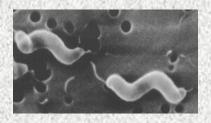
#### New approaches to source attribution: their role in reducing campylobacteriosis notifications in New Zealand



Nigel French EFSA December 2008



http://epicentre.massey.ac.nz/







#### Outline

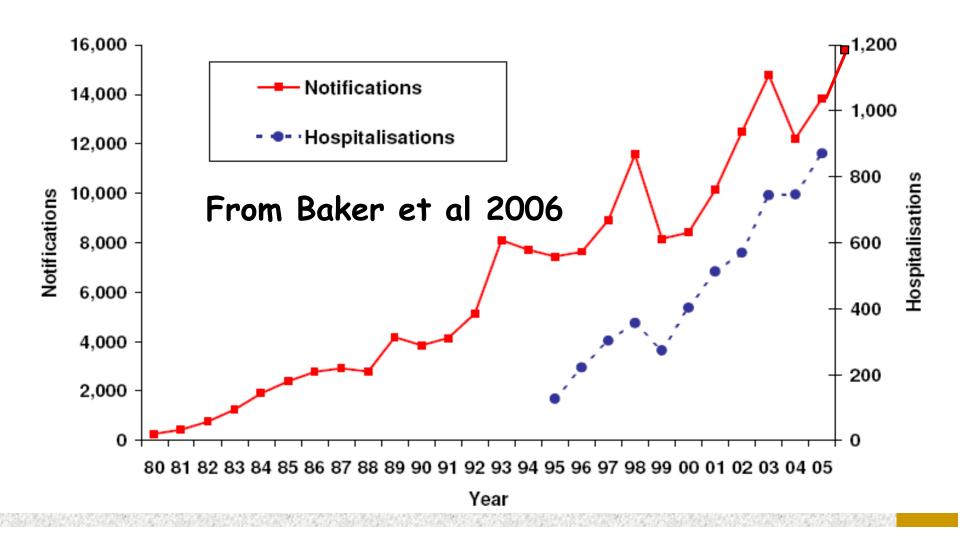
- Epidemiology
  - Recent studies of human case data
- · Genotyping human and animal reservoirs
  - MLST
- · Source attribution modelling
- · Recent trends post intervention



#### **National Surveillance Data** 12-Monthly Notification Rate Changes (1) 6 Campylobacteriosis rate per 1,000 40 Pertussis rate per 10,000 Salmonellosis Giardiasis Gastroenteritis Cryptosporidiosis **Yersiniosis Tuberculosis Disease** Meningococcal Disease **Shigellosis Acute Rheumatic Fever** VTEC Infection 0> Leptospirosis Source: ESR

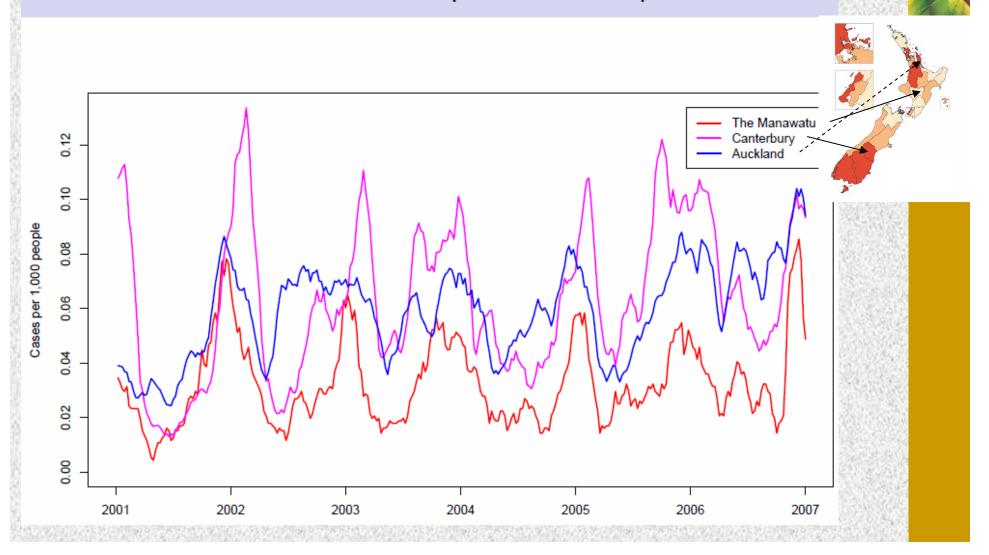
### Campylobacteriosis in NZ

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



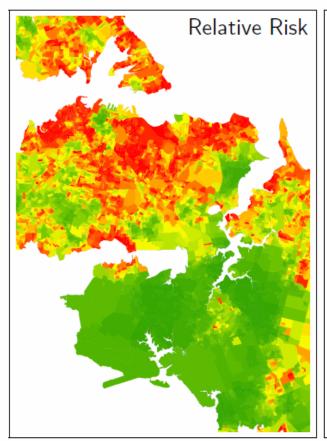
# Epidemiology: seasonal pattern

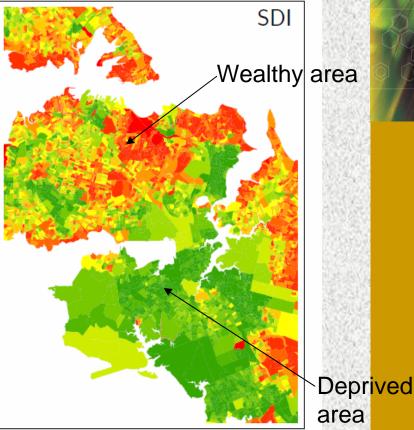
Smoothed Time Series: Cases per 1,000 People



