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PROKARYOTES

Draft Genome Sequences of Three *Coxiella burnetii* Strains Isolated from Q Fever Patients

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ABSTRACT In the current study, we determined the draft genome sequences of three *Coxiella burnetii* human disease isolates. The *Coxiella burnetii* Turkey (RSA315) and Dyer (RSA345) strains were isolated from acute Q fever patients, while the Ko (Q229) strain was isolated from a Q fever endocarditis patient.

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Coxiella burnetii is an intracellular bacterium that causes the zoonosis Q fever. The majority of human infections are acquired through contact with infected domestic ruminants or their products. Following primary infection, approximately 60% of individuals are asymptomatic. Symptomatic acute disease usually presents as a flu-like illness but can also manifest as pneumonia or hepatitis. Less frequent are persistent focalized infections (formally grouped as chronic Q fever) that typically present as endocarditis or vascular disease (1). Here, we report draft genome sequences of three historical human Q fever disease isolates, Dyer (RSA345), Turkey (RSA315), and Ko (Q229). The Dyer (RSA345) strain, also referred to in early reports as the American strain (2), was isolated from the blood of an acute disease patient infected with the Nine Mile phase I (RSA493) strain in 1938 (3). The Turkey (RSA315) strain was isolated from the blood of an acute disease patient in Turkey in 1948 (4). The Dyer (RSA345) and Turkey (RSA315) strains are serologically in phase II (5–7), reside in genomic group I (5), and have a multispacer sequencing typing (MST) 16/26 genotype (8). The Ko (Q229) strain was isolated from a heart valve of an endocarditis patient in Nova Scotia, Canada, in 1982 (9). It is serologically in phase I (5–7), resides in genomic group V (5), and has an MST 21 genotype (8). Genomic group I strains are more virulent than genomic group V strains in animal models of Q fever (10, 11). The genome sequences presented here will expand our knowledge of *C. burnetii* strain variation and pathogenic potential.

Strains were grown in acidified citrate cysteine medium-2 (ACCM-2) (12), and DNA was isolated using an MoBio 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 SPAdes genome assembler version 3.9.1, with -careful flag and kmer lengths of 21,33,55,77,99,127. Contigs with coverage less than 2 and shorter than 200 bp were discarded. The draft genomes were submitted to GenBank for annotation using the 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 chromosome of the *C. burnetii* Ko (Q229) strain and the QpH1 plasmid and chromosome of

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
Dyer (RSA345)	34	100	144	NOLQ00000000	1,969,263	2,143	37,446	50
Ko (Q229)	40	95	No plasmid	NOLP00000000	1,974,020	2,157	No plasmid	No plasmid
Turkey (RSA315)	33	108	165	NOLO00000000	1,969,057	2,144	37,446	49

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

the Dyer (RSA345) and Turkey (RSA315) strains have been deposited in DDBJ/ENA/GenBank under the accession numbers shown in Table 1.

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