Moredun

Genome Sequencing Project

Conducting deep genome sequencing of* C. abortus *strains to investigate strain variation in collaboration with the Sanger Institute
(BBSRC BB/E018939/1)

As part of a multi collaborative project funded under the BBSRC Combating Endemic Diseases of Farmed Animal Species initiative (BB/E018939/1) to investigate the heterogeneity in carriage and expression of a novel group of autotransporter proteins of chlamydia species; a large number of *C. abortus* strains of different geographical origin (European, US and N. African) and host animal species (sheep, cattle, goat and pig) have been collected from collaborators to examine diversity. The strains have been sequenced using Illumina Genome Analyzer II or HiSeq 2000 technologies in collaboration with Professor Nick Thomson and Dr Helena Seth-Smith of the Wellcome Trust Sanger Institute.

70 strains have been collected from Europe (UK [n=21], France [n=12], Germany [n=26] and Greece [n=4]), N. Africa (n=5) and the US (n=2) (see Sequenced strains *[hyperlink to attachment]* in attachments) and have been sequenced. Genome sequences have been analysed to gain an insight into the variability of the field strains with reference to host species and geographical location, and to provide important information on our understanding of how this pathogen differs in its ability to induce disease when compared to other chlamydial pathogens, particularly another important pathogen of ruminants *C. pecorum*. Ultimately this will help in the development of improved disease control strategies.

In 2010 a paper was published (Wheelhouse, N. et al., 2010) providing evidence of the OEA attenuated vaccine strain 1B in the placentas of vaccinated ewes that had aborted using a newly developed molecular DIVA test that could differentiate the vaccine strain from wild-type infections. No other wild-type strains were present in these placentas and the number of organisms present were typical of a normal field infection, suggesting that the vaccine was responsible for the abortion. In order to further clarify this likely causal role of the vaccine strain in cases of OEA, isolates were obtained from aborted animals that had been vaccinated for sequencing and whole genome comparative analysis.

Selected publications:

Sait, M., Livingstone, M., Clark, E.M., Wheelhouse, N., Spalding, L., Markey, B., Magnino, S., Lainson, F.A., Myers, G.S.A. and Longbottom, D. (2014). Genome sequencing and comparative analysis of three Chlamydia pecorum strains associated with different pathogenic outcomes. BMC Genomics 15:23.

Seth-Smith, H.M.B., Sait, M., Sachse, K., Wolfgang, G., Longbottom, D. and Thomson, N.R. (2013). Genome sequence of Chlamydia psittaci strain 01DC12 originating from swine. Genome Announcements 1, e00078-12.

Sait, M., Clarke, E.M., Wheelhouse, N., Livingstone, M., Yaga, R., Spalding, L., Siarkou, V.I., Vretou, E., Smith, D.G.E., Lainson, F.A., and Longbottom, D. (2011). Genome sequence of the Chlamydophila abortus variant strain LLG. Journal of Bacteriology 193, 4276-7.

Wheelhouse, N., Aitchison, K.D., Laroucau, K., Thomson, J. and Longbottom, D. (2010). Evidence of Chlamydophila abortus vaccine strain 1B as a possible cause of Ovine Enzootic Abortion. Vaccine 28, 5657-63.

Thomson, N.R., Yeats, C., Bell, K., Holden, M.T., Bentley, S.D., Livingstone, M., Cerdeño-Tárraga, A.M., Harris, B., Doggett, J., Ormond, D., Mungall, K., Clarke, K., Feltwell, T., Hance, Z., Sanders, M., Quail, M.A., Price, C., Barrell, B.G., Parkhill, J. and Longbottom, D. (2005). The Chlamydophila abortus genome sequence reveals an array of variable proteins that contribute to interspecies variation. Genome Research 15, 629-40.