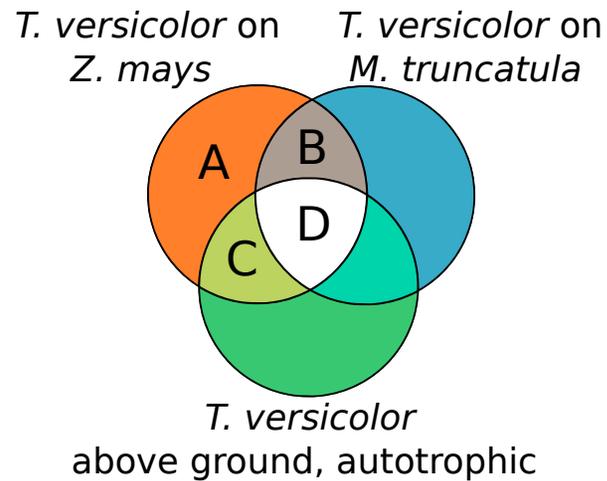
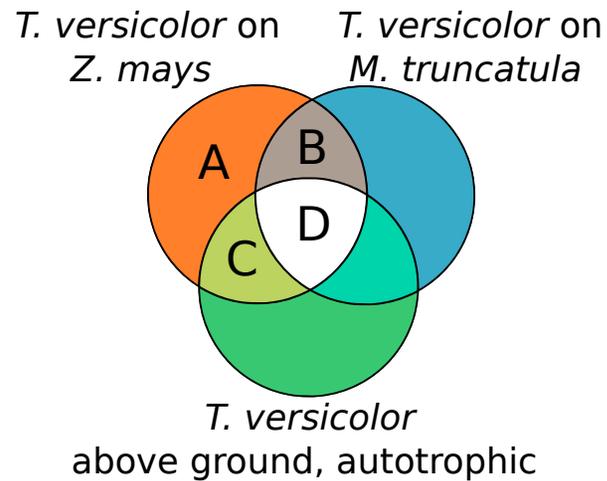


Additional file 4: Figure S3. A) GO Slim Function category analysis for the interface transcriptome of *T. versicolor* grown on *Z. mays*. Chi-Square test ($P \ll 0.0001$) of GO Slim terms represented in the indicated regions (A-D) of the Venn. The numbers of unigenes in each GO category for regions A-D are indicated in the table. Cells with strongly positive residual values (>4) are indicated as **bold+** and strongly negative residual values (<-4) are indicated as **bold-**.



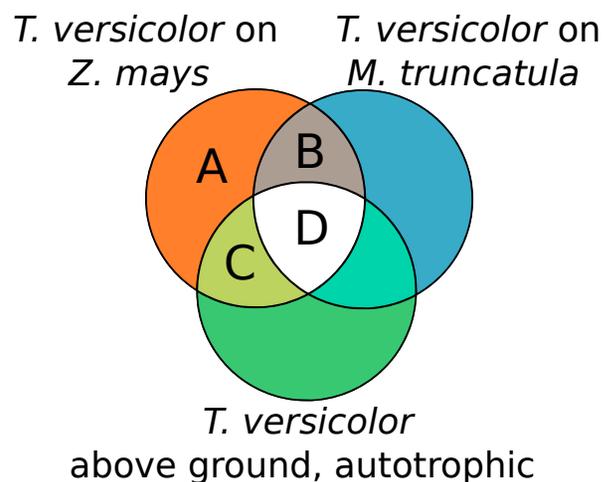
GO Function	A	B	C	D
DNA or RNA binding	24	43	80	515
hydrolase activity	62	177	187	1688
kinase activity	33	70	51	889
nucleic acid binding	3	13	11	152
nucleotide binding	19	20-	34	441
other binding	107	205	147	1298
other enzyme activity	66	146-	159	1791
other molecular functions	227	581+	497	3642
protein binding	32	55	42	644
receptor binding or activity	1	2	0	37
structural molecule activity	1-	12-	18	465-
transcription factor activity	61+	157+	63	531
transferase activity	25-	78-	91	1182
transporter activity	21	66-	57	974
No GO Function	123+	237+	121	768-

Additional file 4: Figure S3. B) GO Slim Component category analysis for the interface transcriptome of *T. versicolor* grown on *Z. mays*. Chi-Square test ($P \ll 0.0001$) of GO Slim terms represented in the indicated regions (A-D) of the Venn. The numbers of unigenes in each GO category for regions A-D are indicated in the table. Cells with strongly positive residual values (>4) are indicated as **bold+** and strongly negative residual values (<-4) are indicated as **bold-**.



GO Component	A	B	C	D
cell wall	7	8	11	55
chloroplast	59	110-	227+	1415
cytosol	0	9	12	185
ER	1	22	10	257
extracellular	3	13	3	40
Golgi apparatus	2	12	2	173
mitochondria	18	42	36	647
nucleus	82	189	129	1148
other cellular components	300	656	504	5455
other cytoplasmic components	11	25	31	493
other intracellular components	17	36	24	378
other membranes	150	406	316	3151
plasma membrane	4	10	12	145
plastid	2	5	15	81
ribosome	1	7-	17	309
No GO Component	148+	312+	209-	1085-

