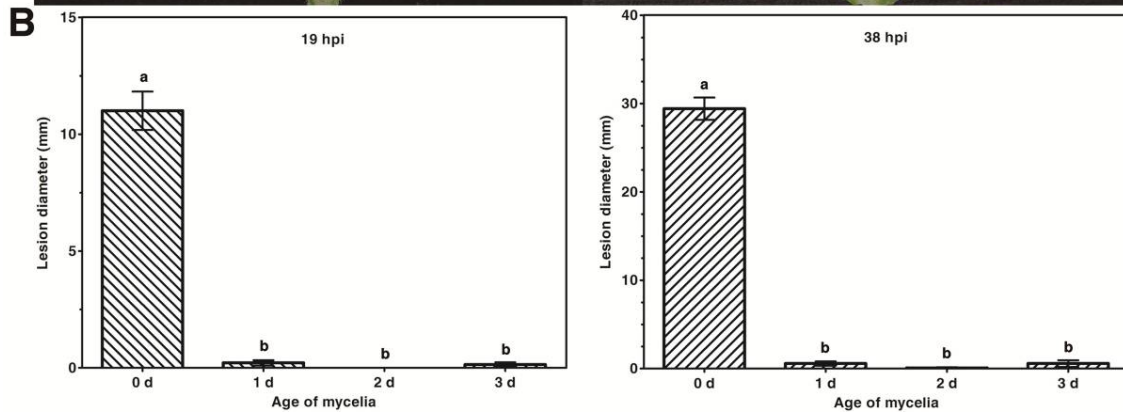


1 Supplemental Materials

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5 **Appendix A** The influence of mycelial age on *S. sclerotiorum* virulence in *Nicotiana benthamiana* leaves.

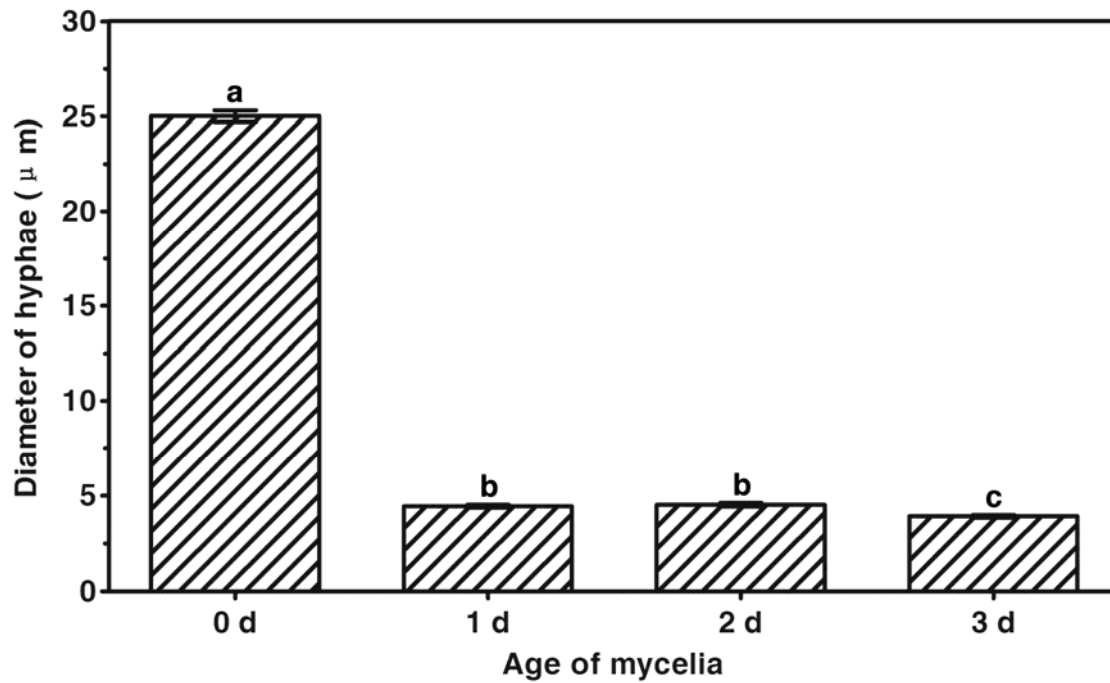
6 A, Necrotic disease symptom in *N. benthamiana* leaves inoculated with *S. sclerotiorum* mycelia at different

7 ages at 19 hpi and 38 hpi. B, Statistical analysis of the lesion diameter of the inoculated leaves. Significant

8 difference between lesion diameter is indicated as small letters ( $P \leq 0.05$ , DMRT).

