P2-130 Perspectives of Real-time Monitoring of *Campylobacter* and *Salmonella* Infections in Free-range Geese for Source Tracing of Human Cases and Risk Mitigating Interventions

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Introduction: Free-range domestic poultry flocks represent challenges in terms of reducing risk of foodborne transmission of *Campylobacter* and *Salmonella* to consumers but also offer unique opportunities to study interference with environmental reservoirs and epidemiological dynamics within flocks.

Purpose: To reveal the feasibility of real-time monitoring of colonization with *Campylobacter* and *Salmonella* in terms of understanding epidemiological dynamics in free-range goose flocks, improvement of traceability of strains from primary poultry production to human outbreak, and assessment of possibilities of risk-mitigating intervention in response to colonization dynamics in management and slaughter planning.

Methods: A complex pattern of splitting and merging of flocks of free-range geese was followed throughout the life of the flocks by collection of droppings and cultivation for *Salmonella* and *Campylobacter*. Isolates of *Salmonella* were identified to the level of serotype and phage type and isolates of *Campylobacter* were preliminarily identified to the level of species by a discriminatory PCR.

Results: While colonization with *Salmonella* tended to decline in the flocks, introduction of *C. jejuni* resulted in permanent colonization in all individuals, and *C. coli* was also frequently introduced to the flock. Colonization with *Salmonella* followed different patterns in different flocks. In one flock, all individuals became infected within one week at 2 to 4 weeks of age with a single strain of *S.* Enteritidis, which once it was introduced, persisted in the flock and from levels below the detection limit was transiently detected again in feces during an incidence of pneumonia in the flock. In another flock a strain of S. Mbandaka became introduced to the flock at 9 weeks of age but it did not spread aggressively. In this flock a multiplicity of serovars transiently appeared at 27 weeks of age.

Significance: The data illustrate the challenge in tracing outbreaks of zoonotic pathogens to primary production. The differences in epidemiology of *Salmonella* in the flocks suggest that risk mitigation in organically-raised poultry flocks based on semi-continuous monitoring is feasible. Monitoring might include control of other infections as well and adequate interventions include relocation of flocks and planning of slaughter time in relation to the course of *Salmonella* infection. However, quantification of colonization in conjunction with real-time monitoring is required to reveal if this is also a possibility for *Campylobacter*.

P2-131 In vitro Assessment of Temperature- and pH-dependent Growth Patterns of *Campylobacter jejuni* and *coli*

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Introduction: Campylobacter spp. are among the main bacterial causes of acute gastroenteritis worldwide. Despite their fragile nature, they survive in the environment and food chain, likely overcoming several stressful challenges. However, little is known about their response to adverse conditions.

Purpose: This study was conducted to investigate the survival of *Campylobacter jejuni* and *coli* at various temperatures (32, 37, 42, and 47°C) and pH ranges (5, 7, and 9) in laboratory media.

Methods: Strains of *C. jejuni* and *C. coli* were cultured separately in tryptic soy broth (TSB). In order to adapt bacteria to a mild stress, broth cultures were further inoculated in TSB at pH 6 and 8. After 24 h, the pH 6 culture was inoculated in TSB at pH 5, while the pH 8 culture in TSB at pH 9. Aliquots of these broths were incubated at 32, 37, 42 and 47°C and a pH 7 culture was used as control. Samples were taken at 0, 2, 4, and 24 h, spread plated onto Campy Cefex agar, and incubated for 48 h at 42°C.

Results: Extreme thermal and pH conditions (i.e., 32 and 47°C, pH 5 and 9, respectively) resulted in variable behavior of *Campylobacter* spp. Although *C. jejuni* and *C. coli* populations at pH 5 and 9 were significantly ($P < 0.05$) lower than those at pH 7, the survival populations still remained high at approximately 6 $\log_{10}$ CFU/ ml. Temperature (37 and 42 °C) did not affect ($P > 0.05$) the growth patterns of *Campylobacter* spp. and no interactions between strain, pH, incubation temperature, and sampling time were detected.

Significance: Results suggest that *C. jejuni* and *C. coli* do not respond well to multiple stresses, but have the ability to adapt to low and high pH. Therefore they can resist typical sanitation practices and persist in the environment leading to human illnesses.

P2-132 Analysis of *Campylobacter jejuni* Whole Genome DNA Microarrays: Significance of Prophage and Hypervariable Regions for Discriminating Isolates

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Introduction: Campylobacter jejuni is a major cause of gastroenteritis in humans and is carried in many common food animals. In order to reduce human infections, a better understanding of *Campylobacter* epidemiology is needed. Identifying genes that enable discriminating between isolates is an important factor in filling this need. A useful technique for this purpose is comparative genome indexing (CGI) using whole genome DNA microarrays.

Purpose: The objective of this study was to use CGI to identify the genes that were most significant for discriminating isolates of *C. jejuni* from humans, chickens, and beef cattle.

Methods: A geographically diverse population of 95 *C. jejuni* strains was selected from a collection of human, cattle and chicken isolates. Genomic DNA from each isolate was labeled and hybridized to microarrays composed of *C. jejuni* strains NCTC 11168 (human; UK, 1980) and RM 1221 (chicken; U.S., 2000) genes. The SAS program was used to analyze the presence or absence of genes and determine which variable genes were most informative.

Results: Statistical analyses of whole genome data from 95 geographically diverse cattle, chicken and human *C. jejuni* isolates identified a total of 142 most informative (i.e., significantly variable) genes. Of this total, 125 (88%) belonged to genomic prophage and hypervariable regions. Prophage and hypervariable genes were identified in isolates from all 3 hosts but were especially common in human isolates.

Significance: The significance of genomic prophage and hypervariable regions in determining *C. jejuni* isolate genomic diversity is emphasized by these results. These genes should prove useful in the development of a more efficient genotyping system for *C. jejuni* as well as furthering our understanding of the epidemiology of this major foodborne pathogen.