

Table S21**Polysaccharide degradation-related genes differentially expressed upon plant infection.**

Expression levels were quantified from microarray hybridization. Comparison was made between RNA isolated from sunflower cotyledons colonized by *B. cinerea* strain T4 and RNA isolated from mycelium of *B. cinerea* strain T4 grown *in vitro*. Only genes that were at least 2-fold statistically increased or decreased in at least one fungus were listed. The different substrate categories are described in Tables S19 and S20.

CAZy genes overexpressed in both fungi					
Gene ID <i>B.cinerea</i>	Gene ID <i>S. sclerotiorum</i>	CAZy family ^a	Substrate category ^b	Fold change infection <i>B. cinerea</i>	Fold change infection <i>S. sclerotiorum</i>
BofuT4_P047740.1	SS1G_04207.1	GH28	P	24.4 *	41.9 *
BofuT4_P005990.1	SS1G_07749.1	GH11	H	14.6	30.5 *
BofuT4_P120850.1	SS1G_03618.1	GH11	H	6.6 *	29.4 *
BofuT4_P014350.1	SS1G_12907.1	CE5	H	43.3 *	25.9 *
BofuT4_P102210.1	SS1G_11992.1	CE12	HP	4.9 *	25.5 *
BofuT4_P118670.1	SS1G_09866.1	GH5	HP [†]	8.9 *	18.5 *
BofuT4_P026900.1	SS1G_04551.1	CE8	P	5.8	15.6 *
BofuT4_P078070.1	SS1G_13255.1	GH3	C or FCW [†]	10.0	15.2 *
BofuT4_P023220.1	SS1G_07039.1	GH28	P	2.1	14.8 *
BofuT4_P023980.1	SS1G_08104.1	CE5	HP	7.1	13.1 *
BofuT4_P026710.1	SS1G_04541.1	GH78	P	4.6 *	12.3 *
BofuT4_P061530.1	SS1G_00746.1	GH5	H [†]	154.2 *	10.6 *
BofuT4_P155280.1	SS1G_11585.1	GH53	HP	10.9 *	9.5
BofuT4_P029340.1	SS1G_02553.1	GH28	P	3.8	9.3 *
BofuT4_P114590.1	SS1G_03387.1	GH5	C or H [†]	9.4 *	8.7 *
BofuT4_P026920.1	SS1G_04552.1	GH28	P	2.2	7.9 *
BofuT4_P059250.1	SS1G_00892.1	GH6	C	60.5 *	7.5 *
BofuT4_P141390.1	SS1G_09392.1	CBM20	E	15.4 *	7.0
BofuT4_P140330.1	SS1G_02760.1	CE5	H	66.6 *	6.6 *
BofuT4_P070230.1	SS1G_03093.1	GH78	P	2.7	6.6 *
BofuT4_P125090.1	SS1G_02334.1	GH7	C	138.5 *	6.5 *
BofuT4_P030130.1	SS1G_02620.1	GH79		2.5	6.1 *
BofuT4_P008190.1	SS1G_10842.1	GH35	H	4.3 *	5.2 *
BofuT4_P067660.1	SS1G_11842.1	GH93	H	3.4	5.0 *
BofuT4_P011980.1	SS1G_10092.1	GH11	H	2.2	4.7 *
BofuT4_P062500.1	SS1G_13386.1	CE5	H	7.6 *	4.6 *
BC1G_01483.1	SS1G_06037.1	GH5	FCW or H [†]	23.7 *	4.0 *
BofuT4_P132770.1	SS1G_08208.1	GH5	H [†]	28.2 *	4.0 *
BofuT4_P035890.1	SS1G_01229.1	GH55	FCW	23.0 *	3.9
BofuT4_P047700.1	SS1G_04200.1	GH92		6.9 *	3.9
BofuT4_P038970.1	SS1G_02462.1	GH54	HP	2.4	3.6 *
BofuT4_P150570.1	SS1G_09020.1	GH7	C	16.7 *	3.5
BofuT4_P078550.1	SS1G_13501.1	GH78	P	4.4	3.3 *
BofuT4_P010470.1	SS1G_03602.1	GH51	HP	2.8	3.1 *
BofuT4_P107060.1	SS1G_01493.1	GH3	HP [†]	3.2	3.0 *
BofuT4_P006540.1	SS1G_07863.1	CBM1	PCW	24.1 *	2.7
BofuT4_P059260.1	SS1G_00891.1	GH5	C	27.0 *	2.6
BofuT4_P103120.1	SS1G_12048.1	CE12	HP	8.6 *	2.6 *
BofuT4_P010370.1	SS1G_03610.1	CE16	H	5.4 *	2.5
BofuT4_P091380.1	SS1G_09821.1	GH61	C	88.0 *	2.4
BofuT4_P103410.1	SS1G_12083.1	GH115	P	9.0	2.4 *
BofuT4_P025430.1	SS1G_14158.1	GH61	C	2.7	2.3 *
BofuT4_P086620.1	SS1G_07162.1	GH3	C or FCW [†]	12.0 *	2.2 *
BofuT4_P003870.1	SS1G_07656.1	GH61	C	19.0 *	2.2
BofuT4_P112910.1	SS1G_08837.1	GH5	C	57.0 *	2.2
BofuT4_P036980.1	SS1G_01572.1	GH35	H or HP [†]	6.0 *	2.2
BofuT4_P143540.1	SS1G_14289.1	CE16	H	12.4 *	2.1
BofuT4_P135380.1	SS1G_12191.1	GH10	H	13.9 *	2.0

