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PROKARYOTES

Draft Genome Sequences of Two *Salmonella* Strains Isolated from Wild Animals on the Eastern Shore of Virginia

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ABSTRACT Antimicrobial-resistant (AMR) *Salmonella* infections pose a significant public health threat. Here, we announce two draft genomes of *Salmonella* strains isolated from wildlife harboring an alarming array of antibiotic resistance genes. Continued investigations of these genomes will provide insight into the possible attribution of AMR *Salmonella* infection of wild animals.

In the United States, antimicrobial-resistant (AMR) nontyphoidal *Salmonella* infections are considered by the CDC to be a serious threat due to the estimated 100,000 cases of AMR nontyphoidal *Salmonella* infections occurring annually (1). While extensive investigations of AMR *Salmonella* infections from clinical settings and livestock exist (2, 3), few studies have focused on wildlife and wild animals, such as deer, geese, ducks, and gulls, and their role in the transmission of AMR *Salmonella*.

In this report, we announce two draft genome sequences from previously characterized *S. enterica* subsp. *enterica* strains isolated from wildlife on the Eastern Shore of Virginia between November 2010 and July 2011 (4).

DNA was extracted from overnight cultures of two *Salmonella* strains, VA-WGS-00333 and VA-WGS-00353, using the Qiagen DNeasy blood and tissue kit (Valencia, CA, USA). Sequencing libraries for each strain were prepared with DNA using the Illumina Nextera XT kit (San Diego, CA, USA). Sequencing was performed on an Illumina MiSeq using the Illumina 500-cycle kit version 2 according to the manufacturer's instructions.

The serotypes of each strain (VA-WGS-00333: Weslaco; VA-WGS-00353: Singapore) were verified using the *in silico Salmonella* serotype prediction tool SeqSero version 1.0 (5). *De novo* assemblies were generated using SPAdes version 3.9.0 (6), and annotation of the draft genomes was performed using the NCBI Prokaryotic Genome Annotation Pipeline (PGAP) (7).

Quality of the *de novo* assemblies was assessed using Quast version 4.5 (8). The N_{50} values of the two assemblies were 278,931 bp and 357,417 bp for VA-WGS-00333 and VA-WGS-00353, respectively. The GC content values (VA-WGS-00333, 52.07%; VA-WGS-00353, 52.18%) and genome lengths (VA-WGS-00333, 4.6 Mb; VA-WGS-00353, 4.7 Mb) were consistent with other reported *Salmonella* genomes (9, 10).

Annotation of VA-WGS-00333 and VA-WGS-00353 revealed multiple genes that encode proteins associated with antibiotic resistance, including RNase BN, a member of the metallo-beta-lactamase family of proteins (11), 6′-*N*-acetyltransferase, a protein conferring aminoglycoside resistance (12), and various multidrug efflux pumps, such as MdtK, MexE, and EmrA (13–15). The identification of these genes from *Salmonella* strains isolated directly from wildlife may provide insight into the modes of transmission and outbreak origins of AMR *Salmonella* strains, particularly when considering the close proximity of migratory birds to agricultural fields. These findings emphasize the importance of continued surveillance and genomic investigations of zoonotic wildlife pathogens and their resistance profiles.

Received 9 April 2018 **Accepted** 9 April 2018 **Published** 10 May 2018

Citation Libuit KG, Turner L. 2018. Draft genome sequences of two *Salmonella* strains isolated from wild animals on the Eastern Shore of Virginia. Genome Announc 6:e00329-18. https://doi.org/10.1128/genomeA.00329-18.

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Accession number(s). The draft genome sequences for VA-WGS-00333 and VA-WGS-00353 have been deposited in DDBJ/EMBL/GenBank under the accession no. NMOO00000000 and NMON00000000, respectively.

ACKNOWLEDGMENTS

This work was funded in part by the Centers for Disease Control and Prevention (CDC) 93.322 Epidemiology and Laboratory Capacity for Infectious Diseases Award (NU50CK000387-04-01) and the U.S. Food and Drug Administration Center for Food Safety and Applied Nutrition GenomeTrakr Program.

Kevin G. Libuit, as an Association of Public Health Laboratories fellow, was supported by a cooperative agreement (no. NU60OE000103) funded by the CDC.

The contents of this report are solely the responsibility of the authors and do not necessarily represent the official views of CDC or the Department of Health and Human Services.

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