Draft Genome Sequence of *Pseudomonas moraviensis* R28-S

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We report the draft genome sequence of *Pseudomonas moraviensis* R28-S, isolated from the municipal wastewater treatment plant of Moscow, ID. The strain carries a native mercury resistance plasmid, poorly maintains introduced IncP-1 antibiotic resistance plasmids, and has been useful for studying the evolution of plasmid host range and stability.

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*P*seudomonas moraviensis R28 is a member of the *Gammaproteobacteria* and was originally reported as *Pseudomonas koreensis* R28. The strain was isolated from activated sludge of the municipal wastewater treatment plant in Moscow, ID, as a transconjugant after a plate mating of a sludge sample with a donor plasmid pB10::*rfp*. The transconjugants were selected on defined aerobic basal (DAB) medium supplemented with succinate, acetate, and citrate and the antibiotics tetracycline (10 mg/liter) and streptomycin (50 mg/liter) (1). In the laboratory, it has been a useful strain for studying the stability and evolution of broad-host-range multidrug resistance plasmids (1–3). The first isolate of the species *P. moraviensis* was collected from oil-polluted soil in the Czech Republic and was shown to hydrolyze diverse carbohydrates and utilize an impressive array of substrates (4). Strain R28-S, a streptomycin-resistant mutant of R28, was identified as a member of this species via an in-house four-gene-based (*atpA*, *glnA*, *rpoB*, and *rpoD*) multilocus sequence analysis (MLSA) scheme, which for each gene undoubtedly showed the highest match with the type strain *P. moraviensis* LMG 24280.

The genome of *P. moraviensis* R28-S was sequenced using a whole-genome shotgun approach, with paired 150-bp reads generated on the MiSeq (Illumina) and 454 (Roche) sequencing platforms. The sequencing adapters and low-quality bases were trimmed using a custom script, and the reads were assembled using Newbler version 2.6. A total of 36 contigs >500 bp were produced. Of these, the largest is 815,593 bp and the N_{50} contig size is 462,409 bp. The assembled contigs were ordered and oriented using a whole-genome map produced by OpGen optical mapping MapIt services. The optical mapping results were corroborated by aligning R28-S contigs against the closely related and so-called *Pseudomonas fluorescens* Pf0-1 (accession no. NC_007492) genome using r2cat (5). Small contigs that could not be scaffolded with the optical map were placed using these alignments. Additional gaps were then closed using the program Gap-Filler (6), and the paired Illumina reads resulted in a final assembly consisting of 12 contigs with a total length of 6,226,470 bp (including estimated gap sizes).

Included in the set of contigs was a native 81,846-bp plasmid, pR28. The replication initiator gene (*repA*) and origin of replication gene (*oriV*) of pR28 bear 89 and 84% nucleotide identities, respectively, to that of the IncP-9θ plasmid pSVS15 isolated from *Pseudomonas putida* (7). Although many IncP-9 plasmids are self-transferable, pR28 does not encode a full conjugative system. Its genome contains multiple transposons, one of which encodes resistance to mercury. Based on its read coverage, its copy number is estimated at 2/cell (1.9× for each chromosome copy).

Nucleotide sequence accession numbers. This whole-genome shotgun project has been deposited at GenBank under the accession no. AYMZ00000000. The version described in this paper is version AYMZ00000000.1. Strain R28-S is available from the LMG culture collection as LMG 28150 (http://bccm.belspo.be/about/lmg.php).

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