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Supplemental material

of

Genomic and secretomic approaches of the newly isolated *Perenniporia fraxinea* SS3 identified CAZymes potentially related to a serious pathogenesis of hardwood trees.

Ruy Matsumoto,^{1†} Jakia Jerin Mehjabin,^{2†} Hideki Noguchi,^{3,4} Toshizumi Miyamoto,⁵ Taichi E. Takasuka,^{5,6} Chiaki Hori,^{1,2*}

Affiliations

- ¹ Research Faculty of Engineering, Hokkaido University, Sapporo 060-8628, Japan
- ² Research Faculty of Environmental Earth Science, Hokkaido University, Sapporo 060-0810, Japan
- ³Center for Genome Informatics, Joint Support-Center for Data Science Research, Research Organization of Information and Systems, Yata 1111, Mishima, Shizuoka 411-8540, Japan
- ⁴Advanced Genomics Center, National Institute of Genetics, Yata 1111, Mishima, Shizuoka 411-8540, Japan
- ⁵Research Faculty of Agriculture, Hokkaido University, Sapporo 060-8589, Japan
- ⁶Global Station for Food, Land and Water Resources, Hokkaido University, Sapporo 060-8589, Japan

[†]These authors are equally contributed

*Corresponding author:

E-mail, chori@ees.hokudai.ac.jp; Tel, +81-11-706-4522; Fax, +81-11-706-4522

1 Table S1. The five monokaryotic strains of *P. fraxinea* isolated from natural environments in
 2 this study.

Name	ITS rRNA Accession#	Top BLASTn hit description_accession #	E-value	Ident. (%)
<i>P. fraxinea</i> SS1	LC556223	Vanderbylia fraxinea voucher HFJAU0492_MN258672	0.0	99.6
<i>P. fraxinea</i> SS2	LC556224	Vanderbylia fraxinea voucher KA17- 0410_MN294841	0.0	99.8
<i>P. fraxinea</i> SS3	LC556225	Vanderbylia fraxinea voucher KA17- 0410_MN294841	0.0	100
<i>P. fraxinea</i> SS4	LC556226	Vanderbylia fraxinea voucher KA17- 0410_MN294841	0.0	99.2
<i>P. fraxinea</i> SS5	LC556227	Vanderbylia fraxinea voucher Dai 5326a_KX081103	0.0	99.8

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1 Table S2. 29 Hypothetical proteins of culture filtrates of *P. fraxinea* SS3 cultivated in glucose,
 2 cellulose and poplar wood powder media for five days.

