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GENOME SEQUENCES

# Genome Sequence of the Black Yeast *Exophiala lecanii-corni*

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**ABSTRACT** The genome sequence of *Exophiala lecanii-corni*, a melanized dimorphic fungus with the capability of degrading several volatile organic compounds, was sequenced using PacBio single-molecule real-time (SMRT) sequencing to assist with understanding the molecular basis of its uncommon morphological and metabolic characteristics. The assembled draft genome is presented here.

Black yeasts belonging to the phylum Ascomycota are of interest due to their ability to cause infections in humans (1). The pathogenesis of these organisms is partly attributed to their stress tolerance, their ubiquity in built environments, their dimorphic growth, and their production of various forms of melanin (2–4). The same features that contribute to virulence in some melanized yeast species, however, render others useful in applications such as bioremediation. One organism that has shown potential for the degradation of pollutants, such as volatile organic compounds, is *Exophiala lecanii-corni* (5). This organism is also notable for its production of large amounts of black melanin via the 1,8-dihydroxynaphthalene (DHN) melanin biosynthesis pathway (6). It was initially discovered associated with the European fruit lecanium scale and named *Torula lecanii-corni*. Subsequently, strains of *E. lecanii-corni* were isolated from cutaneous lesions on humans (7). Due to a lack of morphological features that distinguish it from related organisms, especially *Exophiala jeanselmei*, it was classified as a distinct species using genetic and physiological analyses (6, 7).

Here, we report the release of the genome sequence of *Exophiala lecanii-corni* CBS 102400, which was originally isolated from a bioreactor set up to treat a toluene-contaminated waste gas stream (5). To obtain these data, high-molecular-weight DNA was extracted from a pure culture of *E. lecanii-corni* grown for 4 days in yeast extract-peptone-dextrose (YPD) medium incubated at 30°C and shaken at 200 rpm using the OmniPrep fungus DNA extraction kit (G-Biosciences, St. Louis, MO). DNA selected from sizes of 3 to 20 kb was used to generate SMRTbell libraries using the standard library protocols of the Pacific Biosciences DNA template preparation kit and was then subjected to long-read single-molecule real-time (SMRT) sequencing with the PacBio RS II instrument (Pacific Biosciences, Menlo Park, CA), generating a total of 419,319 filtered reads with an average length of 10,516 bp and approximately 132× coverage. The resulting sequence data were assembled using the Hierarchical Genome Assembly Process version 3 (8), producing a genome sequence 34.46 Mb in size consisting of 13 contigs with an $N_{50}$ value of 2.95 Mbp and a GC content of 48.91%. The presence of telomeric repeats (TTAGGGn) at both ends of 12 contigs suggests that they likely represent entire chromosomes, while high identity of the 13th contig with the mitochondrial genome of the closely related melanized fungus *Cladophialophora bantiana* (GenBank accession number KX257489) suggests that it represents the mitochondrial genome sequence of *E. lecanii-corni*.

Melanized yeasts related to *Exophiala* species were previously separated into six clades, that is, the *jeanselmei*, *salmonis*, *bantiana*, *dermatitidis*, *carrionii*, and *Rhinocla-*

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*diella mackenzei* clades (4). Along with some shared physiological characteristics, such as the ability to reduce nitrate and a lack of growth at 37°C, the size of the *E. lecanii-corni* genome is similar to species within the *jeanselmei* clade, which range from 28.0 Mb to 38.0 Mb (4, 7), suggesting that it is a member of this clade. Using protein sequences from the toluene-degrading black yeast *Cladophialophora immunda* to perform a pBLAST search against the protein database translated from the *E. lecanii-corni* genome, we determined that *E. lecanii-corni* possesses genes for the proteins involved in each of the 12 steps of the fungal toluene degradation pathway (8, 9). These genes represent excellent candidates for future studies seeking to develop *E. lecanii-corni* for the degradation of volatile organic compounds (5).

**Data availability.** The genome sequences described here have been deposited in DDBJ/EMBL/GenBank under the accession numbers CP034370 to CP034382. The version described in this paper is the first version. The raw sequencing reads have been deposited in the NCBI SRA under the accession number SRX5145602.

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