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## ***Differential transcript response to infection to host-specific and host-generalist Salmonella enterica serotypes in pigs***

### ABSTRACT

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Salmonellosis is prevalent worldwide and Salmonella most serotype has a broad host range. The classic salmonella of pigs is *S. enterica* serotype Choleraesuis (SC) and *S. enterica* serotype Typhimurium (ST), the latter of which can also infect humans. The former can cause septicemia, enterocolitis, pneumonia and/or hepatitis whereas the latter only results in mild enterocolitis. Understanding the porcine systemic transcriptional response to SC and ST has significance for both animal disease resistance and human food safety. Mesenteric lymph nodes tissue (MLN; n=3) was collected from uninfected controls as well as MLN from pigs infected for 48 hours or for 21 days with each *S. enterica* serotype. The porcine Affymetrix microarray chip, which contains 23,937 probe sets were used to hybridize with MLN RNA. At the acute phase, 48h post-infected with SC, 1014 genes showed differential expression ( $p < 0.01$ ; false discovery rate (FDR) = 5 %; fold change > 2), while at the chronic phase (21d), 163 genes were differentially expressed ( $p < 0.01$ ; FDR = 13 %; fold change > 2). At 48h post-infection with ST, 126 genes showed differential expression ( $p < 0.01$  level; FDR = 21.9 %; fold change > 2); for the 21d post-infection, there are 133 genes differentially expressed ( $p < 0.01$ ; FDR = 16 %). The host specific response at the same time course in two Salmonella infection were compared and results showed that at 48h post-infection, 33 genes were differentially expressed in both SC and ST studies, while only 6 genes showed differential expression at 21d post-infection (both  $p < 0.01$ ). Functional classification revealed that these differentially expressed genes are involved in the DNA, RNA and protein binding genes, immune responsible genes, ubiquitin-proteasome pathway genes, apoptosis genes and some hypothetical protein genes. Some important genes will be selected to confirm their expression profile by the Q-PCR. This data is the first step to help us to understand the mechanism of Salmonella-host specific response in pigs.