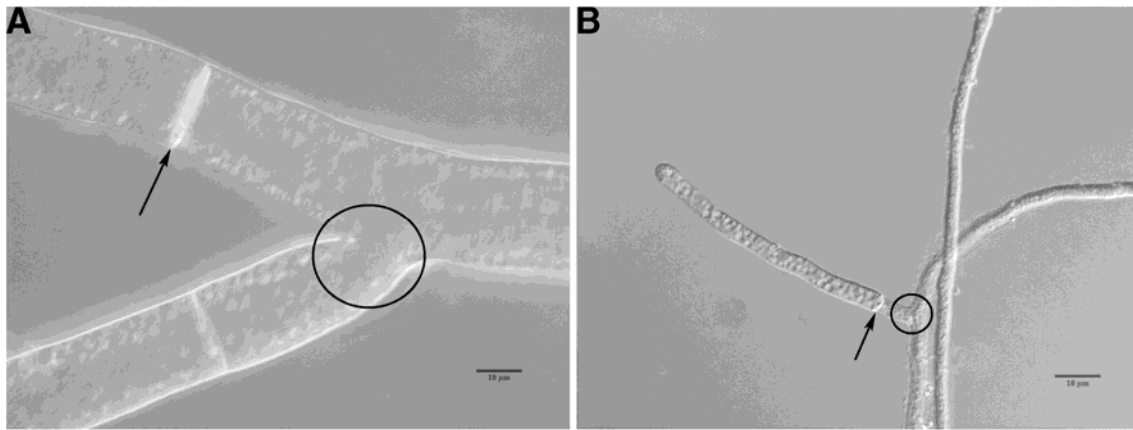
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**Appendix B** Comparison of the diameter of *S. sclerotiorum* hyphae at different culture time/ages. The hyphal diameter was measured under light microscopy using the Image-Pro Plus software. Data were analyzed using SPSS. Error bars indicate SD. Letters indicate significant differences ( $P \leq 0.05$ , DMRT).



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39 **Appendix C** Comparison of the structure of young vegetative and aerial hyphae of *S. sclerotiorum*.

40 Morphological structure of young vegetative (A) and aerial hyphae (B) of *S. sclerotiorum*. The septa and

41 branches were indicated by arrows and circles respectively. Bar=10 µm.

42 **Appendix D** List of the identified 95 proteins differentially expressed between young (0 day-old) and old (3 day-old) mycelia of *S. sclerotiorum*

Sample No	Spot No	Fold change (Aerial/Young vegetative) <sup>a</sup>	Protein	Accession number (NCBI or UNIPROT)	Predicted MW/PI	Score	Functional classification
s104	1951	(-)10000	Gamma-glutamyltransferase, protein SS1G_14127 [Sclerotinia sclerotiorum 1980]	gi 156031038	52564.9/5.46	148	Amino acid biosynthesis-Glu /antioxidation
s19	4402	(+)2.4	Gamma-glutamyltransferase, protein SS1G_14127 [Sclerotinia sclerotiorum 1980]	gi 156031038	52564.9/5.46	132	Amino acid biosynthesis-Glu /antioxidation
s70	661	(+)3.4	Gamma-glutamyltransferase, protein SS1G_14127 [Sclerotinia sclerotiorum 1980]	gi 156031038	52564.9/5.46	138	Amino acid biosynthesis-Glu /antioxidation
s71	732	(+)10.4	Gamma-glutamyltransferase, protein SS1G_14127 [Sclerotinia sclerotiorum 1980]	gi 156031038	52564.9/5.46	139	Amino acid biosynthesis-Glu /antioxidation
s30	165	(-)10000	DAHP synthetase I family, conserved hypothetical protein [Sclerotinia sclerotiorum 1980]	gi 156058015	39262.4/6.47	391	Amino acid biosynthesis-aromatic amino acid
s46	951	(-)10000	Dihydroxy-acid dehydratase, protein SS1G_08852 [Sclerotinia sclerotiorum 1980]	gi 156048242	65063.2/6.16	712	Amino acid biosynthesis-branched chain amino acid
s7	815	(-)10000	Ketol-acid reductoisomerase, mitochondrial precursor [Sclerotinia sclerotiorum 1980]	gi 156059686	44114.4/8.78	767	Amino acid biosynthesis-branched chain amino acid

