.83	0.00990	<i>L. esculentum</i>
TMV resistance protein N - tobacco	3.82	0.00358	<i>N. glutinosa</i>
rbohF	3.78	0.00245	<i>N. tabacum</i>
NADPH cytochrome P450	3.70	0.00037	<i>Vigna radiata</i>
superoxide dismutase [Fe]	3.68	0.00828	<i>L. esculentum</i>
probable cinnamyl-alcohol dehydrogenase	3.67	0.00252	<i>L. esculentum</i>
putative AtMlo-h1 protein	3.67	0.00037	<i>A. thaliana</i>
Avr9 elicitor response protein	3.66	0.00053	<i>N. tabacum</i>

0902172A carboxylase/oxygenase,RBP	3.58	0.00648	<i>N. tabacum</i>
anionic peroxidase	3.56	0.00111	<i>N. tabacum</i>
cytochrome c oxidase	3.54	0.00440	<i>N. tabacum</i>
endo-1,4-beta-glucanase	3.54	0.00089	<i>N. tabacum</i>
wound-inducible carboxypeptidase	3.50	0.00084	<i>L. esculentum</i>
PPO	3.46	0.00196	<i>N. tabacum</i>
protoporphyrinogen oxidase PX-1	3.45	0.00098	<i>N. tabacum</i>
CYP71D21	3.43	0.00961	<i>N. tabacum</i>
WI9	3.34	0.00195	<i>N. tabacum</i>
cytosolic cysteine synthase	3.31	0.00662	<i>S. tuberosum</i>
nitrate reductase	3.31	0.00307	<i>N. tabacum</i>
Al-induced protein	3.31	0.01005	<i>N. tabacum</i>
putative geranyl diphosphate synthase (GPPS) (dimethylallyltransferase)	3.28	0.00034	<i>A. thaliana</i>
cytochrome P450 like_TBP	3.25	0.00112	<i>N. tabacum</i>
endochitinase	3.16	0.00213	<i>N. sylvestris</i>
THLP	3.16	0.00301	<i>N. tabacum</i>
VAP27-1	3.15	0.00347	<i>A. thaliana</i>
putative amine oxidase 1	3.02	0.00292	<i>A. thaliana</i>
F-box protein family	3.00	0.00057	<i>A. thaliana</i>
Transcription factor			
NtHSF1	4.68	0.00256	<i>N. tabacum</i>
LBM4	4.55	0.00539	<i>N. tabacum</i>
TOM (target of myb1)-like protein	4.45	0.01026	<i>A. thaliana</i>
TIZZ	4.26	0.00031	<i>N. tabacum</i>
BAC98495.1 AG-motif binding protein-5	4.18	0.00150	<i>N. tabacum</i>
WRKY2	4.07	0.00908	<i>N. tabacum</i>
NtWRKY3	3.99	0.01054	<i>N. tabacum</i>
LBM1	3.82	0.00043	<i>N. tabacum</i>
LBM3	3.74	0.00092	<i>N. tabacum</i>
Tsi1	3.59	0.00607	<i>N. tabacum</i>
TGA2.2	3.47	0.00146	<i>N. tabacum</i>
putative CCAAT-binding transcription factor subunit	3.42	0.00562	<i>A. thaliana</i>
DNA-binding protein NtWRKY3	3.41	0.00150	<i>N. tabacum</i>
DNA binding protein TGA1b	3.39	0.00488	<i>N. tabacum</i>
DNA-binding WRKY-like protein	3.32	0.00408	<i>A. thaliana</i>
heat shock transcription factor 34	3.18	0.00196	<i>Glycine max</i>

Kinase/Phosphatase

NPK1	4.38	0.00312	<i>N. tabacum</i>
NQK1	4.38	0.00157	<i>N. tabacum</i>
NRK1	4.20	0.00052	<i>N. tabacum</i>
NtMEK1	4.16	0.00138	<i>N. tabacum</i>
Ser/Thr specific protein phosphatase 2A	4.09	0.00220	<i>M. sativa subsp. varia</i>
NtCDPK3	3.87	0.00330	<i>N. tabacum</i>
calcium/calmodulin-dependent protein kinase CaMK1	3.60	0.00296	<i>N. tabacum</i>
WAPK	3.59	0.00267	<i>N. tabacum</i>
calcium-dependent protein kinase	3.38	0.00106	<i>Fragaria ananassa</i>
purple acid phosphatase	3.21	0.00191	<i>N. tabacum</i>
NtCDPK2	3.20	0.01048	<i>N. tabacum</i>
putative protein kinase	3.18	0.00100	<i>A. thaliana</i>
shaggy-like kinase	3.17	0.00192	<i>Ricinus communis</i>

