



Whole-Genome Sequences of Variants of *Bacillus anthracis* Sterne and Their Toxin Gene Deletion Mutants

A. Staab,^a R. D. Plaut,^b C. Pratt,^c S. P. Lovett,^c M. R. Wiley,^c T. D. Biggs,^d
R. C. Bernhards,^{d,e} L. C. Beck,^a G. F. Palacios,^c S. Stibitz,^b K. L. Jones,^f
B. G. Goodwin,^f M. A. Smith,^f S. Sozhamannan^{f,g}

Naval Surface Warfare Center Dahlgren, CBR Defense Division, Dahlgren, Virginia, USA^a; Division of Bacterial, Parasitic and Allergenic Products, Center for Biologics Evaluation and Research, Food and Drug Administration, Silver Spring, Maryland, USA^b; Center for Genome Sciences, U.S. Army Medical Research Institute for Infectious Diseases, Fort Detrick, Maryland, USA^c; U.S. Army Edgewood Chemical Biological Center, Aberdeen Proving Ground, Maryland, USA^d; Defense Threat Reduction Agency, Fort Belvoir, Virginia, USA^e; Defense Biological Product Assurance Office, Frederick, Maryland, USA^f; The Tauri Group, LLC, Alexandria, Virginia, USA^g

ABSTRACT Here, we report the draft genome sequences of three laboratory variants of *Bacillus anthracis* Sterne and their double (Δ lef Δ cya) and triple (Δ pag Δ lef Δ cya) toxin gene deletion derivatives.

The pathogenicity of *Bacillus anthracis*, the bacterium that causes anthrax, has been attributed to the presence of two plasmids in its genome, pXO1, which encodes the anthrax toxin genes, and pXO2, which encodes the capsular genes (1). Strains that lack pXO2 (e.g., Sterne) are exempt from select agent regulations and have been used as vaccines (2). Sterne is also the workhorse of laboratory research, and different laboratories have used and propagated Sterne strains over many years; consequently, these strains appear to have accumulated laboratory-specific adaptations. Here, we report the whole-genome draft sequences of three Sterne strains and four toxin gene deletion derivatives.

Libraries were prepared using the Illumina Nextera XT kit and sequenced on an Illumina NextSeq 500 desktop sequencer (V2 mid-output 2 × 151 bp). Adapter sequences were removed with Cutadapt (3) and assembled using SPAdes v3.9 (4). The genome was annotated with the NCBI Prokaryotic Genome Annotation Pipeline v4.2 (5), and reference mapping was done with Bowtie2 v2.0.6 (6).

Accession number(s). Accession numbers and sequence statistics of the seven genomes are listed in Table 1.

Received 29 September 2017 Accepted 16 October 2017 Published 9 November 2017

Citation Staab A, Plaut RD, Pratt C, Lovett SP, Wiley MR, Biggs TD, Bernhards RC, Beck LC, Palacios GF, Stibitz S, Jones KL, Goodwin BG, Smith MA, Sozhamannan S. 2017. Whole-genome sequences of variants of *Bacillus anthracis* Sterne and their toxin gene deletion mutants. *Genome Announc* 5:e01231-17. <https://doi.org/10.1128/genomeA.01231-17>.

This is a work of the U.S. Government and is not subject to copyright protection in the United States. Foreign copyrights may apply.

Address correspondence to S. Sozhamannan, shanmuga.sozhamannan.ctr@mail.mil.

TABLE 1 Genome sequence details of *B. anthracis* Sterne variants and their derivatives

Strain	Description	GenBank accession no.	Assembly size (bp)	No. of contigs	No. of CDSs ^a	Coverage (×)	
						Chr ^b	pXO1 ^c
BA500	Sterne 34F2_FDA	NRIZ00000000	5,358,909	44	5,882	176	1,057
BAP482	BA500 (Δ lef Δ cya)	NRJA00000000	5,357,360	53	5,889	183	1,014
BAP417	BA500 (Δ pag Δ lef Δ cya)	NRJB00000000	5,354,685	60	5,888	166	953
BA663	Sterne 7702	NRIW00000000	5,362,963	60	5,897	195	1,287
BA721	BA663 (Δ lef Δ cya)	NRIX00000000	5,347,571	50	5,882	200	1,268
BA781	BA663 (Δ pag Δ lef Δ cya)	NRJY00000000	5,345,676	50	5,877	202	1,244
34F2_Sterne	USAMRIID	NRIV00000000	5,364,310	69	5,905	147	512

^aCDSs, coding sequences.

^bNCBI reference sequence NC_005945 (chromosome).

^cNCBI reference sequence NC_001496 (plasmid).

REFERENCES

1. Hambleton P, Carman JA, Melling J. 1984. Anthrax: the disease in relation to vaccines. *Vaccine* 2:125–132. [https://doi.org/10.1016/0264-410X\(84\)90003-3](https://doi.org/10.1016/0264-410X(84)90003-3).
2. Sterne M. 1946. Avirulent anthrax vaccine. *Onderstepoort J Vet Sci Anim Ind* 21:41–43.
3. Martin M. 2011. Cutadapt removes adapter sequences from high-throughput sequencing reads. *EMBnet j* 17:10–12. <https://doi.org/10.14806/ej.17.1.200>.
4. Bankevich A, Nurk S, Antipov D, Gurevich AA, Dvorkin M, Kulikov AS, Lesin VM, Nikolenko SI, Pham S, Prjibelski AD, Pyshkin AV, Sirotkin AV, Vyahhi N, Tesler G, Alekseyev MA, Pevzner PA. 2012. SPAdes: a new genome assembly algorithm and its applications to single-cell sequencing. *J Comput Biol* 19:455–477. <https://doi.org/10.1089/cmb.2012.0021>.
5. Tatusova T, DiCuccio M, Badretdin A, Chetvernin V, Nawrocki EP, Zaslavsky L, Lomsadze A, Pruitt KD, Borodovsky M, Ostell J. 2016. NCBI prokaryotic genome annotation pipeline. *Nucleic Acids Res* 44:6614–6624. <https://doi.org/10.1093/nar/gkw569>.
6. Langmead B, Salzberg SL. 2012. Fast gapped-read alignment with Bowtie 2. *Nat Methods* 9:357–359. <https://doi.org/10.1038/nmeth.1923>.