

# Genome Sequence of *Stenotrophomonas maltophilia* RR-10, Isolated as an Endophyte from Rice Root

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***Stenotrophomonas maltophilia* is an endophyte which plays important roles in agricultural production as a plant growth-promoting bacterium. Here, we present the draft genome sequence of strain RR-10, which was isolated from a rice root in a rice field of China.**

*Stenotrophomonas maltophilia*, formerly *Xanthomonas maltophilia* (10), is widely found on or in plants and has a worldwide distribution (2). Although *S. maltophilia* is also known as the third most common of the nosocomial nonfermenting Gram-negative bacilli that cause human disease as a result of its ability to colonize immunocompromised patients (1, 11, 12), many strains of this species can produce antibiotics that protect plants, as well as generate factors that can promote plant growth (3, 4), and have long been used for biocontrol in agriculture. *S. maltophilia* has been isolated as a beneficial bacterial species from the roots of many plant species, including rice (8). Strains of *S. maltophilia* not only produce volatile organic compounds with antifungal activity but also have an extraordinarily high hydrolytic potential (11). Both chitinolytic and proteolytic activities contribute to the biocontrol activity of *S. maltophilia* (15, 16).

For this paper, we sequenced and annotated the draft genome of *Stenotrophomonas maltophilia* RR-10, which was isolated as an endophyte from a rice root in Zhejiang Province, China. The genomic DNA, isolated with a Wizard genomic DNA purification kit (Promega, Madison, WI), was subjected to whole-genome sequencing using an Illumina HiSeq 2000 sequencing system. This resulted in 13,363,534 high-quality filtered reads with an average length of 80 bp and coverage equivalent to about 200-fold. Quality filtered reads were assembled *in silico* with Velvet and SOAPdenovo software (6, 14). Based on the reference genome of *Stenotrophomonas maltophilia* K279a (1), a draft genome of RR-10 was completed. By subsequent PCR and resequencing, 107 genome gaps were closed but 70 scaffolds remained.

The draft genome sequence of strain RR-10 comprises 4,660,562 bases representing more than 99.9% of the estimated genome size of the RR-10, with G+C content of 66.3%. A total of 4,292 coding sequences (CDSs) were predicted using GLIMMER (13). Putative functions of encoding genes were automatically identified using the GenDB annotation engine (9). The chromosome has five rRNA operons and 50 tRNAs as predicted by RNAmmer and tRNAscan (5, 7). Furthermore, 89.8% of the open reading frames (ORFs) have orthologs in the *S. maltophilia* K279a reference strain (BLASTP < 1e-5), but 421 ORFs were not found in the released genomes of bacteria of the *Stenotrophomonas* genus; of these, 162 ORFs did not give hits in current public databases.

The *S. maltophilia* RR-10 genome contains a repertoire of antimicrobial and antibiotic metabolism-associated genes such as those encoding the ABC-type antimicrobial peptide transport sys-

tem and resistance-nodulation division (RND)-type efflux pumps as well as a large number of epiphytic fitness genes such as those associated with pili, fimbriae, and adhesions. Type I, II, IV, and V as well as TaT system genes are present in RR-10, although type III secretion genes are not. Overall, the genome sequence of *S. maltophilia* RR-10 provides a foundation for plant disease control research.

**Nucleotide sequence accession numbers.** This whole-genome shotgun project has been deposited at DDBJ/EMBL/GenBank under accession number [AGRB000000000](https://www.ncbi.nlm.nih.gov/nuccore/AGRB000000000). The version described in this paper is the first version, AGRB010000000.

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