

# Draft Genome Sequence of *Alcaligenes faecalis* subsp. *faecalis* NCIB 8687 (CCUG 2071)

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***Alcaligenes faecalis* subsp. *faecalis* NCIB 8687, the betaproteobacterium from which arsenite oxidase had its structure solved and the first “arsenate gene island” identified, provided a draft genome of 3.9 Mb in 186 contigs (with the largest 15 comprising 90% of the total) for this opportunistic pathogen species.**

*Alcaligenes faecalis* subsp. *faecalis* strain NCIB 8687 was reported as an arsenite-oxidizing bacterial isolate (6). The collection number was NCIB 8687 (National Collection of Industrial Bacteria, Scotland), and results were published under that strain number (1, 5) (GenBank accession AY297781). However, the strain is no longer available in the United Kingdom or in the ATCC in the United States; it is now available as strain LMG 3368 (Belgian Coordinated Collection of Microorganisms, Ghent) and as strain CCUG 2071 (Culture Collection, University of Göteborg, Sweden; metabolic characteristics are posted on the Culture Collection website [<http://www.ccug.se>]).

*A. faecalis* NCIB 8687 was obtained from G. Anderson and R. Hille (1) and grown in the LB broth medium (4) at 30°C with shaking. Cells in late-log-phase growth were harvested and lysed by EDTA, lysozyme, and detergent treatment, followed by proteinase K and RNase digestion. DNA isolation was by phenol-chloroform-isoamyl alcohol extraction and repeated isopropanol-ethanol precipitation (4). DNA purity was measured by the  $A_{260}/A_{280}$  ratio, and a single DNA band with a size of over 20 kbp was observed (data not shown) after agarose gel electrophoresis. The genome was sequenced using the Illumina HiSeq 2000 sequencing platform, with a random subset of 7 million paired-end reads (171× coverage) used for assembly with MIRA v3.4.0 into 186 contigs that are in GenBank. The genome was independently analyzed on the RAST server (2). The 3.9-Mb draft genome with 186 contigs contains 3,632 coding sequences (CDSs) plus 62 RNAs for a total of 3,694 genes and a G+C content of 57.1%. There are 3,744,806 bp in the largest 22 contigs. Half of these contigs are over 100 kbp in length, totaling 3.2 Mb, and the other half are between 20 kbp and 100 kbp in length.

The sequence of the 16S rRNA gene (1,471 bp) of *A. faecalis* strain NCIB 8687 that is reported here (GenBank accession number AKMR01000044; 6,924 bp) is 99% identical (1,419/1,438) to that of *A. faecalis* strain IAM12369 (ATCC 8750; NCBI NR\_043445), the type strain for this species. This is within a 5,937-bp “ribosomal operon” with genes for 5S rRNA, 23S rRNA, tRNA-Ala-TGC, tRNA-Ile-GAT, tRNA-Val-GAC, and 16S rRNA in order. This draft genome appears to be the first available for this common soil and frequent opportunistic human-pathogenic betaproteobacterium.

It is of interest to analyze potential genes involved in arsenic metabolism and resistance, particularly for the sequence deposited under GenBank accession number AY297781, a sequence with 71,383 bp and the only sequence previously available for

strain NCIB 8687. The sequence listed under GenBank accession number AY297781 includes 69 CDSs, of which 29 were suggested (5) to constitute the first large “arsenic resistance gene island” reported. The 71 kbp of the sequence are now found from positions 409,462 to 480,844 in the sequence deposited under GenBank accession number AKMR01000013 (675,818 bp in length, the second largest in the current draft genome). The arsenite oxidase gene names have (unfortunately) been assigned different mnemonics by different groups; however, there was recently an agreement (3) to use *aioABSX* for arsenite oxidase and the genes for its regulation.

**Nucleotide sequence accession numbers.** The draft genome of *A. faecalis* subsp. *faecalis* strain NCIB 8687 was deposited in GenBank (<http://www.ncbi.nlm.nih.gov/projects/WGS/WGSprojectlist.cgi>) under accession numbers AKMR01000001 through AKMR01000186.

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