Gene	Function	Best hit species of Blastp search	Detected in
mRNA1518_trans	Hypothetical proteins	<i>Lentinus tigrinus</i> ALCF2SS1-6	Glc; Cel; Wood
mRNA1196_trans	Hypothetical proteins	<i>Lentinus tigrinus</i> ALCF2SS1-6	Glc; Cel; Wood
mRNA4734_trans	Hypothetical proteins	<i>Lentinus tigrinus</i> ALCF2SS1-6	Glc; Cel; Wood
mRNA2392_trans	Hypothetical proteins	<i>Polyporus brumalis</i>	Glc; Cel; Wood
mRNA4547_trans	Hypothetical proteins	<i>Ganoderma leucocontextum</i>	Glc; Cel; Wood
mRNA4582_trans	Hypothetical proteins	<i>Earliella scabrosa</i>	Glc; Cel; Wood
mRNA4223_trans	Hypothetical proteins	<i>Trametes cinnabarina</i>	Glc; Cel; Wood
mRNA1380_trans	Hypothetical proteins	<i>Ganoderma Sinens</i>	Glc; Cel; Wood
mRNA5563_trans	Hypothetical proteins	<i>Dichomitus squalens</i>	Glc; Cel; Wood
mRNA7720_trans	Hypothetical proteins	<i>Dichomitus squalens</i>	Glc; Cel; Wood
mRNA4929_trans	Hypothetical proteins	<i>Cubamyces</i> sp.	Glc; Cel; Wood
mRNA6140_trans	Hypothetical proteins	<i>Ganoderma leucocontextum</i>	Glc; Cel; Wood
mRNA6029_trans	Hypothetical proteins	<i>Cubamyces</i> sp.	Glc; Cel; Wood
mRNA5919_trans	Hypothetical proteins	<i>Lentinus tigrinus</i> ALCF2SS1-6	Glc; Cel;
mRNA3734_trans	Hypothetical proteins	<i>Daedaleopsis nitida</i>	Glc; Cel;
mRNA6809_trans	Hypothetical proteins	<i>Fomes fomentarius</i>	Glc; Wood
mRNA5118_trans	Hypothetical proteins	<i>Earliella scabrosa</i>	Glc; Wood
mRNA7591_trans	Polyketide synthase	<i>Daedaleopsis nitida</i>	Cel; Wood
mRNA6710_trans	Hypothetical proteins	<i>Trametes cinnabarina</i>	Glc
mRNA3879_trans	Hypothetical proteins	<i>Cerioporus squamosus</i>	Glc
mRNA4445_trans	Hypothetical proteins	<i>Dichomitus squalens</i>	Glc
mRNA7049_trans	Hypothetical proteins	<i>Polyporus brumalis</i>	Glc
mRNA1567_trans	Hypothetical proteins	<i>Lentinus tigrinus</i> ALCF2SS1-6	Glc
mRNA1662_trans	Hypothetical proteins	<i>Earliella scabrosa</i>	Glc
mRNA1214_trans	Hypothetical proteins	<i>Earliella scabrosa</i>	Glc
mRNA2407_trans	Hypothetical proteins	<i>Lentinus tigrinus</i> ALCF2SS1-6	Glc
mRNA3141_trans	Hypothetical proteins	<i>Daedaleopsis nitida</i>	Wood
mRNA4377_trans	Hypothetical proteins	<i>Cerioporus squamosus</i>	Wood
mRNA1660_trans	Hypothetical proteins	<i>Earliella scabrosa</i>	Wood

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1 Table S3. Top 10 abundant proteins of culture filtrates of *P. fraxinea* SS3 and *P.*
2 *chrysosporium* RP78 cultivated in glucose, cellulose and poplar wood powder media for five
3 days. emPAI value was calculated from biological triplicates as expression level of the detected
4 protein.

Strain	Carbon source	Accession ProteinID	CAZy family	Putative function	Cover (%)	# Unique Peptides	calc. MW (kDa)	calc. pI	emPAI
Pfr	Glucose	mRNA5136		Phosphoglycerate mutase	24.5	6	40.7	4.74	67.1
		mRNA569		Amine oxidase	51.9	17	56.6	4.86	50.8
		mRNA5813		Acid protease	43.0	10	43.8	5.17	40.2
		mRNA6925	AA1_1	Laccase	27.3	12	56.4	5.06	36.3
		mRNA3519	GH25	Lysozyme	59.1	6	24.8	6.37	36.3
		mRNA2484		Acid protease	50.1	11	42.1	5.17	30.6
		mRNA5306	GH17	β -1,3-glucosidase	31.2	12	39.6	5.45	27.9
		mRNA5962	AA1_1	Laccase	29.3	13	56.0	5.67	26.4
		mRNA6029		Hypothetical	61.7	6	20.2	5.71	25.8
		mRNA1786	GH13_15	α -amylase	40.5	11	46.5	5.71	21.8
	Cellulose	mRNA6940	GH7	CBH/EG	78.3	32	49.2	5.16	1556
		mRNA3133	GH7	CBH/EG	46.5	16	48.8	4.84	665.1
		mRNA4140	CBM1, GH6	CBH/EG	48.1	17	47.0	5.02	116.9
		mRNA6025	GH45	EG	19.0	4	20.9	5.71	55.2
		mRNA6069	CBM1, GH10	Xylanase	53.5	13	43.0	5	41.2
		mRNA5626	GH7	CBH/EG	41.0	12	49.1	4.5	34.5
		mRNA5111	GH28	Pectinase	61.5	13	37.5	5.17	33.1
		mRNA3447	GH28	Pectinase	42.3	12	46.5	6.52	22.7
		mRNA6067	CBM1, GH10	Xylanase	35.3	8	42.2	5.19	22.7
		mRNA1259	AA9	LPMO	37.7	6	24.2	6.79	20.5
	Wood	mRNA6940	GH7	CBH/EG	69.3	25	49.2	5.16	90.5
		mRNA6925	AA1_1	Laccase	28.1	13	56.4	5.06	50.8
		mRNA3133	GH7	CBH/EG	37.7	9	48.8	4.84	24.8
		mRNA6916	CBM1, GH10	Xylanase	46.3	14	39.7	6.54	14.4
		mRNA6067	CBM1, GH10	Xylanase	28.9	5	42.2	5.19	14.4
		mRNA1259	AA9	LPMO	37.7	7	24.2	6.79	11.9
		mRNA4140	CBM1, GH6	CBH/EG	30.0	11	47.0	5.02	9.0
		mRNA7753	GH12	EG	24.4	4	26.2	5.78	9.0
		mRNA3519	GH25	Lysozyme	26.7	4	24.8	6.37	9.0
		mRNA70	CBM50, CBM50	Hypothetical	22.8	2	14.0	4.13	9.0
Pch	Glucose	3003339	GH152	β -1,3-glucanase	30.4	5	26.8	4.59	62.1
		2983557	GH152	β -1,3-glucanase	30.1	5	27.2	5.08	38.8
		3014452		Expansin	26.2	6	26.0	5.06	30.6
		2962130		Cerato-platanin	33.1	2	14.7	4.88	20.5
		3006885	GH55	β -1,3-glucanase	16.3	11	82.0	5.8	19.3
		2990416		Hypothetical	46.5	4	14.4	4.46	14.8
		3005609		Hypothetical	39.3	6	20.1	4.6	13.7
		4931		Hypothetical	31.1	9	38.5	4.69	13.3
		1998089		Hypothetical	65.0	6	15.9	6.64	12.3
		2986625		Calmodulin-related	51.0	7	16.8	4.28	11.6
	Cellulose	2983557	GH152	β -1,3-glucanase	30.1	5	27.2	5.08	99.0

