

CAMPYLOBACTER JEJUNI

**CAMPYLOBACTER SPP. ENUMERATION IN BROILER FECES AND PROCESSED CARCASSES
(N. J. Stern and M. C. Robach)**

Enumeration of *Campylobacter* spp. on Campy-Cefex agar from 50 carcasses, before and after chilling, was conducted in both 1995 and 2001. One day prior to processing, feces were also collected from each of the broilers for enumeration. A significant reduction in the levels of the organism on freshly processed broiler carcasses was observed from 1995 ($10^{4.11}$ cfu/carcass) to 2001 ($10^{3.05}$ cfu/carcass). Levels of *Campylobacter* spp. found in production and processing were not strongly correlative and suggested the existence of complex parameters involving production factors and variables associated with flock transport and the processing of the broilers.

**RELATIONSHIP OF CAMPYLOBACTER SPP. IN ICELANDIC POULTRY OPERATIONS
AND INCIDENCE OF HUMAN CAMPYLOBACTERIOSIS**

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Domestic cases of human campylobacteriosis in Iceland during 1999 reached peak levels of 116 cases per 100,000 population. Over the same period, 62% of broiler carcass rinses were contaminated with *Campylobacter* spp. The incidence of campylobacteriosis in humans decreased to 33 cases per 100,000 population in 2000, and only 15% of the broiler flocks tested *Campylobacter* spp. positive. Several factors account for the large reduction in poultry-borne campylobacteriosis and include public education, enhanced on-farm biological security measures, and carcass freezing. Additional information is being sought to understand the decline in campylobacteriosis such that a risk model for *Campylobacter* spp. transmission may be generated for this well-defined system.

**GENOTYPE ANALYSES OF CAMPYLOBACTER ISOLATED FROM THE GASTROINTESTINAL TRACTS
AND THE REPRODUCTIVE TRACTS OF BROILER BREEDER ROOSTERS**

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The pathways involved in *Campylobacter* contamination of poultry flocks, horizontal transmission and/or vertical transmission, remain unclear. In this study, *Campylobacter* isolated from feces, cloacal swabs, ceca, semen, and vas deferens of 12 breeder roosters were genotyped by both flagellin A short variable region (*flaA* SVR) DNA sequence analysis and repetitive element (rep)-polymerase chain reaction (PCR). *Campylobacter* was isolated from multiple sites in 9 of 12 roosters. *Campylobacter* isolated from five of the nine roosters demonstrated closely related M SVR DNA sequences as well as rep-PCR patterns. These isolates were collected from both the gastrointestinal and the reproductive tracts or from the gastrointestinal tract alone. Isolates from two of the remaining four roosters originated from both the gastrointestinal tract and the reproductive tracts and were distinct by both typing methods. Distinct isolates from the remaining two roosters originated from only the reproductive tract. No relationships between the genotypes and the sample type could be determined. Additional studies will need to be conducted to determine if the presence of *Campylobacter* within the rooster leads to contamination of the broiler offspring via the fertilized egg.

**INTESTINAL CARRIAGE OF CAMPYLOBACTER AND SALMONELLA IN TURKEYS
IN RESPONSE TO SUB-THERAPEUTIC LEVELS OF ANTIMICROBIALS IN FEED
(N. A. Cox, S. E. Craven, M. T. Musgrove, M. E. Berrang, and N. J. Stern)**

Since the 1950s, antimicrobials have been added to poultry feed at sub-therapeutic levels to minimize illness and promote growth. Despite the benefits to the agricultural industry and domestic animals, there are fierce debates worldwide on whether or not this practice carries a consequence in terms of human health. Turkeys and broilers provided these additives have increased weight gain, muscle yield, and feed conversion, in part due to decreases in

diseases such as coccidiosis and necrotic enteritis. Benefits achieved by adding these compounds to animal feeds are attributed in part to a shift in the gut microflora. However, studies have been published in which it was determined that competitive exclusion cultures, administered to birds to control colonization by human pathogens such as *Salmonella*, can be negatively affected by antimicrobials commonly used in poultry rations. Other published studies have reported an increase in *Salmonella* levels when experimentally challenged birds were fed diets containing low levels of antimicrobials. This study demonstrated that although naturally occurring populations of *Campylobacter* were virtually unaffected by antimicrobial feed additives, *Salmonella* populations were significantly decreased when commercial turkeys were fed rations containing flavomycin, virginiamycin, or monensin.

**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.

**DIRECT MICROSCOPIC OBSERVATION AND VIABILITY DETERMINATION
OF *CAMPYLOBACTER JEJUNI* ON CHICKEN SKIN
(W. Chantarapanont, M. Berrang, and J. F. Frank)**

The objective of this study was to develop a method to determine survival of *Campylobacter jejuni* at specific sites on chicken skin and to use this method to observe survival of *C. jejuni* at various locations on the skin during storage. This method employs confocal laser scanning microscopy (CSLM) to visualize *Campylobacter jejuni* transformed with a green fluorescent protein plasmid (GFP-*Campylobacter*) and stained with 5-cyano-2,3-ditolyl tetrazolium chloride (CTC). The green fluorescence of *C. jejuni* cells and the red fluorescent CTC-formazan in viable *Campylobacter* cells were clearly visible on chicken skin. GFP-*Campylobacter* remaining on the chicken skin surface after rinsing were mostly located in crevices, entrapped inside feather follicles with water, and entrapped in the surface water layer. Most viable cells were entrapped with water in the skin crevices and feather follicles. These sites provide a suitable microenvironment for GFP-*Campylobacter* to survive. The population of *C. jejuni* on chicken skin decreased by 1 log₁₀ unit during storage at 25°C for 24 h. *Campylobacter jejuni* located in sites 20-30 μm beneath the chicken skin surface maintained viability during incubation at 25°C. *C. jejuni* on chicken skin stored at 4°C maintained constant numbers during 72 h of incubation with no significant changes in population of feather follicles or crevices. Live and dead cells were initially retained with water on the skin and penetrated into skin follicles and channels during storage. Microscopic observations of GFP-producing cells allowed identification of survival niches for *C. jejuni* present on chicken skin.