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Draft Genome Sequence of Alkaliphilic Exiguobacterium sp. Strain HUD, Isolated from a Polymicrobial Consortia

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An alkaliphilic microorganism from the genus Exiguobacterium, non-spore-forming Gram-positive microorganisms within the phylum Firmicutes were first described by Collins et al in 1983 (1). Exiguobacterium spp. have been isolated from a range of habitats including: permafrost, glaciers, soils, fresh and salt waters, hydrothermal vents, and brine shrimp (2). Their presence in these diverse environments is reflected in their ability to survive and grow in extremes of temperature (−12 to 55°C) and pH (5 to 11) and to survive under stresses generated by UV irradiation (3), antibiotics (4), and heavy metals (5, 6). Members of this genus are also noted for their ability to utilize a range of substrates, particularly for the bioremediation of azo dyes, and as a result of this, the reservoir of enzymes produced by these organisms has received considerable attention (7, 8).

Here, we present the draft genome sequence of Exiguobacterium sp. Strain HUD isolated from an anaerobic microcosm operating at pH 10 described previously (S. P. Rout, C. J. Charles, C. Doulgeris, A. J. McCarthy, D. J. Rooks, P. Loughnane, A. P. Laws, and P. N. Humphreys, unpublished data), where products from the anaerobic alkaline degradation of cellulose, including the enzymes produced by these organisms has received considerable attention.

The contigs were linked and placed into scaffolds or supercontigs. The orientation, order, and distance between the contigs was estimated using the insert size between the paired-end and/or mate-pair reads using the SSPACE Premium scaffolder version 2.3 (9). Whole-genome sequencing generated 826 contigs with a draft genome 3,359,295-bp in length and G+C content of 51.1%. The draft genome contained a total of 3,484 coding sequences (CDS), where 19 pseudogenes, 9 genes coding for rRNA (5S, 16S, 23S), 69 genes coding for tRNAs, and 1 noncoding RNA (ncRNA) were present. Further analysis using RAST (10) revealed the presence of a number of genes encoding proteins involved in both aerobic and anaerobic carbohydrate metabolism. As previous authors have noted with other members of this genus, genes encoding stress response proteins were also observed (11). The genome also suggests resistance to a range of metals (As, Cd, Cr, Hg) as well as the potential for multidrug resistance.

Nucleotide sequence accession number. This whole-genome shotgun project has been deposited at DDBJ/EMBL/GenBank under the accession no. JQG100000000.

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Further information regarding the C14-BIG project can be found at: http://www.hud.ac.uk/c14-big.

REFERENCES


