Genes for Resistance to Salmonella in Poultry

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Summary and Implications

A unique chicken resource population was used to determine that variation in several genes is associated with either resistance to colonization with the food-safety pathogen, Salmonella, or with efficiency of vaccine response to this bacterium. Knowledge of genetic variation in genes, and their associations with traits related to Salmonella response, will help to improve the wholesomeness of the food supply and to improve animal health.

Introduction

Contamination with Salmonella is one of the leading causes of food poisoning in the United States. *Salmonella enterica* serovar enteritidis (SE) can contaminate both poultry meat and eggs. Comprehensive disease control programs utilize many approaches. As consumers are increasingly objecting to use of antibiotics in animal production, the importance of alternative strategies increases. One of these strategies is enhancing the genetic resistance of animals to infection and/or colonization with disease-causing organisms. Discovering genetic associations between genes and Salmonella response traits can lead to development of molecular markers that can be used to improve the resistance of poultry to colonization with Salmonella. This will reduce morbidity in the production populations and will reduce the possibility of entry of disease-causing bacteria into the food chain.

Materials and methods

A unique resource population, the Iowa Salmonella Response Resource Population (ISRRP), was established by crossing broiler sires with dams from unrelated highly inbred lines (Leghorn and Fayoumi). Some birds were vaccinated with SE vaccine, and blood samples were later taken to measure the antibody levels as an estimate of vaccine response. Other birds, unvaccinated, were placed into biosecure facilities and challenged with live bacteria. They were humanely killed one week later, and the level of bacterial burden in the gut (cecum) and the spleen were measured by culture of the bacteria. Samples were taken from all birds to analyze the genetic material (DNA) at the molecular level.

Candidate genes, with variation originating from the broiler line, were investigated to uncover the genetic control of Salmonella response traits. The candidate genes were: inducible nitric oxide synthase (*INOS*), tumor necrosis factor related apoptosis inducing ligand (*TRAIL*), transforming growth factor beta 2 (*TGFβ2*), transforming growth factor beta 3 (*TGFβ3*), and immunoglobulin G light chain (*IgL*). Primers were designed from database sequences for the candidate genes. In other species or in other studies in chickens, these genes are reported to influence immune response. Gene fragments were amplified and sequenced. Then molecular diagnostic tests were developed to screen the resource population.

Results and Discussion

Because the inbred dam lines always contributed one copy of the same allele, the heterozygous sire allele effects could be assessed in the F1 generation (Table 1). Association analyses revealed significant effects of sire allele of *TRAIL* on spleen SE bacterial load. Significant effects were found on cecum bacterial load for *TRAIL* and *TGF*β*3*. Moderate to highly significant association was found for SE vaccine antibody response for all genes. This is the first reported study on the association of *INOS*, *TRAIL*, *TGFβ2*, *TGF*β*3*, and *IgL* with chicken response to SE. Identification of candidate genes to improve immune response may be very useful for genetic marker-assisted selection to enhance disease resistance.

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Table 1. Associations between *INOS, TRAIL, TGFβ2, TGFβ3* and *Ig* genes and SE respones.

	P values		
	Bacterial Load		
Gene	Spleen (N[1])	Cecum (N)	Vaccine Antibody (N)
INOS	0.15	0.57	0.21
	51	51	134
TRAIL	**0.07**	**0.0002**	0.20
	12	**12**	68
IgL	0.90	0.24	**0.05**
	36	36	**77**
TGF-β2	0.90	0.90	**0.07**
	45	45	**119**
TGF-β3	0.92	**0.04**	0.17
	40	**40**	34

[1] N=number of phenotyped F1 offspring of sires heterozygous for SNP evaluated for this gene.