

Response of *Sclerotinia sclerotiorum* to long exposure of isothiocyanates by transcriptomics approach

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List of differentially expressed genes (DEGs) which show protein-protein interaction forming a single network in the comparison AITC vs Control. Blue and yellow colors indicate up and down-regulated DEGs, respectively.

Name	Description
ergosterol and lipids synthesis	
erg7	Lanosterol synthase
erg10	Acetyl-CoA acetyltransferase
erg11	Lanosterol 14-alpha demethylase erg11
sts1	C-24(28) sterol reductase
plh1	Phospholipid:diacylglycerol acyltransferase
are1	acyl-coA-sterol acyltransferase
SPAC1A6.05c.1	Triacylglycerol lipase ptl3
SPAC22A12.16.1	Probable ATP-citrate synthase subunit 2
met26	5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase
SPAC23A1.14c.1	Uncharacterised trans-sulfuration enzyme
pi047	Adenosylhomocysteinase
fas2	Fatty acid synthase subunit alpha
fas1	Fatty acid synthase subunit beta
glutathione synthesis	
glt1	Putative glutamate synthase [NADPH]
ggt2	Glutathione hydrolase proenzyme 2
ggt1	Glutathione hydrolase proenzyme 1
gst1	Glutathione S-transferase 1
proteasome	
cpc2	Guanine nucleotide-binding protein subunit beta-like protein
pre10	Probable proteasome subunit alpha type-7
pup3	Probable proteasome subunit beta type-3
pre3	Probable proteasome subunit beta type-1
pts1	Probable proteasome subunit beta type-5

rpn11	26S proteasome regulatory subunit rpn11
SPAC6G10.04c.1	Probable proteasome subunit alpha type-6
SPAC13C5.01c.1	Probable proteasome subunit alpha type-3

ribosome

mrps17	Mitochondrial ribosomal protein subunit S17
rps2602	40S ribosomal protein S26
rpl44	60S ribosomal protein L28/L44
rps801	40S ribosomal protein S8
imp3	U3 small nucleolar ribonucleoprotein protein imp3
fib1	rRNA 2'-O-methyltransferase fibrillarin
SPAC25H1.08c.1	Ribosome biogenesis protein Sqt1

Cell cycle, replication, cytoskeleton organization

top2	DNA topoisomerase 2
klp5	Kinesin-like protein 5
dad1	DASH complex subunit
mph1	Serine/threonine-protein kinase
mad3	Mitotic spindle checkpoint component
mad2	Mitotic spindle checkpoint component
atb2	Tubulin alpha-2 chain
klp9	Kinesin-like motor protein 9
nda2	Tubulin alpha-1 chain
alp4	Spindle pole body component
tea2	Kinesin-like protein
slp1	WD repeat-containing protein; Required for mad2-dependent spindle checkpoint activation
suc1	Cyclin-dependent kinases regulatory subunit
rnh201	Ribonuclease H2 subunit A
pds5	Sister chromatid cohesion protein
cut3	Structural maintenance of chromosomes protein 4

pol1	DNA polymerase alpha catalytic subunit
cdc22	Ribonucleoside-diphosphate reductase large chain
mcm7	DNA replication licensing factor mcm7
rqh1	ATP-dependent DNA helicase hus2/rqh1
pcn1	Proliferating cell nuclear antigen
ctf18	Chromosome transmission fidelity protein 18
msh6	DNA mismatch repair protein msh6
pku70	ATP-dependent DNA helicase II subunit 1
ung1	Uracil-DNA glycosylase
swi10	Mating-type switching protein
rhp14	DNA repair protein rad14
rhp7	DNA repair protein rhp7
pmh1	RNA polymerase II transcription factor B subunit 3
uba5	NEDD8-activating enzyme E1 regulatory subunit
orc2	Origin recognition complex subunit 2
prw1	RbAp48-related WD40 repeat-containing protein
hat1	Histone acetyltransferase type B catalytic subunit
cia1	Histone chaperone
alp13	Chromatin modification-related protein
hhf1	Histone H4
mst1	Histone acetyltransferase
htb1	Histone H2B-alpha
ago1	Protein argonaute; Required for G1 arrest and mating in response to nitrogen starvation
cdc15	Cell division control protein 15
myp2	Myosin type-2 heavy chain 2
myo2	Myosin type-2 heavy chain 1
cdc4	Myosin regulatory light chain cdc4
SPAC144.05	ATP-dependent DNA helicase/ ubiquitin ligase E3