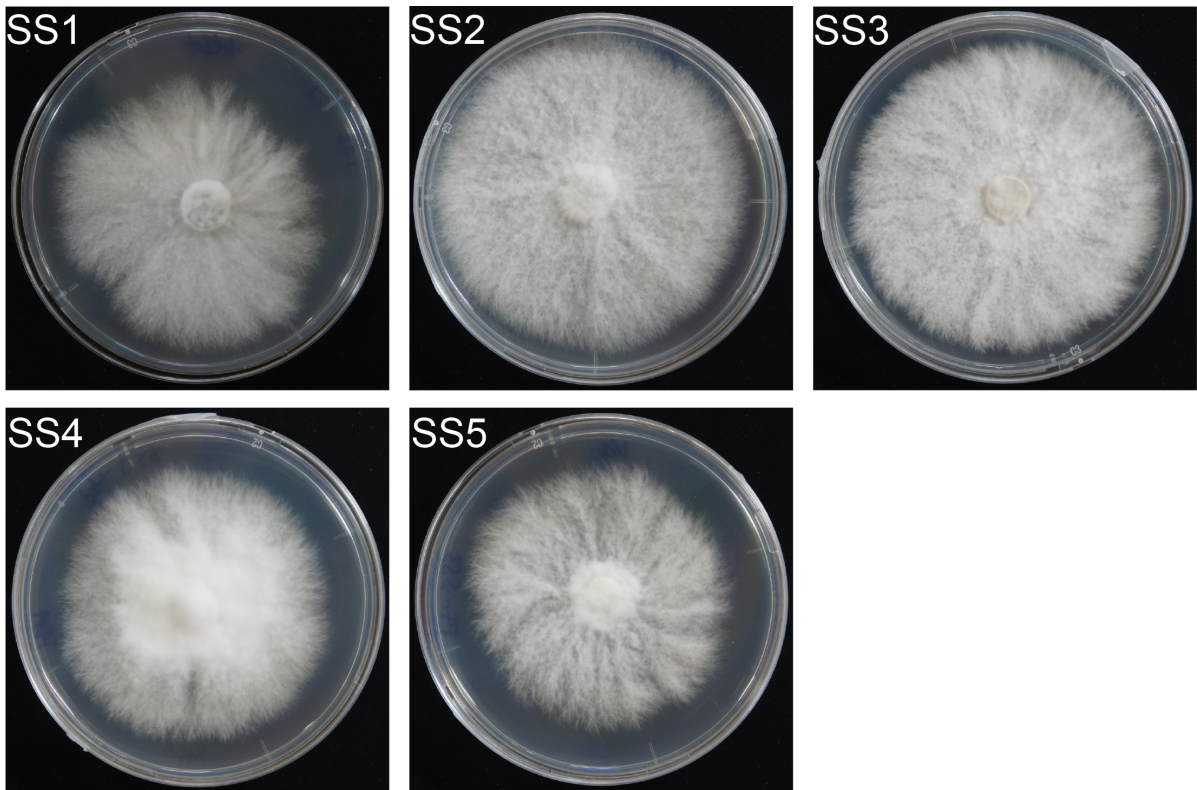
	2971601	GH7, CBM1	CBH/EG	49.2	16	54.9	5.3	47.3
	3003339	GH152	β -1,3-glucanase	30.4	5	26.8	4.59	38.8
	3030351	CBM1, GH10	Xylanase	54.7	9	40.1	6.86	28.3
	2975821	AA9	LPMO	80.7	9	24.9	7.53	27.5
	2962130		Cerato-platanin	33.1	2	14.7	4.88	20.5
	137372	GH7, CBM1	CBH/EG	40.7	11	58.1	5.21	19.0
	3024676		Lipase	44.6	8	31.4	5.24	16.8
	1998089		Hypothetical	65.0	6	15.9	6.64	16.8
	131440	CBM1	Hypothetical	40.4	4	23.2	4.54	16.8
Wood	2983557	GH152	β -1,3-glucanase	30.1	5	27.2	5.08	250.2
	3003339	GH152	β -1,3-glucanase	30.4	5	26.8	4.59	62.1
	2975821	AA9	LPMO	83.6	11	24.9	7.53	52.4
	2971601	GH7, CBM1	CBH/EG	47.7	16	54.9	5.3	47.3
	3006885	GH55	β -1,3-glucanase	20.4	12	82.0	5.8	27.9
	137372	GH7, CBM1	CBH/EG	36.7	13	58.1	5.21	24.1
	4931		Hypothetical	31.6	11	38.5	4.69	23.2
	1998089		Hypothetical	65.0	6	15.9	6.64	22.7
	3030351	CBM1, GH10	Xylanase	54.7	15	40.1	6.86	20.5
	2962130		Cerato-platanin	33.1	2	14.7	4.88	20.5

