

# Genome Sequence of the Rice-Pathogenic Bacterium *Acidovorax avenae* subsp. *avenae* RS-1<sup>∇</sup>

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***Acidovorax avenae* subsp. *avenae* is a phyto bacterium which is the causative agent of several plant diseases with economic significance. Here, we present the draft genome sequence of strain RS-1, which was isolated from rice shoots in a rice field in China. This strain can cause bacterial stripe of rice.**

*Acidovorax avenae* subsp. *avenae*, formerly *Pseudomonas avenae* (10), can cause diseases in many plants with economic importance, including rice, corn, oats, sugarcane, millet, and foxtail (9). In rice, this pathogen can cause bacterial brown stripe and has been reported in many countries in Asia, Africa, the Americas, and Europe (11). The symptoms start as brown stripes on the bottom of stems 5 days after emergence and frequently extend into the sheaths, spreading along the leaf midrib and throughout the seedling at the one-leaf stage (3). As *A. avenae* subsp. *avenae* is a widely distributed seed-borne pathogen of rice (8–9), the rice seeds contaminated with this pathogen are important sources of the primary inoculum and a means of dissemination of the pathogen to new areas (1, 8). Therefore, this pathogen has been gaining increasing attention in China.

We sequenced and annotated the draft genome of *A. avenae* subsp. *avenae* strain RS-1, a strain isolated from a diseased rice sheet in Zhejiang province in 2010 (3). The genomic DNA, isolated with a Wizard genomic DNA purification kit (Promega, Madison, WI), was whole-genome sequenced by using an Illumina HiSeq 2000 sequencing system. This resulted in 17,300,242 high-quality filtered reads with an average read length of 96 bp and coverage equivalent to about 200×. Quality filtered reads were assembled *in silico* with SOAPdenovo and the GapCloser program (4). Based on the reference genome of *A. avenae* subsp. *avenae* ATCC 19860 (sequenced by JGI; isolated from maize leaf), a draft genome of RS-1 was completed. By subsequent PCR and resequencing, 62 genome gaps were closed, but 156 contigs remained.

The draft genome sequence of strain RS-1 comprises 5,522,282 bases, representing approximately more than 99.9% of the estimated genome of RS-1. The genome of this strain has a high G+C content, 68.7%. A total of 5,043 coding sequences (CDSs)

were predicted using GLIMMER (7). Putative functions of encoding genes were automatically identified using the GenDB annotation engine (6). The chromosome has three rRNA operons and 43 tRNAs predicted by RNAmmer and tRNAscan (2, 5). Furthermore, 90.4% of the open reading frames (ORFs) have orthologs in the reference strain *A. avenae* subsp. *avenae* ATCC 19860 (BLASTP value < 1e-5), but 301 ORFs were not found in the released genomes of members of the genus *Acidovorax*. Interestingly, many of these ORFs are clustered together. The result suggested that these regions may be genomic islands in *A. avenae* subsp. *avenae* RS-1.

Pathogenicity-related genes (such as those involved in hypersensitive response and the type III secretion system-related proteins), which are essential for many plant-pathogenic bacteria, are found in RS-1. Meanwhile, several loci encoding proteins for fimbrial biosynthesis, adhesion-type proteins, and RND efflux system proteins were also found. Overall, the genome sequence of *A. avenae* subsp. *avenae* RS-1 provides a foundation for both basic and agricultural applied research.

**Nucleotide sequence accession numbers.** This whole-genome shotgun project has been deposited at DDBJ/EMBL/GenBank under accession number AFPT00000000. The version described in this paper is the first version, AFPT01000000.

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