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GENOME ANNOUNCEMENT

Draft Genome Sequences of the *Pseudomonas fluorescens* Biocontrol Strains Wayne1R and Wood1R

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***Pseudomonas fluorescens* strains Wayne1R and Wood1R have proven capacities to improve plant health. Here we report the draft genome sequences and automatic annotations of both strains. Genome comparisons reveal similarities with *P. fluorescens* strain Pf-5, reveal the novelty of Wood1R, and indicate some genes that may be related to biocontrol.**

Pseudomonas fluorescens strains Wayne1R and Wood1R are rifampin-resistant variants of wild-type strains isolated from the rhizospheres of corn and soybeans (3). They harbor the *phlD* gene, which is essential for biosynthesis of 2,4-diacetylphloroglucinol (DAPG) in *Pseudomonas* spp. (2). Both strains can improve plant health under field conditions, a trait that appears to be common among *phlD*$^+$ bacteria (8). Soybeans treated with Wayne1R have greater stands and yields in the field than those grown from untreated seeds (3). Also, seed treatment with Wood1R ameliorates nutrient stress of field-grown corn grown in acidic soil (6).

The genomic DNAs of Wayne1R and Wood1R were isolated, and libraries were prepared from sheared DNA fractions of ~300 bp using Illumina paired-end sample preparation kits. These were sequenced on a Genome Analyzer II (Illumina, San Diego, CA). The short-read sequences were assembled into assemblies with hash lengths of 37 nucleotides (nt) (Wayne1R) and 31 nt (Wood1R) and a minimum contig length of 300 nt using Velvet version 0.7.55 (9, 10). The assemblies were uploaded to an automated annotation platform, the rapid annotation using subsystems technology (RAST) server (1), and visualized with the SEED viewer (4).

The Wayne1R assembly has a total of 6,858,374 nt spread across 90 contigs. Some 6,228 protein-encoding genes (PEGs) were annotated on 75 contigs, with an average sequence coverage of ~20-fold. rRNA genes were not fully assembled. However, 52 tRNA sequences were identified. In the amino acid sequence-based comparisons to other *Pseudomonas fluorescens* strains in the public SEED database, 5,112 to 5,814 (82 to 93%) of the annotated PEGs of Wayne1R were mapped to the genomes of *P. fluorescens* strains Pf-5 (5), Pf0-1, and SBW25 (7), with an average DNA sequence identity of 74%. Of the 414, 1,079, and 1,116 PEGs predicted to be unique to Wayne1R when compared with Pf-5, Pf0-1, and SBW25, respectively, 117 (28.2%), 756 (70.0%), and 801 (71.8%) PEGs, respectively, were identified (i.e., not assigned as "hypothetical proteins").

The Wood1R assembly has a total of 6,681,319 nt spread across 1,437 contigs. Some 5,897 PEGs were annotated on 1,304 contigs, with an average sequence coverage of ~13-fold. The assembly did not adequately reconstruct the rRNA genes, but 30 tRNA sequences were identified. In the amino acid sequence-based comparisons to other *Pseudomonas fluorescens* strains in the public SEED database, ~85% of the annotated PEGs of Wood1R were mapped to the genomes of Pf0-1, SBW25, and Pf-5, with an average DNA sequence identity of 74 to 77%. Of the 852, 914, and 916 PEGs predicted to be unique to Wood1R when compared with Pf0-1, SBW25, and Pf-5, respectively, 433 (48.9%), 475 (52.0%), and 459 (50.1%) PEGs, respectively, were identified.

The *phlD* genes in the Wayne1R and Wood1R genomes showed similarities of 99.6% and 78.4%, respectively, to the *phlD* gene in Pf-5 (PFL5957) (5). In keeping with the *phlD*-based classification of these strains, the *plt* cluster (pyoluteorin biosynthesis) was found in Wayne1R and the *hcn* locus (biosynthesis of hydrogen cyanide) was found in both Wayne1R and Wood1R.

Nucleotide sequence accession numbers. The assembled short-read genome sequences of the two *Pseudomonas fluorescens* strains were deposited in the European Nucleotide Archive (http://www.ebi.ac.uk/genomes/wgs.html) under the accession numbers CADX01000001 to CADX01000090 (Wayne1R) and CAFF01000001 to CAFF01001437 (Wood1R).

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