

Genome Sequence of the Biocontrol Strain *Pseudomonas fluorescens* F113

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***Pseudomonas fluorescens* F113 is a plant growth-promoting rhizobacterium (PGPR) that has biocontrol activity against fungal plant pathogens and is a model for rhizosphere colonization. Here, we present its complete genome sequence, which shows that besides a core genome very similar to those of other strains sequenced within this species, F113 possesses a wide array of genes encoding specialized functions for thriving in the rhizosphere and interacting with eukaryotic organisms.**

Pseudomonas fluorescens F113 is a Gram-negative, rod-shaped member of the genus *Pseudomonas*, isolated from the sugar-beet rhizosphere (19). *P. fluorescens* F113 can colonize a wide range of plants and is used as a model strain to study rhizosphere colonization (7, 21). It also exhibits biocontrol activity against phytopathogens, such as the oomycetes *Pythium ultimum* and *Phytophthora cactorum* and the fungus *Fusarium oxysporum* in several plant crops, including sugar-beet (13), tomato, and strawberry (6) and is antagonistic toward the potato-cyst nematode *Globodera rostochiensis* (11). This biocontrol activity is linked to the production of secondary metabolites, including diacetylphloroglucinol (DAPG) and hydrogen cyanide, and this strain has been widely used to study the regulation of secondary metabolism in *P. fluorescens* (1, 2, 13, 15). Bioremediation derivatives of this strain able to degrade biphenyl and polychlorinated biphenyls have also been constructed (8, 22) and tested *in situ* (12). To gain insight into ecological traits, to improve its biotechnological applications, and to better understand its evolution, we sequenced the complete genome of this bacterium.

The sequence of the *P. fluorescens* F113 genome was determined by using a combination of Illumina Solexa GAIIx (7e+6 single reads 36 nucleotides [nt] long) and Roche 454 Titanium (7e+5 reads 400 nt long). The reads were assembled into 83 contigs with 30× sequence coverage using MIRA software (9). These contigs were further assembled into 4 supercontigs by using the ends of an ordered bacterial artificial chromosome (BAC) library and using BLAST (4) against the genomes of other *P. fluorescens* strains (14, 17, 20). The remaining gaps were closed by PCR and subsequent Sanger sequencing. Open reading frame (ORF) calling and annotation were first performed automatically using the RAST pipeline (5) and then manually curated using the Blast2GO package (10).

The genome of F113 consists of a single circular chromosome of 6,845,832 bp with an average GC content of 60.8%. This genome is predicted to contain 5,862 protein-coding genes, 8 non-coding RNAs (ncRNAs), 5 rRNA operons, and 66 tRNA loci. Although the genome shows a high degree of homology and synteny with the chromosomes of other sequenced *P. fluorescens* strains, such as Pf0-1, Pf5, SBW25, and WH6, its closest relative is the genome of *Pseudomonas brassicacearum* subsp. *brassicacearum* NFM421 (16), a pseudomonad isolated from the plant rhizo-

sphere in Australia. It is interesting to note that these two strains show infrequent common traits, such as a similar phase variation process during rhizosphere colonization (3, 18) and genes for denitrification with identical genetic organization.

The genome of F113 contains genes encoding proteins that correlate with its plant growth promotion (PGPR) and biocontrol traits, for example, 1-aminocyclopropane-1-carboxylate deaminase, secreted protease, and biosynthesis of secondary metabolites, such as DAPG and hydrogen cyanide. The importance of motility for this bacterium is highlighted by the presence of genes encoding two sets of different flagellar apparatus and three complete chemotaxis systems. Finally, one of the most striking features of the F113 genome is the large number of potential secretory systems, including gene clusters similar to the Hrp1 and SPI-1 type 3 secretion systems (T3SS) and three complete T6SS loci related to HSI-1, HSI-2, and HSI-3.

Nucleotide sequence accession number. The *P. fluorescens* F113 genome sequence and annotation data have been deposited in GenBank under accession number [CP003150](https://doi.org/10.1093/jb/jbr011).

ACKNOWLEDGMENTS

Sequencing of this genome has been funded by grants MICROAMBIENTE-CM (to R.R.), BIO2009-08254 (to M.M.), 08/GEN/1319 (to J.P.M.), TSR 3 (Agribiotics project) (to D.D.), and Marie Curie MIGENOF113 (to M.S.-C. and R.R.). This research was supported in part by grants awarded to F.O. by the Science Foundation of Ireland (07/IN.1/B948, 08/RFP/GEN1295, 08/RFP/GEN1319, and SFI09/RFP/BMT2350), by the Department of Agriculture, Fisheries and Food (RSF grants 06-321 and 06-377 and FIRM grants 06RDC459, 06RDC506, and 08RDC629), and by the European Commission (MTKD-CT2006-042062, Marie Curie TOK: TRAMWAYS, EU256596), IRCSET (05/EDIV/FP107/INTERPAM, EMBARK), the Marine Institute Beaufort award (C&CRA 2007/082), the Environmental Protection Agency (EPA 2006-PhD-S-21 and EPA 2008-PhD-S-2), and the HRB (RP/2006/271, RP/2007/290, and HRA/2009/146).

We also acknowledge the Centro de Computación Científica in Uni-

Received 30 November 2011 Accepted 19 December 2011

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doi:10.1128/JB.06601-11

versidad Autónoma de Madrid for providing the computing facilities used in the assembly process.

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