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Draft Genome Sequences of the Avirulent *Coxiella burnetii* Dugway 7D77-80 and Dugway 7E65-68 Strains Isolated from Rodents in Dugway, Utah

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ABSTRACT Here, we present the draft genome sequences of the *Coxiella burnetii* Dugway 7D77-80 and Dugway 7E65-68 strains, which were isolated from rodents in Dugway, UT, in the 1950s. The strains reside in a distinct genomic group of *C. burnetii* and are considered avirulent despite having the largest genomes of the *Coxiella* genus.

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Coxiella burnetii, the bacterial cause of human Q fever, has an impressive range of animal hosts, with the majority of human infections acquired by inhalation of contaminated aerosols generated by infected domestic livestock (1). *C. burnetii* strains display a range of virulence in rodent models of infection (2, 3). There are also correlations between genetic content and disease outcome in humans (4, 5). Five strains (5J108-111, 7D77-80, 7E9-12, 7E22-57, and 7E65-68) were isolated in 1957 in Dugway, UT, from either a deer mouse (*Peromyscus maniculatus*) or a kangaroo rat (*Dipodomys ordii* or *Dipodomys microps*) (2, 6). All were initially shown to be avirulent for guinea pigs via an intraperitoneal route of infection (2). More recently, it was demonstrated that the Dugway 5J108-111 strain is avirulent for guinea pigs via the aerosol route and that infection of CB-17 mice induces low levels of proinflammatory cytokines compared with those induced by infections by genomic group I strains, such as African (RSA334), a human acute disease isolate (3). The Dugway strains constitute a unique genomic group (group VI) (7–9). Genomic sequencing of Dugway 5J108-111 revealed the largest *C. burnetii* chromosome (2,158 kbp) and plasmid (54.2 kbp), which together contain 2,052 genes (excluding pseudogenes). This is 203 more genes than found in the highly virulent Nine Mile (RSA493) reference strain (8). Phylogenetically, the Dugway strains appear to represent a more primitive genomic group that has not undergone the genome reduction associated with pathogenic *C. burnetii* strains (8, 10). Dugway-like strains have not been isolated from human Q fever patients nor pathological animal infections, such as those causing abortions in sheep or goats (1, 10). Thus, it is interesting to speculate that the novel gene content of the Dugway isolates enables persistent subclinical infection of animal hosts with perhaps a specific tropism for rodents (10, 11). The purpose of this study was to expand our knowledge of the genome content of *C. burnetii* Dugway strains.

Strains were grown in acidified citrate cysteine medium-2 (ACCM-2) (12), and DNA was isolated using a Mo Bio PowerMicrobial DNA extraction kit. DNA was sequenced using an Illumina MiSeq instrument to generate 2 × 300-bp read pairs. Raw FASTQ reads for each sample were quality trimmed using Trimmomatic version 0.3 (13). Quality-trimmed reads were then assembled into contiguous sequences (contigs) using

TABLE 1 Genome statistics

Strain	No. of contigs	Genome coverage (×)	Plasmid coverage (×)	GenBank accession no.	Chromosome size (bp)	Total no. of chromosome genes[a]	Plasmid size (bp)	Total no. of plasmid genes
Dugway 7D77-80	33	75	168	NOLN00000000	2,138,428	2,286	53,590	67
Dugway 7E65-68	35	114	185	NOLM00000000	2,138,988	2,280	53,586	67

[a]Total gene count includes coding genes, RNAs (tRNA, noncoding RNA [ncRNA], and rRNA), and pseudogenes.

SPAdes genome assembler version 3.9.1, with the -careful flag and k-mer lengths of 21, 33, 55, 77, 99, and 127. Contigs with coverage of less than 2 and shorter than 200 bp were discarded. The draft genomes were submitted to GenBank for annotation using the NCBI Prokaryotic Genome Annotation pipeline (PGAP). The assembly properties and annotation statistics for each genome are given in Table 1.

Accession number(s). The annotated draft whole-genome sequences of the chromosome and QpDG plasmid of *Coxiella burnetii* Dugway 7D77-80 and 7E65-68 strains have been deposited in DDBJ/ENA/GenBank under the accession numbers shown in Table 1.

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