Project number: 5427
Funding source: Safefood 04-RESR-04

Date: June, 2011
Project dates: April 2006 – Sept 2009

Campylobacter control on broiler farms

Key external stakeholders:

Poultry farmers, poultry processors, scientists, regulatory personnel, medical doctors, veterinarians, epidemiologists, microbiologists, consumers, EFSA

Practical implications for stakeholders:

Up-to-date information on sources of *Campylobacter* on broiler farms will facilitate improvements in biosecurity. New information on antibiotic resistance will be used to assess the likely success or otherwise of different control strategies.

Main results:

Adjacent cattle and transport crates used during thinning are important sources of *Campylobacter* in broiler houses. Quinolone and macrolide antibiotic resistance in Irish *Campylobacter* isolates is mutation based.

Opportunity / Benefit:

This project provides data for risk analysis that may be used to provide the scientific basis for improved biosecurity of broiler farms and in the formulation of strategies to control the emergence and dissemination of antibiotic resistance determinants in *Campylobacter*.

Collaborating Institutions:

University College Dublin and Cork County Council.

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Teagasc project team: Dr. Declan Bolton (PI)

External collaborators: Prof. Seamus Fanning (University College Dublin) and Mr. Jim Buckley (Cork County Council).

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1. Project background:

Campylobacter is the most commonly reported food-borne bacterial pathogen in Ireland and in Europe and the incidence of campylobacteriosis is growing year on year thus constituting an increased burden on public health services. As poultry is the largest source of *Campylobacter* for human populations, it appears that programmes aimed at reducing the incidence of *Campylobacter* carriage in poultry are falling short of expectations. A significant reduction in prevalence at flock level could have a considerable impact on prevalence rates in consumer products. Research was therefore undertaken to identify sources of *Campylobacter* on broiler farms that could be specifically targeted as part of enhanced biosecurity measures.

In the last decade antibiotic resistance in *Campylobacter* has emerged and spread rapidly. Many studies have attributed this resistance to the use of antimicrobial agents in poultry production. Regardless control of the emergence and dissemination of antimicrobial resistance in *Campylobacter* requires a fundamental understanding of the molecular basis of the observed phenotypes. Studies were therefore undertaken to establish the molecular basis of quinolone and macrolide resistance in Irish *Campylobacter* isolates.

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2. Questions addressed by the project:

- What are the main sources of *Campylobacter* on broiler farms?
- What are the main routes of dissemination?
- What is the molecular basis of observed quinolone and macrolide antibiotic resistance in *Campylobacter* isolates?

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3. The experimental studies:

Farm surveys were undertaken on 3 broiler farms over the course of 12 months. A total of 1,480 samples were collected and processed in the laboratory using conventional methods and a method for the identification of emerging species of *Campylobacter*. All isolates were speciate and genotyped using MLST and *flaA*-SVR typing. All isolates were screened for antibiotic resistance and the molecular basis of observed quinolone and macrolide resistance determined using PCR and gene sequencing methods.

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4. Main results:

Similar MLST genotypes were isolated from poultry in the broiler house, on transport crates and in cattle in an adjacent field. High-level resistance to quinolones (nalidixic acid) was attributed to amino acid substitutions Thr-86-Ile and Asn-203-Ser in GyrA in some but not all isolates. Strains displaying a high-level of resistance to macrolides (erythromycin) carried the 23S rRNA transition mutation A2075G and/or carried mutations in the L4 and /or L22 ribosomal-encoding proteins.

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5. Opportunity/Benefit:

The data generated in this research should be used to revise current biosecurity measures on broiler farms. Our research also supports the hypothesis that quinolone and macrolide antibiotic resistance in *Campylobacter* is mutation based. While this trait may not be transferred horizontally from one organism to another, it is relatively stable in the *Campylobacter* population and can be passed vertically between parents and offspring cells. The use of antibiotics during food production will confer a selective pressure promoting the survival and proliferation of resistant strains while susceptible organisms are eliminated from the microflora with inevitable adverse consequences for therapeutic intervention (in severe cases) and public health.

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6. Dissemination:

Dissemination was primarily achieved through peer reviewed publication and presentation at national and international conferences including:

Bolton, D. Patriarchi, A. and Fanning, S. (2011) The molecular basis for antibiotic resistant Campylobacter phenotypes from intensive poultry flocks. Oral presentation at the 16th International Campylobacter, Helicobacter and Related Organisms (CHRO) 2011 Conference, 28th August to 1st September, Vancouver, Canada, Abstract A148, page 89.

Main publications:

Patriarchi, A., Maunsell, B., Fox, Á., Fanning, S. and Bolton, D. (2009) Prevalence of *Campylobacter* spp. in a subset of intensive poultry flocks in Ireland. Letters in Applied Microbiology, 49 (3) 305-310.

Patriarchi, A., Maunsell, B., Fox, Á., Fanning, S. and Bolton, D. (2011) Molecular characterisation and environmental mapping of *Campylobacter* in a subset of intensive poultry flocks in Ireland. Foodborne Pathogens and Disease 8 (1), 99-108.

Bolton, D., Patriarchi, A., Fox, Á. and Fanning, S. (2012) The Molecular Basis for Antibiotic Resistant *Campylobacter* Phenotypes from Intensive Poultry Flocks. Food Control (submitted).

7. Compiled by: Dr. Declan Bolton