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Complete Genomic Sequences of Two *Salmonella enterica* subsp. *enterica* Serogroup C2 (O:6,8) Strains from Central California

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ABSTRACT *Salmonella enterica* subsp. *enterica* strains RM11060, serotype 6,8:d:−, and RM11065, serotype 6,8:−:e,n,z_{15}, were isolated from environmental samples collected in central California in 2009. We report the complete genome sequences of these two strains. These genomic sequences are distinct and will provide additional data to our understanding of *S. enterica* genomics.

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Salmonella enterica subsp. *enterica* outbreaks have been caused by a variety of foods, indicating broad survival strategies for the organism. It is commonly found in the environment among water, sediment, and wildlife (1–3). Serotype designation in *Salmonella* is based on antisera reactions to O (lipopolysaccharide) and H (flagellar) antigens (4). Strains RM11060 (serotype 6,8:d:−) and RM11065 (serotype 6,8:−:e,n,z_{15}) were isolated from water and coyote feces, respectively, during an environmental survey (1). Both strains belong to the C2 (O:6,8) serogroup, which includes serovars often implicated in outbreaks, such as Newport and Muenchen. Serotype 6,8:d:− was found in water samples, and 6,8:−:e,n,z_{15} was found in soil, sediment, and wildlife samples. Subsequent surveys indicate that serotype 6,8:d:− is endemic to the region (2, 3).

Sequencing was performed using Pacific Biosciences (PacBio) RSII and Illumina MiSeq platforms. The PacBio reads were assembled using an RS hierarchical genome assembly process (HGAP) version 3.0 in single-molecule real-time (SMRT) analysis version 2.2.0 (Pacific Biosciences). A final base call validation was performed using Illumina MiSeq reads with Geneious software (v10.2.3) (Biomatters, Ltd., Auckland, New Zealand). The final coverage for each strain was >200×. Protein-, rRNA-, and tRNA-coding genes were initially annotated using the NCBI Prokaryotic Genomes Automatic Annotation Pipeline (PGAAP) (http://www.ncbi.nlm.nih.gov/genomes/static/Pipeline.html) with additional manual annotation based on the genome of *Salmonella* Typhimurium LT2 and the O-antigen serogroup C2 locus (accession numbers AE006468 and X61917, respectively).

The chromosomes for strains RM11060 (serotype 6,8:d:−) and RM11065 (serotype 6,8:−:e,n,z_{15}) were 4,892,239 bp and 4,991,140 bp, respectively. The RM1160 chromosome is predicted to carry 4,873 coding sequences (CDS), 7 rRNA operons, and 84 tRNAs. The RM11065 chromosome is predicted to possess 5,120 CDS, 7 rRNA operons, and 85 tRNAs. Both genomes contained two plasmids, as RM11060 contained pRM11060-1 (66,623 bp, 80 CDS) and pRM11060-2 (271,721 bp, 314 CDS), while RM11065 contained pRM11065-1 (143,770 bp, 152 CDS) and pRM11065-2 (132,606 bp, 104 CDS). Bacteriophages were identified using PHASTER (http://www.phaster.ca) (5, 6). The chromosome of RM11060 was found to contain 3 intact, 1 questionable, and 1 incomplete prophage, while each

RM11060 plasmid (pRM11060-1 and pRM11060-2) had an intact prophage. The chromosome of RM11065 contained 7 intact, 2 questionable, and 3 incomplete prophages, pRM11065-1 had 2 incomplete prophages, and pRM11065-2 had an intact and an incomplete prophage. The presence of integrated elements (IE) via the presence of additional integrases demonstrated that the chromosomes had 4 IEs and 7 IEs for RM11060 and RM11065, respectively. The presence of insertion sequences (IS) was determined using IS Finder (https://www-is.biotoul.fr/) (7), and 18 IS were found in RM11060 (chromosome, 14 IS; pRM11060-2, 4 IS) and 23 IS in RM11065 (chromosome, 14 IS; pRM11065-1, 4 IS; and pRM11065-2, 5 IS). Interestingly, the chromosome of RM11060 has an approximately 34,000-bp deletion, which includes the envelope stress response gene *cpxPAR*. This region is found on pRM11060-1.

Accession number(s). The whole-genome sequences were deposited with GenBank under the following accession numbers: for strain RM11060, CP022658 (chromosome), CP022659 (pRM11060-1), and CP022660 (pRM11060-2) (BioProject, PRJNA393473; BioSample, SAMN07334224), and for strain RM11065, CP022663 (chromosome), CP022661 (pRM11065-1), and CP022662 (pRM11065-2) (BioProject, PRJNA393473; BioSample, SAMN07334225).

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