

# 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*, *Exiguobacterium* sp. strain HUD was isolated from a fermentative, methanogenic polymicrobial microcosm operating at pH 10. The draft genome shows the presence of genes encoding for the metabolism of a range of carbohydrates under both aerobic and anaerobic conditions.**

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Members of 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. 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(S. P. Rout, C. J. Charles, C. Doulgeris, A. J. McCarthy, D. J. Rooks, P. Loughnane, A. P. Laws, and P. N. Humphreys, unpublished data), where products from the anaerobic alkaline degradation of cellulose, including the  $\alpha$  and  $\beta$  forms of isosaccharinic acid, were used as a carbon source. The original inoculum for the microcosm was obtained from a mesophilic near surface anaerobic sediment from a canal (Huddersfield, United Kingdom). Microcosm effluent was used as an inoculum, where 10  $\mu$ L of suspension was streaked out onto fastidious anaerobic agar (pH 10, LabM, United Kingdom) under a stream of nitrogen and incubated under anaerobic conditions (10% H<sub>2</sub>:10% CO<sub>2</sub>:80% N<sub>2</sub>; DW Scientific, United Kingdom) for 48 h. A single colony was selected from the plate and purified through further subculture before total genomic DNA was isolated using a commercial kit (UltraClean microbial isolation kit; Mo-Bio, USA).

A draft whole-genome sequence was obtained using a whole-genome shotgun (WGS) sequence strategy. Paired-end 125 cycles sequence reads were generated using the Illumina HiSeq 2500 system (BaseClear, The Netherlands). FASTQ sequence files were generated using the Illumina Casava pipeline version 1.8.3 and the assembly prepared using CLC Genomics Workbench version

7.0.4. 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. [JQGI00000000](https://www.ncbi.nlm.nih.gov/nuccore/JQGI00000000).

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

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