

# Genome Sequence of the Biocontrol Agent *Microbacterium barkeri* Strain 2011-R4

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***Microbacterium barkeri* strain 2011-R4 is a Gram-positive epiphyte which has been confirmed as a biocontrol agent against several plant pathogens in our previous studies. Here, we present the draft genome sequence of this strain, which was isolated from the rice rhizosphere in Tonglu city, Zhejiang province, China.**

*Microbacterium barkeri* is one of the species in the genus *Microbacterium*, which belongs to the high-GC-content phylum *Actinobacteria* (13). It has been reported that *Microbacterium* strains can cause human, animal, and plant diseases (1, 7, 9). However, *Microbacterium* spp. have frequently been isolated from the soil and used as biocontrol agents (2, 16, 18). Some reports have demonstrated that *Microbacterium barkeri* strains are strong in plant colonization (17) and play a very important role in biocontrol. Cottyn et al. isolated several *Microbacterium barkeri* strains with potential biocontrol ability from rice seeds (5, 6). These results suggested that *Microbacterium barkeri* may be useful to further explore the commercial potential for biocontrol in rice fields, and genome-wide sequence analysis could play an important role for genetic studies of this bacterium.

In this research, we sequenced and annotated the draft genome of *Microbacterium barkeri* 2011-R4 isolated as an epiphyte from the rice rhizosphere of Tonglu city, Zhejiang province. The bacterial genomic DNA, isolated using a QIAamp DNA minikit (Qiagen, Germany), was paired-end whole-genome shotgun sequenced using Illumina HiSeq 2000 with a 500-bp inserted library. This resulted in 20,513,376 high-quality filtered reads with a 95-bp average read length and coverage equivalent to about 1,000×. Paired-end reads were assembled *in silico* with IDBA-UD 1.0.9 (15). Assembled contigs were scaffolded using SSPACE Basic 2.0 (3). Based on the reference genome of *Microbacterium testaceum* StLB037 (13), a draft genome of 2011-R4 was completed. By subsequent PCR and resequencing, 35 genome gaps were closed but 142 contigs remained.

The draft genome sequence of strain *Microbacterium barkeri* 2011-R4 comprises 3,637,250 bases representing approximately >99.9% of the estimated genome size of 2011-R4. The genome of this strain has a high G+C content of 69.1%. A total of 3,817 coding sequences (CDSs) were predicted using Prodigal v2.6 with default parameters (8). The functions of encoding genes were automatically identified by the GenDB annotation engine (12). The chromosome has eight rRNA operons and 47 tRNAs predicted by RNAmmer and tRNAscan (10, 11). Furthermore, 68.2% of the open reading frames (ORFs) have orthologs in the reference strain *M. testaceum* StLB037 (BLASTP, <1e−5), but 1,213 ORFs were not found in the released genomes of the *Microbacterium* genus. Of these previously unreported ORFs, 1,057 ORFs did not generate hits in current public databases (NCBI nr database).

The *Microbacterium barkeri* 2011-R4 genome contains a reper-

toire of antimicrobial-, antibiotic-, and metabolism-associated pathways and epiphytic fitness genes which were identified by KEGG databases (14). Until now, only two *Microbacterium* genome sequences have been released (4, 13); therefore, it is very hard to predict the potential biocontrol functions of many genes in our strain. Overall, the genome sequence of *S. maltophilia* RR-10 provides a foundation not only for plant disease control research but also for *Microbacterium* genomics and comparative genomics research.

**Nucleotide sequence accession numbers.** This Whole Genome Shotgun project has been deposited at DDBJ/EMBL/GenBank under the accession number [AKVP000000000](https://www.ncbi.nlm.nih.gov/nuccore/AKVP000000000). The version described in this paper is the first version, AKVP01000000.

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