# Epidemiology: spatial pattern

Comparison of Relative Risk vs SDI

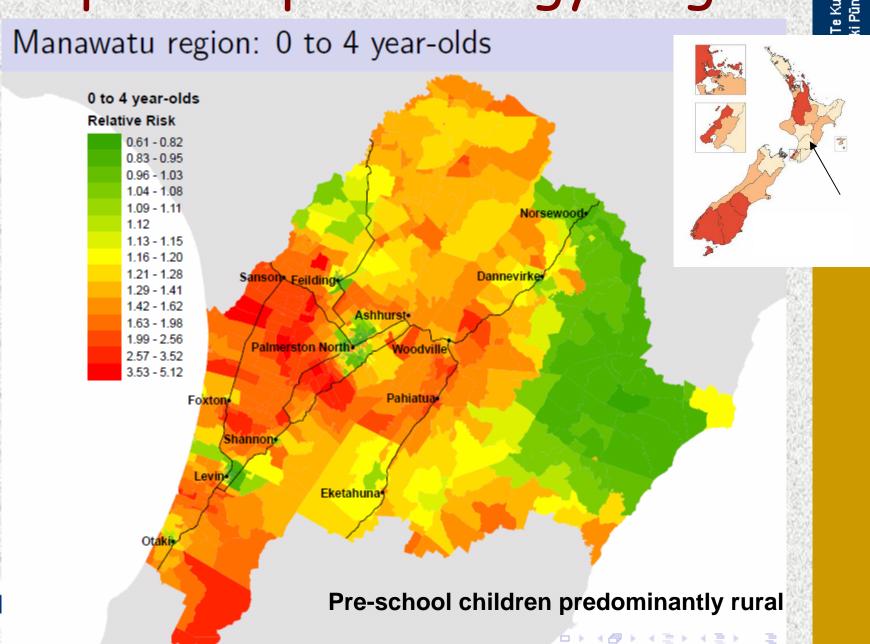




>1M pop<sup>n</sup>

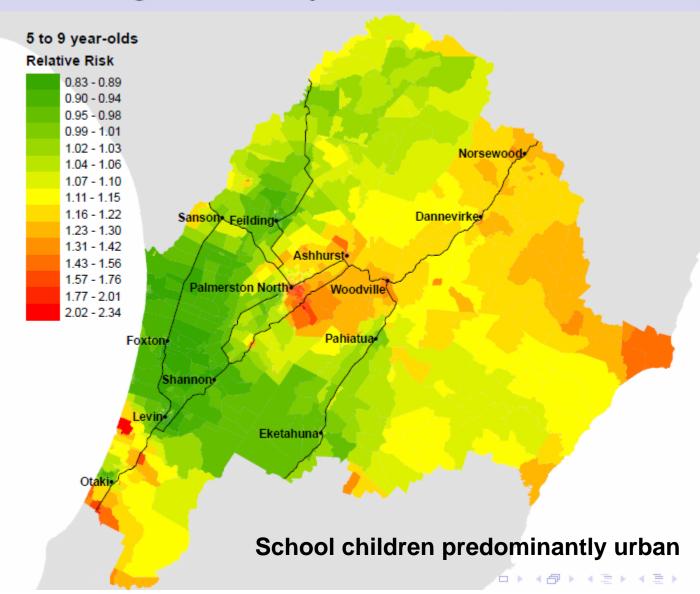


### Spatial epidemiology - age



## Spatial epidemiology - age

Manawatu region: 5 to 9 year-olds





# Interventions in poultry industry demanded

# THE NEW ZEALAND MEDICAL JOURNAL

Vol 119 No 1243 ISSN 1175 8716

2006



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



### Source attribution

- · Essential for:
  - Managing public health risks
  - Prioritising resources
  - Directing research effort



# Approaches to 'source attribution'

- (Analytical) epidemiology
  - · Population-based epidemiological studies
- Simulation modelling / Risk assessment
- Molecular epidemiology
  - · Microbial subtyping / source tracking
  - Applying molecular tools, population genetics and epidemiological modelling to inform public health policy
  - · NZFSA and industry funded



# Approaches to 'source attribution'

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# Population-based epidemiological studies

- Cross-sectional, cohort, case-control, case-case.
- Can estimate relative risk / odds ratios / PAF for different exposures
  - e.g. Campylobacter and eating poultry, foreign travel, environmental, occupational

Source/ disease exposure



#### Issues with case-control studies

- · Can be very valuable but...
- Prone to reporting bias
  - "I must have eaten chicken...."
- If high level immunity, similar exposures in cases and controls - low power



# Chicken - confusing / conflicting evidence?

Risk/Protective factor	Odds ratio (CI)
Eating undercooked poultry (risk)	4.94 (1.03, 23.62)
Poultry eaten at a friend's house (risk)	3.18 (1.0, 10.73)
Consuming fresh chicken (as opposed	1.8 (0.82, 3.82)
to frozen) (risk)	
Eating poultry at home (protective)	0.36 (0.14) 0.9)
Freezing fresh chicken before	0.58 (0.18, 1.83)
consuming (protective)	
Buying frozen chicken (protective)	0.71 (0.34, 1.31)

