



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

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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, goats and cattle), the infection is mainly asymptomatic, but can lead to abortions. 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 correlates with an observed group-specific virulence, identified using rodent infection models. The pathogenic differences may be a result of a variable expression of virulence factors and predisposing factors of the individual host.

Our project is part of the Q-GAPS zoonosis network (**Q** fever **Ger**M**A**n Interdisciplinary **P**rogram for **re**Search) 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.