

Draft Genome Sequence of *Frankia* sp. Strain BCU110501, a Nitrogen-Fixing Actinobacterium Isolated from Nodules of *Discaria trinevis*

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***Frankia* forms a nitrogen-fixing symbiosis with actinorhizal plants. We report a draft genome sequence for *Frankia* sp. strain BCU110501, a nitrogen-fixing actinobacterium isolated from nodules of *Discaria trinevis* grown in the Patagonia region of Argentina.**

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The genus *Frankia* forms a symbiotic nitrogen-fixing association with woody trees and shrubs, resulting in a root nodule formation (1–3). *Frankia* exists either in a free-living state in the soil or in symbiosis with actinorhizal plants. These actinorhizal plants comprise over 200 different plant species belonging to 8 distinct plant families. Because of symbiosis, these globally distributed actinorhizal plants are able to colonize harsh environmental terrains under diverse ecological conditions. Phylogenetic studies have shown that *Frankia* has four major lineages or clusters that can also be defined by physiology, host specificity, and mode of infection of the host plant (4–7). Genomes for representatives from each of these clusters have been sequenced (8–13) and have provided essential baseline information for genomic approaches toward understanding these novel bacteria.

Frankia strains from cluster III have the greatest metabolic versatility, are known to associate with five plant families (*Betulaceae*, *Myricaceae*, *Elaeagnaceae*, *Rhamnaceae*, and *Casuarinaceae*), and are considered broad-host-range symbionts. Many of these strains have adapted to harsh environmental conditions. *Frankia* sp. strain BCU110501 (also called Dtl1 and T1) was isolated from a field nodule of *Discaria trinevis* growing wild in a semiarid steppe (40°41'S, 71°10'W) of the Argentinian Reserve and National Park “Parque Nacional Nahuel Huapi,” located in the northwest of Patagonia (14). The physiology and infectivity of this strain have been well studied (15–20), and it uses an intercellular route of plant infection (18). *Frankia* sp. strain BCU110501 was chosen for sequencing as another cluster III representative with broad-host-range properties and an intercellular infection route. Strain BCU110501 was sequenced to provide information about the potential ecological roles of the *Frankia* strains and their interactions with actinorhizal plants.

The draft genome of *Frankia* sp. strain BCU110501 was generated at the Department of Energy (DOE) Joint Genome Institute (JGI) using Illumina technology (21). An Illumina standard shotgun library was constructed and sequenced using the Illumina HiSeq 2000 platform, which generated 12,553,550 reads totaling 1,883.0 Mbp. All techniques for DNA isolation, library construction, and sequencing were performed according to JGI standards and protocols (<http://www.jgi.doe.gov>). The Illumina sequence data were assembled using Velvet (version 1.1.04) (22) and Allpaths-LG (version r41043) (23). The final draft assembly contained 207 contigs in 207 scaffolds. The total size of the genome is 7.9 Mbp and the final assembly is based on 950.8 Mbp of Illumina data, which provides an average 120.4× coverage of the genome.

The draft genome of *Frankia* BCU110501 was resolved to 207 scaffolds consisting of 7,891,711 bp with a G+C content of 72.39%, 6,742 candidate protein-encoding genes, 47 tRNA genes, and 2 rRNA regions.

Nucleotide sequence accession numbers. The *Frankia* sp. strain BCU110501 genome sequence has been deposited at DDBJ/EMBL/GenBank under the accession number [ARDT00000000](https://www.ncbi.nlm.nih.gov/nuccore/ARDT00000000). The version described in this paper is the first version, [ARDT01000000](https://www.ncbi.nlm.nih.gov/nuccore/ARDT01000000).

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