

Draft Genome Sequence of *Delftia tsuruhatensis* MTQ3, a Strain of Plant Growth-Promoting Rhizobacterium with Antimicrobial Activity

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***Delftia tsuruhatensis* MTQ3 is a plant growth-promoting rhizobacterium (PGPR) isolated from tobacco rhizosphere. Here, we report the draft genome sequence of *D. tsuruhatensis* MTQ3. Several functional genes related to antimicrobial activity and environment adaption have been found in the genome. This is the first genome sequence of *D. tsuruhatensis* related to PGPR.**

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Delftia tsuruhatensis, the type species of *Delftia*, is considered a plant growth-promoting rhizobacterium (PGPR) (1–3), an organic pollutant degradation strain (4, 5), and an opportunistic pathogenic bacterium to the human body (6, 7). *D. tsuruhatensis* is widespread in rhizosphere soil, activated sludge, and polluted environments. Although some researchers have reported the antimicrobial activity of *D. tsuruhatensis*, its antimicrobial substance and relevant synthesis mechanisms are still unclear. *D. tsuruhatensis* MTQ3 was isolated from the soil of tobacco rhizosphere in Guizhou, China, and it has shown antimicrobial activity against pathogens of soilborne plant diseases such as *Ralstonia solanacearum* and *Phytophthora nicotianae*.

Here, we report the draft genome sequence of *D. tsuruhatensis* MTQ3. Genomic DNA was extracted and sequenced using the Illumina HiSeq 2500 platform. The whole shotgun sequencing produced 8,206,833 paired-end reads with an average insert size of 580 bp (over 780-fold coverage). Another mate-paired (MP) library containing 3- to 5-kb inserts was constructed, and 13,462,994 paired-end reads were produced. All these raw data were then filtered by Trimmomatic v 0.30 (8). Filtered reads were assembled, scaffolded, and gap filled with Velvet v. 1.2/08 (9), SSPACE v. 2.0 (10), and GapFiller v. 1.11 (11). Final assembly consisted of 12 scaffolds (length \geq 500 bp) with an N_{50} length of 742,938 bp, an average length of 522,672 bp, and the largest length of 1,608,022 bp. The genome sequence was annotated using the NCBI Prokaryotic Genome Automatic Annotation Pipeline (PGAAP) (http://www.ncbi.nlm.nih.gov/genome/annotation_prok/).

The genome consists of 6.27 Mb, with a G+C content of 66.79%. A total of 5,005 coding sequences (CDS), 13 pseudogenes, 72 tRNA genes, 1 noncoding RNA (ncRNA), and 10 rRNA genes were identified. Average nucleotide identity (ANI) analysis (12) revealed that *D. tsuruhatensis* MTQ3 is phylogenetically related to *D. tsuruhatensis* 391 (98.34%) (GenBank accession no. JNWH00000000), *D. acidovorans* CCUG 274B (97.96%) (AGYX00000000), *D. acidovorans* SPH-1 (94.94%) (NC_010002), *Delftia* sp. 670 (94.30%) (JNWI00000000),

D. acidovorans CCUG 15835 (92.70%) (AGYY00000000), and *Delftia* sp. Cs1-4 (91.37%) (NC_015563).

Many genes involved in the antimicrobial activity of *D. tsuruhatensis* MTQ3 were identified in the genome, such as the bacteriocin gene (AA671_02705), polyketide synthase (PKS) gene (AA671_12420), nonribosomal peptide synthetase (NRPS) gene (AA671_12430), balhimycin synthesis gene (AA671_12395), quinolinate synthesis gene (AA671_01765), and phenazine synthesis gene (AA671_00865). Some genes responsible for the processing and transport of antibiotics were identified in the genome, including antibiotic biosynthesis monooxygenase gene (AA671_01400, AA671_17345), macrolide transporter gene (AA671_00980), and antibiotic ABC transporter substrate-binding gene (AA671_25335).

In addition, *D. tsuruhatensis* MTQ3 possesses genes with likely relevance to rhizosphere competence and adaptation in polluted environments. Specifically, quercetin dioxygenase (AA671_16710, AA671_18600) is likely a plant microbe-signaling bacterium involved in degrading plant-produced antimicrobial root exudates (13, 14). Protocatechuate dioxygenase (AA671_06970, AA671_06975, AA671_20040, AA671_20045, AA671_25085, AA671_25090) may be related to the degradation of aromatic acid (15). Genes related to the degradation of phenylacetic acid (AA671_06085, AA671_20955, AA671_23770, AA671_24525, AA671_24535) and hydroxyatrazine (AA671_03765) were also identified.

Nucleotide sequence accession numbers. The whole-genome shotgun project of *D. tsuruhatensis* MTQ3 has been deposited in DDBJ/ENA/GenBank under the accession number [LCZH00000000](https://www.ncbi.nlm.nih.gov/nuccore/LCZH00000000). The version described in this paper is the first version, LCZH01000000.

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