Ikram 1994, New Zealand Campylobacter study



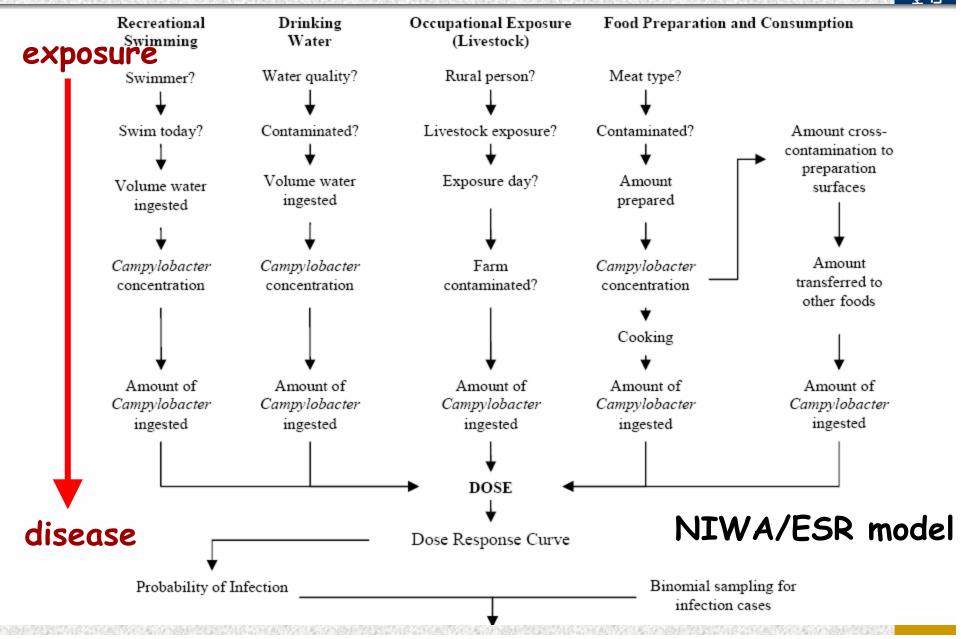
# Approaches to 'source attribution'

- (Analytical) epidemiology
- Simulation (RA) modelling
  - · Multiple pathways / exposures
  - Food and environmental sources
  - Simulation of propagation of pathogen along pathway
  - Hazard or risk based (need D-RR)
  - · Good for assessing interventions
- Molecular epidemiology



#### Environment

#### Food



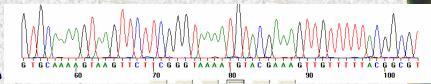
# Approaches to 'source attribution'

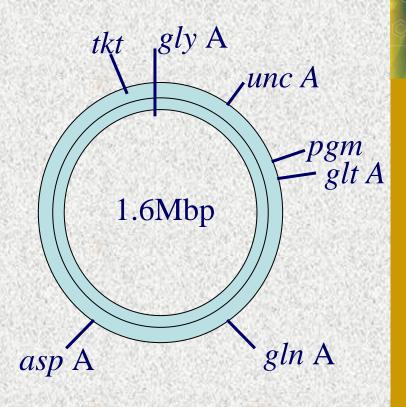
- (Analytical) epidemiology
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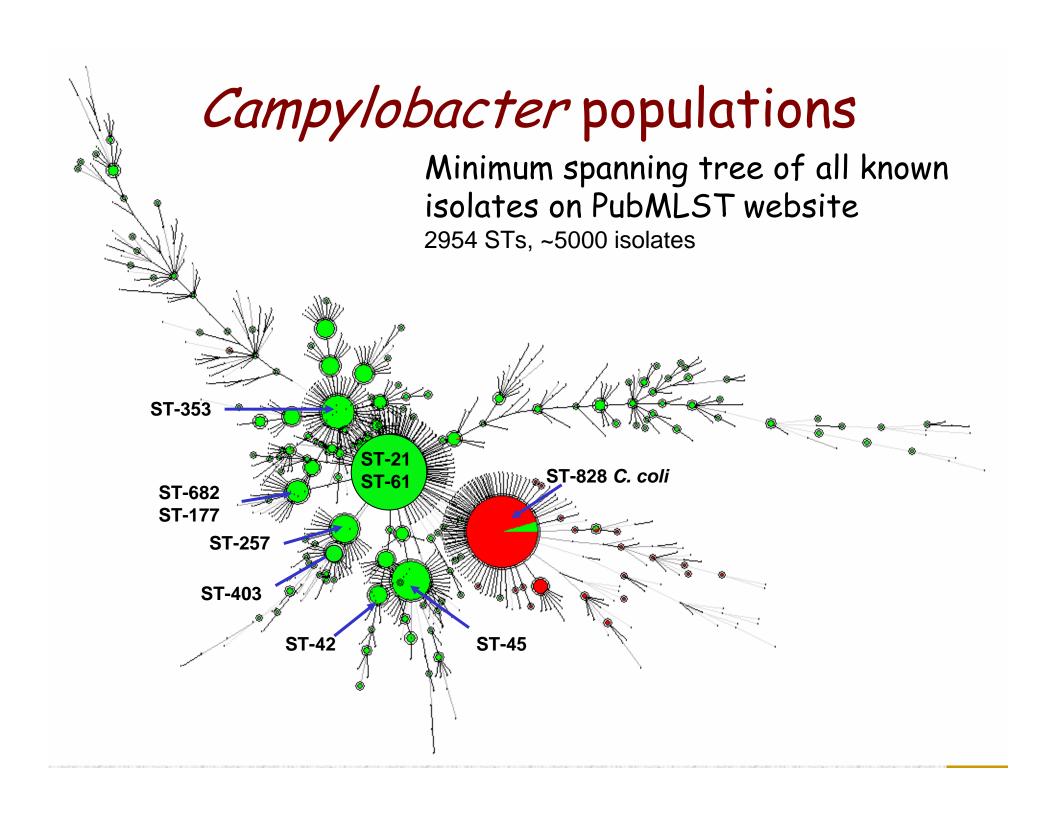
# Multi Locus Sequence Typing