rhp6	Ubiquitin-conjugating enzyme E2 2
hob1	Has a role in DNA damage signaling as a part of stress response processes
wsp1	Wiskott-Aldrich syndrome protein homolog 1
SPAPJ696.02.1	Actin cortical patch component Lsb4
sid2	Serine/threonine-protein kinase
hsp9	Heat shock protein
vip1	RNA-binding protein
ish1	Stress response protein
rds1	Protein rds1; May have a function in stress-related responses of the cell
tps2	Trehalose-phosphatase
SPAC15E1.02c.1	UPF0591 membrane protein C15E1.02c; DUF1761 family protein
SPAC32A11.02c.1	Uncharacterized protein
mug190	Meiotically up-regulated gene 190 protein
SPBC24C6.09c.1	Phosphoketolase family protein
SPAC4H3.03c.1	Glucan 1,4-alpha-glucosidase
SPACUNK4.10.1	Glyoxylate reductase
icl2	Mitochondrial 2-methylisocitrate lyase
dao1	D-amino acid oxidase
sou1	Sorbose reductase
SPBC725.04	Putative 2-hydroxyacyl-CoA lyase
erv1	Mitochondrial FAD-linked sulfhydryl oxidase
cyc1	Cytochrome c
SPBC36.03c	MFS family transmembrane transporter
cox2	Cytochrome c oxidase subunit 2
hri2	Eukaryotic translation initiation factor 2-alpha kinase 2
elf1	mRNA export factor
rex2	Probable oligoribonuclease; 3'-to-5' exoribonuclease specific for small oligoribonucleotides
trx1	Thioredoxin-1

mrx1	Peptide methionine sulfoxide reductase
SPBC216.04c.1	Peptide-methionine (R)-S-oxide reductase MsrB
SPAPB24D3.08c.1	Zinc-type alcohol dehydrogenase-like protein
SPAPB24D3.06c.1	UPF0613 protein; DUF1749 family protein
SPAPB24D3.02c.1	Amino-acid permease
sty1	Mitogen-activated protein kinase
prz1	Transcriptional regulator
vcx1	Vacuolar calcium ion transporter
ras1	Ras-like protein 1
SPAC8E11.04c.1	Acyl-protein thioesterase 1
sck2	Serine/threonine-protein kinase
ppe1	Serine/threonine-protein phosphatase
ste20	Target of rapamycin complex 2 subunit ste20; Component of TORC2
gtr1	GTP-binding protein
slm1	Cytoskeletal signaling protein; Effector of the TORC2- and calcineurin-signaling pathways
SPCC736.15	Probable sphingolipid long chain base-responsive protein

List of differentially expressed genes (DEGs) which show protein-protein interaction forming two networks in the comparison AITC vs Control. Blue and yellow colors indicate up and down-regulated DEGs, respectively.

Name	Description
Network 1	
ase1	Anaphase spindle elongation protein 1
mad2	Mitotic spindle checkpoint component
pcs1	Monopolin complex subunit pcs1
ndc80	Kinetochore protein ndc80; Acts as a component of the NMS super complex
klp9	Kinesin-like motor protein 9
mug190	Meiotically up-regulated gene 190 protein

SPAC32A11.02c.1	Uncharacterized protein C32A11.02c; Conserved fungal protein
ish1	Stress response protein; Has a role in maintaining cell viability during stationary phase induced by stress response
SPCC594.04.1	Steroid oxidoreductase superfamily protein
SPAC26F1.07.1	Glucose 1-dehydrogenase (NADP+)
hsp90	Heat shock protein 90 homolog
SPAC13C5.04.1	Putative glutamine amidotransferase-like protein
SPBC216.04c.1	Peptide-methionine (R)-S-oxide reductase MsrB
hsp9	Heat shock protein Hsp9
SPBC1711.08.1	Chaperone activator Aha1

Network 2

leu1	3-isopropylmalate dehydrogenase
leu2	3-isopropylmalate dehydratase
SPCC1827.06c.1	Probable aspartate-semialdehyde dehydrogenase
SPBC19F5.04.1	Probable aspartokinase; Aspartate kinase (predicted); Belongs to the aspartokinase family
met6	Homoserine O-acetyltransferase
met7	Probable folylpolyglutamate synthase

List of diferentially expressed genes (DEGs) which show protein-protein interaction forming two networks in the comparison AITC vs I3C. Blue and yellow colors indicate up-regulation by AITC or I3C, respectively.

