

Table S1: Number of proteins identified in each major category of protein found in extracts of degraded wood from *Postia placenta*, *Gloeophyllum trabeum*, *Trametes versicolor*, and *Stereum hirsutum*. This data was used to construct Figure 1.

Brown rot Category	<i>Postia placenta</i> Number of Proteins ¹			<i>Gloeophyllum trabeum</i> Number of Proteins ¹		
	0-5	15-20	30-35	0-5	15-20	30-35
Hypothetical Proteins	14	18	10	78	28	34
Glycoside Hydrolase	10	15	13	24	20	16
Oxidoreductase	2	3	2	15	3	3
Esterase/Lipase	2	4	2	12	12	9
Peptidase	4	9	7	15	12	9
Other	6	5	5	23	8	10
Total	38	54	39	167	83	81
White rot Category	<i>Trametes versicolor</i> Number of Proteins			<i>Stereum hirsutum</i> Number of Proteins		
	0-5	15-20	30-35	0-5	15-20	30-35
Hypothetical Proteins	42	20	24	2	9	8
Glycoside Hydrolase	18	32	33	0	6	17
Oxidoreductase	22	26	29	5	8	5
Esterase/Lipase	0	8	11	0	1	4
Peptidase	17	19	19	5	12	13
Other	16	9	9	1	2	2
Total	115	114	125	13	38	49

¹Number of proteins found in wafer sections 0-5, 15-20, and 30-35 mm from the hyphal front. Number of proteins were quantified from all technical replicates of protein samples from each section type.

Table S2: Carbohydrate esterase (CE) and glycoside hydrolase (GH) families identified in aspen wafer sections degraded by *Postia placenta* taken from 0-5, 15-20, 30-35 mm from the advancing hyphal front.

Protein ID ¹	Allele	CE/GH ²	Putative Function ³	Signal P ⁴	Observations ⁵		
					0-5	15-20	30-35
20448	50078	CE 10	Lipase	no	6	7	0
106710		CE 16	No strong hits	no	0	2	0
108959		CE 16	Carboxylesterase	21-22	0	2	0
125801		CE 16	Carboxylesterase	20-21	14	17	12
107557		GH 3	β -glucosidase	no	69	124	132
103675	117690	GH 5	Endoglucanase	22-23	13	16	29
95568		GH 5	Endo- β -1,4-mannosidase	20-21	0	5	0
121831	134772	GH 5	Endo- β -1,4-mannanase	no	16	24	32
115648	108962	GH 5	Endoglucanase	22-23	16	53	49
113670		GH 10	Endo- β -1,4-xylanase	18-19	3	1	0
112658	121191	GH 12	Endo- β -1,4-glucanase	18-19	0	0	2
112941	61809	GH 16	Endo- β -1,3(4)-glucanase	25-26	0	8	5
116903	128334	GH 16	Endo- β -1,3(4)-glucanase	17-18	1	9	0
128150	98662	GH 27	α -galactosidase	23-24	9	67	53
111730	43189	GH 28	Pectinase	18-19	13	0	0
115593	46679	GH 47	α -1,2-mannosidase	24-25	0	4	2
100251		GH 51	α -arabinofuranosidase	no	2	1	14
108648		GH 55	Exo- β -1,3-glucanase	17-18	1	6	3
119394		GH 55	Exo- β -1,3-glucanase	21-22	0	5	5
105490		GH 55	Endo- β -1,3-glucanase	21-22	0	7	6
111332		GH 79	β -glucuronidase	no	0	5	18

¹Protein ID numbers from the DOE JGI MycoCosm database (1).

²Carbohydrate esterase and glycoside hydrolase families as defined in the CAZy database (2).

³Putative functions determined by BLAST searches of SWISS PROT database (3).

⁴Secretion signals for detected protein sequences were detected using Signal P algorithm (4).

⁵Unique peptide counts for proteins found in wafer sections 0-5, 15-20, and 30-35 mm from the hyphal front.

Number of observations were quantified from equal portions of protein from each section type.

Table S3: Carbohydrate esterase (CE) and glycoside hydrolase (GH) families identified in aspen wafer sections degraded by *Gloeophyllum trabeum* taken from 0-5, 15-20, 30-35 mm from the advancing hyphal front.

