ACTINOBACILLUS PLEUROPNEUMONIAE TRANSCRIPTOME ANALYSIS DURING EARLY INFECTION – COPING WITH A HOSTILE ENVIRONMENT

***Actinobacillus pleuropneumoniae* transcriptome analysis during early infection – coping with a hostile environment**

Aim: To obtain an increased understanding of how the porcine lung pathogen *Actinobacillus pleuropneumoniae* (Ap) establish infection in the host. Understanding the means by which a pathogen establishes and maintains infection in the host organism is the first step towards controlling disease.

Methods: The local *in vivo* genetic response of Ap during the early phase of infection in porcine lungs was detailed using pangenomic microarray analysis. The global transcriptional patterns of Ap serotype 2 and 6 isolated from lung tissue biopsies of 25 experimentally infected pigs were compared at four time points between 6 and 48 hours post infection.

Results: We identified 310 genes ($p < 1.0 \times 10^{-8}$) that were differentially expressed during the first 48 hours of infection. Most of these genes appeared to be up-regulated at 6 hours post inoculation after which the expression gradually declined over the next 42 hours. Functional analysis identified a number of putative virulence genes to be initially up-regulated.

Conclusions: This is the first study monitoring the development of Ap response in the porcine host during early infection. The ability of pathogenic bacteria to adjust gene expression in response to environmental stimuli is critical for bacterial survival within the host. The genes identified as differentially expressed in this study may represent a core set of genes which are mobilized to cope with the host immune response and adapt to the hostile environment. The potential virulence genes identified may represent valuable candidates for vaccine development.