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Whole-Genome *De Novo* Sequencing of the Lignin-Degrading Wood Rot Fungus *Phanerochaete chrysosporium* (ATCC 20696)

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ABSTRACT *Phanerochaete chrysosporium* (ATCC 20696) has a catabolic ability to degrade lignin. Here, we report whole-genome sequencing used to identify genes related to lignin modification. We determined the 39-Mb draft genome sequence of this fungus, comprising 13,560 predicted gene models. Gene annotation provided crucial information about the location and function of protein-encoding genes.

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Phanerochaete chrysosporium, model white rot basidiomycete, is well known to secrete lignin peroxidase and manganese peroxidase for lignin degradation (1). In addition, *P. chrysosporium* performs lignin degradation using various extracellular enzymes related to H_2O_2 production (2, 3) and intracellular enzymes, including cytochrome P450 monooxygenase (4–6). This complex fungal catalysis system demonstrates potential biotechnological applications as a novel biocatalyst in numerous industries for the development of proteome and genome analysis techniques (7).

Our previous study found that *P. chrysosporium* (ATCC 20696) degraded monolignols and synthetic lignin to succinic acid (8). This finding suggested that *P. chrysosporium* (ATCC 20696) catalyzed not only reactions involving side chains of lignin compounds, but also ring cleavage, indicating that this fungus uses a unique catabolic system in lignin modification.

Despite these useful properties, the complete genome of *P. chrysosporium* remains unknown. To enhance lignin-related reactions in white rot fungus, molecular biological information is necessary. Thus, we sequenced the genome of this organism using a PacBio sequencing strategy with longer reads. Here, we present the whole-genome *de novo* sequencing and gene annotation of *P. chrysosporium* (ATCC 20696).

Long reads (mean subread length, 7,249 bp) were produced using the PacBio RSII system (Pacific Biosciences). Whole-genome *de novo* assembly was performed using the FALCON method (FALCON version0.2.1), and 174 contigs were generated, with an N_{50} contig length of 966,363 bp. The complete genome of 39,205,125 bp (39 Mb) was obtained. The GC content of the assembly was 56.47%. Finally, 13,560 gene models were predicted by combining the results of transcriptome and protein sequence alignments.

According to the genome annotation, *P. chrysosporium* (ATCC 20696) contains many genes for lignolytic enzymes, such as lignin peroxidase (15 genes), manganese peroxidase (5 genes), and copper radical oxidase (7 genes). We also identified seven multicopper oxidase-related genes, which have been reported to modulate the Fenton reaction through Fe^{2+} oxidation with ferroxidase activity (9, 10). In addition, numerous intracellular enzymes related to the oxidation of aromatic compounds were detected in *P. chrysosporium* (ATCC 20696). Genes for cytochrome P450 monooxygenase (18 genes), 1,4-benzoquinone reductase (2 genes), aryl alcohol dehydrogenase (1 gene), and

homogentisate 1,2-dioxygenase (1 gene) were also identified. These results provide insight into the complex extra- and intracellular enzyme systems of *P. chrysosporium* (ATCC 20696). Based on this complex enzyme pool, *P. chrysosporium* has an excellent catabolic ability to convert aromatics to acid compounds, which supports the biodegradation mechanism of lignin by *P. chrysosporium* suggested in our previous study (8).

In conclusion, our whole-genome data of *P. chrysosporium* (ATCC 20696) will be useful for the research community studying lignin biodegradation to better understand the molecular basis of lignin degradation by the fungus and facilitate its potential applications in lignin valorization.

Accession number(s). The complete genome sequence of *P. chrysosporium* (ATCC 20696) has been deposited at DDBJ/ENA/GenBank under accession number MJGA00000000. The version described in this paper is version MJGA01000000. The database for the *P. chrysosporium* (ATCC 20696) strain is available at http://112.220.192.2/mpc.

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