

## POULTRY

### **Evaluation of *Salmonella* Reduction in Broilers from Breeders Vaccinated with Live and Killed *Salmonella*: A Field Study** (S.D. Young, O. Olusanya, K.H. Jones, T. Liu, K.A. Liljebjelke, and C.L. Hofacre)

*Salmonella* reduction in broilers from commercial broiler breeders vaccinated with live and killed salmonella vaccines was evaluated. Broiler breeders were vaccinated with Poulvac ST (Fort Dodge, Overland Park, KS) live *Salmonella typhimurium* vaccine at day of age and then repeated at 2 and 6 weeks of age. The breeders were then administered a killed autogenous vaccine, containing *S. kentucky*, *S. heidelberg* and *S. hadar* (Merial, Gainesville, GA), at 10 and 18 weeks of age. Between the ages of 36-52 weeks of age, eggs from the breeder flocked were hatched and progeny were challenged at day of age by oral gavage with either  $1 \times 10^6$  cfu/chick in 4 separate experiments by either *S. kentucky*, *S. heidelberg*, *S. hadar*, or *S. enteritidis* each containing resistance to naladixic acid at 32 µg/ml. At 17-21 days of age, the broilers were sacrificed and one side of the cecum was cultured for *Salmonella* and the other side of the cecum was used for enumeration on positive samples. *Salmonella* was confirmed by O-antisera grouping. This study indicated a difference in *Salmonella* incidence and enumeration between the vaccinated and non-vaccinated breeder groups for certain species. When challenged with serotypes *S. kentucky*, *S. hadar* and *S. heidelberg*, protection was noted with a reduction of 28%, 17%, and 11%, respectively, when compared to the control groups. However, protection was not seen when challenged with *S. enteritidis*. Under the conditions of this study, live and killed vaccination of commercial broiler breeders with *Salmonella* contributes some protection to progeny when challenged at day of age.

### **THE MICROBIAL COMMUNITY STRUCTURE OF THE CHICKEN INTESTINE** (M.D. Lee)

The intestinal microbiota is composed of a complex bacterial community that is influenced by the host's age, physiology, and diet. Consequently, the microbial community structure is important in the maintenance of intestinal health. The long-term goal of our research is to identify the mechanisms involved in the interaction between the bacterial intestinal communities and intestinal health. Colonization with certain bacterial species is necessary for normal development of the mucosa and mucosal immune responses. Compositional analysis of bacterial communities is increasing in interest because of new technologies that enable broad surveys of diverse environments. There are 2 methods used to assay the composition of microbial communities. The culture method is recognized to have significant weaknesses due to the inability to culture many of the abundant organisms in some environmental samples. A molecular method, analysis of 16S rRNA genes present among the community DNA, is currently used because of this gene's discriminatory ability in identifying bacteria to the genus, and frequently species, level.

Using this molecular approach, we have characterized the bacterial community of the intestine of chickens fed a corn-soy diet over a standard commercial grow out period. In this study, we sequenced 1200 clones obtained from the community DNA of the ileum and cecum of broilers at different ages. The cecum contained a very high diversity of lactobacilli and clostridia as well as streptococci, enterococci, proteobacteria, and *Bacterioides*. We detected many species of bacteria in each cecal community DNA library and the abundance of each ranged from 1-56% of the total clone population. The ileum contained some of the same phylotypes of bacteria as the cecum, however, the diversity and abundance was much different with the ileal community being dominated by lactobacilli. The composition of the community also varied considerably by age of the bird. In addition, the *Clostridiaceae* were significantly abundant in

the ileum during all sampling times, however, the birds did not exhibit any gross signs of intestinal inflammation.

A molecular approach to characterizing the microbial community of the intestine is revealing weaknesses in our view of the bacteria composing this community. We have commonly viewed the clostridia as pathogens and have failed to evaluate their potential role as intestinal symbionts. A reevaluation of the composition of the commensal community of the chicken will aid in new paradigms of evaluating intestinal health and probiotic formulation.

