Controlling campylobacteriosis

Nigel French
and the Molecular Epidemiology and Public Health Laboratory

MAF Massey Meeting
June 2010
mEpiLab: Molecular Epidemiology and Public Health Laboratory

- Formerly half of the EpiCentre
- We work on:
  - Food safety
  - (Veterinary) Public Health
  - Surveillance
  - Molecular epidemiology of zoonoses
    - *Campylobacter*
    - VTEC (*E. coli* O157)
    - *Cryptosporidium, Giardia*
    - *Leptospira*
    - *Salmonella*
    - *...others*

http://mepilab.massey.ac.nz/default.htm
Campylobacteriosis in NZ

Figure 1. Annual number of notifications (1980–2005) and hospitalisations (1995–2005) for campylobacteriosis in New Zealand

From Baker et al 2006
An International Comparison... (A Sears)

Interventions in poultry industry demanded

Regulation of chicken contamination urgently needed to control New Zealand’s serious campylobacteriosis epidemic

Michael Baker, Nick Wilson, Rosemary Ikram, Steve Chambers, Phil Shoemack, Gregory Cook

Poultry ~ 40% of meat consumption, no imports or exports
Thu Jul 5: Campylobacter revisited; Oil rig kidnapping; The final curtain

Campylobacter
A year ago an Otago University report described fresh chicken meat as the cheap, dirty food of New Zealand. That report suggested it was largely responsible for our high rate of campylobacter infections. Researcher Dr Michael Baker even called for it to be withdrawn from sale. It made the headlines, but has anything really changed? Well, one year later Close Up put fresh chicken to the test. Paul Henry talks to Dr Michael Baker about what the results mean, and to Andrew McKenzie from the New Zealand Food Safety Authority about what steps are being taken to protect consumers from:
Manawatu sentinel surveillance site

• Interdisciplinary collaboration between:
  – MedLab Central
  – Public Health Unit
  – Human health surveillance unit: ESR
  – Regulator: NZFSA
  – Industry body: PIANZ / suppliers
  – Dairy and sheep farmers
  – Regional council
  – Institutes at Massey University
Manawatu study 2005-2010...

- Sentinel site (5 yrs)
Numbers of samples/isolates: **C. jejuni**

- **Human**: 520 (770 samples)
- **Poultry**: 562 samples 75% +ve
- **Red meat**: 1312 samples 12% +ve
- **Ruminant faeces**: 278 samples 58% +ve
- **Env. Water**: 335 samples 30% +ve
- **Wild bird**: 192 samples 13% +ve

March 1st 2005 to Feb 29th 2008
Multi Locus Sequence Typing
MLST

- PCR highly conserved genes
- 7 housekeeping genes
- Used to define:
  - ST = sequence type – unique pattern of 7 genes
  - Clonal complex = group of related STs

- Website: Oxford University
  
  http://campylobacter.mlst.net
Host associated sequence types in NZ

Ruminant associated

Poultry associated

ST 61

ST 2026

ST 422

ST 474

ST 48

ST 257

Poultry
Human
Sheep tissues
Lamb mince
Lamb liver
Cattle tissues
Beef mince
Beef liver

Number of isolates

Number of isolates

Number of isolates

Number of isolates

Number of isolates

Number of isolates
Need for good epidemiological data
EpiSurv, PHU
Molecular and spatial epidemiology of human campylobacteriosis: source association and genotype-related risk factors

Outbreak identification

Census Area Unit

Water supply regions
Identifying potential outbreaks in water supply regions
## Tararua outbreak in 2008

### Water flow

![Water flow graph](image)

