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.

Non-typhoidal *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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