

### **Analysis of the *Coxiella burnetii* isolate-specific pathogenic potential using proteomics**

Jennifer Andrack<sup>1</sup>, Jiri Dresler<sup>2</sup>, Heinrich Neubauer<sup>1</sup>, Katja Mertens-Scholz<sup>1</sup>

<sup>1</sup> Institute of Bacterial Infections and Zoonoses (IBIZ), Friedrich-Loeffler-Institut, Jena, Germany,

<sup>2</sup> Military Health Institute, Prague, Czech Republic

Q fever is a disease caused by *Coxiella (C.) burnetii*, an obligate intracellular zoonotic pathogen, which affects humans and animals. In ruminants (e.g. sheep, goat and cattle) the infection can lead to abortions, whereas in humans flu-like symptoms and pneumonia (acute) and/or endocarditis (chronic) may occur.

*C. burnetii* isolates are genetically heterogeneous and originally classified into six genomic groups. This classification is based on the observed group-specific virulence, identified using rodent infection models. The genetic and pathogenic differences may be a result of a variable expression of virulence factors.

Our project is part of the Q-GAPS zoonosis network (Q fever GermAn Interdisciplinary Program for reSearch) and focuses on isolate-specific differences in pathogenicity and virulence. The hypothesis of our work is that the genetic differences of various *C. burnetii* isolates correlates with differential expression of virulence factors. For determining the isolate-specific differences, the data from whole genome sequencing, cell culture infection models for replication fitness and corresponding proteome analysis will be compared. This will be used for the identification of protein markers for virulence determinants and may contribute to future development of new diagnostic tests and vaccines.

Contact:

Jennifer Andrack

[Jennifer.Andrack@fli.de](mailto:Jennifer.Andrack@fli.de)