CBU_1932: A HYPOTHETICAL DNA-BINDING PROTEIN OF THE Q FEVER PATHOGEN *COXIELLA BURNETII* (POSTER)

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Coxiella burnetii is an obligate intracellular bacterial pathogen that resides within a lysosome-like acidic compartment of the eukaryotic host cell and may cause acute and chronic human infections. Our recent transcriptome analysis of C. *burnetii* demonstrated that the CBU_1932 open reading frame displayed an exceptionally high transcript level at 11,481 transcripts per million (TPM), well above average transcript quantity for remaining ORFs in the genome. Due to it's high transcript level we hypothesize the corresponding protein may play an important role for *Coxiella*. Analysis of the CBU_1932 locus indicates that one of the adjacent ORFs, CBU_1933 is a hypothetical DNA binding protein. The protein encoded by CBU_1932 ORF consists of 66 amino acid residues with an unusually high percentage (42%) of residues being basic, including 20 lysines. Using BLAST algorithms we found CBU_1932 had no similarity with currently defined proteins, but has orthologues in other human intracellular pathogens such as *Legionella* and *Chlamydia*. Due to the high number of basic residues in CBU_1932, and linkage with a hypothetical DNA binding protein (CBU_1933), we hypothesize that CBU_1932 may also encode a protein involved with binding DNA or other negatively charged substrates. To address this hypothesis, we are in the process of cloning the 201-base pair CBU_1932 ORF into pMAL-c5x expression plasmid and analyzing the recombinant protein using DNA-binding protocols including electrophoretic mobility-shift assay EMSA. We are confident that characterization of this high-level transcript/highly basic protein will lead to a better understanding of the unique metabolism of *Coxiella* and other intracellular pathogens.