s40	524	(-)10000	Homoserine dehydrogenase, hypothetical protein SS1G_14424 [Sclerotinia sclerotiorum 1980]	gi 156030657	38815.4/5.93	315	Amino acid metabolism
s85	1696	(+)2.0	Glutathione S-transferase, hypothetical protein SS1G_08210 [Sclerotinia sclerotiorum 1980]	gi 156049007	27833.1/5.01	487	Antioxadation, detoxification
s2	443	(-)2.6	Ascorbate peroxidase, hypothetical protein SS1G_12928 [Sclerotinia sclerotiorum 1980]	gi 156036478	40669.3/9.01	798	Antioxidation
s72	748	(+)3.6	Catalase, hypothetical protein SS1G_05200 [Sclerotinia sclerotiorum 1980]	gi 156055696	34663.1/5.71	730	Antioxidation
s23	4372	(+)3.4	Cerato-platanin family protein, hypothetical protein SS1G_10096 [Sclerotinia sclerotiorum 1980]	gi 156043986	13970.8/4.6	423	Fungus-plant interaction
s97	611	(-)10000	F-actin capping protein alpha subunit, hypothetical protein SS1G_13400 [Sclerotinia sclerotiorum 1980]	gi 156034194	26507.6/6.54	739	Growth-actin filament capping
s27	3847	(+)5.6	Chromosome segregation protein SMC, primarily archaeal type, hypothetical protein SS1G_02331 [Sclerotinia sclerotiorum 1980]	gi 156060385	47965.3/5.15	545	Growth-cell division
s14	194	(-)10000	Hex1-like Woronin body major protein, hypothetical protein SS1G_03527 [Sclerotinia sclerotiorum 1980]	gi 156059030	18148.3/6.51	465	Growth-cell integrity

s28	2533	(+)10.3	Ricin-type beta-trefoil lectin domain-containing Agglutinin [A7XUK7]; predicted protein [Sclerotinia sclerotiorum 1980]	gi 156045299	16729.4/6.41	201	Growth-cell recognition and adhesion
s58	1804	(-)10000	Tropomyosin like, hypothetical protein SS1G_03072 [Sclerotinia sclerotiorum 1980]	gi 156061853	18609.4/4.84	232	Growth-morphogenesis
s21	1688	(+)2.8	Myosin-1 [Aspergillus terreus NIH2624]	gi 115401584	137094.3/9.48	80	Growth-polarized movement and transport
s54	1586	(-)10000	EB1-like microtubule-associated protein, hypothetical protein SS1G_07164 [Sclerotinia sclerotiorum 1980]	gi 156051514	27367.7/4.94	589	Growth-promoting microtubule polymerisation
s12	1949	(-)10000	Hydrophobic surface binding protein A, hypothetical protein SS1G_09270 [Sclerotinia sclerotiorum 1980]	gi 156045988	17951.6/4.64	213	Hydrophobic surface degradation
s82	1581	(+)4.1	Hydrophobic surface binding protein A, hypothetical protein SS1G_09270 [Sclerotinia sclerotiorum 1980]	gi 156045988	17951.6/4.64	116	Hydrophobic surface degradation
s94	1495	(+)3.9	Hydrophobic surface binding protein A, hypothetical protein SS1G_09270 [Sclerotinia sclerotiorum 1980]	gi 156045988	17951.6/4.64	208	Hydrophobic surface degradation
s95	3145	(+)7.0	Hydrophobic surface binding protein A, hypothetical protein SS1G_09270 [Sclerotinia sclerotiorum 1980]	gi 156045988	17951.6/4.64	213	Hydrophobic surface degradation

