



# Complete Genome Sequence of *Curtobacterium* sp. Strain TXMA1, Isolated from a Grapevine in Texas, USA

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**ABSTRACT** The genome of *Curtobacterium* sp. strain TXMA1, isolated from a grapevine in Texas showing leaf marginal necrosis symptoms, was sequenced. The TXMA1 genome has a 3,454,876-bp, circular chromosome with a GC content of 71.74%, 3,213 open reading frames (ORFs), 47 tRNAs, and 4 complete rRNA operons (5S, 16S, and 23S).

*Curtobacterium* is a cosmopolitan genus of Gram-positive bacteria in the order *Actinomycetales* (1). While some strains are plant pathogenic (2), endophytic *Curtobacterium* strains have been reported in many crops, such as rice (3), potato (4), and citrus (5, 6). There has been strong interest among the scientific research community to explore the use of endophytes for biocontrol of plant pathogens, including *Xylella fastidiosa*, a bacterial pathogen causing Pierce's disease (PD) of grapevine in the United States. Here, we report a whole-genome sequence of *Curtobacterium* sp. strain TXMA1, isolated from a grapevine in Texas.

In September 2019, grape leaves with marginal necrosis symptoms resembling those of PD were collected from the cultivar Blanc du Bois grown in an experimental plot in Monte Alto, TX. PCR experiments (7) did not detect *X. fastidiosa*. Leaf petioles were surface-sterilized in 1% (vol/vol) sodium hypochlorite, followed with rinses in sterile, deionized water. Xylem sap was collected, streaked onto periwinkle wilt (PW) medium (8), and incubated at 28°C. While *X. fastidiosa* colonies were not recovered, yellow-pigmented colonies (YPCs) were observed within 7 days. The YPCs were cloned using three rounds of single colony isolation. DNA from one YPC culture was extracted using the Qiagen DNeasy blood and tissue kit (Qiagen) and amplified through PCR using the primer set fD1/rD1 targeting the 16S rRNA gene (9). Amplicons were sequenced using the Sanger method. A BLASTn search using amplicon sequences against the GenBank database showed a sequence identity of >96% to multiple strains of *Curtobacterium* sp. The YPC strain was designated *Curtobacterium* sp. strain TXMA1.

For genome sequencing, strain TXMA1 was cultured at 28°C on PW plates for 2 to 3 days. Bacterial DNA was extracted from a cell culture as above, quantified using a Qubit fluorometer (Invitrogen), and sheared to 8 kb using a Covaris g-TUBE device (Woburn, MA). A library was prepared using a ligation sequencing kit (LSK109, Oxford Nanopore Technologies, UK) and sequenced on a MinION device using an R9.4.1 flow cell (Oxford Nanopore Technologies). Base calling was performed using Guppy v5.0.11 with the parameters `-c dna_r9.4.1_450bps_fast.cfg --min_qscore 7`. A total of 80,465 sequence reads with an  $N_{50}$  value of 12,442 bp were generated. The TXMA1 genome was assembled using Flye v2.9 with `--genome-size 3.5M` (10). The assembly was polished using medaka v1.4.3 with the r941\_min\_fast\_g507 model (<https://github.com/nanoporetech/medaka>) and rotated using Circlator v1.5.5 (11) so that the first base corresponded to the start of *dnaA*. The assembly quality was evaluated using the CheckM v1.1.2 lineage\_wf pipeline (12), estimating 99.45% completeness and no contamination or heterogeneity.

The TXMA1 genome consists of one circular contig of 3,454,876 bp, with ~110× coverage and a GC content of 71.74%. No plasmids were identified. Sequence annotation using

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the NCBI Prokaryotic Genome Annotation Pipeline (PGAP) (13) predicted that the TXMA1 genome had 3,213 open reading frames (ORFs), 47 tRNAs, 4 complete rRNA operons (5S, 16S, and 23S), and 3 noncoding RNAs. The average nucleotide identity (ANI) to the genome assemblies of 138 *Curtobacterium* strains deposited in GenBank was determined using FastANI v1.1 (14). TXMA1 has >98% ANI to two *Curtobacterium oceanosedimentum* strains, NS263 (GenBank accession number [GCF\\_001475745.1](https://doi.org/10.1093/nar/gkw569)) and NS359 ([GCF\\_001476135.1](https://doi.org/10.1093/nar/gkw569)), and >95% ANI to *Curtobacterium* sp. strain SGAir0471 ([NZ\\_CP027869](https://doi.org/10.1093/nar/gkw569)).

**Data availability.** This whole-genome shotgun project has been deposited at GenBank under the accession number [CP083910](https://doi.org/10.1093/nar/gkw569), the BioProject accession number [PRJNA764237](https://doi.org/10.1093/nar/gkw569), and the BioSample accession number [SAMN21487717](https://doi.org/10.1093/nar/gkw569). The version described here is the first version, [CP083910.1](https://doi.org/10.1093/nar/gkw569).

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