<table>
<thead>
<tr>
<th>Lab ID</th>
<th>Source Type</th>
<th>ST</th>
<th>OnsetDt</th>
<th>Outbrk</th>
<th>CurrWSCode</th>
<th>CurrWSpec</th>
</tr>
</thead>
<tbody>
<tr>
<td>H775</td>
<td>Human</td>
<td>61</td>
<td>20/07/2008</td>
<td>No</td>
<td>PAH001PA</td>
<td></td>
</tr>
<tr>
<td>H791</td>
<td>Human</td>
<td>190</td>
<td>5/08/2008</td>
<td>No</td>
<td>PAH001PA</td>
<td>Muddier than usual &quot;toxic in its self&quot;</td>
</tr>
<tr>
<td>H787</td>
<td>Human</td>
<td>190</td>
<td>5/08/2008</td>
<td>No</td>
<td>PAH001PA</td>
<td>smells of dirt, brown</td>
</tr>
<tr>
<td>H788</td>
<td>Human</td>
<td>190</td>
<td>5/08/2008</td>
<td>No</td>
<td>PAH001PA</td>
<td>water been brown, &quot;crap&quot;</td>
</tr>
<tr>
<td>H804</td>
<td>Human</td>
<td>3793</td>
<td>6/08/2008</td>
<td>Yes</td>
<td>PAH001PA</td>
<td></td>
</tr>
<tr>
<td>H803 D</td>
<td>Human</td>
<td>50</td>
<td>6/08/2008</td>
<td>No</td>
<td>PAH001PA</td>
<td></td>
</tr>
<tr>
<td>H795</td>
<td>Human</td>
<td>190</td>
<td>7/08/2008</td>
<td>No</td>
<td>PAH001PA</td>
<td></td>
</tr>
<tr>
<td>H798</td>
<td>Human</td>
<td>50</td>
<td>9/08/2008</td>
<td>Yes</td>
<td>PAH001PA</td>
<td></td>
</tr>
<tr>
<td>H801</td>
<td>Human</td>
<td>61</td>
<td>9/08/2008</td>
<td>Yes</td>
<td>PAH001PA</td>
<td></td>
</tr>
</tbody>
</table>
Source attribution

- Source attribution – used 4 approaches
  - Proportional similarity
    - Simple, area of overlap
  - Dutch model
    - Simple assignment
  - Hald model
    - Complex, epidemiology based
  - Island model
    - Complex, population genetics based
Island model

- Used to find out source of human infections
- Flow into the human “island” from animal “islands”
- Same approach used to identify source of contamination of river water

Tracing the Source of Campylobacteriosis

Daniel J. Wilson¹ a*, Edith Gabriel² b, Andrew J. H. Leatherbarrow³, John Cheesbrough⁴, Steven Gee⁴, Eric Bolton⁵, Andrew Fox⁴,5, Paul Fearnhead¹, C. Anthony Hart⁶, Peter J. Diggle²
Now have information on many sources...
Campylobacteriosis Notifications and Hospitalisations

Year

Notifications

Hospitalisations

Campylobacter in Poultry – Risk Management Strategy 2007 - 2010

...2006-2009, now 2008-2011
National Micro Database results

<table>
<thead>
<tr>
<th>NMD Results</th>
<th>Number of carcasses tested</th>
<th>Prevalence %</th>
<th>Mean Log Count all samples</th>
</tr>
</thead>
<tbody>
<tr>
<td>Q2 2007</td>
<td>890</td>
<td>57</td>
<td>3.07</td>
</tr>
<tr>
<td>Q3 2007</td>
<td>936</td>
<td>53.8</td>
<td>3.06</td>
</tr>
<tr>
<td>Q4 2007</td>
<td>916</td>
<td>45.1</td>
<td>2.75</td>
</tr>
<tr>
<td>Q1 2008</td>
<td>1309</td>
<td>45</td>
<td>2.70</td>
</tr>
<tr>
<td>Q2 2008</td>
<td>1528</td>
<td>30.6</td>
<td>2.41</td>
</tr>
</tbody>
</table>

Target: 1 log reduction in contamination. Action depends on number of non-compliances.
Modelling post intervention change in attribution

N=670 human cases

Cases attributed

2005 2006 2007 2008

Dynamic Hald model

Poultry
Bovine
Ovine
Env
The changing epidemiology of campylobacteriosis in New Zealand

Reduction in case rates most marked in urban adults.

<table>
<thead>
<tr>
<th></th>
<th>% cases rural</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>2000-6 ave</td>
</tr>
<tr>
<td>Total</td>
<td>11.19</td>
</tr>
<tr>
<td>Under 5's</td>
<td>27.11</td>
</tr>
</tbody>
</table>
New focus on non-poultry transmission routes

*Campylobacter* in Manawatu rivers

Where do these *campylobacters* come from???
Manawatu catchment dairy and beef

Dairy=227,658
Beef=181,196
Prevalence of presumptive *Campylobacter* spp.

