






# First Genome Sequence of *Brucella abortus* Biovar 3 Strain BAU21/S4023, Isolated from a Dairy Cow in Bangladesh

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**ABSTRACT** We report the genome sequence of *Brucella abortus* biovar 3 strain BAU21/S4023, isolated from a dairy cow that suffered an abortion in Savar, Dhaka, Bangladesh. The genome sequence length is 3,244,234 bp with a 57.2% GC content, 3,147 coding DNA sequences (CDSs), 51 tRNAs, 1 transfer messenger RNA (tmRNA), and 3 rRNA genes.

Since its first description in 1906 (1), *Brucella abortus* remains one of the most important zoonotic and endemic diseases in several parts of the world (2). *Brucella* species are a group of aerobic, intracellular, small, non-spore-forming, nonencapsulated, and nonmotile Gram-negative coccobacilli (2, 3). They infect all livestock—avian, bovine, caprine, camelid, equine, ovine, and porcine (4, 5) and also wild animals (6, 7) and marine mammals (8). Human brucellosis causes a significant global public health and economic burden (9). Some species are subdivided into biovars; i.e., *B. abortus* species include eight biovars (1 to 7 and 9) (3). *B. abortus* causes infection predominantly in cattle, leading to substantial economic losses in dairy animals through stillbirths and decreased milk production (10). In Bangladesh, *B. abortus* infection is endemic in livestock and was reported to cause brucellosis in humans (11–13).

The genome sequence of *B. abortus* isolates from Bangladesh is essential because of its potential animal and public health impacts in this region. It allows in-depth analysis of genomic structure and will help us to understand its virulence, pathogenesis, host specificity, biotyping difference, and phylogenetic relationships and help to identify potential targets for the development of vaccines and diagnostics to prevent and control brucellosis.

Here, we report the first whole-genome sequence of *B. abortus* biovar 3 strain BAU21/S4023, isolated from a crossbred dairy cow (*Bos taurus*) in Bangladesh in March 2017. The *Brucella* strain was isolated from cow number 4023 (which suffered an abortion on a dairy farm in Savar, Bangladesh) by the streaking of a uterine discharge sample onto *Brucella* selective agar (HiMedia, India), which was then incubated at 37°C for 7 days in the presence of 5% CO<sub>2</sub>. Conventional bacteriological methods, classical biotyping, and enhanced AMOS-ERY PCR analysis confirmed the isolate as *B. abortus* biovar 3 (14, 15).

For genome sequencing, DNA was extracted from a single colony of strain BAU21/S4023 using a GeneJET genomic DNA purification kit (Thermo Fisher Scientific). DNA concentrations were quantitated using the Qubit 2.0 fluorometer for a double-stranded DNA high-sensitivity assay kit (Thermo Fisher Scientific, MA). Genomic libraries were

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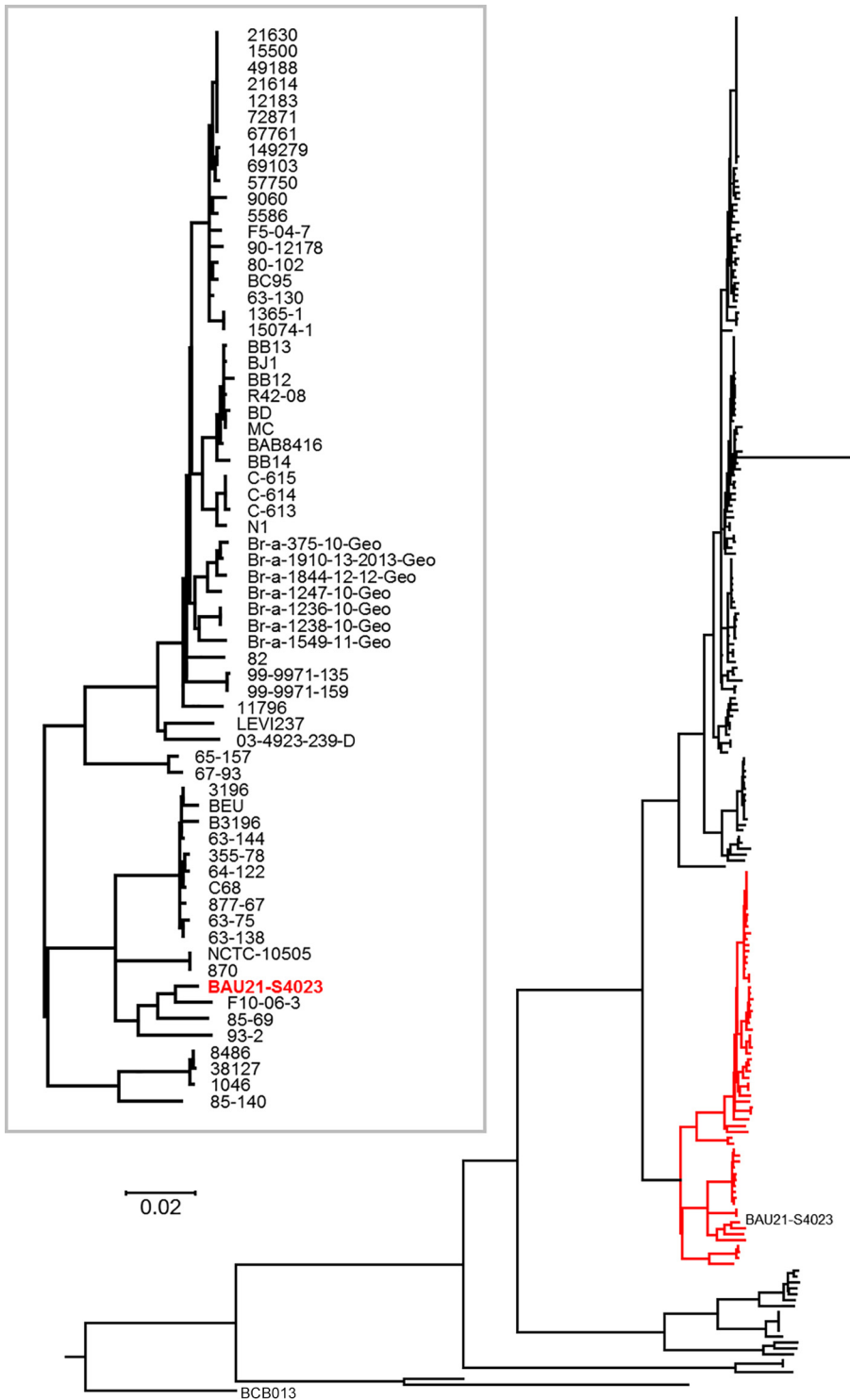
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**FIG 1** Phylogenetic tree of 229 *B. abortus* genome sequences based on core genome single nucleotide polymorphisms as identified using ParSNP. The position of the *B. abortus* BAU21/S4023 genome sequence is indicated in the tree, which was rooted with the genome sequence of *B. abortus* BCB013. The inset shows the part of the tree where the *B. abortus* BAU21/S4023 genome sequence clusters, with the closest relatives named.