Heat shock protein and ubiquitin

chaperonin 21 precursor	4.63	0.00902	<i>L. esculentum</i>
heat shock protein 70	4.37	0.00067	<i>Oryza sativa (indica cultivar)</i>
putative heat-shock protein	3.98	0.00934	<i>A. thaliana</i>
non-cell-autonomous heat shock cognate protein 70	3.58	0.00546	<i>Cucurbita maxima</i>
chaperonin 21 precursor	3.54	0.00983	<i>L. esculentum</i>
molecular chaperone Hsp90-2	3.39	0.00360	<i>N. benthamiana</i>
polyubiquitin	3.81	0.00135	<i>Pinus sylvestris</i>
SUMO protein	3.49	0.00316	<i>Lycopersicon esculentum</i>
putative ubiquitin-specific protease	3.45	0.00112	<i>Oryza sativa (japonica cultivar)</i>
ubiquitin-activating enzyme E1	3.15	0.00244	<i>N. tabacum</i>

Phytohormone

GAST-like gene product	4.38	0.00560	<i>Fragaria ananassa</i>
putative auxin response factor protein	3.28	0.00185	<i>Arabidopsis thaliana</i>
putative IAA amidohydrolase	3.02	0.00526	<i>Oryza sativa (japonica cultivar)</i>

Cell wall and cytoskeleton

putative pectinacetylase	12.17	0.00167	<i>A. thaliana</i>
GDP-D-mannose pyrophosphorylase	5.24	0.00680	<i>N. tabacum</i>
fructose-1,6-bisphosphate aldolase	4.72	0.00076	<i>Pisum sativum</i>

similar to dTDP-D-glucose 4,6-dehydratase	4.66	0.00001	<i>A. thaliana</i>
putative actin-binding protein	4.65	0.00095	<i>Malus domestica</i>
putative microfibril-associated protein	4.00	0.00110	<i>A. thaliana</i>
actin-depolymerizing factor 2	4.00	0.00095	<i>Petunia hybrida</i>
glucose-6-phosphate isomerase	3.96	0.00167	<i>Spinacia oleracea</i>
kinesin-like protein	3.82	0.00054	<i>N. tabacum</i>
pectinesterase-like protein	3.77	0.00066	<i>A. thaliana</i>
Ntbfruc1	3.74	0.00880	<i>N. tabacum</i>
beta-galactosidase	3.67	0.00207	<i>Prunus armeniaca</i>
putative pyrophosphate--fructose-6-phosphate 1-phosphotransferase	3.54	0.00280	<i>A. thaliana</i>
putative syntaxin protein	3.50	0.00353	<i>Oryza sativa (japonica cultivar)</i>
LOB DOMAIN 15 [<i>Arabidopsis thaliana</i>]	3.50	0.00416	<i>N. tabacum</i>
putative expansin	3.41	0.00184	<i>C. annuum</i>
alpha-tubulin	3.36	0.00320	<i>N. tabacum</i>
xyloglucan endotransglycosylase	3.22	0.00599	<i>Malus domestica</i>
cellulose synthase catalytic subunit	3.05	0.01331	<i>N. alata</i>
alpha-galactosidase-like protein	3.29	0.00103	<i>Arabidopsis thaliana</i>
fructose-biphosphate aldolase	3.25	0.00281	<i>Mesembryanthemum crystallinum</i>
fructose-bisphosphate aldolase	3.23	0.00504	<i>Persea americana</i>
putative 6-phosphogluconolactonase	3.22	0.00071	<i>Elaeis guineensis</i>
beta-galactosidase like protein	3.14	0.00219	<i>A. thaliana</i>
beta-D-xylosidase	3.06	0.00194	<i>Prunus persica</i>
putative nucleotide sugar epimerase	3.02	0.00038	<i>A. thaliana</i>
Transcription/ Translation-regulatory protein			
translation initiation factor eIF3-like protein	6.63	0.00369	<i>A. thaliana</i>
translation initiation factor	4.85	0.00204	<i>Pisum sativum</i>
putative cleavage and polyadenylation specificity factor 73 kDa subunit	4.25	0.01415	<i>A. thaliana</i>
elongation factor 1B gamma	4.01	0.00278	<i>Oryza sativa</i>
putative replication factor C	3.82	0.00800	<i>A. thaliana</i>
putative NifU-like metallocluster assembly factor	3.81	0.00853	<i>A. thaliana</i>
RNA-directed RNA polymerase	3.76	0.00393	<i>N. tabacum</i>
putative arginine/serine-rich splicing factor	3.68	0.00296	<i>M. sativa</i>
replication factor, putative; 74998-73295	3.44	0.01085	<i>A. thaliana</i>
putative RNA-binding protein MEI2	3.37	0.00330	<i>A. thaliana</i>
chloroplast elongation factor TuB (EF-TuB)	3.17	0.00602	<i>N. sylvestris</i>

