

Transcriptomic response in symptomless roots of clubroot infected kohlrabi mirrors resistant plants

Supplementary Tables

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Table S1: Total (raw) and good quality reads of the sequenced libraries. Only reads with a minimum length of 75 bp and a sliding window of 5 bp and an average quality score > 20 were kept. Illumina adapters were removed.

Library	Total reads	Good quality reads
C	35470516	18724257
SL-1	25749647	17112091
SL-2	26086772	15292763
SL-3	22998692	13487038
WG-1	23140251	15398974
WG-2	21623635	13055601
WG-3	30159869	16748310
BG-1	27662722	15482391
BG-2	33728086	17655530
BG-3	31782654	19236687
Total	278402844	162193642

Table S2: Kohlrabi DEGs compared across the three root tissue types.

Type of DEGs	SL vs WG	SL vs BG	WG vs BG
Up-regulated DEGs	1619	942	6
Down-regulated DEGs	2280	2571	13
Total DEGs	3899	3513	19

Table S3: Kohlrabi DEGs per COG category in infected plants. Total DEGs of SL vs WG, SL vs BG, and WG vs BG are given. Individual DEGs can occur in more than one comparison but are counted only once. The five categories containing most DEGs are highlighted in bold. Orange: Information and Storage Processing; Green: Metabolism; Blue: Cellular Process and Signalling; Grey: Poorly Characterized.

COG category	# of DEGs
A: RNA processing and modification	74
B: Chromatin structure and dynamics	30
C: Energy production and conservation	130
D: Cell cycle control and mitosis	87
E: Amino acid metabolism and transport	179
F: Nucleotide metabolism and transport	42
G: Carbohydrate metabolism and transport	388
H: Coenzyme metabolism	46
I: Lipid metabolism	170
J: Translation	136
K: Transcription	479
L: Replication and repair	71
M: Cell wall/membrane/envelop biogenesis	52
N: Cell motility	0
O: Post-translational modification, protein turnover, chaperon functions	349
P: Inorganic ion transport and metabolism	195
Q: Secondary Structure	251
R: General function prediction only	0
S: Function unknown	1435
T: Signal transduction	538
U: Intracellular trafficking and secretion	136
V: Defence mechanisms	30
W: Extracellular structures	3
X: Multiple function	127
Y: Nuclear structure	1
Z: Cytoskeleton	49
N/A: Unassigned	206

Table S4: Complete list of kohlrabi DEGs between BG and WG. The Functional annotations are given as returned by eggNOG mapper. Up-regulated genes are highlighted in red, down-regulated genes in blue.

Transcript ID	Functional annotation	log₂ fold change
Bol 94671.3.1.4	F-box kelch-repeat protein	10.18
Bol 99971.0.1.7	Acyl-CoA synthetase long-chain family	8.88
Bol 76700.1.2.2	chitinase	8.72
Bol 97623.1.1.1	Aspartyl protease family protein	8.19
Bol 94026.0.2.1	GDE1 homolog	8.13
Bol 159044.0.1.1	inhibitor	5.20
Bol 99469.1.6.8	Glutamate decarboxylase	-3.77
Bol 93718.3.1.2	Indole-3-acetic acid-amido synthetase	-6.15
Bol 134791.0.1.1	expressed protein	-7.21
Bol 100433.0.1.1	Armadillo/beta-catenin-like repeat	-8.09
Bol 85918.1.1.4	May negatively regulate the SNF1 kinase	-8.15
Bol 96726.0.1.1	Farnesyl-diphosphate farnesyltransferase	-8.24
Bol 99205.7.2.8	NA	-8.36
Bol 96830.0.1.6	phosphatase 2C	-8.38
Bol 96394.0.1.1	glycosyltransferase family 14 protein	-8.40
Bol 98490.1.1.3	RNA recognition motif containing protein	-8.53
Bol 96780.1.1.3	AUX/IAA family	-8.57
Bol 99251.0.2.4	Cytochrome P450	-8.62
Bol 64904.0.1.1	Plastocyanin-like domain	-10.61

Table S5: DEGs between the uninfected control plant and the three tissue types of infected kohlrabi plants (SL, WG, BG).

Type of DEGs	SL vs C	WG vs C	BG vs C
Up-regulated DEGs	4606	8347	6031
Down-regulated DEGs	1721	5075	5390
Total DEGs	6327	13422	11421

Table S6: Kohlrabi DEGs per COG category between infected and control plants. Total DEGs of SL vs C, WG vs C, and BG vs C are given. Individual DEGs can occur in more than one comparison but are counted only once. The five categories containing most DEGs are highlighted in bold. Orange: Information and Storage Processing; Green: Metabolism; Blue: Cellular Process and Signalling; Grey: Poorly Characterized.

