

## ANTIBIOTIC RESISTANCE

### ANTIMICROBIAL RESISTANCE IN *CAMPYLOBACTER JEJUNI* IN POULTRY (M. D. Lee, U. Idris, A. Fairchild, J. J. Maurer, S. Sanchez, and C. Hofacre)

*Campylobacter jejuni* is the most common cause of sporadic bacterial enteritis in the United States. Consumption of undercooked poultry has been identified as a significant risk factor. Antibiotic-resistant *Campylobacter* have recently been of concern because of their resistance to fluoroquinolone antibiotics, the drugs of choice for treating infections. While resistance to quinolones is mediated by point mutations in their DNA gyrase, resistance to other antibiotics requires their acquisition of specific resistance genes from the microbiota present on the farm. We examined the population dynamics of *Campylobacter* on a poultry farm with regards to drug resistance. The antibiotic-resistance of *C. jejuni* did not appear to correlate with treatment history of the flock. Tetracycline-resistant isolates were commonly cultured but none of the isolates were collected from treated flocks. In contrast, *Campylobacter* cultured from an oxytetracycline-treated flock did not show an increase in resistance. Similar results were seen among fluoroquinolones-resistant isolates cultured from the flocks. A more thorough examination of the strain types present on each farm may illuminate the source of the resistant isolates.

### ANTIMICROBIAL RESISTANCE OF INTESTINAL COMMENSAL BACTERIA FROM POULTRY (M. D. Lee, J. Smith, A. Fairchild, J. J. Maurer, S. Sanchez, and C. Hofacre)

Commensal bacteria of the intestine are believed to serve as a reservoir of resistance genes that may be transferred to pathogenic bacteria. Many resistance genes reside on mobilizable elements and pathogens can acquire these elements by conjugation or transformation while transiently passing through the intestine. We have investigated the prevalence of common resistance elements, such as integrons and tetracycline resistance genes, among intestinal microflora of chickens. Integrons are often present at a high prevalence (> 50% of isolates) among commensal *E. coli*. Although some integrons do not appear to contain resistance cassettes, most of the integrons contained a streptomycin resistance gene and most *E. coli* isolates were streptomycin-resistant. Similarly tetracycline resistance genes are found and are expressed at a high prevalence among *E. coli* and *Enterococcus* species isolated from the chicken intestine. Some of the *tet* determinants that are present on transposons, *Tn10* and *Tn916* for example, may therefore conceivably be transferred among many genera present in the intestinal microflora.

### HEMOLYTIC AND NON-HEMOLYTIC VANCOMYCIN-RESISTANT *ENTEROCOCCUS FAECALIS* FROM BEEF IMPORTED TO MALAYSIA (N. Fifadara, S. Radu, Z. Hassan, L. R. Beuchat, and G. Rusul)

Reservoirs for antibiotic resistant enterococci have been described. There are two suspected routes of origin of vancomycin-resistant enterococci (VRE). One is from clinical sources resulting from the use of vancomycin in human therapy. Another source is foods of animal origin. Of the VRE isolated from food animal sources, most of the parent vancomycin-susceptible strains were originally endogenous and nonpathogenic to animals. When animals consume avoparcin-supplemented feeds, vancomycin-susceptible strains may undergo selection for resistance to the antibiotic. Vancomycin resistant strains may not necessarily be pathogenic because the genes for vancomycin resistance and virulence may be different. Resistant strains can serve as a reservoir pool for vancomycin-resistant genes at the interspecies, intraspecies, and genus level.

*Enterococcus faecalis* is an opportunistic human pathogen, and a significant percentage of clinical isolates are hemolytic. Various factors have been shown to contribute to virulence. Only a few studies have been done to determine phenotypic and genotypic relationships of VRE originating from foods of animal origin. Beef is a major food of animal origin in Malaysia and most beef products are imported. This study was undertaken to survey frozen beef and beef products imported to Malaysia for the presence of VRE. The VRE isolates were characterized for resistance to antibiotics, hemolysin production, plasmid profile, and genetic diversity by random amplified polymorphic DNA (RAPD) analysis.

Twenty-two strains of vancomycin-resistant *Enterococcus faecalis* were isolated from 9 of 150 (6%) samples of frozen beef and beef products imported to Malaysia. Isolates were from eight samples of frozen beef and one sample of minced beef patties. None was isolated from frankfurters. Twelve of the 22 isolates (54.5%) were  $\beta$ -hemolytic and all isolates harbored the *vanA* gene. All vancomycin-resistant isolates were also resistant to streptomycin, erythromycin, kanamycin, bacitracin, ceftazimide, gentamycin, tetracycline, nalidixic acid, and teicoplanin; 95.4% were resistant to trimethoprim-sulfamethoxazole, 68.8% were resistant to chloramphenicol and 41% were resistant to ampicillin and penicillin. Small plasmids ranging from 1.5 to 5.8 Kb were detected in 8 of 22 (36.4%) strains. The 22 isolates were differentiated into twenty RAPD-types. Isolates segregated into two groups, each with subclusters, which may reflect clonal lineage. It is concluded that several clones of vancomycin-resistant *E. faecalis* are represented in the isolates from beef imported to Malaysia.