- PCR highly conserved genes
- · 7 housekeeping genes
- Use allelic variation to describe subtypes:
  - ST = sequence type unique pattern of 7 alleles
  - Clonal complex = group of related STs identified by progenitor ST
  - Website: Oxford University
    http://campylobacter.mlst
    .net









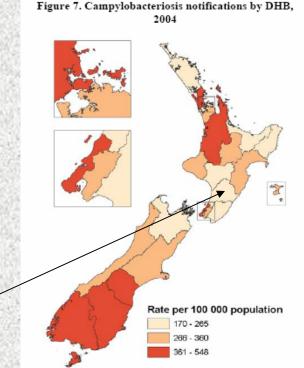
# ST-61 complex

source	Frequency	Percentage
human stool	62	35.2%
cattle	53	30.1%
sheep	17	9.7%
ruminant offal/ meat	8	7.9%
lamb	8	4.5%
Chicken	3	1.7%

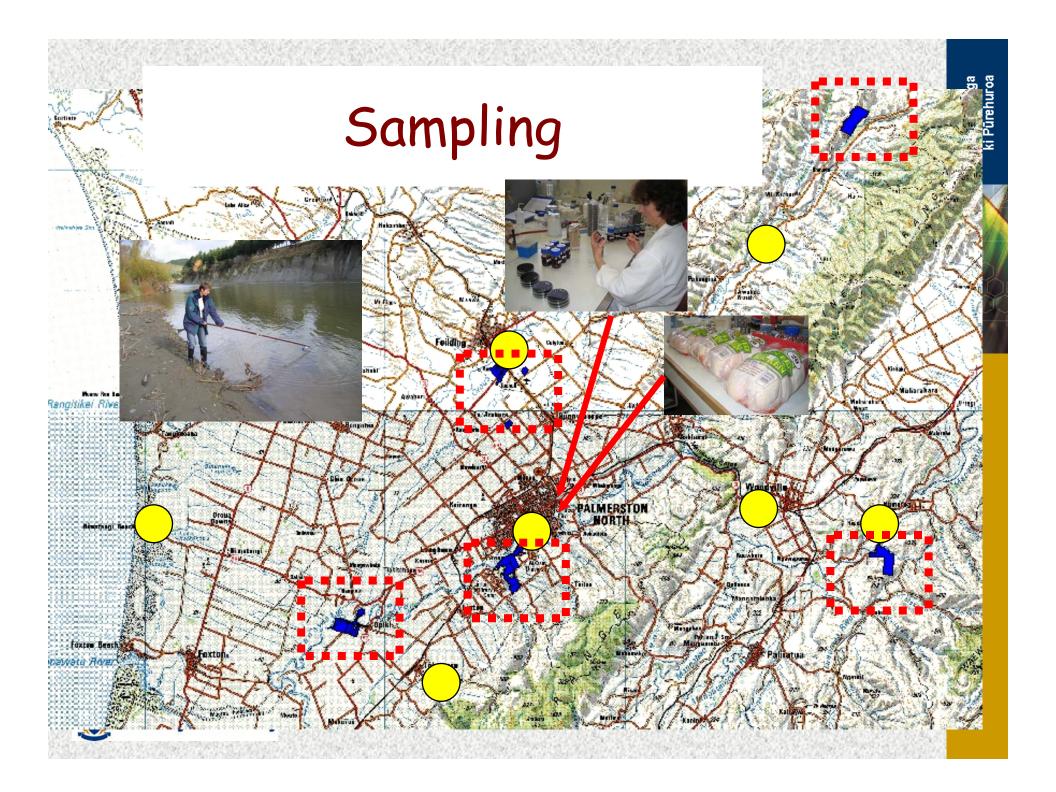


## NZ Manawatu study 2005-

- Are human isolates the same as those found in different sources?
- Identify genotypes common to particular sources
- Modelling (risk attribution)
- Feasibility study: useful approach to embed within surveillance in NZ?







### 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 1<sup>st</sup> 2005 to Feb 29<sup>th</sup> 2008



		#21443123011	
ST	# of cases	%	2006 rank
474	66	27.3	1
48	24	9.9	2
190	18	7.4	4
45	17	7.0	3
53	13	5.4	8
42	11	4.5	5
61	10	4.1	10
50	9	3.7	7
2026	9	3.7	11

