

Lawrence Berkeley National Laboratory

Recent Work

Title

Whole Genome Annotation and Comparative Analysis of whiterot fungus *Pleurotus ostreatus*

Permalink

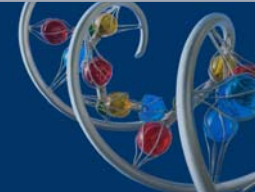
<https://escholarship.org/uc/item/3219170h>

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Publication Date

2009-03-25



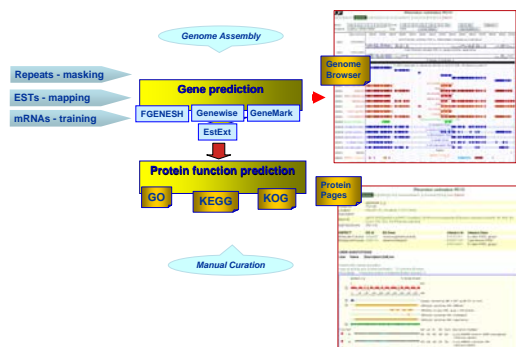
Abstract

The whiterot fungus *Pleurotus ostreatus* actively degrades lignin—the second most abundant biopolymer on Earth and an important biomass component of wood and agricultural waste. This edible oyster mushroom also degrades a variety of polycyclic aromatic hydrocarbons and has potential for *in situ* bioremediation of contaminated soil. JGI sequenced, assembled, and annotated the haploid *Pleurotus ostreatus* PC15 strain with 8.7x sequencing depth coverage of the resulting 34.3 megabase draft assembly. Annotation using the JGI Annotation pipeline yielded over 11,000 gene models. Approximately 97% of over 27,000 sequenced ESTs were mapped to the assembly and supported about one quarter of the predicted gene models. The *P. ostreatus* assembly and gene families were compared with other basidiomycetes including *Phanerochaete chrysosporium*, *Postia placenta*, and *Laccaria bicolor*.

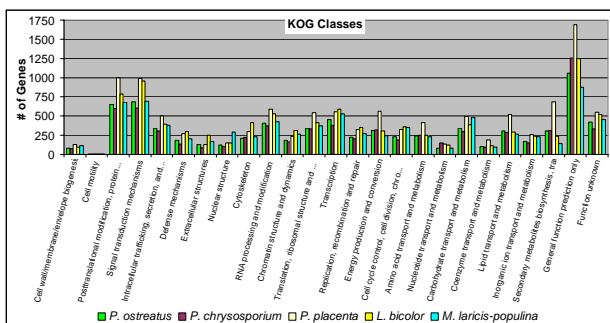


Photo: *P. ostreatus*, Genetics and Microbiology Research Group, Public University of Navarre

Annotation Pipeline Schematic



Functional Classifications



Genome Statistics

Nuclear Genome Size	34.3 Mbp
Sequencing read coverage depth	8.67 x
# of Contigs	249
# of Scaffolds	19
# of Scaffolds > 2Kbp	18
Scaffolds N50	5
Scaffolds L50	3.3 Mbp

Sequences	# of sequences	% mapped to genome
<i>P. ostreatus</i> EST cluster consensus sequences	9,132	95%
<i>P. ostreatus</i> PC15 ESTs	13,184	98%
<i>P. ostreatus</i> PC9 ESTs	13,931	97%

	<i>Pleurotus ostreatus</i>	<i>Phanerochaete chrysosporium</i>	<i>Postia placenta</i>	<i>Laccaria bicolor</i>	<i>Melampsora laricis-populina</i>
Gene length	1,772	1,667	2,075	1,533	1,623
Transcript length	1,377	1,366	1,439	1,134	1,242
Protein length	445	455	458	367	383
Exon length	217	234	212	210	256
Intron length	78	64	112	93	101
Exons per Gene	4.4	5.9	6.8	5.4	4.9

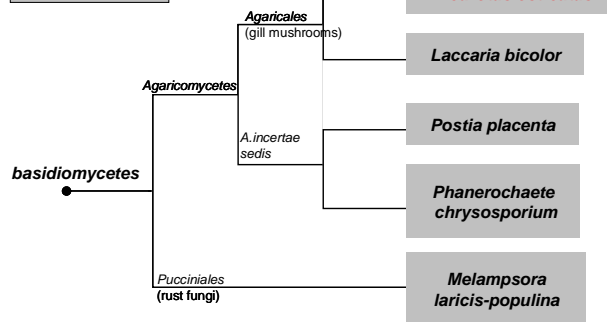
	<i>Pleurotus ostreatus</i>	<i>Phanerochaete chrysosporium</i>	<i>Postia placenta</i>	<i>Laccaria bicolor</i>	<i>Melampsora laricis-populina</i>
Scaffolds (Mbp)	34.3	35.1	90.9	64.9	101.1
Gaps (Mbp)*	0.31 (0.9%)	2.6 (7.5%)	21.9 (24.1%)	6.2 (9.6%)	3.4 (3.4%)
Repeats (Mbp)*	1.6 (5.7%)	0.32 (0.9%)	4.96 (5.46%)	14.4 (22.2%)	49.4 (48.9%)
Gene length (Mbp)*	20.5 (59.6%)	16.8 (47.9%)	35.6 (39.2%)	31.6 (48.7%)	25.0 (24.7%)
# of genes	11,603	10,048	17,173	20,614	15,410
Density (genes/Mbp)	338	286	189	318	152
Assembly Date	2008-07	2005-02	2006-09	2006-05	2007-11

