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Draft Genome Sequences for Two Metal-Reducing *Pelosinus fermentans* Strains Isolated from a Cr(VI)-Contaminated Site and for Type Strain R7

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***Pelosinus fermentans* 16S rRNA gene sequences have been reported from diverse geographical sites since the recent isolation of the type strain. We present the genome sequence of the *P. fermentans* type strain R7 (DSM 17108) and genome sequences for two new strains with different abilities to reduce iron, chromate, and uranium.**

Pelosinus fermentans strain R7 was isolated as a representative iron-reducing bacterium from Russian kaolin clays and as the type strain for a new genus (11). *P. fermentans* 16S rRNA gene sequences dominated iron-reducing enrichments derived from geochemically different soils obtained from the Melton Branch Watershed, near Oak Ridge, TN, which suggests physiological flexibility within the species (4). Subsurface microbial communities from an Oak Ridge, TN, field site contaminated with uranium were stimulated *in situ* with a slow-release vegetable oil substrate; subsequently, bacteria related to *Pelosinus* species dominated, and in turn their fermentation end products were proposed to stimulate other community members (3). *Pelosinus* strain UFO1 was isolated from pristine sediments at a background field site in Oak Ridge, TN, and was found to have the ability to facilitate hexavalent uranium removal via reduction and phosphate precipitation mechanisms (10).

P. fermentans 16S rRNA gene sequences have been reported from uranium- and heavy-metal-contaminated soils in Germany (12), and phylogenetic analysis indicated bacteria closely related to *Pelosinus* in Portuguese soil enrichments capable of uranium reduction (7). *Sporotalea propionica*, an isolate from the intestinal tract of a soil-feeding termite, has been transferred to the genus recently (8).

Metal-reducing *Pelosinus* species dominated electron acceptor-limited enrichments that used lactate as the main carbon source and electron donor and inocula from contaminated groundwater samples drawn from the U.S. Department of Energy's H-100 well in Hanford, WA (9). Sixteen isolates obtained from the chemostat studies via fluorescence-activated cell sorting (FACS) were identified as being 99 to 100% identical to *P. fermentans* strain R7 at the 16S rRNA gene level (9). The three strains sequenced in this study were assayed for their abilities to reduce different metals and all reduced soluble Fe(III) but not solid-phase iron (9). Strain A11 was notable as being the only isolate able to reduce hexavalent uranium (9).

The draft genome sequences for strains A11, B4, and R7 were generated using a combination of Illumina (1) and 454 technologies (6) with HiSeq2000 and GS FLX instruments, respectively. All data sets were from paired-end DNA libraries, with approximate insert sizes of 500 bp and 3 kb for the Illumina and 454 libraries,

respectively. Illumina sequence data were trimmed for quality (CLC Genomics Workbench version 4.7.1) and then assembled with Velvet (version 1.1.04) (13), and hybrid assemblies were generated as described previously (2).

There were 65, 76, and 134 contigs greater than 500 bp that constituted the draft genome sequences for strains R7, B4, and A11, respectively, and their estimated genome sizes ranged from approximately 4.9 to 5.1 Mb. Draft genome sequences were annotated at Oak Ridge National Laboratory using an automated annotation pipeline, based on the Prodigal gene prediction algorithm (5).

These *P. fermentans* draft genome sequences will facilitate comparative and functional genomic studies and will permit a better assessment of their functions and relationships within microbial community structures in the future.

Nucleotide sequence accession numbers. The genome sequences have been deposited at DDBJ/EMBL/GenBank under the accession numbers [AKVN000000000](#), [AKVM000000000](#), and [AKVJ000000000](#) for strains R7 (DSM 17108), A11, and B4, respectively. The versions described in this paper are the first versions, [AKVN000000000](#), [AKVM000000000](#), and [AKVJ000000000](#).

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