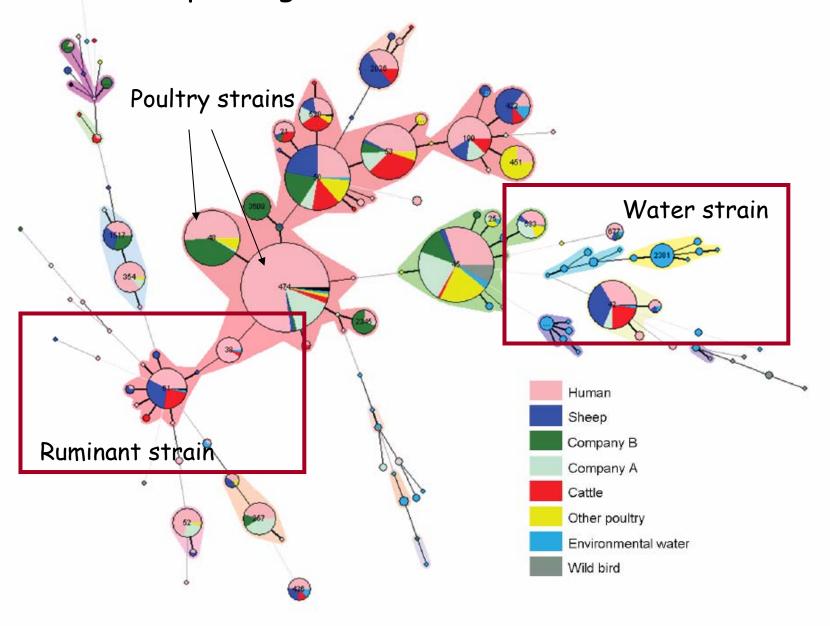
Rare internationally

## MLST Human cases in Manawatu

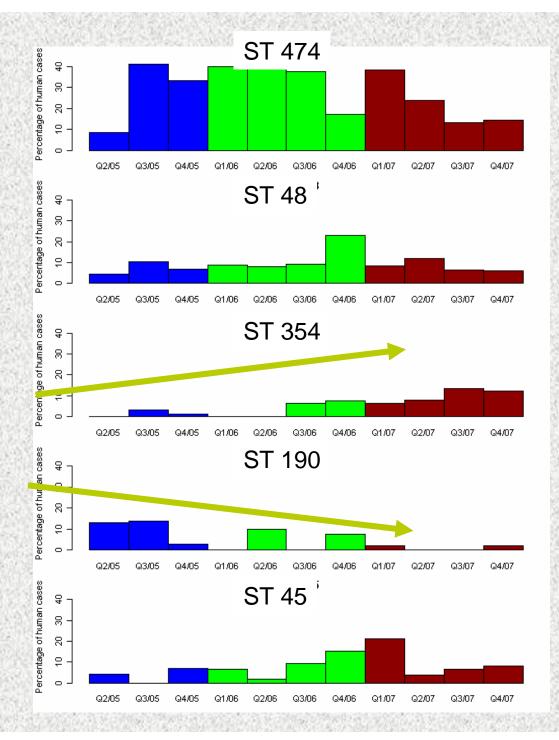
Red = Ruminant associated strains



#### Minimum spanning tree: isolates from