Protein ID ¹	CE/GH ²	Putative Function ³	Signal P ⁴	Observations ⁵		
				0-5	15-20	30-35
117128	CE 1	Acetyl xylan esterase	21-22	0	19	16
46545	CE 15	4-O-methyl-glucuronyl methylesterase	19-20	17	238	150
48624	CE 16	Carbohydrate esterase family 16	21-22	20	53	5
56205	CE 16	Carbohydrate esterase family 16	19-20	9	19	0
32318	CE 4	Chitin deacetylase	20-21	5	0	0
112531	CE 8	Pectinesterase	20-21	10	2	0
115191	GH 2	β -Mannanase	19-20	26	25	5
75899	GH 3	β -glucosidase	no	9	0	0
69843	GH 3	β -glucosidase	18-19	55	164	55
122002	GH 3	Exo- β -1,4-xylosidase	21-22	75	112	46
114574	GH 5	Endo- β -1,4-mannanase	20-21	2	13	0
110405	GH 5	Endo- β -1,4-mannanase	22-23	4	21	0
135369	GH 5	Endo- β -1,4-mannanase	18-19	0	8	0
63180	GH 5	Endo- β -1,4-glucanase	20-21	14	78	35
140289	GH 10	Endo- β -1,4-xylanase	18-19	0	1	3
46499	GH 10	Endo- β -1,4-xylanase	no	81	435	545
138821	GH 12	Xyloglucan Endo- β -1,4-glucanase	20-21	6	212	328
52752	GH 16	β -glucan synthesis protein	no	2	0	0
122074	GH 18	Chitinase	22-23	0	5	0
77583	GH 20	β -N-acetylglucosaminidase	22-23	14	0	0
116582	GH 20	β -N-acetylglucosaminidase	19-20	28	15	0
117566	GH 27	α -galactosidase	21-22	14	15	1
6650	GH 28	Pectinase	no	8	0	0
120615	GH 28	Pectinase	18-19	23	0	0
110574	GH 28	Pectinase	17-18	22	20	2
141329	GH 31	α -xylosidase	23-24	2	0	0
111095	GH 35	β -galactosidase	23-24	12	0	0
112205	GH 47	α -1,2-mannosidase	22-23	7	0	0
134804	GH 51	α -arabinofuranosidase	23-24	0	4	0
126879	GH 55	Exo- β -1,3-glucosidase	22-23	29	33	3
113553	GH 72- CBM43	β -1,3-glucanosyltransferase	24-25	1	2	0
116837	GH 79	β -glucuronidase	no	0	6	2
81814	GH 92	Glycosidase	19-20	8	0	0
121307	GH 115	No strong hits	21-22	4	1	2
121308	GH 115	No strong hits	21-22	55	108	42

¹Protein ID numbers from the DOE JGI Mycosm database (1).

²Carbohydrate esterase and glycoside hydrolase families as defined in the CAZy database (2).

³Putative functions determined by BLAST searches of SWISS PROT database (3).

⁴Secretion signals for detected protein sequences were detected using Signal P algorithm (4).

⁵Unique peptide counts for proteins found in wafer sections 0-5, 15-20, and 30-35 mm from the hyphal front. Number of observations were quantified from equal portions of protein from each section type

Table S4: Carbohydrate esterase (CE) and glycoside hydrolase (GH) families identified in aspen wafer sections degraded by *Trametes versicolor* taken from 0-5, 15-20, 30-35 mm from the advancing hyphal front.