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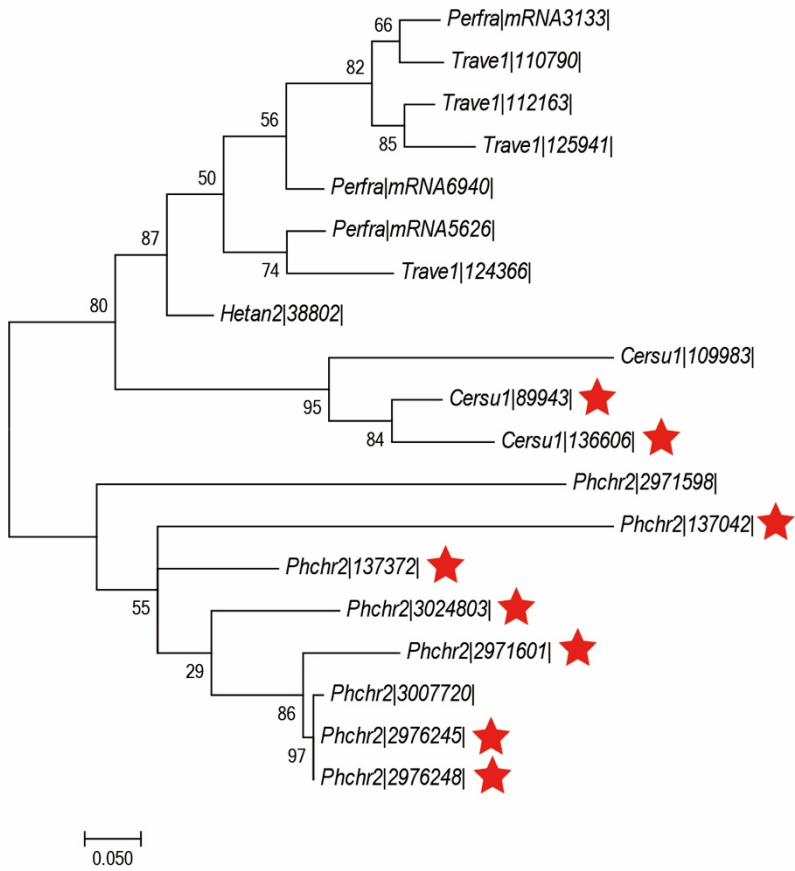
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4 Figure S1. Mycelial growth of the five *P. fraxinea* strains SS1 to SS5 isolated from a *P.*