the Manawatu

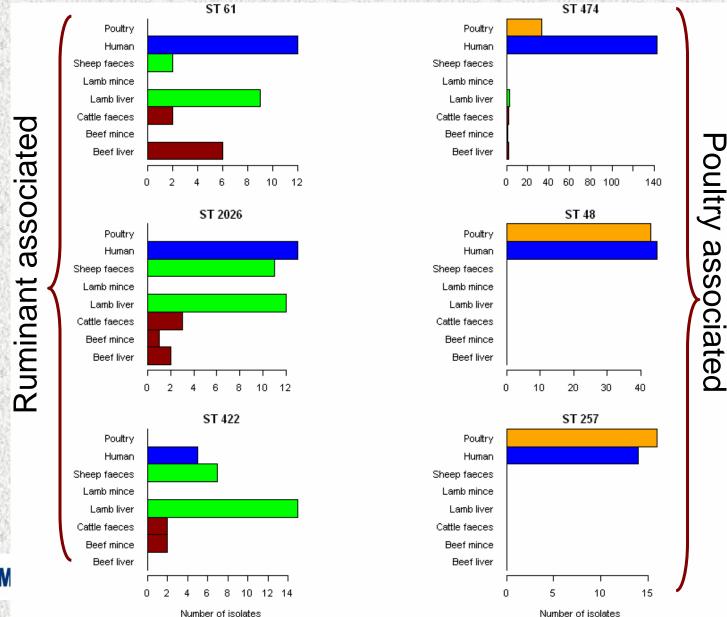


# Human cases over 3-year period

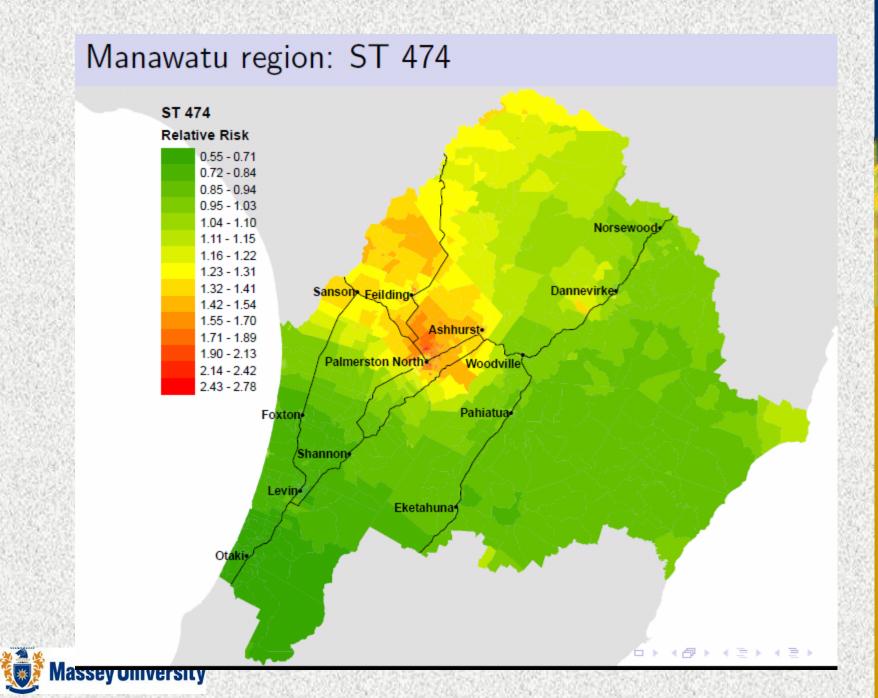




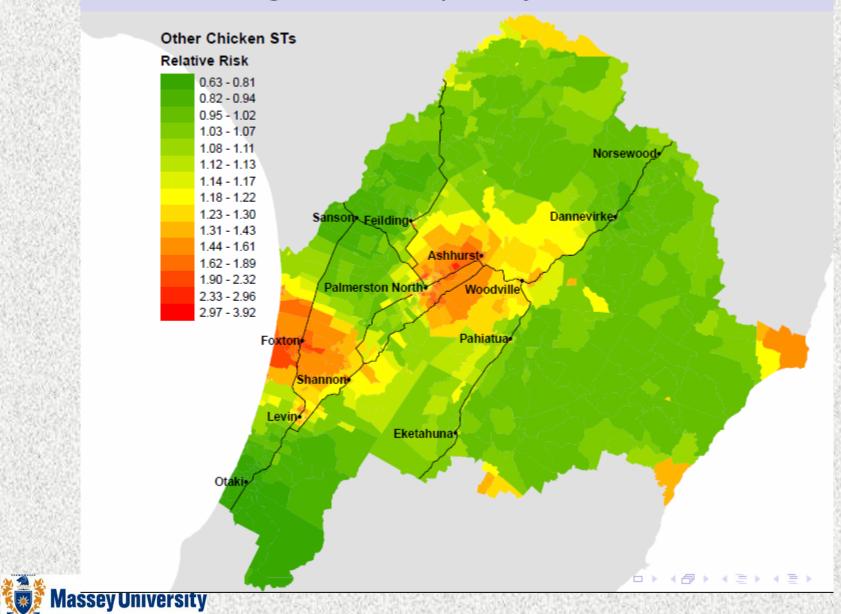
### Host associated sequence types in NZ