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s98	1383	(-)10000	Hydrophobic surface binding protein A, hypothetical protein SS1G_09270 [Sclerotinia sclerotiorum 1980]	gi 156045988	17951.6/4.64	220	Hydrophobic surface degradation
s101	1978	(-)10000	2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily, hypothetical protein SS1G_07964 [Sclerotinia sclerotiorum 1980]	gi 156050753	31713.1/5.29	609	Metabolism
s47	1062	(-)10000	2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily, hypothetical protein SS1G_07964 [Sclerotinia sclerotiorum 1980]	gi 156050753	31713.1/5.29	559	Metabolism
s87	1812	(+)2.8	Alpha/beta hydrolase family, hypothetical protein SS1G_07096 [Sclerotinia sclerotiorum 1980]	gi 156051378	24795.5/4.74	90	Metabolism
s79	1386	(+)2.7	Alpha-mannosidase, hypothetical protein SS1G_04148 [Sclerotinia sclerotiorum 1980]	gi 156056835	122701.4/5.92	223	Metabolism
s99	1421	(-)10000	Alpha-mannosidase, hypothetical protein SS1G_04148 [Sclerotinia sclerotiorum 1980]	gi 156056835	122701.4/5.92	603	Metabolism
s26	3741	(+)3.8	Haloacid dehalogenase-like hydrolases, subfamily IA, variant 3 with third motif having DD or ED, hypothetical protein SS1G_00721 [Sclerotinia sclerotiorum	gi 156065421	27042.8/5.1	509	Metabolism

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			1980]					
s42	534	(-2.9	Metallo-beta-lactamase superfamily, hypothetical protein SS1G_00290 [Sclerotinia sclerotiorum 1980]	gi 156064565	33505.9/6.19	130	Metabolism	
s18	3010	(+)2.3	NADP-dependent Mannitol dehydrogenase, hypothetical protein SS1G_08799 [Sclerotinia sclerotiorum 1980]	gi 156048136	28333.1/5.79	361	Metabolism	
s75	769	(+)2.7	NADPH-dependent FMN reductase, hypothetical protein SS1G_14285 [Sclerotinia sclerotiorum 1980]	gi 156031009	25967.1/5.64	339	Metabolism	
s3	1259	(-5.9	Nitroreductase-like family 4, hypothetical protein SS1G_09615 [Sclerotinia sclerotiorum 1980]	gi 156044853	29804.5/9.2	469	Metabolism	
s51	1426	(-)10000	Nitroreductase-like family 4, hypothetical protein SS1G_09615 [Sclerotinia sclerotiorum 1980]	gi 156044853	29804.5/9.2	126	Metabolism	
s31	173	(-)10000	Putative NADP-dependent oxidoreductases (dehydrogenase), hypothetical protein SS1G_06287 [Sclerotinia sclerotiorum 1980]	gi 156054878	37833.6/6.48	539	Metabolism	
s35	327	(-)7.8	Acetate-CoA ligase (acetyl-CoA synthetase) [Sclerotinia sclerotiorum 1980]	gi 156055998	73986.8/6.11	628	Metabolism- Acetyl CoA biosynthesis	

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s29	128	(-)2.8	Acetyl-CoA C-acetyltransferase / thiolase, hypothetical protein SS1G_12152 [Sclerotinia sclerotiorum 1980]	gi 156040271	41558.8/6.68	284	Metabolism- Acetyl CoA fatty acid (ketogenesis -first step, acetyl CoA reduction)
s90	1479	(+)2.3	3-hydroxy-3-methylglutaryl-CoA synthase, hypothetical protein SS1G_14433 [Sclerotinia sclerotiorum 1980]	gi 156030675	50551.1/5.89	570	Metabolism- Acetyl CoA (ketogenesis -2nd step, acetyl CoA reduction)
s57	1779	(-)10000	mitochondrial F1 ATPase subunit alpha [Magnaporthe grisea 70-15]	gi 39972915	59538.2/9.28	96	Metabolism- energy
s68	257	(+)2.8	3-ketoacyl-(acyl-carrier-protein) reductase, hypothetical protein SS1G_13315 [Sclerotinia sclerotiorum 1980]	gi 156034759	29547.2/5.9	391	Metabolism- fatty acid biosynthesis
s73	754	(+)3.1	Acyl-CoA synthetases (AMP-forming)/AMP-acid ligases II, hypothetical protein SS1G_09846 [Sclerotinia sclerotiorum 1980]	gi 156045315	65526.8/5.71	491	Metabolism- lipid
s6	489	(-)10000	S-adenosylmethionine synthetase (EC 2.5.1.6)[Botryotinia fuckeliana (strain B05.10)]	gi 154315126	43095.2/5.91	716	Metabolism-miscellaneous
s39	484	(-)10000	S-adenosylmethionine synthetase [Botryotinia fuckeliana B05.10]	gi 154315126	43095.2/5.91	856	Metabolism-miscellaneous
s24	2316	(+)3.8	Citrate synthase, mitochondrial precursor [Sclerotinia sclerotiorum 1980]	gi 156063018	50072.9/7.21	882	Metabolism-oxalic acid
s5	200	(-)10000	Citrate synthase, mitochondrial precursor	gi 156063018	50072.9/7.21	779	Metabolism-oxalic acid

