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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 a biological gene cluster is associated with either resistance to colonization with the food-safety pathogen, Salmonella, or with efficiency of vaccine response to this bacterium. Examination of sequence variations within genes and their associations with Salmonella response traits will help to improve the safety of food and increase animal well-being.

Introduction

Salmonella, a food-borne bacterial pathogen, detrimentally affects animal and human health. *Salmonella enterica* serovar enteritidis (SE) is one of the most common serotypes of Salmonella in the US and can contaminate both poultry meat and eggs. With increasing concerns about the use of antibiotics in animal production, alternative strategies must be considered. One of these strategies is enhancing the genetic resistance of animals to infection and/or colonization with disease-causing organisms through natural variations in the animals. Discovering genetic associations between genes and Salmonella response traits can identify molecular markers that can be used to improve the resistance of poultry to colonization with Salmonella. This will increase animal health in the production populations and will reduce the potential for entry of disease-causing bacteria into the food chain and production systems.

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. One week later, 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 non-inbred broiler line, were investigated to uncover the genetic control of Salmonella response traits. The candidate genes were: *Gallinacin* 2 (*Gal2*), *Gallinacin* 3 (*Gal3*), *Gallinacin* 4 (*Gal4*), and *Gallinacin* 5 (*Gal5*), and *Gallinacin 7* (*Gal7*). Primers were designed from database sequences for the candidate genes. These genes are reported to have a role in the immune response in chickens and are analogous to genes in other species such as humans. Gene fragments were amplified and sequenced. Then molecular diagnostic tests were developed to screen the resource population.

Results and Discussion

Heterozygous sire allele effects could be examined in the F1 generation due to the resource population design, in which the inbred dam lines always contribute one copy of the same allele. Association analyses revealed significant effects of sire allele of *Gal3* and *Gal7* on SE vaccine antibody response (Table 1). Moderate association was found for SE vaccine antibody response and *Gal5*. Moderate association of *Gal2* variation was found with spleen bacterial load, and of *Gal3* and *Gal5* with cecum bacterial load. This is the first demonstration of an association of a *Gallinacin* gene SNP with SE response in poultry. Identification of candidate genes to improve immune response may be useful for genetic marker-assisted selection to enhance disease resistance.

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Table 1. Associations between *Gallanacin* genes and SE responses in chickens.

	P values		
	Bacterial Load		
	Spleen	Cecum	Vaccine Antibody
Gene	N[1]	N	N
Gal2	0.10	0.26	0.66
	65	65	74
Gal3	0.57	0.12	0.03
	116	114	84
Gal4	0.24	0.45	0.79
	63	63	26
Gal5	0.45	0.13	0.11
	126	127	68
Gal7	0.72	0.19	0.02
	90	88	79

[1] N = number of phenotyped F1 progeny from sires that were heterozygous for the SNP evaluated for this gene.