

Genome Sequence of the Soviet/Russian *Bacillus anthracis* Vaccine Strain 55-VNIIVViM

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ABSTRACT

Bacillus anthracis strain 55-VNIIVViM is a live-attenuated nonencapsulated Soviet/Russian veterinary anthrax vaccine strain. We report here the genome of 55-VNIIVViM and confirm its phylogenetic placement in the global population structure of *B. anthracis*.

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GENOME ANNOUNCEMENT

Bacillus anthracis, the causative agent of anthrax, is a Gram-positive, spore-forming bacteria that can cause acute infectious disease in livestock and wild ungulates (1). Humans are generally incidental hosts that acquire infection through handling contaminated meat or other animal products. Historically, *B. anthracis* was a subject of state-sponsored biowarfare research and currently poses a risk for illicit use as an agent of bioterrorism (2). *B. anthracis* exhibits global distribution and continues to present a significant public and animal health risk.

B. anthracis virulence is associated with two megaplasms, pXO1 and pXO2 (3, 4). Toxigenic but attenuated live spore anthrax vaccines, lacking either of the virulence plasmids, have been in wide use since the 1930s. The most prevalent livestock vaccine is the live, nonencapsulated (pXO2) spore suspension of the Sterne strain developed in 1937 (5). In the Soviet Union, live-attenuated anthrax vaccine spore suspensions were also developed (6). Russian anthrax vaccine strains such as the Tsiankovskii-I strain and strain 55-VNIIVViM were developed for use in livestock. The Georgian/Soviet ST1 strain was also used as a livestock vaccine (6), in addition to its use in human vaccination, but was subsequently replaced by the 55-VNIIVViM strain in 1985. Currently, both commercial and national production facilities in the former Soviet Union maintain and distribute formulations of strain 55-VNIIVViM for regular use in veterinary vaccination programs. We report here the genome of *B. anthracis* strain 55-VNIIVViM.

A commercial preparation of strain 55-VNIIVViM was prepared for full-genome sequencing at the National Centers for Disease Control Lugar Center. Genomic DNA was extracted from colony culture using a Qiagen DNA mini prep kit, sheared to 350 bp. Whole-genome shotgun sequencing on the Illumina MiSeq platform produced 4,104,958 paired-end reads. Mapped and *de novo* read assemblies were analyzed using CLC Bio (<http://www.clcbio.com>) and Geneious version 7.0 (7) referenced against the Ames ancestor (NC_007530). *De novo* assembly yielded 31 chromosomal contigs and four contigs for the pXO1 plasmid. The 55-VNIIVViM draft genome was approximately 5,227,484 bp for the chromosome and 181,756 bp for the pXO1 plasmid with coverages of 188× and 481× for the chromosome and pXO1 plasmid, respectively. The RAST annotation server (8) and the NCBI Prokaryotic Genome Annotation Pipeline (9) were used for functional annotation using the

Ames ancestor as a reference taxon.

Comparative sequence analyses identified at least 355 chromosomal polymorphisms that distinguish strain 55-VNIIVViM from the Ames ancestor. *In silico* canonical single-nucleotide polymorphism (canSNP) analysis placed 55-VNIIVViM within the trans-Eurasia group in the A.Br.008/009 lineage (10, 11). The B.Br.003 canSNP allele state in the strain 55-VNIIVViM genome reported here (B.Br.003=G) differs from that reported by Afanas'ev et al. (B.Br.003=A) (12). In addition, preliminary whole-genome comparisons suggest strain 55-VNIIVViM falls within the newly identified STI group (13). The genome of strain 55-VNIIVViM has been made available for further cross-strain comparisons with other global representatives of *B. anthracis*.

Accession number(s). The whole-genome shotgun project for strain 55-VNIIVViM has been deposited at DDBJ/ENA/GenBank under the accession number [MLJX00000000](#). The version described in this paper is the first version, MLJX01000000.

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FOOTNOTES

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