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			[Sclerotinia sclerotiorum 1980]				
s69	460	(+)3.9	Citrate synthase, mitochondrial precursor [Sclerotinia sclerotiorum 1980]	gi 156063018	50072.9/7.21	225	Metabolism-oxalic acid
s74	761	(+)3.4	Citrate synthase, mitochondrial precursor [Sclerotinia sclerotiorum 1980]	gi 156063018	50072.9/7.21	422	Metabolism-oxalic acid
s66	137	(+)4.2	Fumarate reductase, hypothetical protein SS1G_06222 [Sclerotinia sclerotiorum 1980]	gi 156054748	68013.5/6.36	539	Metabolism-oxalic acid
s17	345	(-)10000	Glyoxysomal and mitochondrial malate dehydrogenase, conserved hypothetical protein [Sclerotinia sclerotiorum 1980]	gi 156032838	35650.9/8.48	576	Metabolism-oxalic acid
s32	181	(-)10000	Glyoxysomal and mitochondrial malate dehydrogenase, conserved hypothetical protein [Sclerotinia sclerotiorum 1980]	gi 156032838	35650.9/8.48	749	Metabolism-oxalic acid
s67	142	(+)5.9	Glyoxysomal and mitochondrial malate dehydrogenase, hypothetical protein SS1G_08975 [Sclerotinia sclerotiorum 1980]	gi 156048488	34499.7/6.77	440	Metabolism-oxalic acid
s37	400	(-)2.2	Isocitrate dehydrogenase, hypothetical protein SS1G_04924 [Sclerotinia sclerotiorum 1980]	gi 156055146	50339.7/7.67	584	Metabolism-oxalic acid
s41	532	(-)2.0	Isocitrate dehydrogenase, hypothetical protein SS1G_04924 [Sclerotinia sclerotiorum 1980]	gi 156055146	50339.7/7.67	848	Metabolism-oxalic acid

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s36	350	(-)10000	Isocitrate lyase [Sclerotinia sclerotiorum 1980]	gi 156055248	60801.6/6.16	840	Metabolism-oxalic acid
s60	1839	(-)10000	Oxaloacetate acetylhydrolase [Aspergillus oryzae RIB40]	gi 169777425	36311.5/5.78	75	Metabolism-oxalic acid
s49	1293	(-)10000	Oxaloacetate acetylhydrolase-like protein, hypothetical protein SS1G_08218 [Sclerotinia sclerotiorum 1980]	gi 156049023	35998.5/5.27	256	Metabolism-oxalic acid
s59	1832	(-)10000	Oxaloacetate acetylhydrolase-like protein, hypothetical protein SS1G_08218 [Sclerotinia sclerotiorum 1980]	gi 156049023	35998.5/5.27	99	Metabolism-oxalic acid
s8	822	(-)10000	Oxaloacetate acetylhydrolase-like protein, hypothetical protein SS1G_08218 [Sclerotinia sclerotiorum 1980]	gi 156049023	35998.5/5.27	352	Metabolism-oxalic acid
s33	201	(-)10000	Glyceraldehyde-3-phosphate dehydrogenase [Sclerotinia sclerotiorum 1980]	gi 156050423	36749.7/5.93	222	Metabolism-respiration
s44	733	(-)10000	hypothetical protein SS1G_03728 [Sclerotinia sclerotiorum 1980], Putative NADH-ubiquinone oxidoreductase ((Botryotinia fuckeliana (strain BcDW1)) [M7UQL0])	gi 156059432	21261.8/6.43	801	Metabolism-respiratory chains (electron transfer)
s10	1040	(-)10000	NADH:ubiquinone oxidoreductase (Nuo) subunit E subfamily, hypothetical protein SS1G_04889 [Sclerotinia sclerotiorum]	gi 156055076	32040.1/8.13	519	Metabolism-respiratory chains (electron transfer)