* Parenthesis show percentage of the nuclear assembly.

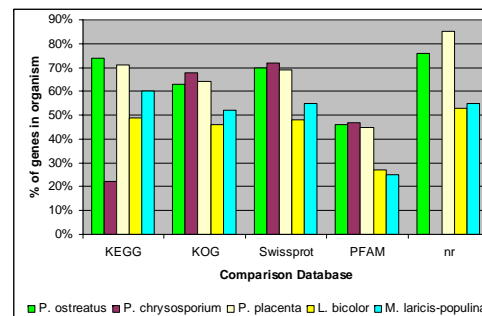
	<i>Pleurotus ostreatus</i>	<i>Phanerochaete chrysosporium</i>	<i>Postia placenta</i>	<i>Laccaria bicolor</i>	<i>Melampsora laricis-populina</i>
FGESH Expressed Sequence Mapping	343 (3.0%)	12 (0.1%)	61 (0.4%)	64 (0.3%)	1377 (8.9%)
homology	5064 (43.6%)	3526 (35.1%)	7549 (43.9%)	13547 (66%)*	8256 (54%)*
ab initio	6196 (53.4%)	6510 (64.8%)	9563 (55.7%)	7003 (34%)	5777 (37.5%)

*Includes counts from EUGene gene predictions.

Phylogeny



Homology to Reference Databases



Clustering and Gene Families

All-against-all protein BLAST alignments
(11,603 genes from *P. ostreatus*)

Symmetric similarity matrix of alignment scores

Tribe MCL clustering

Table 6. *P. ostreatus* Gene Family Clustering

	MCL Inflation (clustering stringency)		
	4.5	2.0	1.5
# Genes in families	11,603	11,603	11,603
# Gene families	9,858	8,606	7,614
# Gene families with >=2 genes	802	1,154	1,326
# genes in families with >=2 genes	2,560	4,164	5,328
% of genes in families with >=2 genes	22%	36%	46%

Functional Domains

Table 7. Most Common Domains in *P. ostreatus*

Pfam Domain ID	<i>P. ostreatus</i>	<i>P. chrysosporium</i>	<i>P. placenta</i>	<i>L. bicolor</i>	PFAM Domain Name
PF00067.13	128	110	214	70	Cytochrome P450
PF00400.23	117	116	142	220	WD domain, G-beta repeat
PF00069.16	108	98	125	111	Protein kinase domain
PF00646.24	91	56	125	115	F-box domain
PF07690.7	76	66	73	40	Major Facilitator Superfamily
PF00271.22	75	56	107	98	Helicase conserved C-terminal domain
PF00096.17	64	38	125	60	Zinc finger, C2H2 type
PF0106.16	63	72	138	41	short chain dehydrogenase
PF00076.13	58	52	71	60	RNA recognition motif. (e.g. RRM/RBD/RNP)
PF00172.9	46	34	43	68	Fungal Zn(2)-Cys(6) binuclear cluster domain

Table 8. Domains Putatively Expanded in *P. ostreatus*

Pfam Domain ID	<i>P. ostreatus</i>	<i>P. chrysosporium</i>	<i>P. placenta</i>	<i>L. bicolor</i>	PFAM Domain Name
PF06985.2	22	0	0	0	Heterokaryon incompatibility protein (HET)
PF00840.11	15	7	0	0	Glycosyl hydrolase family 7
PF01609.12	6	1	0	0	Transposase DDE domain
PF00544.10	6	0	2	0	Pectate lyase
PF04616.5	5	2	0	0	Glycosyl hydrolases family 43
PF08531.1	4	0	0	0	Alpha-L-rhamnosidase N-terminal domain
PF08519.3	4	0	0	1	Replication factor RFC1 C-terminal domain
PF04438.7	4	0	0	2	HIT zinc finger
PF03211.4	3	0	0	0	Pectate lyase
PF0593.5	3	0	0	0	RHS Repeat

*Domains present in >1 copy in *P. ostreatus*, compared to median copy number in other basidiomycetes