



Draft Genome Sequences of Historical Strains of *Coxiella burnetii* Isolated from Cow's Milk and a Goat Placenta

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ABSTRACT Here, we report draft genome sequences of historical strains of *Coxiella burnetii* derived from cow's milk and the placenta of a goat that had aborted. The California and Ohio milk strains display a different sequence type than do contemporary milk strains.

The intracellular bacterium *Coxiella burnetii* causes human Q fever, a zoonotic disease that normally manifests as a severe flu-like illness. *C. burnetii* has an impressive range of animal reservoirs, but most human infections are caused by contact with infected dairy cows, goats, and sheep. Large numbers of stable *C. burnetii* are shed into the environment by infected livestock, especially in birth products, which promotes aerosol transmission of Q fever (1).

The California 16 (RSA350) and 33 (RSA329) strains were isolated from cow's milk in California in 1947 (2, 3) and are serologically in phase II and phase I, respectively (3–5). They are in genomic group I (3) and have a multispacer sequence typing (MST) 16/26 genotype (6). The Ohio (RSA270) strain was isolated from cow's milk in Ohio in 1956 (7). It is serologically in phase I (3–5), resides within genomic group I (3), and has an MST 16/26 genotype (6). Ohio 314 (RSA338) is a passage history variant of Ohio 314 (RSA270) that is serologically in phase II (3). Phase I variants of California and Ohio milk strains are highly virulent for guinea pigs (8–10). Indeed, California milk strains were historically associated with large human Q fever outbreaks (11) and fixed organisms were efficacious as human vaccines (12, 13). Interestingly, contemporary cow milk strains circulating in the United States now display an MST20 genotype, which is rarely associated with human disease (14, 15). The Idaho goat (Q195) strain was isolated from the placenta of dairy goat that had aborted in Idaho in 1976 (16). It is serologically in phase I (3–5), resides in genomic group III (3), and has an MST20 genotype (6). It is weakly virulent for guinea pigs (16). These genome sequences provide insight into host adaptation and virulence potential of *C. burnetii*.

Strains were grown in acidified citrate cysteine medium-2 (ACCM-2) (17) 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 (18). Quality trimmed reads were then assembled into contiguous sequences (contigs) using SPAdes Genome Assembler, version 3.9.1, with -careful flag and kmer lengths of 21, 33, 55, 77, 99, and 127. Contigs with coverage less than 2 and shorter than 200 bp were discarded. The draft genomes were submitted to GenBank for annotation using the

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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
California 33 (RSA329)	34	82	144	NOLV00000000	1,968,897	2,146	37,374	50
California 16 (RSA350)	34	75	96	NOLU00000000	1,968,786	2,146	37,374	50
Ohio 314 (RSA270)	34	103	164	NOLT00000000	1,968,781	2,146	37,446	49
Ohio 314 (RSA338)	34	109	140	NOLS00000000	1,968,786	2,147	37,446	49
Idaho goat (Q195)	39	130	242	NOLR00000000	1,968,263	2,162	37,457	50

^aTotal gene count includes coding genes, RNAs (tRNAs, noncoding RNAs [ncRNAs], and rRNAs), and pseudogenes.

NCBI Prokaryotic Genome Annotation pipeline (PGAP). Assembly properties and annotation statistics for each genome are given in Table 1.

Accession number(s). The annotated draft whole-genome sequences of the QpH1 plasmid and chromosome of *C. burnetii* California, Ohio, and Idaho goat strains have been deposited in DDBJ/ENA/GenBank under the accession numbers shown in Table 1.

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