




# Draft Genome Sequence of *Aspergillus terreus* High-Itaconic-Acid-Productivity Mutant TN-484

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**ABSTRACT** Itaconic acid is an important organic acid used in the chemical industry. *Aspergillus terreus* strain TN-484 is a high-itaconic-acid-productivity mutant derived from strain IFO6365. Here, we report the draft genome sequence of strain TN-484, advancing the understanding of the biosynthesis of itaconic acid in filamentous fungi.

Itaconic acid is an unsaturated dibasic acid that is widely used as a raw material, food additive, and industrial product additive in synthetic resins and printing inks. Itaconic acid is known to be produced by filamentous fungi such as *Aspergillus itaconicus* and yeasts such as *Candida tsukubaensis*. *Aspergillus terreus* is used for industrial production of itaconic acid due to its high compound production (1). Itaconic acid is a relatively expensive organic acid, and further application expansion can occur with cost decreases (2). To more efficiently produce itaconic acid, we developed an itaconic acid-resistant strain, TN-484, by treating *A. terreus* IFO6365 with *N*-methyl-*N'*-nitro-*N*-nitrosoguanidine (NTG) and screened for an itaconic acid-resistant and high-itaconic-acid-productivity mutant (3). In addition, we cloned and analyzed the CAD1 gene encoding *cis*-aconitic acid decarboxylase (CAD). We showed that *A. terreus* CAD produced itaconic acid using *cis*-aconitic acid as the substrate (4). We previously showed that itaconic acid productivity was affected by medium pH and metal ion concentration in *A. terreus* (reviewed in reference 5). However, many itaconic acid biological functions remain unclear, and elucidating its underlying biosynthetic control will help clarify its functions.

TN-484 cells cultured in potato dextrose broth were homogenized using a bead crusher, and genomic DNA was isolated using a NucleoSpin plant II kit (TaKaRa Bio, Inc.). TN-484 genomic DNA was isolated from a liquid-submerged culture grown in potato dextrose broth at 30°C. Using the NEBNext Ultra II FS DNA library prep kit for Illumina (New England BioLabs [NEB], MA, USA), a 500-ng DNA aliquot was fragmented using DNA Fragmentase to generate DNA fragments (average, 600 bp) for library preparation. The DNA was end repaired and A tailed, adaptors were ligated, PCR was performed, and library purification was done according to the manufacturer's instructions. Sequencing

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of the TruSeq DNA library (paired-end  $2 \times 300$ -bp reads) generated 18,647,110 reads. Removal of the sequencing primers and low-quality read trimming were conducted using CLC Genomics Workbench version 12.0.2 (Qiagen, Valencia, CA, USA), with default parameters. *De novo* assembly was performed using CLC Genomics Workbench, with default parameters. After *de novo* assembly, the reference-guided scaffolding of draft genomes was conducted using RaGOO version 1.1 (6), with default parameters, and *A. terreus* NIH2624 genome sequences (GenBank accession number [GCA\\_000149615](https://doi.org/10.1093/nar/gkt418)). The resulting genome assembly had a length of 29,733,777 bp divided into 24 contigs. The  $N_{50}$  contig length was 1,952,528 bp, the GC content was 52.5%, and the genome coverage was  $174.9\times$ . The coding regions of the chromosomes were predicted using AUGUSTUS version 3.2.2 (7) and implemented in OmicsBox version 1.1.164 (Qiagen), with default parameters, using *A. terreus* as a gene model (the *A. terreus* model is contained in the AUGUSTUS package). The estimated number of genes in the draft genome was 10,301. This genomic information could provide insight into the genetic basis of itaconic acid production by this strain.

**Data availability.** The draft genome sequence for strain TN-484 has been deposited in GenBank/ENA/DBJ under the accession number [BKZM00000000](https://doi.org/10.1093/nar/gkt418) (BKZM02000001 to BKZM02000024). The SRA/DRA/ERA accession number is [DRA008975](https://doi.org/10.1093/nar/gkt418).

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