

Draft Genome Sequence of *Bacillus anthracis* BF-1, Isolated from Bavarian Cattle

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***Bacillus anthracis* BF-1 was isolated from a cow in Bavaria (Germany) that had succumbed to anthrax. Here, we report the draft genome sequence of this strain, which belongs to the European B2 subclade of *B. anthracis*. The closest phylogenetic neighbor of strain BF-1 is a strain isolated from cattle in France.**

Cases of the zoonosis anthrax are rare in Western Europe. Nevertheless, the causative agent of the disease, *Bacillus anthracis*, is of concern because it had been misused as an agent of state-sponsored warfare (2, 3) and bioterrorist weapon (6). The Gram-positive, endospore-forming bacterium produces several virulence factors required for successful establishment of infections in animal and human hosts. Hosts succumb through the action of two binary toxins named lethal toxin and edema toxin. Additionally, for full virulence an antiphagocytic poly- γ -D-glutamic acid capsule is required (4). In the environment, especially soil, endospores can persist for extended periods. However, to complete its natural life cycle the organism requires a propagation phase as vegetative cells in wildlife or livestock. In 2009, five cows were infected in Bavaria, probably through ingested spore-laden pasture grass. Strain BF-1 was isolated from one of these cows that had died from anthrax. In our ongoing efforts to elucidate worldwide phylogenetic relationships between *B. anthracis* isolates, the genome of strain BF-1 was sequenced.

Whole-genome shotgun (WGS) sequencing of *B. anthracis* BF-1 was performed by Ion Torrent sequencing technology (Ion Torrent Systems, Inc.). For the WGS library, 2,358,141 reads with a total of 423,285,348 bp were generated. About 96.7% of the reads containing 98.4% of the bases were assembled into 82 contigs using Newbler version 2.6 (Roche) to reach 76.4-fold coverage. The assembled contigs were submitted to the RAST annotation server for subsystem classification and functional annotation (1). Coding sequences (CDSs) were assigned using BLASTp with KEGG Orthology (KO). The G+C content was calculated using an in-house Perl script. The NCBI Prokaryotic Genomes Automatic Annotation Pipeline (PGAAP) was employed for gene annotation in preparation for submission to GenBank (<http://www.ncbi.nlm.nih.gov/genomes/static/Pipeline.html>).

The total length of the draft genome shotgun sequence of *B. anthracis* BF-1 was 5,434,529 bp, and the mean GC content was 35.09%. Its chromosomal sequence contained 45 contigs totaling 5.16 Mbp with 67.4-fold coverage, and the assembled genome consists of 56 large contigs (>500 bp) with an average contig size of 97,045 bp. The plasmids pXO1 and pXO2 comprised 10 and 1 contigs with 134.6- and 79.7-fold coverage, respectively. The genome encodes 5,700 putative coding sequences (CDSs), of which 4,022 CDSs have functional predic-

tions. The draft genome sequence contains 4 rRNAs, 2 5S rRNAs, and 73 tRNA loci. For the CDSs, 69.2% corresponding to 3,946 proteins could be assigned to Cluster of Orthologous Groups (COG) families (7).

Strain BF-1 is associated with the B2 clade of *B. anthracis*, as determined by phylogeny via canonical single nucleotide polymorphisms (canSNP) (8) and multilocus variable number of tandem repeats (VNTR) analysis (MLVA) (8; M. Antwerpen, unpublished data). In comparison, strain BF-1 is most closely related to a strain isolated from diseased cattle of the French Savoie department in 1997 (5). As more strains from Western Europe become genome sequenced, new insights into the exact phylogeny of this group of organisms can be expected.

Nucleotide sequence accession numbers. This Whole Genome Shotgun project has been deposited in DDBJ/EMBL/GenBank under accession no. [AMDT000000000](https://www.ncbi.nlm.nih.gov/nuccore/AMDT000000000). The version described in this paper is the first version, [AMDT010000000](https://www.ncbi.nlm.nih.gov/nuccore/AMDT010000000).

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