Draft Genome Sequence of the Wood-Staining Ascomycete *Chlorociboria aeruginascens* DSM 107184

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**ABSTRACT** *Chlorociboria aeruginascens* DSM 107184 is a wood-decomposing ascomycetous fungus known to produce the bluish-green dimeric naphthoquinone derivative xylindein. Here, we present the first draft genome sequence, which contains 588 contigs with a total length of 33.1 Mb. Altogether, 8,648 protein-coding genes were predicted.

The bluish-green-colored ascomycete *Chlorociboria aeruginascens* belongs to the Helotiaceae family. It is well known for its characteristic spalting of infected wood during deadwood decomposition. *C. aeruginascens* is a sequential wood decomposer, i.e., a soft rot fungus, colonizing different deciduous tree species (hardwood), with a worldwide distribution (1). Chemical derivatization and spectroscopic analyses of the bluish-green pigment xylindein revealed its absolute configuration and its tautomeric structure as a dimeric naphthoquinone (2), and most of its total synthesis has been reported (3). The chemical characteristics of xylindein, like stability or insolubility, in common organic solvents, as well as its electronic properties (4), make xylindein an interesting subject of biotechnological research. Bluish-green wood has been utilized for artistic purposes since the 15th century (5, 6). However, large-scale production of the pigment using *C. aeruginascens* is difficult due to slow growth and difficult handling of the fungus (1, 7).

The present draft genome sequence of *C. aeruginascens* will help identify the genes coding for proteins involved in the biosynthesis of the pigment xylindein and for extracellular enzymes involved in the decomposition of the lignocellulosic complex.

The strain DSM 107184 (ribosomal cistron GenBank accession number MK480517) was isolated from a fruiting body growing on *Fagus sylvatica* deadwood (Lackenwald Weyer, Austria; 47°26′24.0″N, 14°18′00.0″E). Mycelium was obtained from 6-week-old malt agar plates (2.5% apple peel). Afterwards, biomass was scraped off, freeze dried, and used to extract the genomic DNA by a standard cetyltrimethylammonium bromide (CTAB)-based method. Genomic DNA was sonographically sheared (S2 ultrasonicator; Covaris, Woburn, MA, USA), and a 200-bp library was constructed using the Ion Plus fragment library kit (Thermo Fisher, Darmstadt, Germany). The genome was sequenced on an Ion Torrent personal genome machine (PGM) using the Ion PGM sequencing 200 kit version 2 and a 318v2 Chip (Thermo Fisher). The resulting 5.9 million reads were filtered to include only lengths of 160 to 280 bp and were assembled using MIRA 4.0 (8) first and Geneious R11 (9) after (parameter highest sensitivity/slow) to join overlapping contigs and to filter for duplicate contigs. The assembly contains 588 contigs (maximum length, 454,753 bp; N⁵₀ value, 110,634) (10) with a total length of 33.1 Mb and a G+C content of 43.1%. AUGUSTUS version 3.2.2 (11) and the predictor set to *Coccidioides immitis* were used to predict 8,648 protein-coding genes. Quantitative genome statistics were analyzed using BUSCO version 3 (12, 13) (fungal data set Ascomycota_odb9), which reported a genome completeness of 98.0% (complete BUSCOs). Specific
enzymes, like lignocellulolytic hydrolases and oxidoreductases (Table 1), were annotated and filtered using Blast2GO version 5.2.2 (BioBam, Valencia, Spain) or identified in the genome using BLASTP searches (BLOSUM62 matrix; E value, 1e⁻¹¹) with known crystal structure-based reference sequences (RCSB PDB). Prediction of carbohydrate-active enzymes (CAZymes) using dbCAN resulted in 497 identified genes (Table 1), among them those encoding enzymes that act on aromatic substrates. Secondary metabolite (SM) biosynthetic gene clusters (BGCs) were predicted using antiSMASH version 4.1.0. A total of 32 BGCs were identified, including BGCs for the production of 14 polyketides, four nonribosomal peptides, one hybrid polyketide-nonribosomal peptide, five terpenes, and eight nonribosomal peptide-like SMs. One of the polyketide BGCs likely controls the production of xylindein.

**Data availability.** This whole-genome shotgun project has been deposited at DDBJ/ENA/GenBank under the accession number NC5K00000000. The version described in this paper is NC5K02000000. The Sequence Read Archive (SRA) accession number is SRR5435769, associated with the BioProject number PRJNA382475.

**ACKNOWLEDGMENTS**

We thank Ulrike Schneider and Britta Büttner for help in the lab. In this context, we thank all managers and initiators of this joint project.

The work was financially and scientifically supported by the European Union (integrated projects INDOX–KBBE 2013.3.3-04 and EnzOx2 H2020-BBI-PPP-2015-2-1-720297), by the DFG project PeroxiDiv HO 1961/8-1, and by the AiF project PeroxyMEER IGF 19636 BG/3. The work has been partly funded by the DFG Priority Program 1374 "Infrastructure-Biodiversity-Exploratories" with projects HO 1961/6-1 and KE 1742/2-1, as well as by the Federal Ministry of Education and Research (BMBF) under grant VnmDiv 031B0627.

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