

ANTIBIOTIC RESISTANCE

FOLLOWING DRUG-RESISTANT *SALMONELLA* THRU THE FOOD CHAIN: A MOLECULAR ECOLOGY APPROACH. (J.J. Maurer)

Antibiotic resistance has become an important food safety issue with the emergence of multi-drug resistant *Salmonella enterica* Typhimurium and Newport. There are several factors that impact on the emergence and maintenance of multi-drug resistance including: 1) antibiotic resistance gene reservoir; and 2) fitness cost. We collected poultry litter from commercial broiler chicken houses and isolated gram-negatives and *Salmonella*. Microbial DNA was isolated from poultry litter and integron associated antibiotic resistance genes were quantified. Poultry litter microflora was used to reconstitute the microflora of one day-old, commercial broiler chickens colonized with *S. ser* Typhimurium Nal^r, Rif^r T1 strain \pm integron. *Salmonella* and antibiotic resistant gram-negatives were enumerated from poultry litter by plating on MacConkey agar supplemented with various antibiotics. *Salmonella* isolated from bird pens were genetically typed by PFGE and screened for several antibiotic resistance genes. Antimicrobial susceptibilities were determined by standard, NCCLS approved methods. There was a significantly large reservoir of integron-associated antibiotic resistance genes in poultry litter, including gram-positive bacteria. Despite this large gene load, there was significant disparity in antibiotic resistance phenotype/genotype of litter *Enterobacteriaceae*. In birds experimentally colonized with *Salmonella*, a greater diversity of antibiotic resistance phenotypes/genotypes in *Salmonella* were associated with birds challenged with integron-positive *S. enterica* T1 strain. However, this *S. ser.* Typhimurium T1 strain lost its resident class 1 integron and was present in poultry litter at levels 2-3 logs less than integron-minus, T1 strain. There is a significantly large reservoir of integron-associated drug resistance genes in the poultry environment and ample opportunities for *Salmonella* to acquire these resistance genes. However, antibiotic resistance carriage may severely impact on *Salmonella*'s fitness in this environment.

Poultry a Food Animal Model for Following Antimicrobial Resistant Enterococci. (J.J. Maurer)

With FDA approval of the streptogramin, Synercid for treating vancomycin-resistant enterococci (VRE), there have been concerns that veterinary use of another streptogramin, may compromise the effectiveness of Synercid to treat VRE infections. However, we do not know if or how virginiamycin usage in food animals impacts on the microflora and resident resistance gene pool present on finished, food product. For three commercial, broiler chicken farms participating in this study, poultry houses were paired into two groups, houses that did not receive growth promoting antibiotics in feed, and those that received virginiamycin. The participating poultry company does not use virginiamycin. Litter was collected from houses and carcasses obtained from processed flocks. Total microbial community DNA was extracted from poultry litter and carcass rinses using soil DNA extraction kit. Composition of the microbial community was determined using terminal restriction fragment length polymorphism (T-RFLP) analysis of 16S rDNA. Streptogramin, macrolide, and tetracycline resistance genes, as well as class 1 integrons were identified from microbial community DNA by PCR. There were no discernable changes in the major bacterial populations in response to virginiamycin. However, there were intra- and inter-farm differences in TRFLP profiles. Streptogramin resistance genes *vatA*, *vatB*, and *vatE*, macrolide-lincosamide-streptogramin B (MLS) resistance genes *ermA* and *ermB*, and tetracycline resistance gene *tetM* were present in microbial community of poultry litter. Only *ermB* and class 1 integrase *intI1* was present consistently among microbial communities present in litter and broiler carcass for the three poultry farms. There was intra- and inter-farm variability in the distribution of *vatA* and *vatE* among litter microbiota. However, there were no differences in their distribution with regards to virginiamycin usage.

Virginiamycin usage does not appear to cause major changes in microbial community structure or affect presence of streptogramin and streptogramin-related resistance genes.

