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Public health significance of emergent *Campylobacter* species in the Irish food Chain



Key external stakeholders:

Pork industry, poultry industry, public health laboratories, Food Safety Authority of Ireland

Practical implications for stakeholders:

Campylobacter spp. is the most common cause of bacterial food borne illness in Ireland. It was considered up the mid 2000's that infection was almost exclusively linked to just two species, *C. jejuni* and *C. coli*, but new methods capable of detecting 15 other species of the pathogen indicated that these emergent species were also causing human illness. This study investigated the occurrence and human virulence potential of emergent *Campylobacter* species in Irish pork, poultry and human clinical stool samples. The key finding was that these emergent species are indeed widely prevalent in the food chain and have virulence factors which indicate their public health importance.

Main results:

- *Campylobacter* was detected in pig gut (caecal) contents (34.7 %), pre chill pork, carcasses (17 %), pork cuts (9.5%) and chicken pieces (68%) with a wide range of species present including *C. coli*, *C. jejuni*, and emergent species *C. lari*, *C. upsaliensis*, *C. mucosalis*, *C. curvus*, *C. sputorum*, *C. concisus*, *Arcobacter butzleri*, *Arcobacter Skirrowii* present across all sample types.
- *Campylobacter* was found in 4.8% of previously undiagnosed human clinical samples with emergent species *C. concisus* the second most common species recovered after known species *C. jejuni*.
- Majority of emergent species isolated had virulence genes typically found in known *C. jejuni* and *coli* giving further evidence of a link to human illness
- *Campylobacter* isolates recovered from poultry and beef were genetically identical to isolates recovered from human stools while isolates recovered from pork were less similar, indicating that the pork has less of a role in transmission of human disease causing strains than other commodities.

Opportunity / Benefit:

Advice, consultancy work and/or research can be provided by Teagasc on *Campylobacter*.

Collaborating Institutions:

Public Health Laboratory at Cherry Orchard Hospital

Teagasc project team:	Geraldine Duffy Claire Cagney Karl Scanlon
External collaborators:	Dr Eleanor McNamara, Public Health Laboratory Dr Anne Carroll, Public Health Laboratory Mr Des McNulty, Public Health Laboratory

1. Project background:

Campylobacter spp. cause more cases of food borne illness in the developed world than any other bacterium. Up to five years ago it was considered that cases of infection were almost exclusively linked to just two species, *C. jejuni* and *C. coli* and routine examination of stool samples from patients and foods only looked for these species. In the mid 2000's as a result of new methods which could detect a wider range of *Campylobacter* species evidence started to emerge from human clinical infections that other emerging species of *Campylobacter* (including *C. concisus*, *C. gracilis*, *C. curvus* and *C. upsaliensis*) and closely related *Arcobacter* spp. were appearing in human gastro-intestinal illness. For example a South African study in 2005 showed that over 60% of *Campylobacter* clinical infections were related to emergent species including *C. concisus*. However no foods had been examined to assess their role in the transmission of these emergent species. This project aimed to apply cultural and molecular methods for emergent *Campylobacter* and *Arcobacter* to assess whether these emergent species were occurring in Irish human clinical diarrhoeal samples and if they were being transmitted through the Irish food supply. The aim was then to genetically characterise the emergent *Campylobacter* isolates from clinical and food sources, to establish whether they carried the same virulence factors, seen in the more well know *C. jejuni* and *coli*. The research proposed to establish the risk posed by emergent *Campylobacter* and *Arcobacter* spp. and inform stakeholders about the food safety risk related to this group of organisms.

2. Questions addressed by the project:

- Are emergent species of *Campylobacter* transmitted through Irish pork and poultry?
- Are emergent species of *Campylobacter* present in previously undiagnosed human clinical diarrhoeal stool samples?
- Do emergent species of *Campylobacter* recovered from human diarrhoeal stools, pork and poultry have the same virulence genes as well known species of *Campylobacter* (*C. jejuni* and *C. coli*)?
- Do emergent species of *Campylobacter* have the same survival characteristics as known species which would indicate a need for particular controls?
- Is there a link between strains of *Campylobacter* isolates from human infection and any particular animal host or food?

3. The experimental studies:

Samples

Between January 2007 and December 2008, samples from the pork chain comprising gut (caecal contents) (n= 389), carcass swabs (pre chill) (n = 382) were taken at a number of Irish commercial pork abattoirs. Pork cuts (n=399) and chicken samples (n=300) were collected from retail establishments throughout Ireland. Between February 2007 and November 2008, a total of 1625 stool samples submitted to the Public Health Laboratory, Dublin from hospital and community based individuals were collected.

