IVD.05 - *In silico* studies of *Coxiella burnetii* outer membrane proteins (OMPs) as basis to Q fever diagnosis development

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Introduction: Q fever is a highly infectious but largely 'neglected zoonosis' caused by Gram-negative bacterium, *Coxiella burnetii*, which is listed as a biological warfare agent and infects a wide range of domestic and wild animals as well as humans. The disease in animals is associated to late abortions, stillbirths and other reproductive disorders. In humans, acute Q fever has a wide clinical spectrum, ranging from asymptomatic to influenza-like or pneumonia cases, and may progress to chronic diseases complicated by endocarditis, meningoencephalitis and/or osteomyelitis. *Coxiella burnetii* survive in environment for months and can spread by aerosolization or ingestion of contaminated milk and derivatives. Considering its severity, Q fever may have a huge impact on livestock and public health, especially in developing countries like Brazil, where meat of cattle, milk and its derivatives are important economic issues and largely consumed. Besides, the true picture of infection remains obscure due to limited diagnostic and surveillance strategies. On this context, outer-membrane proteins (OMPs) emerge as targets to novel diagnosis reactive, once previous studies showed the reactivity of members of these proteins against serum of humans and animals infected by C. burnetii. However, in order to avoid cross-reactions with other bacterial pathogens, *in silico* analysis of OMPs rise as a promising approach to identification of highly specific immunogenic regions on *Coxiella burnetii* targets.

Objective: This study aimed to identify potential B-cell epitopes on OMPs (Omp-H, Omp-P1, Omp-Com1) of *Coxiella burnetii*.

Methodology: To predict linear B-cell epitopes, sequences of OMP-H, Omp-Com1 and Omp-P1 were obtained from Uniprot and explored by three prediction algorithms (BCpred,BepiPred-1.0,EMINI-Surface-Accessibility-Prediction). All sequences predicted by at least two algorithms and with more than 9 mers were analyzed by VaxiJen, to predict its immunogenicity. Moreover, the conservation degree of predicted epitopes was evaluated by comparison (BLASTp) between each sequences and correlated bacteria (*Francisella tularensis, Legionella pneumophila, Escherichia coli, Pseudomonas aeruginosa, Rickettsia rickettsia, Ehrlichia chaffeensis,Bartonella henselae, Brucella melitensis, Afipia felis, Campylobacter jejuni*). Finally, the 3D structures of OMP-H, OMP-P1 and OMP-Com1 were predicted by Robetta algorithm and its oligomeric structures predicted by Galaxy Protein Modelling Program.

Results: Firstly, in each studied OMP, two sequences were predicted as linear B-cell epitope (OmpH-E1, OmpH-E2, OmpC-E1, OmpC-E2, OmpP-E1, and OmpP-E2). Among these sequences, OmpH-E2, OmpC-E1, OmpP-E1 and OmpP-E2 were predicted as immunogenic epitopes and evaluated for its conservation degree. Remarkably, all sequences predicted as immunogenic linear B-cell epitopes were specific of *Coxiella burnetii*, once that presented a low conservation degree in comparison with correlated bacteria. Moreover, all immunogenic predicted epitopes are exposed on surface of proteins, reinforcing their potential as diagnostic target.

Conclusion: We identified four immunogenic B-cell epitopes highly specifics to *Coxiella burnetii*. If experimentally validated, these sequences can be used in the development of novel diagnosis and surveillance tools to Q fever.

Keywords: Q FEVER; Diagnostic; *Coxiella burnetii*