NETWORK 1

Name	Description
Ribosome synthesis and translation	
rps2	40S ribosomal protein S2
rps3	40S ribosomal protein S3
rps401	40S ribosomal protein S4
rps5	40S ribosomal protein S5
rps601	40S ribosomal protein S6
rps801	40S ribosomal protein S8

SPAC144.11.1	40S ribosomal protein S11
rps1201	40S ribosomal protein S12
SPAC3H5.05c.1	40S ribosomal protein S14
rps1701	40S ribosomal protein S17
rps1901	40S ribosomal protein S19
rps20	40S ribosomal protein S20
rps21	40S ribosomal protein S21
rps23	40S ribosomal protein S23
rps2401	40S ribosomal protein S24
rps2502	40S ribosomal protein S25
rps2602	40S ribosomal protein S26
rps2801	40S ribosomal protein S28
rpl901	60S ribosomal protein L9
rpl13	60S ribosomal protein L13
rpl14	60S ribosomal protein L14
rpl15	60S ribosomal protein L15
rpl2401	60S ribosomal protein L24
rpl2702	60S ribosomal protein L27
rpl44	60S ribosomal protein L28/L44
rpl35	60S ribosomal protein L35
rpl3703	60S ribosomal protein L37-A
rpl4301	60S ribosomal protein L37a
rpl3802	60S ribosomal protein L38
rpp203	60S acidic ribosomal protein P2-C
mrpl6	Mitochondrial ribosomal protein subunit L16
mrps17	Mitochondrial ribosomal protein subunit S17
fib1	rRNA 2'-O-methyltransferase fibrillarin
rpa12	DNA-directed RNA polymerase I subunit RPA12

rpc37	DNA-directed RNA polymerase III subunit rpc5
ltv1	Non-ribosomal factor required for efficient nuclear export of the ribosomal 40S subunit
ran1	Negative regulator of sexual conjugation and meiosis
aps1	Diphosphoinositol polyphosphate phosphohydrolase
btf3	Nascent polypeptide-associated complex (NAC) subunit beta
ppn	Endopolyphosphatase
Steroids and lipids synthesis	
erg10	Acetyl-CoA acetyltransferase
erg11	Lanosterol 14-alpha demethylase
erg25	Methylsterol monooxygenase
sts1	C-24(28) sterol reductase
SPAC22A12.16.1	Probable ATP-citrate synthase subunit 2
plh1	Phospholipid:diacylglycerol acyltransferase
Leucine synthesis	
leu1	3-isopropylmalate dehydrogenase
leu2	3-isopropylmalate dehydratase
oac1	Mitochondrial oxaloacetate transporter
fsf1	Mitochondrial citrate transporter
SPAC19G12.05.1	Mitochondrial citrate transporter
Others	
gpd1	Glycerol-3-phosphate dehydrogenase
SPAC26F1.07.1	Glucose 1-dehydrogenase (NADP+)
tpi1	Triosephosphate isomerase
pi047	Adenosylhomocysteinase
met26	5-methyltetrahydropteroyltriglutamate-homocysteine methyltransferase
SPCC338.14	Adenosine kinase
SPBC24C6.09c.1	Phosphoketolase family protein
rds1	May have a function in stress-related responses of the cell

SPAC139.03

SPBC2A9.02

NETWORK 2

ung1

rhp14

rev1

rhp6

ubc11

ubc7

cia1

hip4

hhf1

mst1

ngg1

Transcriptional factor
NAD dependent epimerase/dehydratase family protein

Uracil-DNA glycosylase
DNA repair protein
DNA repair protein
Ubiquitin-conjugating enzyme E2 2
Ubiquitin-conjugating enzyme E2-20 kDa
Ubiquitin-conjugating enzyme E2-18 kDa
Histone chaperone
Histone promoter control protein 2
Histone H4
Histone acetyltransferase
Chromatin-remodeling complexes subunit