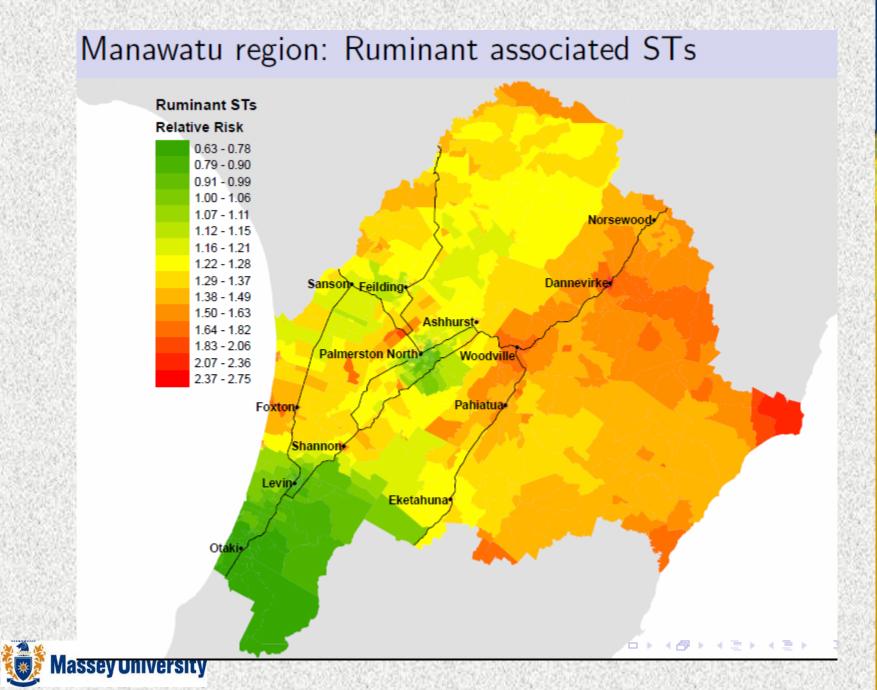


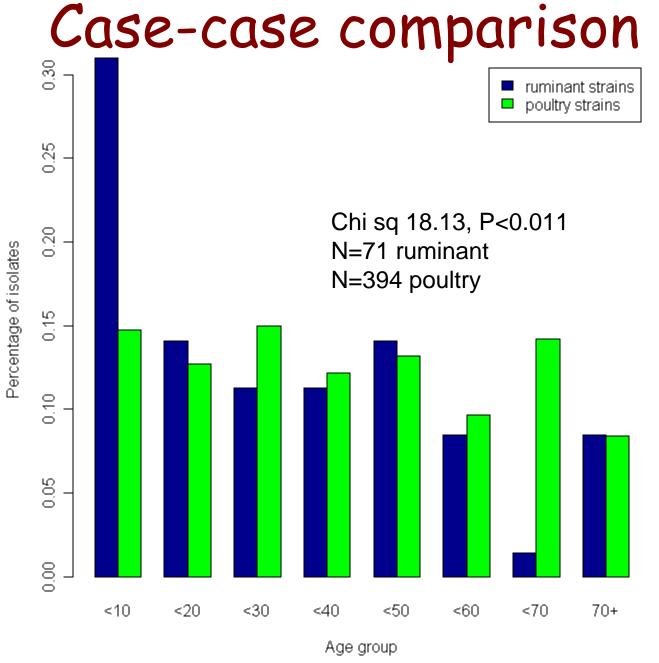




#### Manawatu region: Other poultry associated STs

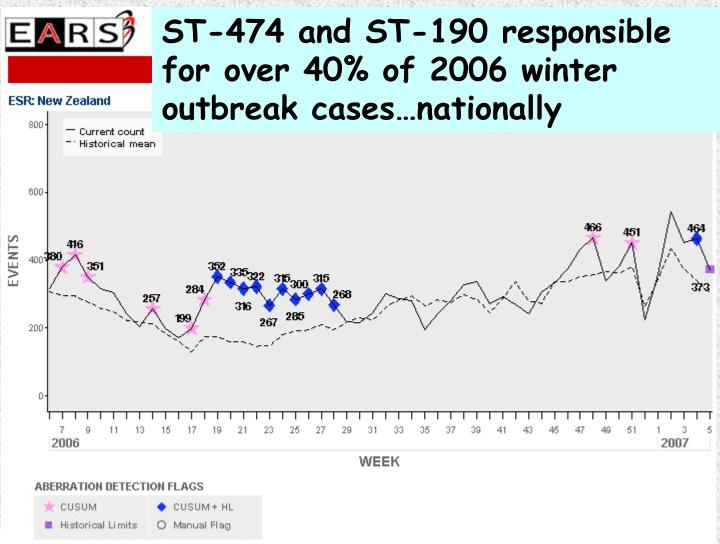






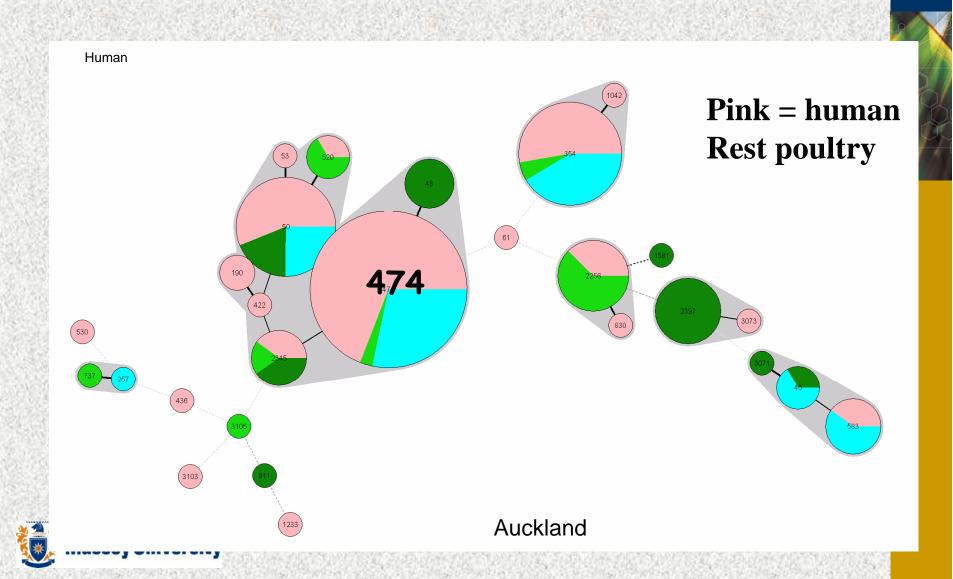


#### Generalised outbreak





# Auckland MLST (T. Wong)



#### Source attribution

- · Molecular tools and modelling
  - Proportional similarity
    - · Area of overlap
  - Dutch model
    - · Simple deterministic assignment



- · Bayesian model assignment with uncertainty
- Island model
  - Population genetics approach

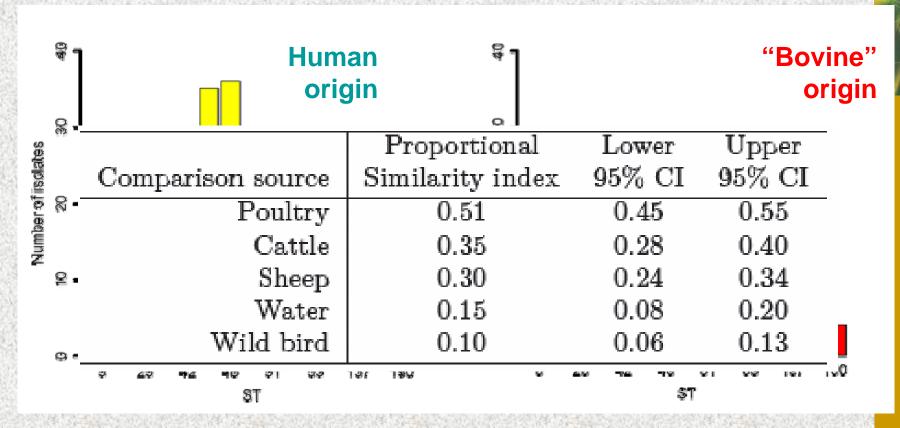


"I need 148 get-well cards."



### Proportional Similarity Index (PS)

The PS estimates the area of overlap between the frequency distributions of e.g. bacterial sub types from different sources.







