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Genome Sequence of the *Chlamydophila abortus* Variant Strain LLG▽

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***Chlamydophila abortus* is a common cause of ruminant abortion. Here we report the genome sequence of strain LLG, which differs genotypically and phenotypically from the wild-type strain S26/3. Genome sequencing revealed differences between LLG and S26/3 to occur in pseudogene content, in transmembrane head/inc family proteins, and in biotin biosynthesis genes.**

Chlamydophila abortus is the etiological agent of enzootic abortion, causing abortion of the fetus in pregnant sheep and other ruminants. *C. abortus* isolates exhibit low genetic heterogeneity, with the exception of two variant strains, LLG and POS, which display genetic heterogeneity (2, 3, 7) and exhibit phenotypic differences in inclusion morphology, polypeptide profiles, antibody cross-reactivity, and cross-protection experiments and in their ability to colonize the placenta and fetus compared to those of wild-type strains (1, 9, 10). Here we report the genome sequence of LLG, which will contribute to the understanding of *C. abortus* pathogenesis and evolution.

The *C. abortus* LLG genome was sequenced using 454 GS-FLX and Solexa 35-bp paired-end sequencing. Reads were assembled by the GenePool genomics facility in the University of Edinburgh using Newbler v2 (Roche) and Velvet v.0.7 (11) and then combined using minimus2. Contigs, providing approximately 50× sequence coverage, were ordered using *C. abortus* S26/3 (GenBank accession no. CR848038) as a reference sequence (8) and finished by PCR and sequencing. Two gaps that were unable to be closed are marked in the annotation. Based on the corresponding region in *C. abortus* S26/3, these gaps have an estimated size of 4,721 bp spanning pmp12G to pmp14G and 3,457 bp spanning pmp17G to pmp16G. Annotation was performed using Artemis (6).

C. abortus LLG is composed of a 1,143,519-bp circular chromosome with a G+C content of 39.5%. There are 963 predicted coding sequences (CDSs), of which 957 have orthologs in S26/3, with an average amino acid identity of 99.4%. There is a single rRNA gene operon and 38 tRNA genes representing all standard amino acids except selenocysteine. *C. abortus* LLG-specific CDSs include six hypothetical proteins (CAB1_0191, CAB1_204, CAB1_0266, CAB1_0609, CAB1_0695, and CAB1_0801). The greatest variation between LLG and S26/3 occurs in the pseudogene content. Genes which are intact in S26/3 but occur as pseudogenes or truncated genes in LLG include bioA (CAB1_0707) and bioD (CAB1_0706), both involved in biotin synthesis, CAB1_0873 (CAB853) which is a hypothetical protein that occurs instead of intimin in *C. abortus* S26/3 (4, 8), and the transmembrane head (TMH)/Inc family protein CAB1_0792 (CAB775), which (based on the corresponding region in S26/3) contains a 962-bp deletion of the N-terminal transmembrane domain and the DUF1539 conserved domain (5, 8). Pseudogenes present in S26/3 that are intact in LLG include three TMH/Inc family proteins CAB1_0782 (CAB760), CAB1_0784 (CAB762), and CAB1_0787 (CAB768) (5, 8).

Nucleotide sequence accession numbers. The Whole Genome Shotgun project has been deposited at DDBJ/EMBL/GenBank under the accession number AFHM00000000. The version described in this paper is the first version, AFHM01000000.

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