Functional Protein

Putative integral membrane protein	8.64	0.00004	<i>A. thaliana</i>
putative germin-like protein (GLP2a) copy2	5.84	0.01272	<i>A. thaliana</i>
Moco containing protein	5.20	0.00042	<i>A. thaliana</i>
putative translationally controlled tumor protein	4.18	0.00305	<i>N. tabacum</i>
putative dim1p	4.09	0.00343	<i>Oryza sativa (japonica cultivar)</i>
14-3-3 protein	4.06	0.00242	<i>N. tabacum</i>
RAD23-like protein	3.85	0.00777	<i>A. thaliana</i>
P69C protein	3.84	0.00273	<i>L. esculentum</i>
urease accessory protein G	3.80	0.00053	<i>S. tuberosum</i>
putative signal recognition particle protein	3.57	0.00207	<i>A. thaliana</i>
putative urease accessory protein F	3.50	0.00464	<i>L. esculentum</i>
RNA-binding protein AKIP1	3.47	0.00833	<i>Vicia faba</i>
transmembrane protein, putative	3.44	0.00093	<i>A. thaliana</i>
putative Ran binding protein	3.41	0.00014	<i>Oryza sativa (japonica cultivar)</i>
germin-like protein	3.40	0.00147	<i>Ananas comosus</i>
putative cytochrome b5	3.36	0.00225	<i>A. thaliana</i>
proline-rich protein family	3.35	0.00047	<i>A. thaliana</i>
stomatin-like protein	3.34	0.00076	<i>A. thaliana</i>
oligouridylate binding protein, putative	3.26	0.01545	<i>A. thaliana</i>
54-kD signal recognition particle (SRP) specific protein	3.24	0.00150	<i>L. esculentum</i>
Putative integral membrane protein	3.22	0.00047	<i>A. thaliana</i>
luminal binding protein (BiP)	3.19	0.00066	<i>N. tabacum</i>
putative transformer serine/arginine-rich ribonucleoprotein	3.15	0.00012	<i>Oryza sativa (japonica cultivar)</i>
Nonclathrin coat protein gamma-like protein	3.04	0.00259	<i>A. thaliana</i>
putative multispinning membrane protein	3.03	0.00056	<i>A. thaliana</i>

Ca²⁺-related and Ion Channel

MRS2-5	4.31	0.00707	<i>A. thaliana</i>
vacular H ⁺ -ATPase	3.71	0.01252	<i>N. tabacum</i>
putative potassium channel regulatory factor	3.46	0.00310	<i>Oryza sativa (japonica cultivar)</i>
MRS2-1	3.44	0.00261	<i>A. thaliana</i>
putative nitrate transporter	3.20	0.00038	<i>A. thaliana</i>
NtCam13	3.07	0.00726	<i>N. tabacum</i>

Metabolism

long-chain-fatty-acid CoA ligase [Arabidopsis thaliana]	4.65	0.01264	<i>A. thaliana</i>
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putative adenosine deaminase	4.65	0.00798	<i>Oryza sativa (japonica cultivar)</i>
catechol O-methyltransferase	4.06	0.00187	<i>A. thaliana</i>
phosphoinositide-specific phospholipase C P12	3.65	0.00090	<i>N. tabacum</i>
aspartic endopeptidase	3.57	0.01297	<i>Cucurbita pepo</i>
putative steroid dehydrogenase [Arabidopsis thaliana]	3.53	0.00462	<i>A. thaliana</i>
glycoprotein endopeptidase-like protein	3.48	0.00538	<i>A. thaliana</i>
phosphoenolpyruvate carboxylase	3.44	0.00107	<i>N. sylvestris</i>
ATP-diphosphohydrolase	3.40	0.00321	<i>N. tabacum</i>
3-hydroxyisobutyryl-coenzyme A hydrolase-like protein	3.39	0.00379	<i>A. thaliana</i>
CDP-diacylglycerol synthetase	3.36	0.00034	<i>S. tuberosum</i>
PLC2	3.27	0.00258	<i>N. tabacum</i>
glycine hydroxymethyltransferase	3.30	0.00813	<i>Flaveria pringlei</i>
S-adenosyl-methionine-sterol-C- methyltransferase	3.20	0.00245	<i>N. tabacum</i>
putative serine carboxypeptidase	3.19	0.00131	<i>Oryza sativa (japonica cultivar)</i>
alpha-rhamnosidase-like protein	3.16	0.00487	<i>Oryza sativa (japonica cultivar)</i>
putrescine N-methyltransferase	3.14	0.00153	<i>N. tabacum</i>
putative subtilisin serine proteinase	3.08	0.01321	<i>A. thaliana</i>
putative mercaptopyruvate sulfurtransferase	3.00	0.00497	<i>A. thaliana</i>
