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Draft Genome Sequence of *Pseudomonas fuscovaginae*, a Broad-Host-Range Pathogen of Plants

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***Pseudomonas fuscovaginae* was first reported as a pathogen of rice causing sheath rot in plants grown at high altitudes. *P. fuscovaginae* is now considered a broad-host-range plant pathogen causing disease in several economically important plants. We report what is, to our knowledge, the first draft genome sequence of a *P. fuscovaginae* strain.**

Pseudomonas fuscovaginae is a Gram-negative fluorescent pseudomonad first identified and reported as a pathogen of rice (*Oryza sativa*) in Japan in 1976 (11). Its symptoms on rice plants are the appearance of brown-black, water-soaked spots on the adaxial side of the flag leaf sheath, with grain discoloration, poor spike emergence, and sterility in severe cases (12). *P. fuscovaginae* is now regarded as a plant pathogen that causes bacterial sheath brown rot disease also on several other cereals, including maize (*Zea mays*), sorghum (*Sorghum bicolor*) (6), and wheat (*Triticum aestivum*) (4). *P. fuscovaginae* is one of the 18 validly described *Pseudomonas* plant-pathogenic species that comprise the oxidase-positive cluster (1, 8).

Here we announce the draft genome sequence of *P. fuscovaginae* UPB0736; this strain was isolated on 26 April 1986 from a sheath brown rot lesion on the rice at Antsirabe (1,550-m elevation) in Madagascar (5). The strain displays particularly high pathogenicity toward rice (5). The strain has been deposited in the BCCM/LMG Culture Collection, Ghent, Belgium.

The genome sequence of *P. fuscovaginae* was determined using a 36-bp paired-end library with the Illumina GA sequencing system as described previously (10). We obtained a total of 33,846,290 pairs of reads, representing approximately 360-fold coverage of the genome. We performed *de novo* assembly using Velvet 1.1.03 (13), generating 102 scaffolds (supercontigs) with a mean length of 65.9 kbp. The total length of the supercontig assembly was 6.7 Mbp, and the N_{50} length was 205.3 kbp, assuming a genome size of 6.7 Mb. The longest scaffold obtained was 605.8 kbp nucleotides long. The G+C content was 61.46%, similar to that of other sequenced *Pseudomonas* genomes. Automated annotation of the *P. fuscovaginae* draft genome sequence using RAST (2) assigned a total of 5,639 candidate protein-coding genes. Among all the predicted genes, a total of 1,077 genes were annotated as encoding hypothetical proteins. A total of 3 rRNA and 48 tRNA genes were also identified in the RAST annotation.

P. fuscovaginae produces three different types of phytotoxic metabolites, syringotoxin, fuscopeptin A (FP-A), and fuscopeptin B (FP-B), that have been shown to be involved in generating the disease symptoms (3, 7). Despite the importance of *P. fuscovaginae* as a plant pathogen on several plant hosts around the world, very few studies of the virulence and biology of this pathogen have been performed. In a previous study we investigated the role of the quorum sensing regulatory system

in causing sheath brown rot by *P. fuscovaginae* (9). In the present study, we report the draft genome information of a very virulent *P. fuscovaginae* strain which, to our knowledge, is the first sequence report of this species.

Nucleotide sequence accession numbers. This Whole Genome Shotgun project has been deposited at DDBJ/EMBL/GenBank under the accession number AIEU00000000. The version described in this paper is the first version, AIEU01000000. The genome project data are also available at GenBank under the genome project ID PRJNA84441.

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