Data in Brief

Draft genome sequence of a monokaryotic model brown-rot fungus Postia (Rhodonia) placenta SB12

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We report the genome of Postia (Rhodonia) placenta MAD-SB12, a homokaryotic wood decay fungus (Basidiomycota, Polyporales). Intensively studied as a representative brown rot decayer, the gene complement is consistent with the rapid depolymerization of cellulose but not lignin.

Specifications

Sex N/A
Organism/cell line/tissue Postia (Rhodonia) placenta Mad-SB12
Sequencer or array type Illumina paired-end, 454 titanium, Sanger

1. Direct links to deposited data

The whole genome project has been deposited at DDJB/EMBL/GenBank under accession NEDQ00000000. The version described in

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this paper is version NEDQ00000000.1. The annotated genome is also available via the Joint Genome Institute fungal portal MycoCosm ([1]; http://genome.jgi.doe.gov/PosplSB12.1).

2. Experimental design, materials and methods

Common inhabitants of forest litter and decaying wood, brown-rot fungi play a key role in carbon cycling. These Basidiomycetes rapidly depolymerize cellulose while leaving the bulk of lignin as a modified residue. The preponderance of evidence supports oxidative mechanisms involving diffusible hydroxyl radicals, but much uncertainty remains. To examine the system more closely, a dikaryotic isolate of the brown-rot fungus, *Postia placenta* (which is also classified in the genus *Rhodonia* [2]), was previously sequenced [3]. The genome has been used for phylogenomic comparisons and for analyses of transcriptomes and secretomes, but investigations are hampered by allelic variation [4–13].

Addressing this problem, single basidiospores were collected from the fruiting dikaryon strain Mad-98B by inverting agar plates containing malt extract medium. The basidiospores were eluted from the lids with sterile water and, after streaking onto agar, individual germinating basidiospores were transferred to new plates. The monokaryotic condition was confirmed by PCR amplification and direct sequencing of genes encoding a glycosyl transferase family 66, and representatives of glycosidase families 55 and 1 [14].

The genome of *P. placenta* MAD-SB12 was sequenced using a combination of platforms: 454 (Roche), Illumina, and Sanger. Firstly, Illumina reads obtained from 300 bp insert size library sequenced in 2 × 72 bp format were assembled using Velvet [15], followed by shredding the velvet assemblies into ~1000 bp fragments. Then, these fragments were assembled with 454 Titanium standard and 2.8 kb insert size paired-end reads as well as Sanger fosmids using Newbler (2.5–internal-10Apr08-1) (Roche). The 42.5 Mbp genome assembly consisted of 549 scaffolds and 1446 contigs (scaffold N50 and L50 were 8

### Table 1
Assembly and annotation features of *P. placenta* SB12.

| Feature                                         | Value     |
|-------------------------------------------------|-----------|
| Genome assembly size (Mbp)                      | 42.45     |
| Sequencing read coverage depth                  | 47.36     |
| # of contigs                                     | 1446      |
| # of scaffolds                                   | 549       |
| # of scaffolds ≥ 2 kbp                          | 549       |
| Scaffold N50                                     | 8         |
| Scaffold L50 (Mbp)                               | 2.10      |
| # of gaps                                        | 897       |
| % of scaffold length in gaps                     | 6.1%      |
| Three largest Scaffolds (Mbp)                    | 4.33, 3.52, 3.23 |
| Gene models                                      | 12,541    |
| Average and median protein length                | 429, 354  |
| Genes with Interpro domains                      | 7221      |
| Genes with GO terms                              | 5937      |

