

Draft Genome Sequences of Eight *Salmonella enterica* Serotype Newport Strains from Diverse Hosts and Locations

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Salmonellosis is a major contributor to the global public health burden. *Salmonella enterica* serotype Newport has ranked among three *Salmonella* serotypes most commonly associated with food-borne outbreaks in the United States. It was thought to be polyphyletic and composed of independent lineages. Here we report draft genomes of eight strains of *S. Newport* from diverse hosts and locations.

Nontyphoid *Salmonella* serotypes cause approximately 1.4 million illness cases (5) and several billion dollars in economic losses (7) annually in the United States. *Salmonella enterica* serotype Newport ranks among the top three *Salmonella* serotypes associated with food-borne outbreaks in the United States (1). The number of *S. Newport* outbreaks has increased markedly since 1995, causing at least 100,000 infections annually (1). Sangal et al. (6) indicated that *S. Newport* was polyphyletic and consisted of three independent lineages. Horizontal gene transfer has played a critical role in its evolution (6). Whole-genome sequencing has been increasingly used as a tool for both evolutionary studies and epidemiological investigations (2, 4). We selected eight *S. Newport* strains from a diverse range of hosts and locations for whole-genome sequencing analysis.

Currently, there are 31 complete genomes and 96 draft genomes of *Salmonella* that have been deposited in GenBank. However, there are only two genomes of *S. Newport* available, namely, *S. Newport* strain SL254 and *S. Newport* strain SL317. In this report, we announce the availability of eight draft genomes for the following *S. Newport* strains: CVM35185 (bison, TN), CVM33953 (ground turkey, MD), CVM21550 (swine, TX), CVM21538 (chicken, GA), CVM37978 (spinach, CO), CVM19593 (cheese, Mexico), CVM19443 (shrimp, India), and CVM19470 (squid, Vietnam). The whole-genome sequence data enable us to better understand the evolutionary history and pathogenicity of these important pathogens.

The eight *S. Newport* strains were sequenced using 454 Titanium pyrosequencing (Roche, Branford, CT) to obtain high-quality draft genomes (18 to 23× coverage). Genomic DNA from each strain was isolated from overnight culture with a DNeasy blood and tissue kit (Qiagen, Valencia, CA). Genomic contigs were assembled (*de novo*) with 454 Life Sciences Newbler software package version 2.3 (Roche). The data for each draft genome are as follows: CVM35185 (95 contigs, 4,708,608 bp and 175,262 bp N_{50} contig size), CVM33953 (88 contigs, 4,801,131 bp and 223,836 bp N_{50} contig size), CVM21550 (73 contigs, 4,919,392 bp and 302,731 bp N_{50} contig size), CVM21538 (70 contigs, 4,927,747 bp and 317,487 bp N_{50} contig size), CVM37978 (49 contigs, 4,796,975 bp and 264,843 bp N_{50} contig size), CVM19593 (74 contigs, 4,654,030 bp and 149,724 bp N_{50} contig size), CVM19443 (70 contigs, 4,807,399 bp and 209,050 bp N_{50} contig size), and

CVM19470 (84 contigs, 4,730,328 bp and 158,282 bp N_{50} contig size). Sequences were annotated with the NCBI prokaryotic genomes automatic annotation pipeline (3). A total of 4,485 (CVM35185), 4,603 (CVM33953), 4,756 (CVM21550), 4,737 (CVM21538), 4,597 (CVM37978), 4,451 (CVM19593), 4,645 (CVM19443), and 4,559 (CVM19470) genes were determined.

A detailed report of the phylogenetic analysis of the eight draft genomes will be included in a future publication.

Nucleotide sequence accession numbers. The draft genome sequences of these eight *S. Newport* strains are available in GenBank under the accession no. [AHTJ00000000](#), [AHTM00000000](#), [AHTT00000000](#), [AHTV00000000](#), [AHUC00000000](#), [AHUD00000000](#), [AHUB00000000](#), and [AHUE00000000](#).

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