

Systematic Analysis of the *Pleurotus ostreatus* Laccase Gene (*PoLac*) Family and Functional Characterization of *PoLac2* Involved in the Degradation of Cotton-Straw Lignin

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Table S1. The predicted secondary structures of 12 putative laccase identified in *P. ostreatus*.

Gene name	α -Helix (%)	Extended strand (%)	β -Turn (%)	Random coils (%)
<i>PoLac1</i>	13.16	34.77	11.47	40.60
<i>PoLac2</i>	16.28	29.69	11.88	42.15
<i>PoLac3</i>	13.68	33.83	12.57	39.93
<i>PoLac4</i>	12.07	30.27	11.11	46.55
<i>PoLac5</i>	22.38	27.14	10.16	40.32
<i>PoLac6</i>	11.44	32.46	10.88	45.22
<i>PoLac7</i>	16.57	28.99	12.23	42.21
<i>PoLac8</i>	16.67	30.90	11.61	40.82
<i>PoLac9</i>	14.37	32.14	11.34	42.16
<i>PoLac10</i>	11.82	32.27	11.63	44.28
<i>PoLac11</i>	15.29	29.10	9.02	46.59
<i>PoLac12</i>	13.26	33.33	12.09	41.33

Table S2. *PoLac* gene-specific primers used for qRT-PCR analysis.

Gene	Transcript identification no. (PC15)	Primer name	Primer sequence (5'- 3')
<i>Lac1</i>	1043420	Fw	CGGTACATCTTAGCACCCAATG
		Rv	GGACAGGGCTCGCTGGTT
<i>Lac2</i>	1067328	Fw	CATGACCTTGCTCCCCAC
		Rv	GATGACAGCGTAAGGGAC
<i>Lac3</i>	1102751	Fw	GTAAGAAGTGCAGGAAGCTCAACA
		Rv	CCCGTTCCGGTGGAAAC
<i>Lac4</i>	1077328	Fw	CCGTGACGTGCCATACGATG
		Rv	GGTCGAAGGGTGCGTGCGG
<i>Lac5</i>	1094975	Fw	CGCATTTGCCGCTTTCTT
		Rv	GGTGACTAGGACTGAGTATCTC
<i>Lac6</i>	1113032	Fw	GTACAACTACGAAAACCCCG
		Rv	CAAGGTCAAGATGCCAGT
<i>Lac7</i>	1077468	Fw	GTTGATAGCCTCCAGATCTTCG
		Rv	GTAGGATGGCGGAGTTGATG
<i>Lac8</i>	1106925	Fw	CATTGGCTGTGACTCGAA
		Rv	GGATCAGAGAATAGCGTTGG
<i>Lac9</i>	1089733	Fw	GCTTACCGGTGTCCTCGTG
		Rv	GTCATATAGGAAGCTGTTC
<i>Lac10</i>	1089723	Fw	GTTCCCTTTCCTTCCACCAAC
		Rv	CTCCAGCTCGTAAATGCTAC
<i>Lac11</i>	1043488	Fw	GTACTIONAGGGCCGTACTTG
		Rv	GTCGGTATTCATGGTCGTG
<i>Lac12</i>	1094965	Fw	CTATACCGCCACCTTGCCCTCG
		Rv	GGAAATTGACCGCTAGACGAC
<i>sar1</i>	1052294	Fw	GGATAGTCTTCCTCGTCGATAG
		Rv	GGGTGCGTCAATCTTGTTAC

Table S3. Detailed information of the 20 motifs in 12 putative *P. ostreatus* laccase proteins.

Motif	Width	Best Possible Match	Domain
1	101	PTPDSTLINGLGRYAGGPTSPLAVINVERGKRYRIRLISISCDPNYTFSIDGHSMTI IEADGENTQPLEVDSIQIFAGQRYSFVLNANQAIGNYWIRANP	Cu-oxidase
2	143	EDPTTTESNSTNPLLETBLVPLENPGAPGPPVPGGADVNINLAFAFDFTTFEFTI NGVPFVPPTAPVLLQILSGASTAASLLPAGSVYTLPPNKVVEJSM	*
3	59	KGDRFQJNVINZLSDTTMLKTTSIHWHGLFQKGTNWADGPAFVTQCPIVPGDS FLYDFK	Cu-oxidase_3
4	57	PDQAGTFWYHSHLSTQYCDGLRGPVVYDPNDPHKSLYDVDDDESTVJTLEDW YHVPA	Cu-oxidase_3
5	22	CHIDWHLEJGLAVVFAEDPAST	Cu-oxidase_2
6	15	DNVTIRFVTDNPGPW	*
7	21	LGSPGFEGGINSAILRYKGAP	*
8	21	GPTADLHIVNKVIAPDGFERS	*
9	15	NPVPAAWDDLCPYB	*
10	11	GTYPGPLIQGN	*
11	20	MFPGARILATLTLALHLLHG	*
12	16	AGKHPFHLHGKFDIV	Cu-oxidase_2
13	10	ALSDEEKGGI	*
14	29	KYYRFRLINISCRPFFFFWIDGHDFDVIE	Cu-oxidase
15	11	KLLMGTTNAJGR	*
16	7	HAQGQFF	*
17	6	NPPRRD	*
18	8	IYFAQRAS	*
19	6	ANKLIE	*
20	8	ELNPPIKE	*

Table S4. Orthologous analyses of laccase genes between *P. ostreatus* and *C. cinerea*.