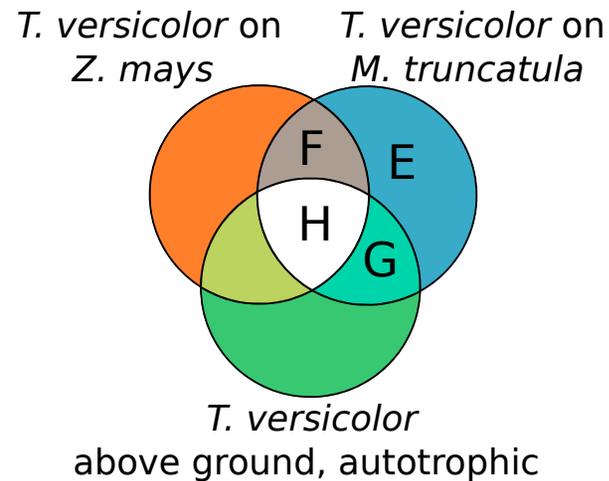
Additional file 4: Figure S3. C) GO Slim Process category analysis for the interface transcriptome of *T. versicolor* grown on *Z. mays*. Chi-Square test ($P \ll 0.0001$) of GO Slim terms represented in the indicated regions (A-D) of the Venn. The numbers of unigenes in each GO category for regions A-D are indicated in the table. Cells with strongly positive residual values (>4) are indicated as **bold+** and strongly negative residual values (<-4) are indicated as **bold-**.



GO Process	A	B	C	D
cell organization and biogenesis	9	27	29	286
developmental processes	14	19	30	145
DNA or RNA metabolism	2	13	5	48
electron transport or energy pathways	21	39	27	298
other biological processes	376	910+	711	5827
other cellular processes	47	124	96	1388
other metabolic processes	147-	357-	398	4393+
protein metabolism	1	2	0	14
response to abiotic or biotic stimulus	12	16	28	230
response to stress	2	6	1	65
signal transduction	5	9	15	148
transcription	0	1	3	42
transport	29	72-	58-	1157+
No GO Process	140+	267+	157	976-

Additional file 4: Figure S3. D) GO Slim Function category analysis for the interface transcriptome of *T. versicolor* grown on *M. truncatula*.

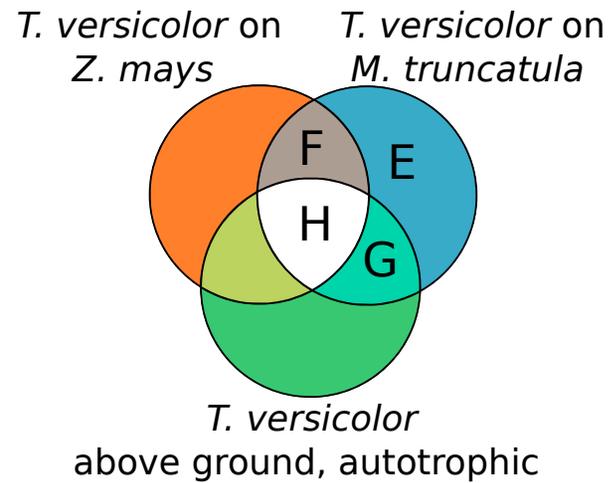
Chi-Square test ($P \ll 0.0001$) of GO Slim terms represented in the indicated regions (E-H) of the Venn. The numbers of unigenes in each GO category for regions E-H are indicated in the table. Cells with strongly positive residual values (>4) are indicated as **bold+** and strongly negative residual values (<-4) are indicated as **bold-**.



GO Function	E	F	G	H
DNA or RNA binding	9	41	11	444
hydrolase activity	33	156	47	1423
kinase activity	39	66	20	718
nucleic acid binding	2	8	4	118
nucleotide binding	15	22	6	353
other binding	51	184	38	1125
other enzyme activity	20	132-	38	1526
other molecular functions	102	568+	111	3172
protein binding	12	51	16	569
receptor binding or activity	0	2	0	28
structural molecule activity	2	10-	7	446
transcription factor activity	30	141+	16	440
transferase activity	25	64-	26	991
transporter activity	9	62	11	795
No GO Function	72+	219+	34	677-

Additional file 4: Figure S3. E) GO Slim Component category analysis for the interface transcriptome of *T. versicolor* grown on *M. truncatula*.

Chi-Square test ($P \ll 0.0001$) of GO Slim terms represented in the indicated regions (E-H) of the Venn. The numbers of unigenes in each GO category for regions E-H are indicated in the table. Cells with strongly positive residual values (>4) are indicated as **bold+** and strongly negative residual values (<-4) are indicated as **bold-**.



GO Component	E	F	G	H
cell wall	1	6	1	53
chloroplast	20	111	45	1211
cytosol	3	8	2	177
ER	0	15	5	247
extracellular	4	14	1	39
Golgi apparatus	0	12	2	137
mitochondria	0	35	6	544
nucleus	44	169	28	941
other cellular components	152	572	128	4578
other cytoplasmic components	5	29	4	407
other intracellular components	8	36	12	359
other membranes	102	402	86	2657
plasma membrane	0	7	1	120
plastid	2	5	2	75
ribosome	2	6-	7	293
No GO Component	78+	299+	55	987-

Additional file 4: Figure S3. F) GO Slim Process category analysis for the interface transcriptome of *T. versicolor* grown on *M. truncatula*. Chi-Square test ($P \ll 0.0001$) of GO Slim terms represented in the indicated regions (E-H) of the Venn. The numbers of unigenes in each GO category for regions E-H are indicated in the table. Cells with strongly positive residual values (>4) are indicated as **bold+** and strongly negative residual values (<-4) are indicated as **bold-**.

