

Genome Sequence of the Rice Pathogen *Pseudomonas fuscovaginae* CB98818

Guanlin Xie,^a Zhouqi Cui,^a Zhongyun Tao,^a Hui Qiu,^a He Liu,^a Muhammad Ibrahim,^a Bo Zhu,^a Gulei Jin,^b Guochang Sun,^c Abdulwareth Almoneafy,^a and Bin Li^a

State Key Laboratory of Rice Biology, Institute of Biotechnology, Zhejiang University, Hangzhou, China^a; Institute of Bioinformatics, Zhejiang University, Hangzhou, China^b; and State Key Laboratory Breeding Base for Zhejiang Sustainable Pest and Disease Control, Institute of Plant Protection and Microbiology, Zhejiang Academy of Agricultural Sciences, Hangzhou, China^c

***Pseudomonas fuscovaginae* is a phytopathogenic bacterium causing bacterial sheath brown rot of cereal crops. Here, we present the draft genome sequence of *P. fuscovaginae* CB98818, originally isolated from a diseased rice plant in China. The draft genome will aid in epidemiological studies, comparative genomics, and quarantine of this broad-host-range pathogen.**

Pseudomonas fuscovaginae belongs to the authentic rRNA group I of pseudomonads pathogenic toward several crop species, such as rice, maize, sorghum, and wheat (1, 4, 5). In rice, this pathogen can cause bacterial sheath brown rot and has been reported in many countries in Asia, Africa, the Americas, and Europe (4, 5, 10). Distinctive symptoms on rice plants are water-soaked, brown-black spots on the adaxial side of the flag leaf sheath, poor spike emergence, and sterility in severe cases (10–12). As *P. fuscovaginae* is a seed-borne and seed-transmitted pathogen of rice, 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 (9–11). Therefore, this pathogen has been gaining increasing attention in China.

We sequenced and annotated the draft genome of *P. fuscovaginae* CB98818, a strain isolated from diseased rice in Zhejiang province, China, in our previous study (11). The genomic DNA, isolated with a Wizard genomic DNA purification kit (Promega, Madison, WI), was whole-genome sequenced by using Roche 454 GS FLX systems. A total of 437,333 reads were generated, with an average read length of 425 bp and coverage equivalent to about 200×. The sequence reads were *de novo* assembled using Geneious Pro v5.5.3 (3) and Newbler Assembler 2.7 (454 Life Science), resulting in a total of 263 contigs. Based on the most closely related reference genome of *P. fuscovaginae* UPB0736 (8), a draft genome of *P. fuscovaginae* CB98818 was generated. Functional annotation was conducted by merging the results obtained from the RAST (rapid annotation using subsystem technology) server (2), tRNAscan-SE 1.21 (7), and RNAmmer 1.2 (6).

Here we announce the draft genome sequence of *P. fuscovaginae* CB98818, which comprises 6,541,443 bp and has a G+C content of 61.4%. A total of 6,290 genes were predicted using Glimmer (9). The draft sequence contains 74 RNAs, including two 23S rRNA genes, seven 5S rRNA genes, and 65 tRNAs. Furthermore, 94.2% of the open reading frames (ORFs) have orthologs in the reference strain *P. fuscovaginae* CB98818 (BLASTP E value of 1E–20), but 372 ORFs were not found in the released genomes of members of the genus *Pseudomonas*.

P. fuscovaginae has the ability to produce three different types of phytotoxic metabolites, syringotoxin, fuscopeptin A, and fuscopeptin B, which are reported to be involved in producing the disease symptoms (8). Furthermore, functional annotation of *P. fuscovaginae* strain CB98818 revealed pathogenicity-related genes

like type VI secretion system, type III and IV secretion system, Hcp- and VgR-like protein, Hrp protein, and flagellin. These genes are virulence associated in many phytopathogenic Gram-negative bacteria (3). Meanwhile, several multidrug resistance efflux pumps, the multidrug transporter MdtB, and ABC transporter subunits were also identified.

Overall, the genome sequence of *P. fuscovaginae* CB98818 will provide the basis for a better understanding of the molecular pathogenesis of rice bacterial sheath brown rot and is an important data resource for epidemiological studies, comparative genomics, and quarantine measures of this important phytopathogen.

Nucleotide sequence accession numbers. This whole-genome shotgun project has been deposited at DDBJ/EMBL/GenBank under the accession number [ALAQ00000000](#). The version described in this paper is the first version, ALAQ01000000.

ACKNOWLEDGMENTS

This project was supported by the Natural Science Foundation of Zhejiang Province (LY12C14007 and Y3090150), the 12th Five-Year Key Programs for Science and Technology Development of China (2012BAK11B02 and 2012BAK11B06), the Zhejiang Provincial Project (2010R10091), the Fundamental Research Funds for the Central Universities, the Agricultural Ministry of China (nyhyzx 201003029 and 201003066), and the State Education Ministry and Key Subject Construction Program of Zhejiang for Modern Agricultural Biotechnology and Crop Disease Control (2010DS700124-KF1101).

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Received 20 July 2012 Accepted 27 July 2012

Address correspondence to Bin Li, libin0571@zju.edu.cn, or Muhammad Ibrahim, ibrahim211@zju.edu.cn.

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doi:10.1128/JB.01273-12

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