

Gene Expression Differences in White Blood Cells after *Escherichia coli* Infection in Chickens

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Erin Sandford, graduate research assistant, Department of Animal Science, ISU;
 Megan Orr, graduate student, Department of Statistics, ISU;
 Xianyao Li, postdoctoral research associate, Department of Poultry Science, Texas A&M University;
 Huaijun Zhou, professor, Department of Poultry Science, Texas A&M University;
 Timothy J. Johnson, professor, Department of Veterinary and Biomedical Sciences, University of Minnesota;
 Subhashinie Kariyawasam, professor, Department of Veterinary and Biomedical Sciences, Pennsylvania State University;
 Lisa K. Nolan, professor, Department of Veterinary Microbiology and Preventive Medicine, and dean, College of Veterinary Medicine;
 Peng Liu, professor, Department of Statistics, ISU;
 Susan J. Lamont, distinguished professor, Department of Animal Science, ISU

Summary and Implications

Avian pathogenic *Escherichia coli* (APEC) infections are detrimental to the poultry industry. White blood cells (WBC) are important in the fight against infection. Global gene expression of WBC in response to APEC infection was measured by microarray. A large number of differences in expression were detected between chicks with a severe response to infection and chicks with either a mild response or non-challenged chicks. A large number of immune response genes including receptors and antibacterial genes experienced expression differences. The genes and pathways identified in this microarray study form the basis for understanding host response to APEC infection and may lead to targets for genetic improvement of resistance to disease.

Introduction

APEC infections result in welfare issues for producers and losses of millions of dollars of production. The pressure to reduce use of antibacterial drugs in farm animals requires greater reliance on genetics for disease resistance. Very little is currently known about how the chicken responds to APEC infection. Microarray technology allows for the assessment of expression levels of thousands of genes, allowing for new insight into response to infection.

Materials and Methods

Commercial male broiler chicks were purchased at 1 day of age. At 2 weeks of age, chicks were either

vaccinated or non-vaccinated against APEC. At 4 weeks of age, chicks were either challenged or non-challenged with APEC. At 1 and 5 days after challenge, blood was collected, chicks euthanized and internal lesions scored to assign pathology. Non-vaccinated, challenged chicks were split by pathology, designated by mild or severe lesions. This created ten unique groups (Figure 1).

White blood cells were isolated from collected blood and RNA isolated from 4 replicates of the 10 groups, 40 samples in total. Global gene expression was assessed by microarray analysis. A linear mixed model was used to calculate *P* values for each contrast. *P* values were converted to *q* values to control the rate of false positives. Genes were declared significant at a *q* value < 0.05.

Results and Discussion

Five contrasts saw significant different expression between treatment groups (Table 1). Most of these contrasts involved the chicks with severe pathology. Vaccination did not significantly impact gene expression, but was able to significantly reduce observed lesions. Many genes related to immune response were found to be significant. In the contrast between pathologies, several immune receptors, Toll-like receptors and cytokine receptors, were more highly expressed in the severe pathology. The avian beta-defensin gene family, antibacterial genes, was only significant between the severe pathology and the non-vaccinated, non-challenged group on day 1, with greater expression in the severe pathology.

Greater knowledge about how the host responds after infection can form the foundation for targeted gene studies. These results demonstrate the importance of pathology in gene expression responses in WBC.

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Figure 1. Flowchart of treatment groups.

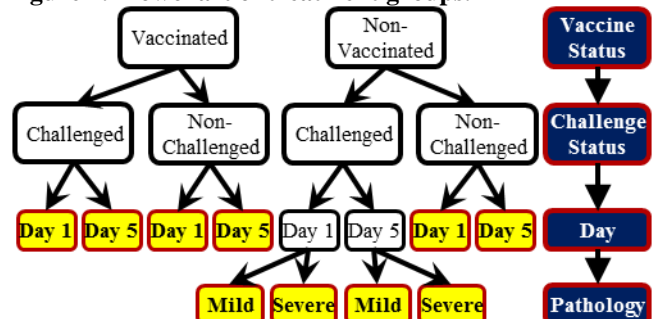


Table 1. Number of significantly differentially expressed genes between treatment groups (q value < 0.05).

Contrast	Number
Non-Vaccinated, Challenged Severe Day 5 vs. Non-Vaccinated, Challenged Mild Day 5	1914
Non-Vaccinated, Challenged Severe Day 5 vs. Non-Vaccinated, Challenged Severe Day 1	107
Non-Vaccinated, Challenged Severe Day vs. Non-Vaccinated, Non-Challenged Day 1	1097
Non-Vaccinated, Challenged Severe Day 5 vs. Non-Vaccinated, Non-Challenged Day 5	506
Vaccinated, Challenged Day 1 vs. Non-Vaccinated, Non-Challenged Day 1	7