



# Complete Genome Sequence of *Terriglobus albidus* Strain ORNL, an Acidobacterium Isolated from the *Populus deltoides* Rhizosphere

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**ABSTRACT** *Terriglobus albidus* strain ORNL is a heterotrophic soil acidobacterium isolated from the rhizosphere of an Eastern cottonwood tree (*Populus deltoides*) in Tennessee. Its 6.4-Mb chromosome was completely sequenced using PacBio long reads, and it encodes 5,010 proteins and 53 RNAs.

**A**cidobacteria are one of the most diverse and abundant bacterial phyla, with members colonizing most soils, in which they represent, on average, one-fifth of the microbial community (1, 2). Among the 14 currently recognized classes in the phylum (3), the class *Acidobacteriia* encompasses the vast majority of the several dozen cultivated members and genomic sequences. The other classes have few isolates and are only represented by culture-independent sequence data from single cells and metagenomes. Here, we report the complete genome sequence of *Terriglobus albidus* ORNL, isolated from a *Populus deltoides* rhizosphere sample in Oak Ridge, Tennessee. Single bacterial cells from a root-associated soil sample were randomly deposited by flow cytometry sorting (4, 5) on Reasoner's 2A (R2A) agar and incubated at 28°C to form colonies, followed by identification by small subunit (SSU) rRNA gene amplicon sequencing (5). Based on ClustalW 2.1 sequence alignment, one colony had 1,459 out of 1,461 nucleotides (nt) identical (99.8%) to those of the sequence of *T. albidus* Ac26B10, a species isolated and described from semiarid savannah soil in Namibia (6). Therefore, our isolate is a strain of *T. albidus*, designated ORNL.

*T. albidus* ORNL was grown in liquid R2A agar for 5 days. Genomic DNA was extracted and purified using a Qiagen DNeasy kit and a Zymo Research DNA Clean & Concentrator kit, followed by shearing with g-Tubes (Covaris, Woburn, MA) to a 10-kb average fragment size. A library was prepared with an SMRTbell template prep kit v1.0 (Pacific Biosciences, Menlo Park, CA) and sequenced on a Pacific Biosciences Sequel instrument. Sequence quality-based filtering and assembly were performed using Hierarchical Genome Assembly Process 4 (HGAP4) software implemented in the PacBio SMRTLink v7 pipeline with a target genome size of 5 Mbp (based on other *Terriglobus* genomes), a minimum confidence of 40, a minimum coverage of 50, and the other options set as defaults. A total of 78,854 filtered subreads ( $N_{50}$  length, 8,759 nt) were assembled into a single polished contig 6,405,582 nt long, with a mean coverage of 553-fold and a G+C content of 58.5%. Using Geneious v11 (7), we determined that the ends of the contig spanned an open reading frame encoding the same potential protein. ClustalW v2.1 was used to align the extracted contig ends with the corresponding sequencing reads. An identical region was identified, indicating a closed circular genome, and the duplicated sequence was manually removed from one of the ends. Gene prediction and functional annotation were performed using the NCBI Prokaryotic Genome Annotation Pipeline (PGAP) v4.8 (8), which identified 5,010 protein coding sequences, 47 tRNAs, 1 rRNA operon, and 3 noncoding RNAs (ncRNAs). A metabolic model was built using KBase (9) and is accessible together with a Rapid

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Annotations using Subsystems Technology (RAST) annotation at <https://narrative.kbase.us/narrative/ws.44746.obj.1>. The genome of *Terriglobus albidus* will help in identifying genes and processes associated with the evolution of plant-microbe associations.

**Data availability.** The *Terriglobus albidus* ORNL genome sequence has been deposited in GenBank under accession number [CP042806](https://ncbi.nlm.nih.gov/nuccore/CP042806). The version described in this paper is the first version, CP042806.1. The PacBio reads have been deposited in the SRA database under accession number [SRR10037938](https://ncbi.nlm.nih.gov/sra/SRR10037938).

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