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Draft Genome Sequences for Ten *Salmonella enterica* Serovar Typhimurium Phage Type 135 Variants

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***Salmonella enterica* serovar Typhimurium (*S.* Typhimurium) is a common cause of gastroenteritis in humans. Here, we report the draft genome sequences of 10 isolates of an *S.* Typhimurium phage type 135 variant that is linked to egg-associated outbreaks in Tasmania, Australia.**

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Salmonella enterica serovar Typhimurium (*S.* Typhimurium) is a common cause of gastroenteritis in humans (1, 2). The first *S.* Typhimurium genome was published in 2001 (3), and only a handful of additional *S.* Typhimurium genomes have been published since (4). In Australia, a variant of *S.* Typhimurium phage type 135 (sometimes referred to as 135a but without the official phage-type designation) is a common form of *S.* Typhimurium that is responsible for food-borne gastroenteritis (5, 6) and has been associated with multiple outbreaks (7, 8). To facilitate studies of *S.* Typhimurium 135a and future outbreak investigations, the genomes of 10 *S.* Typhimurium 135a isolates linked to egg-associated outbreaks in Tasmania were sequenced. These include five isolates from 2005, one from 2006, two from 2007, and three from 2008.

Sequencing was performed on Illumina HiSeq (10 isolates multiplexed in one lane), generating paired-end 100-bp reads. Reads were assembled using Velvet and Velvet Optimizer (9), resulting in a median of 240 contigs per genome (range, 210 to 284 contigs), covering a median of 4.69 Mbp of sequence (range, 4.64 to 4.73 Mbp), with N_{50} of 99 kbp to 250 kbp and a mean read depth of 300× to 1,000×.

Read mapping to the available finished *S.* Typhimurium reference sequences (10) revealed the closest reference for all isolates was *S.* Typhimurium SL1344 (phage type DT44; accession no. NC_016810.1). Each set of contigs was ordered against *S.* Typhimurium SL1344 using ABACAS (http://abacas.sourceforge.net/) and annotated using the NCBI Prokaryotic Genome Automated Annotation Pipeline (PGAAP). Prophage sequences were identified using PHAST (11).

Between 4,780 and 4,859 protein-coding genes were annotated in each genome, with the exception of STm2, which carries 4,943 genes due to the presence of an additional ~95 kbp of novel sequence with high similarity to the colicin plasmid PColIb-P9 (accession no. AB021078.1) and carries the structural and immunity genes of colicin Ib (12). Multiple alignment of the assemblies using Mauve (13) revealed that the novel *S.* Typhimurium genomes were nearly identical in DNA content, were identical in prophage content, and each carried a copy of the *S.* Typhimurium virulence plasmid pSLT (accession no. NC_003277 [3]). The novel *S.* Typhimurium genomes were very similar in gene content to that of DT44 strain SL1344, with just a few differences in prophage content. The Gifsy-2 and ST64B prophage sequences of SL1344 (SLP105, SLP203) were present and intact at the same locations within the *S.* Typhimurium phage type 135 genomes. The latter also contained a divergent copy of the Gifsy-1 prophage (SLP272) of SL1344 in the same location as in SL1344 and a novel 42.5-kb prophage sequence occupying the same insertion site as the SopEΦ-P4 prophage sequences of SL1344 (SLP285 linked to SLP289). The novel phage consists of a 32-kbp P2 phage with 50.5% G+C content, linked directly to a 10.2-kbp P4 phage with 47.5% G+C content that is identical to SLP289 in *S.* Typhimurium SL1344. The P2 phage has no homology with SopEΦ but shows significant levels of homology with phage sequences in *S. enterica* serovar Newport strain SL254 and *S. enterica* serovars Paratyphi A, Paratyphi C, and Heidelberg.

TABLE 1 Accession numbers of the annotated *S.* Typhimurium whole-genome sequences

S. Typhimurium isolate	Accession no.	Version described here
STm1	AMDX00000000	AMDX01000000
STm2	AMDY00000000	AMDY01000000
STm3	AMEB00000000	AMEB01000000
STm4	AMEC00000000	AMEC01000000
STm6	AMED00000000	AMED01000000
STm8	AMDZ00000000	AMDZ01000000
STm9	AMEA00000000	AMEA01000000
STm10	AMEE00000000	AMEE01000000
STm11	AMEF00000000	AMEF01000000
STm12	AMEG00000000	AMEG01000000

Nucleotide sequence accession numbers. The annotated *S.* Typhimurium whole-genome sequences were deposited as

Whole-Genome Shotgun projects at DDBJ/EMBL/GenBank under the accession numbers listed in Table 1.

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