5 *fraxinea* fruiting body in this study.

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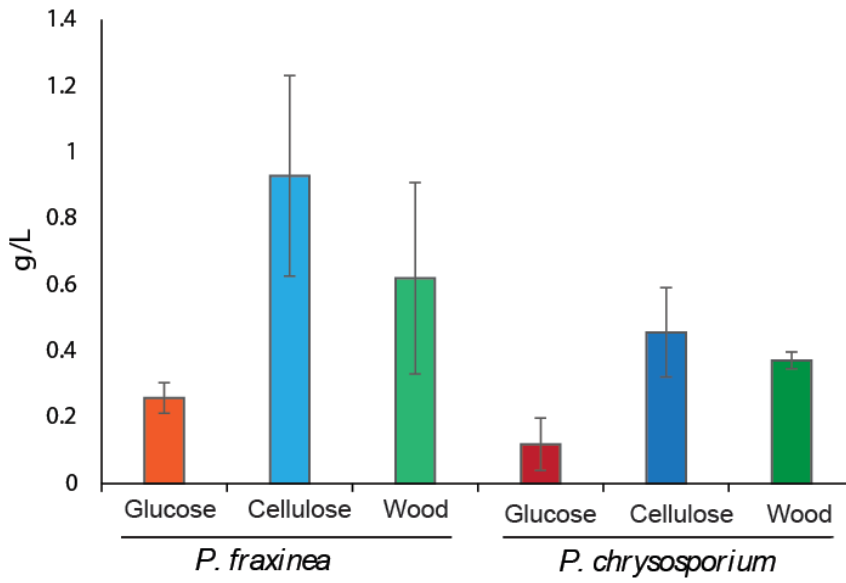
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Figure S2. Phylogenetic tree of the GH7 family protein sequences of *P. fraxinea* SS3 and other fungi. Perfr, *P. fraxinea* SS3 Phach, *Phanerochaete chrysosporium* RP78 ver 2.2; Cersu, *Ceriporiopsis subvermispora*, Trave, *Trametes versicolor*; Hetan, *Heterobasidion annosum*. Star indicates the GH7 genes contain the CBM1 domain.

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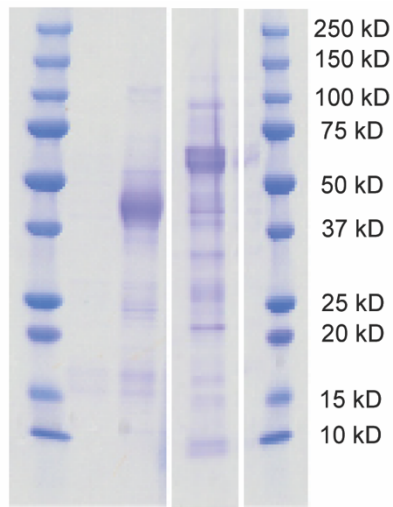
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4 Figure S3. Protein concentrations of culture filtrates of *P. fraxinea* SS3 and *P. chrysosporium*
5 RP78 cultivated in glucose, cellulose, and poplar wood powder media for five days. The
6 average and standard deviation were calculated by three independent biological replicates.
7 Student's T-test was performed in each medium between *P. fraxinea* SS3 and *P.*
8 *chrysosporium* RP78, and there is no significant difference.

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4 Figure S4. SDS-PAGE analysis of culture filtrates of *P. fraxinea* SS3 (left lane) and *P.*

5 *chrysosporium* RP78 (right lane) cultivated in cellulose media for five days.

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