

# Genome Sequences of Five *Salmonella enterica* Serovar Heidelberg Isolates Associated with a 2011 Multistate Outbreak in the United States

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***Salmonella enterica* serovar Heidelberg has caused numerous outbreaks in humans. Here, we report draft genomes of five isolates of serovar Heidelberg associated with the recent (2011) multistate outbreak linked to ground turkey in the United States. Isolates 2011K-1110 and 2011K-1132 were recovered from humans, while isolates 2011K-1138, 2011K-1224, and 2011K-1225 were recovered from ground turkey. Whole-genome sequence analysis of these isolates provides a tool for studying the short-term evolution of these epidemic clones.**

*Salmonella enterica* is recognized as one of the most common bacterial causes of food-borne illness worldwide (3) and causes approximately 1.0 million cases of illness in humans resulting in 19,336 hospitalizations and >378 deaths each year in the United States (4). Within the last several years, *S. enterica* serovar Heidelberg has been identified as one of the top serovars responsible for numerous human outbreaks (2, 5). Recently, the Centers for Disease Control and Prevention (CDC) investigated a multistate (34 states) outbreak of *Salmonella* Heidelberg infections with 136 confirmed cases between 27 February and 13 September 2011. Among 94 ill persons for whom information was available, 37 (39%) had been hospitalized, and 1 death was reported. Collaborative investigative efforts of state and federal public health and regulatory agencies implicated ground turkey as the likely source of this outbreak, necessitating the largest product recall in history of 36 million tons of ground turkey meat (1).

To date, whole-genome sequences of two *Salmonella* serovar Heidelberg strains SL476 and SL486 are available in GenBank. In this report, we announce the availability of five draft genomes of *Salmonella* serovar Heidelberg associated with the recent (2011) multistate outbreak linked to ground turkey in the United States. Strains 2011K-1110 (XbaI pattern JF6X01.0058; BlnI pattern JF6A26.0076) (resistant to ampicillin [AMP], tetracycline [TET], streptomycin [STR], and gentamicin [GEN]) and 2011K-1132 (XbaI pattern JF6X01.0058; BlnI pattern JF6A26.0076) (resistant to AMP, STR, TET, and GEN) were isolated from humans, while strains 2011K-1138 (XbaI pattern JF6X01.0032; BlnI pattern JF6A26.0076) (resistant to AMP, TET, STR, and GEN), 2011K-1224 (XbaI pattern JF6X01.0058; BlnI pattern JF6A26.0017) (resistant to kanamycin [KAN], TET, and STR), and 2011K-1225 (XbaI pattern JF6X01.0032; BlnI pattern JF6A26.0076) (resistant to AMP, TET, STR, and GEN) were isolated from ground turkey.

Genomic DNA from each strain was isolated from overnight cultures using DNeasy blood and tissue kit (Qiagen). The genomes were sequenced using the Genome Sequencer FLX 454 Life Sciences (Roche, Branford, CT) using the GS FLX titanium se-

quencing kit XLR70 according to the manufacturer's recommended protocol to generate between 23- and 38-fold coverage. *De novo* assemblies were performed using Roche Newbler software version 2.6. The draft genome sequences of strains 2011K-1110, 2011K-1132, 2011K-1138, 2011K-1224, and 2011K-1225 consisted of 96, 179, 75, 196, and 126 contigs, respectively, each comprising 4,920,073 bp, 4,913,393 bp, 4,892,102 bp, 4,982,800 bp, and 4,903,677 bp, respectively, with an  $N_{50}$  contig size of 184,125 bp, 68,391 bp, 233,730 bp, 89,037 bp, and 163,931 bp, respectively, and an overall GC content between 53.16% and 53.29%. Sequences were annotated using the NCBI Prokaryotic Genomes Automatic Annotation Pipeline (PGAAP) (<http://www.ncbi.nlm.nih.gov/genomes/static/Pipeline.html>) and have been deposited at DDBJ/EMBL/GenBank. A total of 4,695 (strain 2011K-1110), 4,687 (2011K-1132), 4,653 (2011K-1138), 4,745 (2011K-1224), and 4,675 (2011K-1225) genes were determined.

A detailed report of the results of a full comparative analysis of the genomes of these strains and other available *Salmonella* serovar Heidelberg strains will be included in future publications.

**Nucleotide sequence accession numbers.** The draft genome sequences for these five *Salmonella* serovar Heidelberg strains have been deposited at DDBJ/EMBL/GenBank under accession numbers [AJGW00000000](#), [AJGX00000000](#), [AJGY00000000](#), [AJGZ00000000](#), and [AJHA00000000](#).

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