



THE UNIVERSITY *of* EDINBURGH

Edinburgh Research Explorer

Genome sequence of the *Chlamydophila abortus* variant strain LLG

Citation for published version:

Sait, M, Clark, EM, Wheelhouse, N, Livingstone, M, Spalding, L, Siarkou, VI, Vretou, E, Smith, D, Lainson, FA & Longbottom, D 2011, 'Genome sequence of the *Chlamydophila abortus* variant strain LLG' *Journal of Bacteriology*, vol 193, no. 16, pp. 4276-7., 10.1128/JB.05290-11

Digital Object Identifier (DOI):

[10.1128/JB.05290-11](https://doi.org/10.1128/JB.05290-11)

Link:

[Link to publication record in Edinburgh Research Explorer](#)

Document Version:

Publisher final version (usually the publisher pdf)

Published In:

Journal of Bacteriology

Publisher Rights Statement:

Freely available in PMC.

General rights

Copyright for the publications made accessible via the Edinburgh Research Explorer is retained by the author(s) and / or other copyright owners and it is a condition of accessing these publications that users recognise and abide by the legal requirements associated with these rights.

Take down policy

The University of Edinburgh has made every reasonable effort to ensure that Edinburgh Research Explorer content complies with UK legislation. If you believe that the public display of this file breaches copyright please contact openaccess@ed.ac.uk providing details, and we will remove access to the work immediately and investigate your claim.



Genome Sequence of the *Chlamydomphila abortus* Variant Strain LLG[∇]

Michelle Sait,^{1*} Ewan M. Clark,^{1†} Nick Wheelhouse,¹ Morag Livingstone,¹ Lucy Spalding,¹
Victoria I. Siarkou,² Evangelia Vretou,³ David G. E. Smith,^{1,4}
F. Alex Lainson,¹ and David Longbottom¹

Moredun Research Institute, Pentlands Science Park, Bush Loan, Edinburgh, Midlothian EH26 0PZ, United Kingdom¹; Laboratory of Microbiology and Infectious Diseases, Faculty of Veterinary Medicine, Aristotle University of Thessaloniki, University Campus, GR-54124, Thessaloniki, Greece²; Laboratory of Biotechnology, Hellenic Pasteur Institute, Vassilissis Sofias Avenue 127, 11521 Athens, Greece³; and Institute of Infection, Immunity and Inflammation, College of Medical, Veterinary and Life Sciences, University of Glasgow, Garscube Estate, Bearsden Road, Glasgow G61 1QH, United Kingdom⁴

Received 13 May 2011/Accepted 6 June 2011

***Chlamydomphila 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.**

Chlamydomphila 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.

This work was funded by grant no. BB/E018939/1 from the Biological and Biotechnology Sciences Research Council (BBSRC) and by the Scottish Government Rural and Environmental Research and Analysis Directorate (RERAD).

REFERENCES

1. Bouakane, A., H. Benchaieb, and A. Rodolakis. 2003. Abortive potency of *Chlamydomphila abortus* in pregnant mice is not directly correlated with placental and fetal colonization levels. *Infect. Immun.* **71**:7219–7222.
2. Laroucau, K., et al. 2009. Genotyping of *Chlamydomphila abortus* strains by multilocus VNTR analysis. *Vet. Microbiol.* **137**:335–344.
3. Pannekoek, Y., et al. 2010. Multi locus sequence typing of *Chlamydia* reveals an association between *Chlamydia psittaci* genotypes and host species. *PLoS One* **5**:e14179.
4. Read, T. D., et al. 2003. Genome sequence of *Chlamydomphila caviae* (*Chlamydia psittaci* GPIC): examining the role of niche-specific genes in the evolution of the Chlamydiaceae. *Nucleic. Acids Res.* **31**:2134–2147.
5. Rockey, D. D., M. A. Scidmore, J. P. Bannantine, and W. J. Brown. 2002. Proteins in the chlamydial inclusion membrane. *Microbes Infect.* **4**:333–340.
6. Rutherford, K., et al. 2000. Artemis: sequence visualization and annotation. *Bioinformatics* **16**:944–945.
7. Siarkou, V., A. F. Lambropoulos, S. Chrisafi, A. Kotsis, and O. Papadopoulos. 2002. Subspecies variation in Greek strains of *Chlamydomphila abortus*. *Vet. Microbiol.* **85**:145–157.

* Corresponding author. Mailing address: Moredun Research Institute, Pentlands Science Park, Bush Loan, Edinburgh, Midlothian EH26 0PZ, United Kingdom. Phone: 44 131 445 5111. Fax: 44 131 445 6235. E-mail: michelle.sait@moredun.ac.uk.

† Present address: BigDNA, Wallace Building, Roslin BioCentre, Roslin, Midlothian, EH25 9PP, United Kingdom.

[∇] Published ahead of print on 17 June 2011.

8. **Thomson, N. R., et al.** 2005. The *Chlamydomophila abortus* genome sequence reveals an array of variable proteins that contribute to interspecies variation. *Genome Res.* **15**:629–640.
9. **Vretou, E., et al.** 1996. Diversity among abortion strains of *Chlamydia psittaci* demonstrated by inclusion morphology, polypeptide profiles and monoclonal antibodies. *Vet. Microbiol.* **51**:275–289.
10. **Vretou, E., et al.** 2001. Identification of protective epitopes by sequencing of the major outer membrane protein gene of a variant strain of *Chlamydia psittaci* serotype 1 (*Chlamydomophila abortus*). *Infect. Immun.* **69**:607–612.
11. **Zerbino, D. R., and E. Birney.** 2008. Velvet: algorithms for de novo short read assembly using de Bruijn graphs. *Genome Res.* **18**:821–829.