

# 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](https://www.ncbi.nlm.nih.gov/nuccore/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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