Protein ID ¹	CE/GH ²	Putative Function ³	Signal P ⁴	Observations ⁵		
				0-5	15-20	30-35
112899	CE 15	Glucuronyl esterase	no	0	2	10
70662	CE 16	Carbohydrate esterase family 16	18-19	0	0	1
168624	CE 16	Acetyl esterase	21-22	0	8	4
39742	CE 16-CBM 1	Carbohydrate esterase family 16	22-23	0	7	6
61724	GH 2	β -mannosidase	18-19	0	0	2
132011	GH 3	Exo- β -1,4-xylosidase	24-25	10	7	6
67879	GH 3	Exo- β -1,4-xylosidase	24-25	14	11	3
127171	GH 3	β -glucosidase	no	0	3	1
68557	GH 3-CBM 1	β -glucosidase	19-20	0	1	2
33056	GH 5-CBM 1	Endo- β -1,4-glucanase	no	0	5	14
151848	GH 5_5-CBM 1	Endoglucanase	21-22	0	3	0
150608	GH 5-CBM 1	Endoglucanase	20-21	0	1	2
63826	GH 6	Cellobiohydrolase	20-21	10	306	334
110790	GH 7	Cellobiohydrolase	18-19	0	1	0
124366	GH 7	Cellobiohydrolase	18-19	0	8	4
112163	GH 7	Cellobiohydrolase	18-19	4	103	225
125941	GH 7, Tvf7	Cellobiohydrolase	18-19	2	128	80
33948	GH 10	Endo- β -1,4-xylanase	18-19	0	21	0
38102	GH 10-CBM 1	Endo- β -1,4-xylanase	19-20	0	6	8
50178	GH 12	Xyloglucan endo- β -1,4-glucanase	19-20	8	0	0
136117	GH 12	Endo- β -1,4-glucanase	18-19	0	22	23
18215	GH 18	Chitinase	no	0	3	0
175547	GH 20	β -hexosaminidase	19-20	3	2	2
135976	GH 20	β -hexosaminidase	18-19	20	16	4
60477	GH 27	α -galactosidase	19-20	0	1	0
171861	GH 28	Pectinase	19-20	89	0	0
62650	GH 28	Rhamnogalacturonase	18-19	0	1	0
52416	GH 28	Pectinase	19-20	45	41	47
66957	GH 30	No strong hits	20-21	0	5	7
58033	GH 31	α/β -glucosidase	24-25	2	0	0
37024	GH 35	β -galactosidase	25-26	0	7	13
58222	GH 43	Endo- α -1,5-L-arabinosidase	22-23	4	0	0
145953	GH 43-CBM 35	No strong hits	19-20	0	6	7
131501	GH 47	α -1,2-mannosidase	24-25	7	2	4

59914	GH 51	α -L-arabinofuranosidase	16-17	14	11	3
143650	GH 53	Endo- β -1,4-galactanase	17-18	0	0	0
26555	GH 79	β -glucuronidase	19-20	2	2	0
75494	GH 92	Uncharacterized glycosidase	23-24	23	2	0
43566	GH 92	Uncharacterized glycosidase	23-24	12	24	20
49304	GH 115	No strong hits	27-28	10	66	28
175614	GH 131	No strong hits	16-17	0	1	3
46975	GH 131-CBM 1	No strong hits	18-19	0	2	4

¹Protein ID numbers from the DOE JGI MycoCosm database (1).

²Carbohydrate esterase and glycoside hydrolase families as defined in the CAZy database (2).

³Putative functions determined by BLAST searches of SWISS PROT database (3).

⁴Secretion signals for detected protein sequences were detected using Signal P algorithm (4).

⁵Unique peptide counts for proteins found in wafer sections 0-5, 15-20, and 30-35 mm from the hyphal front. Number of observations were quantified from equal portions of protein from each section type.

Table S5: Carbohydrate esterase (CE) and glycoside hydrolase (GH) families identified in aspen wafer sections degraded by *Stereum hirsutum* taken from 0-5, 15-20, 30-35 mm from the advancing hyphal front.

Protein ID ¹	CE/GH ²	Putative Function ³	Signal P ⁴	Observations ⁵		
				0-5	15-20	30-35
127673	CE 1, CBM 1	Acetyl xylan esterase	21-22	0	0	4
172051	CE 12	Rhamnogalacturonan acetyl esterase	21-22	0	0	3
96554	CE 15, CBM 1	Glucuronyl esterase	20-21	0	0	12
144289	GH 3	β -glucosidase	25-26	0	0	2
65746	GH 5	Endoglucanase	17-18	0	2	8
136401	GH 5, CBM 1	Acetate buturate ligase	19-20	0	0	6
165557	GH 5, CBM 1	Endoglucanase	20-21	0	0	2
92249	GH 6, CBM 1	Cellobiohydrolase	19-20	0	6	187
62237	GH 7	Cellobiohydrolase	19-20	0	0	103
49403	GH 10, CBM 1	Endo- β -1,4-xylanase	20-21	0	0	5
91607	GH 10, CBM 1	Endo- β -1,4-xylanase	20-21	0	0	6
123978	GH 15, CBM 20	Glucoamylase	23-24	0	0	2
58599	GH 15, CBM 20	Glucoamylase	17-18	0	0	8
49482	GH 18, CBM 5	No strong hits	24-25	0	0	2
61806	GH 18, CBM 5	No strong hits	no	0	0	3
91437	GH 18, CBM 5	Chitinase	25-26	0	0	2
150302	GH 28	Exopolysaccharidase	18-19	0	1	2
130790	GH 28	Polygalacturonase	19-20	0	0	67
82112	GH 72 CBM 43	β -1,3-glucanosyl transferase	20-21	0	1	6
112437	GH 75	Endo-chitosanase	23-24	0	2	0
128057	GH 79	β -glucuronidase	22-23	0	2	2

