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Draft Genome Sequence of *Pseudomonas* sp. nov. H2

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We report the draft genome sequence of *Pseudomonas* sp. nov. H2, isolated from creek sediment in Moscow, ID, USA. The strain is most closely related to *Pseudomonas putida*. However, it has a slightly smaller genome that appears to have been impacted by horizontal gene transfer and poorly maintains IncP-1 plasmids.

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Pseudomonas sp. nov. H2 is a member of the *Gammaproteobacteria*. The strain was isolated from creek sediment in Moscow, ID, as a transconjugant after a plate mating of a sediment sample with an auxotrophic donor of the IncP-1β plasmid pB10. Transconjugants were selected on M9 medium supplemented with 0.1% gluconic acid and the antibiotics tetracycline (20 mg/liter) and amoxicillin (150 mg/liter) (1). Based on its 16S rRNA sequence, it was provisionally called *P. putida* H2. While *P. putida* strains are generally quite capable of maintaining IncP-1 plasmids, strain H2 was reported as an unfavorable host to broad-host-range IncP-1 plasmids, and as such has been used in several plasmid-host evolution and persistence studies (1–4).

Genomic DNA (gDNA) was isolated using a GenElute bacterial genomic DNA kit (Sigma-Aldrich) as per manufacturer's instructions. The gDNA was sequenced using a whole-genome shotgun approach with paired 150 bp reads generated on MiSeq (Illumina) at the IBEST Genomics Resources Core at the University of Idaho, ID, USA. Sequencing adapters and low-quality bases were trimmed using custom scripts, and reads were assembled using Newbler v2.6. A total of 95 contigs >500 bp were produced (total number of contigs is 132). Of these, the largest was 281,547 bp and the N_{50} contig size was 127,674 bp.

Strain H2 was identified as a potential new *Pseudomonas* species using an in-house, four-gene (*glnA*, *gyrB*, *rpoB*, and *rpoD*) multilocus sequence analysis (MLSA) scheme. The *glnA*, *gyrB*, and *rpoD* genes of H2 were highly similar to those of *P. putida* LMG 14676. Previously, strain LMG 14676 was regarded as a member of *P. putida* biotype A based on phenotypic data (5) and SDS PAGE profiles of whole cell proteins (6), but it clearly separates from the *P. putida* type strain on the basis of ribopatterning (7). The *rpoB* gene sequence of strain H2 was incongruent to the *glnA*, *gyrB*, and *rpoD* gene sequences. Comparison among the 11 completely sequenced *P. putida* chromosomes showed that the H2 genome, estimated at 5.79 Mb, is with one exception, smaller than all *P. putida* genomes (the median for *P. putida* is 6.03 Mb, and the smallest and largest genomes are 5.73 and 6.87 Mb). Unsurprisingly, the H2 genome contains fewer predicted protein coding sequences (CDSs) (4,985) than most *P. putida* genomes (the median number of CDSs is 5,321, and the minimum and maximum are 4,960 and 6,357). Finally, the G+C contents of the H2 genome vary between 28 and 75%, with a median of 62.6% (500-bp sliding window). Combined with the MLSA results, these data suggest that the H2 genome has been considerably impacted by horizontal gene transfer. Because of the few clear distinctions from *P. putida*, we define strain H2 here as a *Pseudomonas* sp. nov.

Nucleotide sequence accession numbers. This whole-genome shotgun project has been deposited at DDBJ/EMBL/GenBank under the accession no. JRPO00000000. The version described here is version JRPO01000000. Strain H2 is available from the LMG culture collection (http://bccm.belspo.be/about/lmg.php, LMG 28719).

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