### Table 2
Genes predicted to be involved in lignocellulose degradation by wood decay fungi.

| CAZy categorya | Brown-rotb | White-rotc |
|----------------|------------|------------|
| Auxiliary Activities Family AA1_1 Laccase       | 4           | 7          |
| Auxiliary Activities Family AA1_2 Ferrooxidase   | 2           | 2          |
| Auxiliary Activities Family AA2 peroxidases      | 0           | 15         |
| Auxiliary Activities Family AA3_1 CDH             | 0           | 1          |
| Auxiliary Activities Family AA3_3 Alcohol oxidase| 5           | 3          |
| Auxiliary Activities Family A6 BQR                | 1           | 4          |
| Auxiliary Activities Family A9 LPMO              | 2           | 16         |
| Total AA-encoding genes                          | 55          | 89         |
| Carbohydrate binding modules family 1 (CBM1)     | 0           | 36         |
| Total CBM-encoding genes                         | 33          | 65         |
| Glycoside hydrolase family GH12                  | 2           | 2          |
| Glycoside hydrolase family GH13                  | 1           | 1          |
| Glycoside hydrolase family GH135                 | 0           | 1          |
| Glycoside hydrolase family GH13                  | 0           | 0          |
| Glycoside hydrolase family GH3                   | 3           | 4          |
| Glycoside hydrolase family GH30_3               | 3           | 2          |
| Glycoside hydrolase family GH12                  | 1           | 2          |
| Glycoside hydrolase family GH5_22               | 2           | 2          |
| Glycoside hydrolase family GH5_31               | 1           | 2          |
| Glycoside hydrolase family GH5_5                | 3           | 2          |
| Glycoside hydrolase family GH51                 | 1           | 2          |
| Glycoside hydrolase family GH6                  | 0           | 0          |
| Glycoside hydrolase family GH7                  | 0           | 0          |
| Glycoside hydrolase family GH7                   | 0           | 0          |
| Glycoside hydrolase family GH74                 | 0           | 4          |
| Glycoside hydrolase family GH78                 | 3           | 3          |
| Glycoside hydrolase family GH7                  | 2           | 8          |
| Glycoside hydrolase family GH9                  | 0           | 1          |
| Total GH-encoding genes                          | 144         | 181        |
| Total GlycosylTransferase (GT)-encoding genes    | 70          | 70         |
| Total Polysaccharide Lyase (PL)-encoding genes   | 5           | 6          |
| Total                                            | 326         | 444        |

a Abbreviations: CAZy, Carbohydrate Active Enzyme classifications [14]; CDH, Cellobiose dehydrogenase; CRO, Copper radical oxidase; BQR, Benzoquinone reductase; LPMO, Lytic polysaccharide monooxygenase.
b Brown-rot genomes: PosplSB12, *P. placenta* monokaryotic strain described here; Pospl1, *P. placenta* dikaryotic strain (http://genome.jgi.doe.gov/Pospl1/Pospl1.home.html); Antsi, *Antrodia sinuosa* (http://genome.jgi.doe.gov/Antsi1/Antsi1.home.html); Daequ, *Daedalea quercina* (http://genome.jgi.doe.gov/Daequ1/Daequ1.home.html); Fompi, *Fomitopsis pinicola* (http://genome.jgi.doe.gov/Fompi3/Fompi3.home.html); Laesu, *Lentinus subvermispora* (http://genome.jgi.doe.gov/Laesu1/Laesu1.home.html); Wolco, *Wolfiporia cocos* (http://genome.jgi.doe.gov/Wolco1/Wolco1.home.html).
c White-rot genomes: Phach, *Phanerochaete chrysosporium* (http://genome.jgi.doe.gov/Phchr2/Phchr2.home.html); Cersu, *Ceriporiopsis subvermispora* (http://genome.jgi.doe.gov/Cersu1/Cersu1.home.html).
and 2.1 Mbp, respectively). Secretion signals were predicted in 1047 sequences and general annotation features are summarized in Table 1.

3. Data description

Consistent with the degradative potential of brown rot fungi, no ligninolytic peroxidases, cellulose binding modules, or members of glycoside hydrolase (GH) families 6 and 7 were detected in the P. placenta SB12 genome (Table 2). Among the brown rot fungi, potential cental ligninolytic peroxidases, cellulose binding modules, or members of 3. Data description sequences. Assembly and general annotation features are summarized and 2.1 Mbp, respectively). Secretion signals were predicted in 1047 domains (Table 2). A total of 326 biohydrolases and endoglucanases are typically fused to family CBM1, and their activity on crystalline cellulose is therefore suspect. In the white rot fungi, these exocellobiohydrolases and endoglucanases are typically fused to family CBM1 domains (Table 2). A total of 326 P. placenta SB12 genes encode carbohydride active enzymes (CAZys), of which 144 are glycoside hydrolases [14].

To recognize single haplotypes within the dikaryon, BLASTN alignments of putative alleles plus 500 bp of upstream regions were used to delete 4996 allelic variants. This resulted in 12,227 total gene predictions [3], an estimate similar to the actual number of haplotypes shown here in the monokaryon (12,541). However, a substantial number of genes involved in lignocellulose degradation were not captured by the computational approach. For example, dikaryotic P. placenta MAD-698 was predicted to encode only 243 CAZys including 129 GHS [3]. Glycosyl transferases were particularly underestimated in the dikaryon, as were 15 GHS and several oxidoreductases (Table 2). Among the latter, alcohol oxidase genes (AA3_3) are particularly important as evidence suggests their peroxide-generating activity may be directly related to the generation of small molecular weight oxidants via Fenton chemistry [16].

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