Numble	orthologous genes	
1	PoLac1	Cclcc11
2	PoLac2	Cclcc17
3	PoLac3	Cclcc10
4	PoLac4	Cclcc7
5	PoLac6	Cclcc7
6	PoLac7	Cclcc10
7	PoLac8	Cclcc6
8	PoLac9	Cclcc7
9	PoLac10	Cclcc11
10	PoLac11	Cclcc9
11	PoLac12	Cclcc11

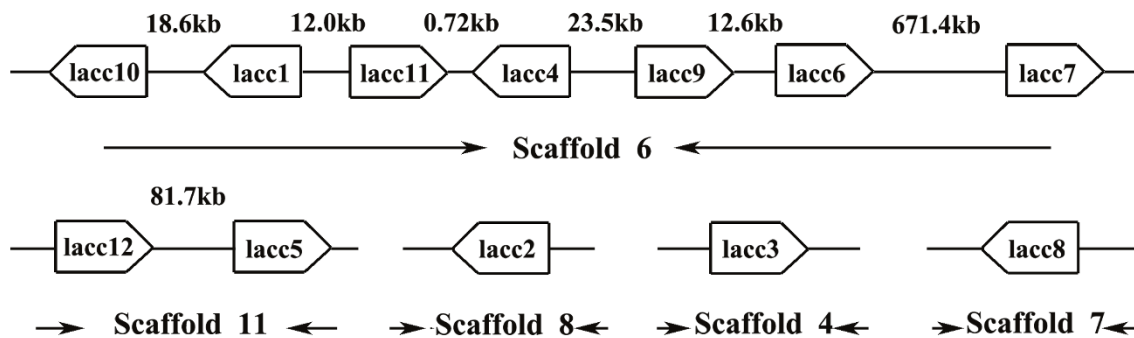


Figure S1. Distribution of laccase genes in the genome of *P. ostreatus* (PC 15). Arrow-shaped boxes indicate the laccase genes, while the direction of arrow shows the direction for each gene. The numerical values above the line show the distances (bp) between the laccase genes.

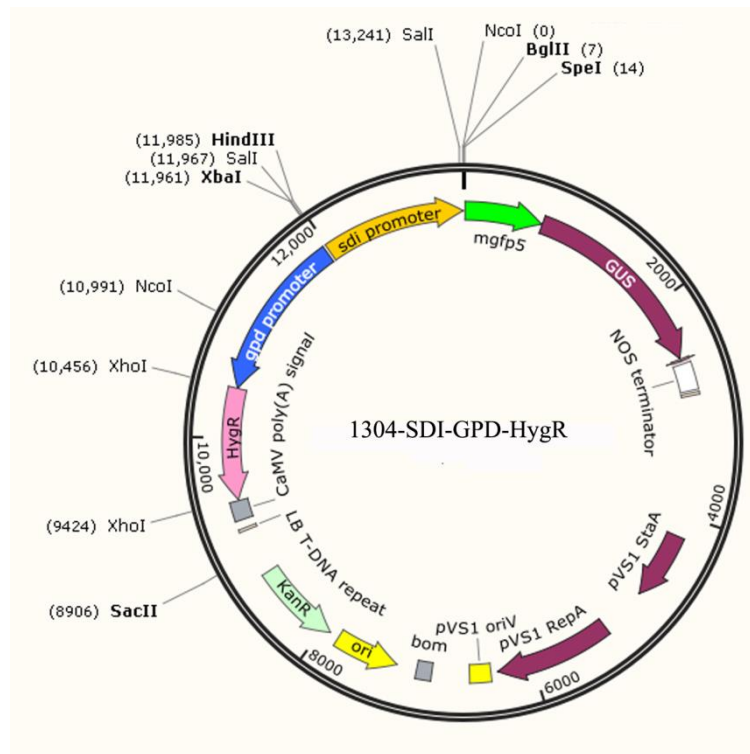


Figure S2. Structures of modified binary vector pCambia 1304-SDI-GPD-HygR. *gusA* and target gene are under the influence of *sdi* promoter, while hygromycin resistance (*HygR*) gene is expressed using GPD promoter.