



Genome Sequences of *Salmonella enterica* subsp. *enterica* Serovar Kentucky Sequence Type 152 Isolated from Dairy Cows in the United States

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ABSTRACT *Salmonella enterica* subsp. *enterica* serovar Kentucky (*S. Kentucky*) is frequently isolated from dairy cows in the United States, but is an infrequent cause of human salmonellosis. To investigate the genomic features of *S. Kentucky* strains isolated from a single dairy farm, the genomes of eight isolates were sequenced and added to the public domain.

Salmonella enterica is a major foodborne and livestock pathogen worldwide. There are over 2,500 recognized serovars of *S. enterica*, and some of these are more frequently associated with specific animal hosts than others (<https://www.cdc.gov/salmonella/reportspubs/salmonella-atlas/serotyping-importance.html>). Several serovars, such as *S. enterica* subsp. *enterica* serovar Kentucky (*S. Kentucky*), are polyphyletic within the *Salmonella* phylogeny (1) and are known to have multiple sequence type (ST) assignments, suggesting that different strains of the same serovar may have different ecologies. This, however, has yet to be fully investigated. *S. Kentucky* ST198 has received the most attention due to the epidemic status of multidrug-resistant strains among humans in Africa, the Middle East, and South Asia, with cases in North America and Europe primarily linked with travel to those regions (2–6). *S. Kentucky* ST152 is rarely isolated from humans but is frequently isolated from asymptomatic cattle and poultry across the United States (7–10).

To further investigate the ecology of *S. Kentucky*, the genomes of eight ST152 isolates collected from different cows at different time points on a single dairy farm in Pennsylvania were sequenced and added to the public database. Isolates were first screened using the PCR-based serogrouping scheme as described by Karns et al. (11) with subsequent serovar level identification done by the National Veterinary Services Laboratories (NVSL; Ames, IA). Confirmed *S. Kentucky* isolates were then grown overnight in Luria-Bertani (LB) broth. DNA was extracted from overnight cultures using a Qiagen DNeasy kit (Qiagen, Valencia, CA). Paired-end libraries were constructed using a Nextera XT kit (Illumina, San Diego, CA), and these libraries were sequenced using Illumina MiSeq technology (Illumina). Genomes were assembled using SPAdes v3.0 (12) into 124 to 365 contigs with an average coverage between 37× and 66× and N_{50} contig lengths ranging between 332,848 and 438,375 bp. The genomes were annotated using the NCBI Prokaryotic Genome Annotation Pipeline. There were between 4,703 and 4,889 genes identified in these genomes.

Acquired antibiotic resistance genes were not identified in any of the genomes using the ResFinder database with the threshold for percent identification (% ID) set at 95% and the minimum alignment length set at 100% (13). Homologues of

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Salmonella pathogenicity islands (SPI) 1, 2, 3, 4, and 8 as well as the centisome 63 pathogenicity island (C63PI) were detected in all genomes using SPIFinder with default parameters (<http://www.genomicpidemiology.org/>). Clustered regularly interspaced short palindromic repeat (CRISPR) types identified in Enterobase were 1,097 (isolates CFSAN011775, CFSAN011776, CFSAN011779, and CFSAN011782) and 3,620 (isolates CFSAN011778, CFSAN011780, CFSAN011781, and CFSAN011777) (<http://enterobase.warwick.ac.uk/>). In a whole-genome multilocus sequence type (wgMLST), all genomes were identified as different sequence types (STs) (ST-26854, ST-26850, ST-26844, ST-26846, ST-26843, ST-26848, ST-26842, and ST-21107), indicating that there is an appreciable level of diversity among *S. Kentucky* isolates from the same herd (<http://enterobase.warwick.ac.uk/>).

Accession number(s). This genome sequence project has been deposited in DDBJ/ENA/GenBank under the accession numbers [LOBM00000000](#), [LOBK00000000](#), [LOBJ00000000](#), [LOBH00000000](#), [LOG00000000](#), [LOBL00000000](#), [LOBF00000000](#), and [LOBI00000000](#). The versions described in this paper are the first versions, LOBM01000000, LOBK01000000, LOBJ01000000, LOBH01000000, LOG01000000, LOBL01000000, LOBF01000000, and LOBI01000000.

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