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s43	726	(-)10000	Diphosphomevalonate decarboxylase, hypothetical protein SS1G_03958 [Sclerotinia sclerotiorum 1980]	gi 156059890	41097.8/5.81	195	Metabolism-secondary
s16	249	(-)10000	Adenosine 5'-phosphosulfate kinase, conserved hypothetical protein [Sclerotinia sclerotiorum 1980]	gi 156030585	23140.1/6.34	279	Metabolism-sulfur
s102	380	(-)10000	20S proteasome alpha subunit E, conserved hypothetical protein [Sclerotinia sclerotiorum 1980]	gi 156045147	26443.2/4.86	266	Protein degradation
s52	1428	(-)10000	20S proteasome subunit alpha type, hypothetical protein SS1G_08759 [Sclerotinia sclerotiorum 1980]	gi 156048056	29109.7/5.12	644	Protein degradation
s55	1607	(-)3.1	FKBP-type peptidyl-prolyl cis-trans isomerase, hypothetical protein SS1G_13012 [Sclerotinia sclerotiorum 1980]	gi 156035617	21185.8/4.94	162	Protein folding
s93	1757	(+)3.1	Hsp70 protein, hypothetical protein SS1G_01888 [Sclerotinia sclerotiorum 1980]	gi 156063540	79224.5/5.07	671	Protein-molecular chaperone
s88	1844	(+)2.5	heat shock 70 kDa protein [Sclerotinia sclerotiorum 1980]	gi 156064253	68490.2/5.07	223	Protein-molecular chaperone
s100	1955	(-)10000	Heat shock protein 90 [Sclerotinia	gi 156051968	79414.6/4.9	706	Protein-molecular

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			sclerotiorum 1980]				chaperone
s92	1631	(+)2.9	Hsp70 protein, hypothetical protein SS1G_01888 [Sclerotinia sclerotiorum 1980]	gi 156063540	79224.5 /5.07	666	Protein-molecular chaperone
s25	4353	(+)3.8	Serine carboxypeptidase, hypothetical protein SS1G_12413 [Sclerotinia sclerotiorum 1980]	gi 156037404	51574.7/4.63	309	Protein-proteolysis
s63	1932	(-)10000	M18 Peptidase Aspartyl aminopeptidase [Nectria haematococca mpVI 77-13-4]	gi 256732839	54407.6/5.44	72	Protein-proteolysis
s64	1963	(-)10000	40S ribosomal protein S17 [Sclerotinia sclerotiorum 1980]	gi 156049137	16885/9.76	276	Protein synthesis
s1	1145	(-)2.1	54S ribosomal protein L4, mitochondrial hypothetical protein SS1G_09769 [Sclerotinia sclerotiorum 1980][A7EWR0]	gi 156045161/A7EWR0	22237.8/4.92	387	Protein synthesis
s13	2008	(-)10000	60S ribosomal protein L11 [Sclerotinia sclerotiorum 1980]	gi 156036374	19981.6/10.07	92	Protein synthesis
s65	1998	(-)10000	Elongation factor 2 [Sclerotinia sclerotiorum 1980]	gi 156062450	87377.6/6.53	652	Protein synthesis
s91	1898	(+)2.6	Eukaryotic translation initiation factor 3 subunit H, hypothetical protein SS1G_01190 [Sclerotinia sclerotiorum 1980]	gi 156062150	41046.7 /5.95	550	Protein synthesis
s4	186	(-)10000	Guanine nucleotide-binding protein beta subunit [Botryotinia fuckeliana (strain	gi 154301805	34909.4/6.55	792	Signal transduction

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			B05.10)]				
s34	280	(-).2.2	Guanine nucleotide-binding protein beta subunit [Botryotinia fuckeliana (strain B05.10)]; Putative uncharacterized protein [Sclerotinia sclerotiorum (strain ATCC 18683/1980/Ss-1)][A7E6H5 ]	gi 154301805/A7E6H5	34909.4/6.55	365	Signal transduction
s53	1515	(-)10000	DNA-directed RNA polymerase subunit A [Coccidioides immitis RS]	gi 119191177	159844.4/8.89	76	Transcriptional regulation
s56	1630	(-)10000	Mitochondrial FMP27 protein, conserved hypothetical protein [Talaromyces stipitatus ATCC 10500]	gi 242761518	331795.7/8.74	84	Transcriptional regulation
s61	1848	(-)10000	Nuclear transport factor 2 [Sclerotinia sclerotiorum 1980]	gi 156052963	13772.8/4.53	164	Transport between nucleus and cytoplasm
s11	1587	(-)10000	Ran-specific GTPase-activating protein, hypothetical protein SS1G_11444 [Sclerotinia sclerotiorum 1980]	gi 156040932	28822.3/5.01	533	Transport between nucleus and cytoplasm
s20	4339	(+)3.0	Cupin_3 domain-containing protein (DUF861) , hypothetical protein SS1G_03393 [Sclerotinia sclerotiorum 1980]	gi 156058762	15230.6/6.29	231	Unknown
s103	481	(-)10000	Cupin_5 domain-containing protein, hypothetical protein SS1G_06228 [Sclerotinia sclerotiorum 1980]	gi 156054760	17484.5/5.39	670	Unknown

