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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 23895. 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 RepeatMasker version 4.0.5 (Institute for Systems Biology, Seattle, WA, USA; http://www.repeatmasker.org), and then gene-calling with AUGUSTUS version 3.0.3 (10, 11), FGENESH version 3.1.2 (SoftBerry) (12), and GeneMark-ES (13). The individual *ab initio* gene predictions were merged into a consensus gene prediction using EVidenceModeler (14), resulting in a total of 9,519 protein-encoding genes serving as the final gene prediction. The genome sequence reported here represents a
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**


