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Journal

Microbiology Resource Announcements, 4(5)

ISSN

2576-098X

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Publication Date

2016-10-27

DOI

10.1128/genomea.00964-16

Peer reviewed

Draft Genome Sequence of *Salmonella enterica* subsp. *enterica* Serovar Bardo Strain CRJJGF_00099 (Phylum *Gammaproteobacteria*)

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Here, we report a 4.87-Mbp draft genome sequence of the multidrug-resistant (MDR) *Salmonella enterica* subsp. *enterica* serovar Bardo strain CRJJGF_00099, isolated from dairy cattle in 2005.

Received 19 July 2016 Accepted 22 July 2016 Published 15 September 2016

Citation Gupta SK, McMillan EA, Jackson CR, Desai PT, Porwollik S, McClelland M, Hiott LM, Humayoun SB, Frye JG. 2016. Draft genome sequence of *Salmonella enterica* subsp. *enterica* serovar Bardo strain CRJJGF_00099 (phylum *Gammaproteobacteria*). *Genome Announc* 4(5):e00964-16. doi:10.1128/genomeA.00964-16.

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Salmonella enterica subsp. *enterica* serovar Bardo is a rarely reported serotype across the globe; however, *S. Bardo* has been reported from chicken carcasses in Portugal (1), pet reptiles in Japan (2), and oysters in the United States (3). *S. Bardo* has also been previously isolated from cattle in the United States (4), and an *S. Bardo* outbreak was reported in Switzerland in 2011 (5). Here, we announce the draft genome sequence of a multidrug-resistant (MDR) *S. Bardo* strain isolated from dairy cattle in 2005.

Standard microbiology techniques were applied to isolate *Salmonella* strains from food animals. Using pulsed-field gel electrophoresis (PFGE), as described by PulseNet (6), the isolate was assigned PFGE pattern TEGX01.0001.ARS. The isolates were serotyped using SMART (7), and sequencing reads were used to determine an antigenic formula to predict the serotype using SeqSero (8), which predicted the antigenic formula of 8:e,h:1,2 designated *S. Bardo*. As *S. Bardo* shares the same antigenic profile with *Salmonella enterica* subsp. *enterica* serovar Newport, *S. Bardo* was confirmed with the help of the PFGE profile, SMART typing pattern, and antigenic formula. Susceptibility testing for the strain was performed using broth microdilution plates for the Sensititre semiautomated antimicrobial susceptibility system (Trek Diagnostic Systems, Inc., Westlake, OH). The results were interpreted according to Clinical and Laboratory Standards Institute (CLSI) guidelines (9).

Genomic DNA was isolated from an overnight culture using the GenElute bacterial genomic DNA kit (Sigma-Aldrich, St. Louis, MO). DNA libraries were constructed using Nextera-XT DNA preparation kit, and paired-end sequencing was performed on the Illumina HiSeq 2500 (Illumina, Inc., San Diego, CA) using a 500-cycle MiSeq reagent kit. A total of 5,050,994 reads were generated. The reads were *de novo* assembled using Velvet (10), which assembled to 190 contigs ≥ 200 bp, with 96-fold average coverage. The combined length of the contigs was 4,875,034 bases, with a G+C content of 52.17% and an N_{50} value of 60.1 kb. The contigs were ordered with Mauve (11) using the *Salmonella* LT2 genome sequences as a reference, and coding sequences were pre-

dicted with Prodigal (12). A total of 4,598 coding sequences (≥ 50 amino acids) were predicted within the genome. Signal peptide, clustered regularly interspaced short palindromic repeat (CRISPR) regions, and prophages were predicted using SignalP (13), CRISPRFinder (14), and PHAST (15), respectively. We identified signal peptides in 449 coding sequences (CDSs), two CRISPR loci, and five intact phage, including Salmon_SP_004 (accession no. NC021774), Gifsy2 (accession no. NC010393), Salmon_SEN34 (accession no. NC028699), and two Gifsy_1 (accession no. NC010392) phage in the analyzed contigs. The MDR isolate was resistant to streptomycin, ampicillin, cefoxitin, ceftiofur, chloramphenicol, sulfisoxazole, and tetracycline, and we identified corresponding resistance genes [*strA*, *strB*, *cmv-94*, *flor*, *sullI*, and *tet(A)*] and a cryptic aminoglycoside resistance gene, *aac6-Iy*, through ARG-ANNOT (16). The data generated from the draft genomes can provide useful information about the genomic variations in this rarely reported serovar.

Accession number(s). The genome sequence of *Salmonella enterica* subsp. *enterica* serovar Bardo strain CRJJGF_00099 has been deposited in the GenBank database (NCBI) under the accession no. [JQWD00000000](https://ncbi.nlm.nih.gov/nucl/JQWD00000000). This paper describes the first version of the genome.

ACKNOWLEDGMENTS

J.G.F. and C.R.J. were supported by USDA Project no. 6040-32000-006-00 and 6040-32000-009-00 and a grant from the American Meat Institute Foundation. M.M. was supported in part by NIH grants R01AI052237, AI039557, AI052237, AI073971, AI075093, AI077645, and AI083646 USDA grants 2009-03579 and 2011-67017-30127, the Binational Agricultural Research and Development Fund, and a grant from the Center for Produce Safety.

We thank Calvin Williams for all the technical support.

The mention of trade names or commercial products in this article is solely for the purpose of providing specific information and does not imply recommendation or endorsement by the U.S. Department of Agriculture.

FUNDING INFORMATION

This work, including the efforts of Charlene R. Jackson and Jonathan Gray Frye, was funded by Foundation for Meat and Poultry Research and Education. This work, including the efforts of Michael McClelland, was funded by HHS | National Institutes of Health (NIH) (R01AI052237, AI039557, AI052237, AI073971, AI075093, AI077645, and AI083646). This work, including the efforts of Charlene R. Jackson and Jonathan Gray Frye, was funded by U.S. Department of Agriculture (USDA) (6040-32000-006-00 and 6040-32000-009-00). This work, including the efforts of Michael McClelland, was funded by U.S. Department of Agriculture (USDA) (2009-03579 and 2011-67017-30127). This work, including the efforts of Michael McClelland, was funded by United States - Israel Binational Agricultural Research and Development Fund (BARD). This work, including the efforts of Michael McClelland, was funded by Center for Produce Safety (CPS).

The funders had no role in study design, data collection and interpretation, or the decision to submit the work for publication.

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