¹Protein ID numbers from the DOE JGI Mycosm database (1).

²Carbohydrate esterase and glycoside hydrolase families as defined in the CAZy database (2).

³Putative functions determined by BLAST searches of SWISS PROT database (3).

⁴Secretion signals for detected protein sequences were detected using Signal P algorithm (4).

⁵Unique peptide counts for proteins found in wafer sections 0-5, 15-20, and 30-35 mm from the hyphal front. Number of observations were quantified from equal portions of protein from each section type.

Table S6: Putative oxidoreductases identified in aspen wafer sections degraded by *Postia placenta* taken from 0-5, 15-20, 30-35 mm from the advancing hyphal front.

Protein ID ¹	OR Description	Putative Function ²	Signal P ³	Observations ⁴		
				0-5	15-20	30-35
127365	Oxidoreductase	Cytochrome b oxidoreductase	no	15	57	25
130375	Oxidoreductase	Cytochrome b oxidoreductase	no	0	5	6
116836	Thioredoxin	Thioredoxin	no	1	1	0

¹Protein ID numbers from the DOE JGI MycoCosm database (1).

²Putative functions determined by BLAST searches of SWISS PROT database (3).

³Secretion signals for detected protein sequences were detected using Signal P algorithm (4).

⁴Unique peptide counts for proteins found in wafer sections 0-5, 15-20, and 30-35 mm from the hyphal front. Number of observations were quantified from equal portions of protein from each section type.

Table S7: Putative oxidoreductases identified in aspen wafer sections degraded by *Gloeophyllum trabeum* taken from 0-5, 15-20, 30-35 mm from the advancing hyphal front.

Protein ID ¹	OR Description	Putative Function ²	Signal P ³	Observations ⁴		
				0-5	15-20	30-35
113068	Aldo/keto reductase	NAD(P)H-xylose reductase	no	9	0	0
75987	Aldo/ketoreductase	Glycerol-2-dehydrogenase	no	7	0	0
111441	Aldo/ketoreductase	Aldo/ketoreductase	no	14	0	0
135963	Cytochrome b5-like	Cytochrome b5	no	10	0	0
140776	Oxidoreductase	Putative oxidoreductase	no	4	0	0
95549	Oxidoreductase-FAD binding	Solanopyrone synthase	26-27	10	0	0
130320	Oxidoreductase-FAD-linked	Uncharacterized oxidoreductase	28-29	9	0	0
46992	Oxidoreductase-glutathione peroxidase	Glutathione peroxidase	no	26	0	0
65654	Oxidoreductase-glyoxal oxidase	Glyoxal oxidase	21-22	2	0	0
74773	Oxidoreductase-GMC	Choline dehydrogenase	19-20	6	0	0
116849	Oxidoreductase-nitrate reductase	Nitrate reductase	no	1	1	0
65680	Oxidoreductase-thioredoxin	Thioredoxin	no	45	0	0
82515	Polyamine oxidase, FAD-containing	Flavin-containing polyamine oxidase	20-21	5	7	0
134939	Thioredoxin	Thioredoxin	no	838	107	8
62178	Thioredoxin reductase	Thioredoxin reductase	no	16	0	0

¹Protein ID numbers from the DOE JGI MycoCosm database (1).

²Putative functions determined by BLAST searches of SWISS PROT database (3).