COG category	# of DEGs
A: RNA processing and modification	504
B: Chromatin structure and dynamics	141
C: Energy production and conservation	469
D: Cell cycle control and mitosis	289
E: Amino acid metabolism and transport	528
F: Nucleotide metabolism and transport	211
G: Carbohydrate metabolism and transport	1149
H: Coenzyme metabolism	203
I: Lipid metabolism	496
J: Translation	681
K: Transcription	1636
L: Replication and repair	403
M: Cell wall/membrane/envelop biogenesis	182
N: Cell motility	0
O: Post-translational modification, protein turnover, chaperon functions	1566
P: Inorganic ion transport and metabolism	605
Q: Secondary Structure	563
R: General function prediction only	0
S: Function unknown	5081
T: Signal transduction	1830
U: Intracellular trafficking and secretion	672
V: Defence mechanisms	102
W: Extracellular structures	11
X: Multiple function	528
Y: Nuclear structure	2
Z: Cytoskeleton	223
N/A: Unassigned	1155

Table S7: Twenty highest expressed genes of *Plasmodiophora brassicae* in WG. Annotation given as predicted with eggNOG mapper. Putative secreted proteins are tagged (●). FPKM: fragments per kilobase (of exons) per million reads. NA: not assigned.

Transcript ID	Functional annotation	FPKM	Secreted
PbraAT 83084.17.1.2	NA	14838	
PbraAT 133546.1.1.1	glutathione-S-transferase	12890	
PbraAT 108093.0.1.1	NA	10438	
PbraAT 146283.0.1.1	heat shock protein	9304	
PbraAT 83084.17.1.1	NA	7262	
PbraAT 83084.18.1.1	NA	7031	●
PbraAT 158899.8.1.1	NA	6733	
PbraAT 100779.1.1.1	PPIases accelerate the folding of proteins	5484	
PbraAT 133446.2.1.1	carboxyl methyltransferase (PbBSMT)	4983	●
PbraAT 120659.1.1.1	ribosomal protein	3330	
PbraAT 108093.5.1.1	ankyrin repeat domain-containing protein	3168	
PbraAT 108221.0.1.1	60s ribosomal protein	3167	
PbraAT 108279.2.1.1	ribosomal protein	3084	
PbraAT 108037.1.1.1	finger protein	3048	
PbraAT 100599.0.1.1	ribosomal protein	2332	
PbraAT 158960.0.1.1	60s ribosomal protein	2271	
PbraAT 158883.0.1.1	NA	2113	
PbraAT 158922.0.1.1	NA	1789	
PbraAT 121753.0.1.1	ribosomal protein L12	1620	
PbraAT 146514.1.1.1	NA	1561	

Table S8: Twenty highest expressed genes of *Plasmodiophora brassicae* in BG. Annotation given as predicted with eggNOG mapper. Putative secreted proteins are tagged (●). FPKM: fragments per kilobase (of exons) per million reads. NA: not assigned.

Transcript ID	Functional annotation	FPKM	Secreted
PbraAT 133546.1.1.1	glutathione-S-transferase	25036	
PbraAT 146283.0.1.1	heat shock protein	18301	
PbraAT 83084.17.1.2	NA	12855	
PbraAT 100779.1.1.1	PPIases accelerate the folding of proteins	8838	
PbraAT 158899.8.1.1	NA	8751	
PbraAT 108093.0.1.1	NA	8468	
PbraAT 133446.2.1.1	carboxyl methyltransferase (PbBSMT)	7182	●
PbraAT 83084.17.1.1	NA	6570	
PbraAT 83084.18.1.1	NA	6020	●
PbraAT 146514.1.1.1	NA	5713	
PbraAT 120659.1.1.1	ribosomal protein	4744	
PbraAT 108279.2.1.1	ribosomal protein	3716	
PbraAT 133396.0.1.1	heat shock protein	3528	
PbraAT 100599.0.1.1	ribosomal protein	3503	
PbraAT 108221.0.1.1	60s ribosomal protein	3366	
PbraAT 158960.0.1.1	60s ribosomal protein	3170	
PbraAT 146422.1.1.1	peroxiredoxin	2950	
PbraAT 158936.0.1.1	10 kda heat shock protein	2929	
PbraAT 158883.0.1.1	NA	2630	
PbraAT 161208.0.1.1	ribosomal protein	2604	

Table S9: *Plasmodiophora brassicae* DEGs between BG and WG. Annotations are given as predicted with eggNOG mapper. Up-regulated genes in BG are highlighted in red, down-regulated genes in BG in blue.

Transcript ID	Functional annotation	log ₂ fold change
PbraAT 71424.0.1.5	heat shock protein	11.45
PbraAT 52700.0.2.1	DNA-directed RNA polymerase	9.56
PbraAT 26420.0.2.1	structural maintenance of chromosomes	9.40
PbraAT 69953.0.1.2	Scl Tall1 interrupting locus	8.82
PbraAT 93256.0.5.1	retrotransposon protein	-8.36