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s76	955	(+)3.4	Cupin_5 domain-containing protein, hypothetical protein SS1G_06228 [Sclerotinia sclerotiorum 1980]	gi 156054760	17484.5/5.39	419	Unknown
s45	906	(-)10000	hypothetical protein SS1G_10556 [Sclerotinia sclerotiorum 1980]; Putative MYG1 (Melanocyte proliferating gene 1) protein (Botryotinia fuckeliana (strain BcDW1)) [M7U0J2]	gi 156043107	39213.8/5.65	697	Unknown
s83	1622	(+)6.1	Hypothetical protein, hypothetical protein SS1G_03084 [Sclerotinia sclerotiorum 1980]	gi 156061877	21001.0/4.42	186	Unknown
s22	1711	(+)3.1	Phosphatidylglycerol/phosphatidylinositol transfer protein , hypothetical protein SS1G_07613 [Sclerotinia sclerotiorum 1980]	gi 156050055	18746.7/5.34	230	Unknown
s50	1377	(-)10000	SAC3/GANP/Nin1/mts3/eIF-3 p25 family, hypothetical protein SS1G_07914 [Sclerotinia sclerotiorum 1980]	gi 156050653	30605.8/5.16	401	Unknown
s78	1358	(+)2.6	SAC3/GANP/Nin1/mts3/eIF-3 p25 family, hypothetical protein SS1G_07914 [Sclerotinia sclerotiorum 1980]	gi 156050653	30605.8/5.16	795	Unknown
s81	1575	(+)10000	Uncharacterized protein conserved in bacteria, hypothetical protein SS1G_12284 [Sclerotinia sclerotiorum 1980]	gi 156040535	10899.4 6.55	187	Unknown

s96	744	(-)2.0	Rossmann-fold oxidoreductase, SS1G_04896	NAD(P)(+)-binding hypothetical protein [Sclerotinia sclerotiorum 1980]	gi 156055090	27400.2/5.88	440	Unknown
s9	909	- 10000	Predicted protein Mad-698-R]	[Postia placenta	gi 242211165	19625.2 /7.62	70	Unknown

43 <sup>a</sup> “+” and “-” indicate up- and down-regulation of the protein in aerial mycelia; while “+10000” and “-10000” mean detection of the protein only in aerial and  
44 young mycelia, respectively.



45 **Appendix E** Retrieved sequences of BLAST searches with the putative *S. sclerotiorum* OAH protein  
 46 (gi|156049023) against *S. sclerotiorum* strain 1980 genome database<sup>a</sup>

Retrieved sequences	Score (Bits)	Expect	Alignment Length	Identities	Positives
SS1G_08218.3: similar to oxaloacetate acetylhydrolase	669.848	0.0	327	327	327
SS1G_04975.3: isocitrate lyase	81.6481	2.69138E-16	92	44	59
SS1G_04900.3: isocitrate lyase	74.7146	3.05198E-14	83	40	53

47 **a.** BLAST searches were performed online with an expectation limit < 1 e-3 against  
 48 database([http://www.broadinstitute.org/annotation/genome/sclerotinia\\_sclerotiorum/MultiHome.html](http://www.broadinstitute.org/annotation/genome/sclerotinia_sclerotiorum/MultiHome.html)).