<table>
<thead>
<tr>
<th>Source Site</th>
<th>Number samples</th>
<th>Number +ve</th>
<th>% +ve</th>
</tr>
</thead>
<tbody>
<tr>
<td>Himatangi</td>
<td>85</td>
<td>26</td>
<td>30.59</td>
</tr>
<tr>
<td>Mangapapa</td>
<td>86</td>
<td>47</td>
<td>54.65</td>
</tr>
<tr>
<td>MR Albert</td>
<td>87</td>
<td>46</td>
<td>52.87</td>
</tr>
<tr>
<td>MR Hopelands</td>
<td>85</td>
<td>25</td>
<td>29.41</td>
</tr>
<tr>
<td>Oroua</td>
<td>86</td>
<td>29</td>
<td>33.72</td>
</tr>
<tr>
<td>Tokomaru</td>
<td>78</td>
<td>19</td>
<td>24.36</td>
</tr>
<tr>
<td>All</td>
<td>507</td>
<td>192</td>
<td>37.87</td>
</tr>
</tbody>
</table>

~ 50% of presumptive +ve are confirmed *C. jejuni* +ve
Novel Clonal Complexes with an Unknown Animal Reservoir Dominate *Campylobacter jejuni* Isolates from River Water in New Zealand

P. E. Carter,1* S. M. McTavish,1† H. J. L. Brooks,2 D. Campbell,3 J. M. Collins-Emerson,4 A. C. Midwinter,4 and N. P. French4

---

**FIG. 1.** Minimum spanning tree of New Zealand water isolates based on sequence types. Clusters are identified by the clonal complex number associated with the sequence types in the cluster.
Water/wild bird: ducks

Water/wild bird: gulls

Water/wild bird: pukeko

Wild bird/starling

Wild bird/starling
Source attribution: water

Most isolates from water are associated with wildlife – even in dairy catchments.

Cattle and sheep isolates more likely to be associated with human infection.
Time series since 2006

Recent increases in central and lower NI

Recent trends

Poultry counts tracking up NB log scale

Need for more work with industry...
Conclusions

- Success of campaign attributable to many factors.
- Manawatu sentinel surveillance site provided an important contribution to the recent success in reducing campylobacteriosis across NZ.
- Wouldn’t have been possible without collaboration and cooperation between many individuals and organisations.
- Many of the findings have been published and the study has been recognised internationally.
- New tools have been developed of use for local and national surveillance.
- Good example of ‘one health’ in action.
Acknowledgements

- Staff – lecturers, RAs
  - Dr Julie Collins-Emerson, Dr Anne Midwinter
  - Dr Simon Spencer, Dr Jonathan Marshall, Dr Patrick Biggs
- Lab team:
  - Rebecca Pattison, Rukhshana Akhter, Errol Kwan, Lynn Rogers, Isabel Li, Jim Learmonth, Anthony Pita, Sarah Moore, Angie Reynolds, Neville Haack
- PhD students
  - Petra Mullner, Vathsala Mohan
- Masters students
  - Particularly Tui Shadbolt, Ann Sears
- MidCentral Public Health
  - Dr Jill McKenzie and team
- MedLab Central
- ESR - Phil Carter, Sharla McTavish, Elaine Moriarty
- AgResearch – Grant Hotter, Adrian Cookson
- CDRP team
  - NIWA – Graham McBride
  - ESR – Rob Lake
  - NZFSA – Peter van de Logt, Dr Donald Campbell
- Michael Baker
- Massey – IMBS, IFNHH, IFS (Dr Barbara Holland, Dr Geoff Jones, Dr Alasdair Noble, Prof Martin Hazelton)
  - Allan Wilson Centre
- Universities of Liverpool, Lancaster, Oxford, Chicago
- Undergraduate student
  - Jeffrey Ling
- Industry

NZFSA, MoH, FRST, Royal Society Marsden and Industry funding
Publications


- + NZFSA website – science for number of reports