Microbiological analyses

All above samples were examined for *Campylobacter* using a novel cultural / molecular method developed by Teagasc (Lynch *et al*, 2010) and capable of detecting 17 different species of *Campylobacter*.

Characterisation

All emergent *Campylobacter* isolates were examined to establish their antibiotic resistance profile, and the presence of a range of virulence genes which are present in *Campylobacter* of know clinical significance (*C. jejuni*, *coli*). All isolates were then characterised by multi-locus sequence analysis and micro-arrays to characterise the genetic relatedness of *Campylobacter* isolates recovered from pork, poultry, beef and human stool samples.

Survival characteristics

The survival of emergent species when heated at a range of temperature was established as was their ability to survive on foods stored at chill temperatures.

4. Main results:

This study investigated the occurrence and human virulence potential of emergent *Campylobacter* and *Arcobacter* species in Irish pork, poultry and human clinical stool samples.

- *Campylobacter* was recovered from pork caecal contents (135/389, 34.70 %), pre chill pork carcasses (65/382, 17.0 %) and pork cuts at retail (38/ 399, 9.5%). A wide range of species were recovered including *C. coli*, *C. jejuni*, *C. lari*, *C. upsaliensis*, *C. mucosalis*, *C. curvus*, *C. sputorum* and *C. concisus* were recovered from samples taken at all stages of the pork chain but the majority of emergent species were recovered from caecal samples.
- *Campylobacter* was recovered from (204/ 300, 68%) of poultry samples at retail with a wide range of species recovered including *C. jejuni*, *C. coli*, and emergent species *C. helveticus* *C. lari*, *C. mucosalis*, *Arcobacter butzleri*, *Arcobacter. skirrowii*
- *Campylobacter* was present in human clinical samples (78/1625 (4.8%) with emergent species *C. concisus* the second most common species recovered after *C. jejuni*. In addition a number of *C. concisus* were multi-drug resistant highlighting their public health significance and potential difficulties with clinical treatment.
- The majority of the emergent isolates had virulence genes typically found in known *C. jejuni* and *coli* indicating a role in human illness
- Genetic fingerprinting (by multi-locus sequence analysis and micro-arrays) showed some isolates recovered from poultry and beef were genetically identical to *Campylobacter* isolates recovered from human stools highlighting the role of both these commodities in transmission of this pathogen. Isolates recovered from pork were less similar to those recovered from human stool samples, indicating that the pork may have less of a role in transmission of disease causing strains.
- Studies on survival of emergent *Campylobacter* when exposed to typical food borne temperature stresses indicated that emergent *Campylobacter* had similar thermal inactivation profiles and survived for similar lengths of time at chilled temperatures to known *C. jeji* and *coli* so current control applied against these two species should also be successful against the emerging species

5. Opportunity/Benefit:

The main output from this project is public good knowledge about the risk posed by an emergent group of food borne pathogens. The results give strong evidence that these emergent species are widely occurring in the food chain and in human stool samples. The results also indicated that poultry followed by beef are considerably more important sources of human clinical *Campylobacter* than pork.

Through the project, the technology for detection and characterisation of emergent *Campylobacter* was transferred from Teagasc to the Public Health Laboratory, Health Service Executive, at Cherry Orchard Hospital

6. Dissemination:

Information from the project has been widely disseminated to researchers and stakeholders

Main publications:

Lynch, O.A., Cagney, C., McDowell, D.A, and Duffy, G. (2010). A method for the growth of 17 species of *Campylobacter* and their recovery from inoculated beef, using common cultural parameters. *J. Microbiological methods* 83, 1-7

Lynch, O.A., Cagney, C., McDowell, D.A, and Duffy, G. (2011). Occurrence of fastidious *Campylobacter* spp. in fresh meat and poultry using an adapted cultural protocol. *Int J Food*; 150 (2-3):171-177

Popular publications:

Duffy, G. (2006). Clamp down on *Campylobacter*. Proceedings of Relay workshop, University

College Cork, September 7th 2006.

Cagney, C. (2007). Emerging *Campylobacter* in the food chain in Ireland. Proceedings of Relay workshop no 47. “*Campylobacter* an Irish’ perspective”, Ashtown Food Research Centre, October 24th 2007.

Mc Nulty, D (2007). Prevalence of emergent *Campylobacter* and *Arcobacter* species in the Irish food chain. Proceedings of Relay workshop no 47. “*Campylobacter* an Irish’ perspective”, Ashtown Food Research Centre, October 24th 2007.

7. Compiled by: Geraldine Duffy
