

Whole-Genome Sequences of Six *Salmonella enterica* Serovar Bovismorbificans Isolates Associated with a 2011 Multistate Hummus-Borne Outbreak

Gopal Gopinath,^a Junia Jean-Gilles Beaubrun,^a Chris Grim,^a Morris Blaylock,^b Reginald Blackwell,^b Sosina Merid,^b Alpha Diallo,^b Darcy Hanes^a

U.S. Food and Drug Administration, Center for Food Safety and Applied Nutrition, Office of Applied Research and Safety Assessment, Division of Virulence Assessment, Laurel, Maryland, USA^a; District of Columbia Public Health Laboratory, Department of Forensic Sciences, Washington, DC, USA^b

We present six draft genome sequences of *Salmonella enterica* serovar Bovismorbificans from isolates associated with the 2011 hummus-borne multistate outbreak. All six genome sequences indicate the presence of two plasmids, one of which demonstrates similarity to the 93-kb pSLT2 IncF-type plasmid of *Salmonella enterica* serovar Typhimurium.

Received 20 December 2013 Accepted 13 February 2014 Published 6 March 2014

Citation Gopinath G, Jean-Gilles Beaubrun J, Grim C, Blaylock M, Blackwell R, Merid S, Diallo A, Hanes D. 2014. Whole-genome sequences of six *Salmonella enterica* serovar Bovismorbificans isolates associated with a 2011 multistate hummus-borne outbreak. *Genome Announc.* 2(2):e01239-13. doi:10.1128/genomeA.01239-13.

Copyright © 2014 Gopinath et al. This is an open-access article distributed under the terms of the [Creative Commons Attribution 3.0 Unported license](https://creativecommons.org/licenses/by/3.0/).

Address correspondence to Junia Jean-Gilles Beaubrun, junia.jean-gillesbeaubrun@fda.hhs.gov.

There are more than 40,000 cases of salmonellosis reported in the United States each year (see the CDC reports of *Salmonella* outbreak investigations [<http://www.cdc.gov/salmonella/outbreaks.html>]). In August through November of 2011, sesame seed paste (tahini) and hummus containing a rare serotype of *Salmonella enterica* caused illness in 23 people in 7 states and the District of Columbia (see the CDC report on *Salmonella* pathogens and protocols [<http://www.cdc.gov/pulsenet/pathogens/salmonella.html>]) (1). Reported cases were largely concentrated in the Mid-Atlantic region, with eight in Washington, DC, seven in Maryland, three in Virginia, and one each in Delaware and New Jersey. Three cases were also reported outside this region—one in California, one in Michigan, and one in New Hampshire (see the CDC report on *Salmonella* pathogens and protocols and reference 1). The *Salmonella enterica* serovar Bovismorbificans strains isolated from the 2011 hummus-associated outbreak demonstrated a pulsed-field gel electrophoresis (PFGE) pattern that was distinctly different from those of other isolates of serovar Bovismorbificans recorded in the Pulse Net Database (see the CDC reports and reference 1). In this report, we announce the availability of six draft genome sequences of *Salmonella* serovar Bovismorbificans from isolates associated with this outbreak: three isolates (SAL609, 610, and 615) from patient stool samples, two from hummus samples (SAL616 and 617) from the District of Columbia Public Health Laboratory, and one clinical isolate (SAL682) from the Michigan Department of Health.

Genomic DNA from each strain was extracted from overnight cultures using QIAcube (Qiagen). The DNA library was constructed according to the Illumina recommended protocol for Nextera XT DNA sample prep and sequenced using Illumina MiSeq (San Diego, CA). CLC bio software version 6.0.1 (Germantown, MD) was used for the trimming and *de novo* assembly of the paired-end reads to 100 contigs. The genomes were annotated by use of the RAST server (2).

The lengths and the GC contents of the draft whole-genome assem-

blies of the strains are as follows: SAL609, 4,896,135 bases and 52.1%; SAL610, 4,856,095 bases and 52.2%; SAL615, 4,845,484 bases and 52.1%; SAL616, 4,863,068 bases and 52.1%; SAL617, 4,870,084 bases and 52.1%; and SAL682 version 02, 4,843,320 bases and 52.2%. All six genomes indicated the presence of two plasmids, one of which demonstrates similarity to the 93-kb pSLT2 IncF-type plasmid of *S. enterica* serovar Typhimurium. In addition to this virulence plasmid, an integration and conjugative element (ICE) similar to ICESb1 found in *Salmonella bongori* (3) has been identified in these outbreak strains. Unlike in other *Salmonella* serovars, in this serovar some phages and type III, IV, and VI secretion systems were observed. A detailed analysis of these isolates of Bovismorbificans from a recent outbreak will shed light on the diversity and distribution of factors contributing to virulence mostly obtained by horizontal transfer.

Nucleotide sequence accession numbers. The draft genome sequence accession numbers for these six *Salmonella enterica* serovar Bovismorbificans strains as deposited in NCBI are [AZKW000000000](https://ncbi.nlm.nih.gov/nucl/AZKW000000000), [AZKX000000000](https://ncbi.nlm.nih.gov/nucl/AZKX000000000), [AZKY000000000](https://ncbi.nlm.nih.gov/nucl/AZKY000000000), [AZKZ000000000](https://ncbi.nlm.nih.gov/nucl/AZKZ000000000), [AZLA000000000](https://ncbi.nlm.nih.gov/nucl/AZLA000000000), and [AZKQ000000000](https://ncbi.nlm.nih.gov/nucl/AZKQ000000000) (the version described here is version 02, AZKQ02000000).

ACKNOWLEDGMENTS

This work was funded by the U.S. FDA Center for Food Safety and Applied Nutrition.

We acknowledge and thank everyone from the Department of Health from the District of Columbia Public Health Laboratory (DC_PHL) for providing the isolates used in this study, and the FDA scientists from the Center for Food Safety and Applied Nutrition (CFSAN), Office of Applied Research and Safety Assessment (OARSA).

REFERENCES

- Centers for Disease Control and Prevention (CDC). 2012. Multistate outbreak of *Salmonella* serotype Bovismorbificans infections associated with hummus and tahini—United States, 2011. *MMWR Morb. Mortal. Wkly. Rep.* 61:944–947.

2. Aziz RK, Bartels D, Best AA, DeJongh M, Disz T, Edwards RA, Formsma K, Gerdes S, Glass EM, Kubal M, Meyer F, Olsen GJ, Olson R, Osterman AL, Overbeek RA, McNeil LK, Paarmann D, Paczian T, Parrello B, Pusch GD, Reich C, Stevens R, Vassieva O, Vonstein V, Wilke A, Zagnitko O. 2008. The RAST server: rapid annotations using subsystems technology. *BMC Genomics* 9:75. <http://dx.doi.org/10.1186/1471-2164-9-75>.
3. Seth-Smith HM, Fookes MC, Okoro CK, Baker S, Harris SR, Scott P, Pickard D, Quail MA, Churcher C, Sanders M, Harmse J, Dougan G, Parkhill J, Thomson NR. 2012. Structure, diversity, and mobility of the *Salmonella* pathogenicity island 7 family of integrative and conjugative elements within *Enterobacteriaceae*. *J. Bacteriol.* 194:1494–1504. <http://dx.doi.org/10.1128/JB.06403-11>.