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Genome Sequence of Talaromyces atroroseus, Which Produces Red Colorants for the Food Industry

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ABSTRACT Talaromyces atroroseus is a known producer of Monascus colorants suitable for the food industry. Furthermore, genetic tools have been established that facilitate elucidation and engineering of its biosynthetic pathways. Here, we report the draft genome of a potential fungal cell factory, T. atroroseus IBT 11181 (CBS 123796).

The genus Talaromyces primarily contains saprophytic fungi and encompasses medically and industrially relevant species such as the opportunistic human pathogen T. marneffei (formerly Penicillium marneffei), species with high production of cellulolytic enzymes, i.e., T. cellulolyticus (1), as well as the interesting pigment-producing species T. atroroseus (2). Several strains of T. atroroseus and closely related species are recognized as potential cell factories for Monascus pigment production, as they may serve as mycotoxin-free alternatives to Monascus spp. (2–4).

T. atroroseus IBT 11181 was originally isolated from red sweet bell pepper bought in a Danish supermarket and is deposited in the CBS collection at CBS-KNAW, Utrecht, the Netherlands, as CBS 123796 and CBS 238.95. We intend to implement this isolate as a model for T. atroroseus by investigating its growth physiology (5), by establishing genetic tools (6), and by reporting here the full-genome sequence of T. atroroseus IBT 11181.

Genomic DNA was extracted from the mycelium with a slightly modified protocol of the cetyltrimethylammonium bromide method used by Fulton et al. (7). The T. atroroseus IBT 11181 genome was sequenced using an Illumina HiSeq 2000 platform on a 180-bp paired-end library and a 6-kb mate-paired library both with reads of 2 × 100 bp by Beijing Genome Institute (BGI), Hong Kong. Sequencing depth was 193×, and assembly of the genome was performed with the ALLPATHS-LG algorithm (8). The final assembly resulted in 48 scaffolds with a G+C content of 44.35% and a total assembly size of 30.85 Mb corresponding to 93% of the estimated genome size from k-mer spectral analysis. The minimum number of sequences making up 50% of the genome assembly was seven, and the N50 length was 1,577,401 bp. The CEGMA pipeline (9) identified 242 of the 248 core eukaryotic genes, assessing the genome assembly completeness to be 97.58%. This indicated that the draft genome assembly was good with a high completeness and was valid to use for whole-genome analysis.

Gene-calling of the genome was performed using a pipeline of first masking the genome with a slightly modified protocol of the cetyltrimethylammonium bromide method used by Fulton et al. (7). The T. atroroseus IBT 11181 genome was sequenced using an Illumina HiSeq 2000 platform on a 180-bp paired-end library and a 6-kb mate-paired library both with reads of 2 × 100 bp by Beijing Genome Institute (BGI), Hong Kong. Sequencing depth was 193×, and assembly of the genome was performed with the ALLPATHS-LG algorithm (8). The final assembly resulted in 48 scaffolds with a G+C content of 44.35% and a total assembly size of 30.85 Mb corresponding to 93% of the estimated genome size from k-mer spectral analysis. The minimum number of sequences making up 50% of the genome assembly was seven, and the N50 length was 1,577,401 bp. The CEGMA pipeline (9) identified 242 of the 248 core eukaryotic genes, assessing the genome assembly completeness to be 97.58%. This indicated that the draft genome assembly was good with a high completeness and was valid to use for whole-genome analysis.

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useful resource for further research into the metabolism of *T. atroroseus* and its potential as a cell factory for colorant production.

**Accession number(s).** This whole-genome shotgun project has been deposited at DDBJ/ENA/GenBank under the accession number LFMY00000000. The version described in this paper is the first version, LFMY01000000.

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**REFERENCES**