³Secretion signals for detected protein sequences were detected using Signal P algorithm (4).

⁴Unique peptide counts for proteins found in wafer sections 0-5, 15-20, and 30-35 mm from the hyphal front.

Table S8: Putative oxidoreductases identified in aspen wafer sections degraded by *Stereum hirsutum* taken from 0-5, 15-20, 30-35 mm from the advancing hyphal front.

Protein ID ¹	OR Description	Putative Function ²	Signal P ³	Observations ⁴		
				0-5	15-20	30-35
74329	Cellobiose dehydrogenase	Cellobiose dehydrogenase	19-20	0	0	3
76915	CRO	Glyoxal oxidase	22-23	11	140	122
129431	Laccase, SHlcc5	Laccase-4	22-23	1	3	0
99490	LPMO	LPMO	18-19	0	0	2
121343	LPMO, CBM 1	LPMO	20-21	0	5	21
142136	MnP, atypical	Versatile peroxidase	22-23	3	2	0
134504	MnP, atypical	Versatile peroxidase	22-23	4	62	13
161701	MnP, atypical	Versatile peroxidase	22-23	0	8	0
134527	MnP, atypical	Versatile peroxidase	22-23	0	25	1
171838	MnP, atypical	Versatile peroxidase	22-23	28	51	0

¹Protein ID numbers from the DOE JGI Mycosm database (1).

²Putative functions determined by BLAST searches of SWISS PROT database (3).

³Secretion signals for detected protein sequences were detected using Signal P algorithm (4).

⁴Unique peptide counts for proteins found in wafer sections 0-5, 15-20, and 30-35 mm from the hyphal front. Number of observations were quantified from equal portions of protein from each section type.

Table S9: Putative oxidoreductases identified in aspen wafer sections degraded by *Trametes versicolor* taken from 0-5, 15-20, 30-35 mm from the advancing hyphal front.

Protein ID ¹	OR Description	Putative Function ²	Signal P ³	Observations ⁴		
				0-5	15-20	30-35
143158	Cytochrome b5	Cytochrome b5	no	21	0	0
48870	DyP1	Dye-decolorizing peroxidase	no	174	57	33
48874	DyP2	Dye-decolorizing peroxidase	no	109	4	7
73596	Iron reductase/GMC oxidoreductase	Cellobiose dehydrogenase	19-20	0	2	1
146232	Laccase, TvLac2	Laccase-2	25-26	41	0	0
138261	Laccase, TvLac3	Laccase	21-22	62	27	14
115295	Laccase, TvLac4	Laccase	22-23	16	0	0
43576	Lignin peroxidase 1	Lignin peroxidase	21-22	8	42	41
114944	Lignin peroxidase 12	Ligninase C	21-22	0	0	0
43578	Lignin peroxidase 2	Lignin peroxidase	21-22	6	34	66
52333	Lignin peroxidase 6	Ligninase C	21-22	0	0	0
134226	Lignin peroxidase 9	Ligninase C	20-21	12	69	34
162601	LPMO	LPMO	18-19	0	23	19
162729	LPMO	LPMO	16-17	0	2	1
51004	LPMO	LPMO	17-18	0	4	4
36998	LPMO	LPMO	20-21	0	33	16
51375	Mn peroxidase 1, short	Mn Peroxidase 3	21-22	53	1	1
112835	Mn peroxidase 2	Mn Peroxidase 3	21-22	2	5	4
131080	Mn peroxidase 3s	Mn Peroxidase 3	21-22	11	0	0
130496	Mn peroxidase 4s	Mn Peroxidase 3	21-22	211	38	30
43477	Mn peroxidase 5	Mn peroxidase	21-22	0	3	0
51455	Mn peroxidase 6	Manganese peroxidase 3	21-22	53	10	5
51457	Mn peroxidase 9	Manganese Peroxidase 3	no	0	0	0
174721	Oxidoreductase, GMC	Pyranose 2 oxidase	no	19	3	0
32746	Thioredoxin	Thioredoxin	no	51	1	21
156571	Thioredoxin	Thioredoxin	no	5	0	0
68124	Xylose reductase	Xylose reductase	no	28	0	0

¹Protein ID numbers from the DOE JGI MycoCosm database (1).

²Putative functions determined by BLAST searches of SWISS PROT database (3).

