

Genetically Distinct Chicken Crosses Differ in Splenic *Salmonella* Colonization and Cytokine RNA Expression

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Summary and Implications

Two advance intercross lines significantly differed in *Salmonella* colonization of the spleen and expression levels of splenic cytokine RNA. These genetic differences in immune response have the potential of improving disease resistance through genetic selection.

Introduction

Unsafe handling of food products can lead to food-borne illness such as salmonellosis. Reduction of microbial burden of the live animal can reduce the amount of pathogen entering the food chain. Enhancement of the immune system through genetic selection has the potential for permanent reduction in pathogen burden. Cytokines are immune signaling proteins and are essential for activation and regulation of the immune response to pathogenic challenge.

Material and Methods

Two genetically diverse chicken crosses were developed by mating an outbred broiler breeder male to females of two highly inbred and genetically diverse lines (Leghorn and Fayoumi). The resulting offspring of each cross were intermated through eight generations producing F8 Advanced Intercross Lines (AIL) of broiler-Leghorn or broiler-Fayoumi origin. At one day of age, 90 chicks from the AIL-F8 generation were either orally challenged with pathogenic *S. enteritidis* or mock challenged with culture medium. At one week of age, chicks were euthanized. The number of *S. enteritidis* in the spleen was determined and spleen tissue was collected for RNA isolation.

The relative expression of four cytokines [Interleukin (IL)-1 β , IL-4, Monocyte Chemoattractant Protein (MCP) and Regulated on Activation, Normal T Expressed and Secreted (RANTES)] were measured by quantitative Polymerase Chain Reaction (qPCR). Level of RNA expression was reported as the Ct value-the point at which the PCR reaction synthesized enough DNA to meet a preset threshold level.

The contribution of chicken cross, *S. enteritidis* challenge, and sample day on *S. enteritidis* burden and cytokine RNA expression levels were analyzed statistically.

Results and Discussion

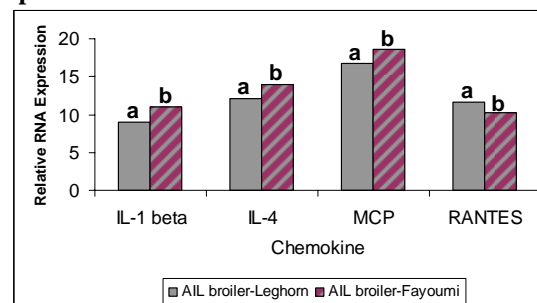
There was significantly ($P < 0.01$) more *S. enteritidis* colonizing the spleens of broiler-Fayoumi cross chicks at one week post-challenge than chicks of the broiler-Leghorn cross. This difference in *S. enteritidis* colonization between two genetic crosses suggests a genetic component of the host immune response to *S. enteritidis*, which arises from differences contributed by Leghorn versus Fayoumi lines.

The broiler-Leghorn cross expressed higher levels of IL-1 β (pro-inflammatory), IL-4 (B-cell activation, anti-inflammatory) and MCP (macrophage activation) RNA than the broiler-Fayoumi cross, while the broiler-Fayoumi cross expressed higher levels of RANTES (pro-inflammatory) than the broiler-Leghorn cross (Figure 1). A comprehensive immune response involves both innate (MCP, RANTES) and acquired (IL-1 β , IL-4) immunity, and is balanced for both pro- and anti-inflammation. The genetic line differences in cytokine RNA expression levels suggest that alternate host immune response pathways may be utilized by the two lines in host immune defense against *S. enteritidis*. This information may lead to more effective genetic selection to improve innate resistance to colonization with food-safety pathogens.

Acknowledgements

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Figure 1. Relative level of cytokine RNA expression in spleens from chickens of two distinct crosses.



Comparisons within chemokine with no common letter significantly differ ($P \leq 0.05$).