CAZy genes overexpressed mainly in one fungus					
Gene ID <i>B.cinerea</i>	Gene ID <i>S. sclerotiorum</i>	CAZy family ^a	Substrate category ^b	Fold change infection <i>B. cinerea</i>	Fold change infection <i>S. sclerotiorum</i>
BofuT4_P031660.1	SS1G_09251.1	GH61	C	74.1 *	1.9
BofuT4_P109330.1	SS1G_01838.1	GH61	C	44.0 *	1.1
BofuT4_P004830.1	SS1G_07847.1	GH3	C or H [†]	39.5 *	1.5
BofuT4_P015800.1	SS1G_00040.1	PL1	P	30.4 *	1.0
BofuT4_P128360.1	SS1G_12622.1	GH1	C or FCW [†]	19.0 *	1.7
BofuT4_P043000.1	SS1G_05832.1	GH28	P	9.9 *	-1.7
BofuT4_P103260.1	SS1G_12057.1	GH28	P	7.3 *	1.5
BofuT4_P152970.1	SS1G_11057.1	GH28	P	6.5 *	-1.2
BofuT4_P019100.1	SS1G_00321.1	GH81	FCW	6.2 *	1.6
BofuT4_P122770.1	SS1G_01373.1	CBM1	PCW [†]	4.3 *	-1.2
BofuT4_P132940.1	SS1G_08229.1	GH28	P	1.5	24.4 *
BofuT4_P030090.1	SS1G_02618.1	GH43	HP	1.6	9.2 *
BofuT4_P118760.1	SS1G_09857.1	GH105	P	-1.5	6.7 *
BofuT4_P150610.1	SS1G_09129.1	GH1		1.7	3.2 *
BofuT4_P113750.1	SS1G_05557.1	GT32		1.4	2.6 *
BofuT4_P089070.1	SS1G_01005.1	GH31	E or FCW [†]	1.3	2.2 *

CAZy genes underexpressed mainly in one fungus					
Gene ID <i>B.cinerea</i>	Gene ID <i>S. sclerotiorum</i>	CAZy family ^a	Substrate category ^b	Fold change infection <i>B. cinerea</i>	Fold change infection <i>S. sclerotiorum</i>
BofuT4_P008230.1	SS1G_10847.1	GT2	FCW [†]	-39.5 *	-1.3
BofuT4_P060820.1	SS1G_14460.1	GH72	FCW	-16.7 *	-1.6
BofuT4_P116560.1	SS1G_01882.1	CE5	H	-7.3 *	-1.2
BofuT4_P008250.1	SS1G_10845.1	GH12	C	-4.5 *	-1.1
BofuT4_P116630.1	SS1G_01889.1	GT2	FCW [†]	-2.3 *	1.5
BofuT4_P063490.1	SS1G_05784.1	GH71	FCW	-1.44	-4.8 *
BofuT4_P034570.1	SS1G_08695.1	GH18	FCW	1.60	-4.4 *
BofuT4_P008430.1	SS1G_10867.1	GH76	FCW	1.54	-4.2 *
BofuT4_P046700.1	SS1G_04062.1	GT4		-1.14	-4.0 *
BofuT4_P116860.1	SS1G_01334.1	GH92		-1.19	-3.1 *
BofuT4_P062560.1	SS1G_13392.1	CBM32		-1.08	-2.9 *
BofuT4_P122270.1	SS1G_01422.1	GH16	FCW or H [†]	-1.83	-2.5 *
BofuT4_P030230.1	SS1G_02625.1	GT17		1.5	-2.0 *

CAZy genes differentially expressed and present in only one fungus					
Gene ID <i>B.cinerea</i>	Gene ID <i>S. sclerotiorum</i>	CAZy family ^a	Substrate category ^b	Fold change infection <i>B. cinerea</i>	Fold change infection <i>S. sclerotiorum</i>
BofuT4_P061870.1		GH28	P	11.59 *	
BofuT4_P059350.1		PL1	P	6.22 *	
BofuT4_P041780.1		GT8		-18.25 *	
	SS1G_07331.1	GH30	E		-2.2 *
	SS1G_02128.1	GH18 + CBM18	FCW		-2.1 *

Red - Positive fold changes upon infection ; **Green** - Negative fold changes upon infection

* The differential expression is statistically significant.

^a CAZy family annotations: GH - Glycoside Hydrolase; CE - Carbohydrate Esterase; CBM - Carbohydrate-Binding Module; GT – Glycosyltransferase; PL - Polysaccharide Lyase.

^b CAZy substrate category: C - cellulose; H - hemicellulose; P - pectin; HP - hemicellulose/pectin side chains; E - energy; FCW-fungal cell wall.

[†] For models from families with a wide substrate preference, a substrate prediction was made by comparison against the sequences of previously characterized proteins in CAZy.