³Secretion signals for detected protein sequences were detected using Signal P algorithm (4).

⁴Unique peptide counts for proteins found in wafer sections 0-5, 15-20, and 30-35 mm from the hyphal front. Number of observations were quantified from equal portions of protein from each section type.

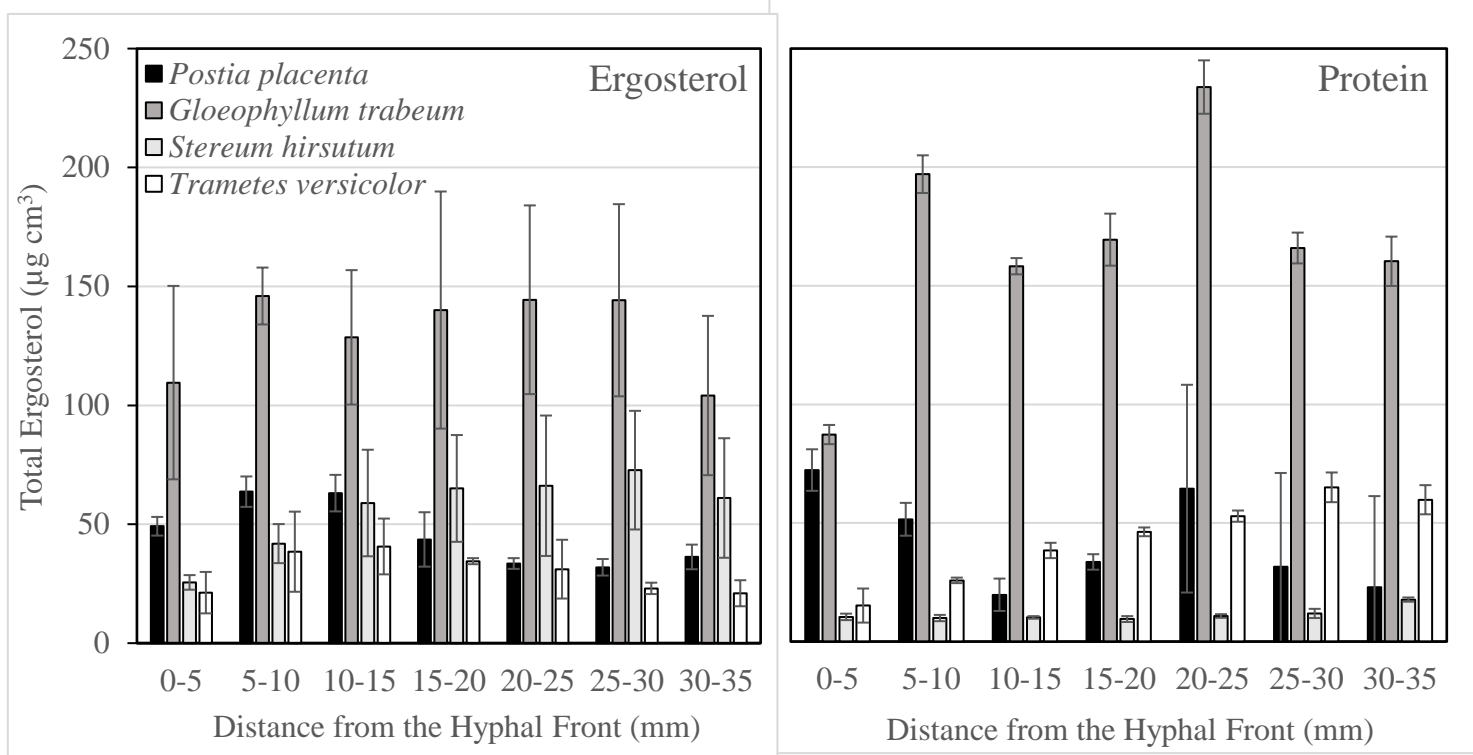


Figure S1: Total ergosterol and protein isolated from 5 mm wafer sections along an advancing hyphal front on aspen wafers. Values were standardized to the volume of wood from which it was extracted. Ergosterol error bars are +/- one standard deviation of three replicate wafer sections and protein error bars are standard deviations of three assays of a single extract of 12 wafer sections.

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