49 **Appendix F** Retrieved sequences of BLAST searches with the *Aspergillus oryzae* RIB40 OAH protein  
 50 (gi|169777425) against *S. sclerotiorum* strain 1980 genome database<sup>a</sup>

Retrieved sequences	Score (Bits)	Expect	Alignment Length	Identities	Positives
SS1G_08218.3: similar to oxaloacetate acetylhydrolase	462.225	0.0	300	220	255
SS1G_04975.3: isocitrate lyase	80.8777	3.88566E-16	122	48	71
SS1G_04900.3: isocitrate lyase	72.4034	1.50227E-13	83	37	55

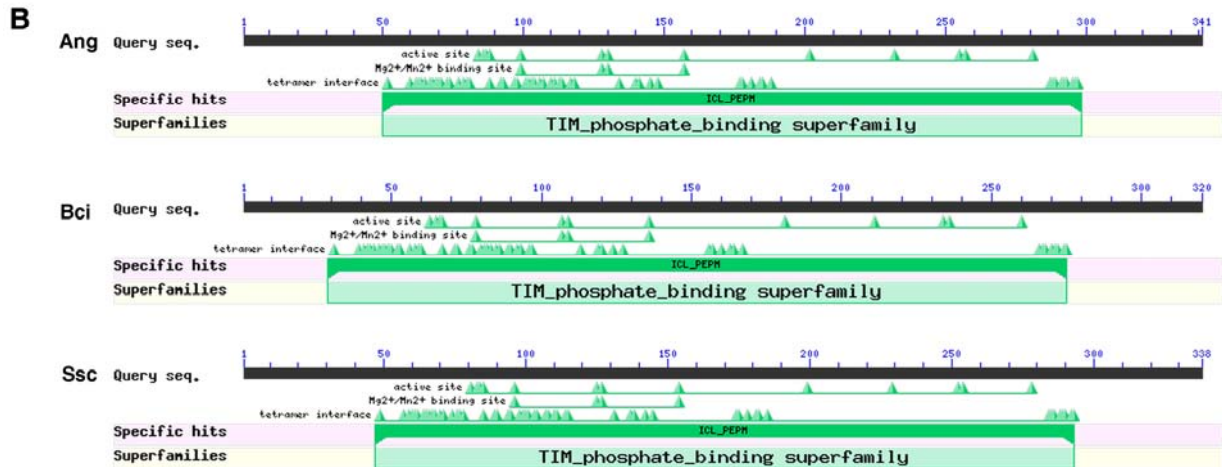
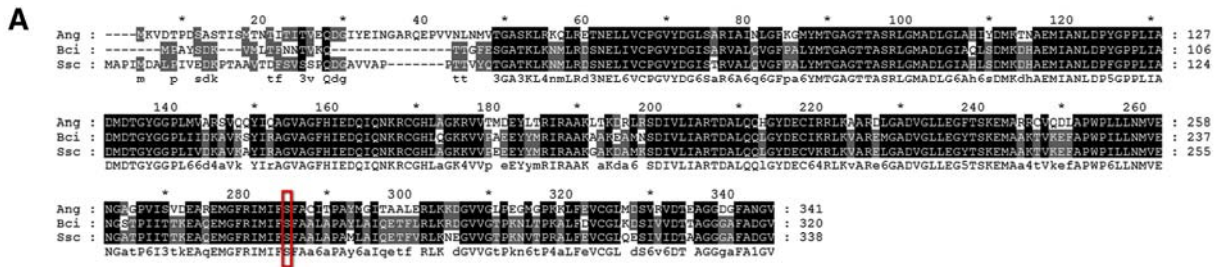
51 **a.** BLAST searches were performed online with an expectation limit < 1 e-3 against database  
 52 ([http://www.broadinstitute.org/annotation/genome/sclerotinia\\_sclerotiorum/MultiHome.html](http://www.broadinstitute.org/annotation/genome/sclerotinia_sclerotiorum/MultiHome.html)).

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54 **Appendix G** OAH proteins in three fungal species

Fungal species	Number of OAH	Protein accession number	Length (aa)
<i>S. sclerotiorum</i> 1980	1	XP_001590478	338
<i>B. cinerea</i> B05.10	1	AAS99938	320
<i>A. niger</i> N400	1	CAD99195	341

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59 **Appendix H** The alignment and domain composition of OAH protein sequences of *Aspergillus niger* (Ang),  
 60 *Botrytis cinerea* (Bci) and *Sclerotinia sclerotiorum* (Ssc). A, The oxaloacetate acetylhydrolase (OAH)  
 61 marker amino acid serine was framed. B, Domain composition analysis was performed against CDD  
 62 database (<http://www.ncbi.nlm.nih.gov/cdd>).

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