constructed using a NEBNext Ultra DNA library prep kit (Illumina, Inc., San Diego, CA). The library size selection was 350 bp, and a paired-end (PE) sequencing strategy (2 × 150 bp) was performed by Apical Scientific (Selangor, Malaysia) using a HiSeq 4000 instrument (Illumina, Inc.). A total of 1,294 Mb (or ~1.3 Gb) raw data reads were

generated, and a total of 1.191 Mb (or ~1.2 Gb) clean reads were obtained using Perl script to trim off Illumina adaptor sequences and remove low-quality reads. A total of 3.97 million reads passed the quality filter; reads averaged 150 bp in length and showed an average quality score above Q30 in more than 90% of the bases. Sequences were assembled using SPAdes version 3.11.0 (16) into 24 contigs at least 200 nucleotides (nt) long and a coverage of  $>10\times$ , for a total of 3,244,234 bp with a GC content of 57.2%, an  $N_{50}$  value of 367,095, and an  $L_{50}$  value of 4 and containing 3,147 coding DNA sequences (CDSs), 51 tRNAs, 1 transfer messenger RNA (tmRNA), and 3 rRNA genes as identified by annotation using Prokka version 1.13 with default settings (17).

A core genome single nucleotide polymorphism (SNP) tree of 228 genomes from GenBank was constructed to determine the relationship between the BAU21/S4023 strain and other available *B. abortus* isolates. *B. abortus* genomes were downloaded from the NCBI genome database using ncbi-genome-download version 0.2.9 (<https://github.com/kblin/ncbi-genome-download>), and core genome SNPs were identified and used for the construction of a phylogenetic tree using ParSNP version 1.2 (18) with the settings “-a 13” and “-x” as described previously (19). The genome of BAU21/S4023 was clustered closely with reference *B. abortus* genomes such as NCTC10505 (biovar 6), 870 (biovar 6), and C68 (biovar 9) (Fig. 1).

**Data availability.** This whole-genome shotgun project has been deposited at DDBJ/ENA/GenBank under the BioProject number [PRJNA529883](https://www.ncbi.nlm.nih.gov/bioproject/PRJNA529883) and accession number [SRJJ00000000](https://www.ncbi.nlm.nih.gov/seq/srj02000000). The version described in this paper is version SRJJ02000000. The sequences have been submitted to the Sequence Read Archive (SRA) under the accession number [SRX5762378](https://www.ncbi.nlm.nih.gov/sra/SRX5762378).

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M.E.E.Z. prepared the manuscript; M.S.I., M.T.R., M.A.I., M.M.K., and S.S. conducted diagnostic tests; A.H.M.V.V. and S.T. performed phylogenetic analysis; and M.E.E.Z., A.H.M.V.V., M.A.I., M.T.R., and A.N. reviewed the manuscript.

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