Number of cases of The Hald model (Hald et al 2004) type i attributable to food source j

 $p_{ij}$  = matrix of prevalence of different strain types  $M_j$ = relative amount of food consumed  $a_j$  = relative 'danger' of food (or environmental) sources.  $q_i$  = relative 'virulence' of strains.

Estimates number of cases with measure of uncertainty (Bayesian inference)

## Modified Hald Model

- Model prevalence uncertainty
- Hierarchical model for bacterial parameters (q)
- Exponential prior for source specific parameters (a)
- Omit food consumption weights (M)
- Include potentially pathogenic subtypes



## Island model (Wilson et al 2008)

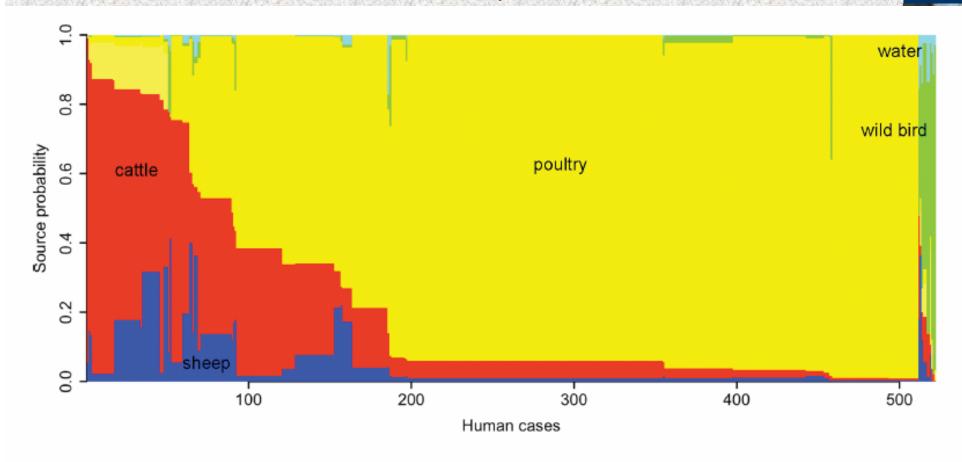
- · Population genetics approach
- · Genealogical method based on 'coalescent'
  - Cross-validation
- Use MLST data in animal populations ("islands") to estimate:
  - Mutation rates
  - Recombination rates
  - Migration rates (inter-host transmission)
- From these estimate 'migration' into human population
  - Source attribution

OPEN & ACCESS Freely available online

PLOS GENETICS

#### Tracing the Source of Campylobacteriosis

# Source attribution in New Zealand: Island model





## Source of human cases, Lancashire, England

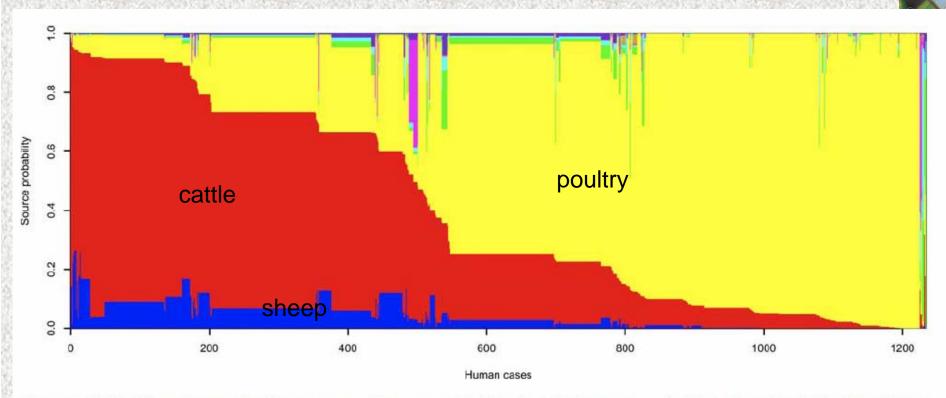
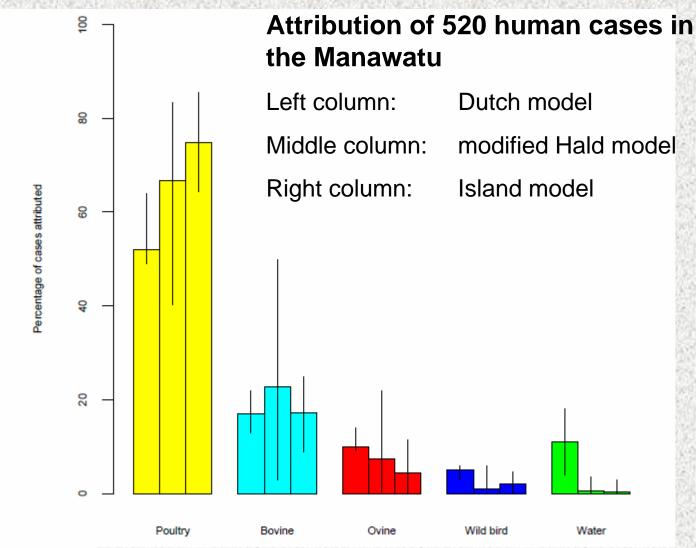


Figure 2. Probability of source for human cases. The source probability for 1,231 human cases (vertical columns) is depicted for Chicken (yellow), Cattle (red), Sheep (blue), Pig (pink), Bird (green), Rabbit (purple), Sand (beige) and Water (cyan). The isolates have been ordered horizontally to aid visualization.



# Source attribution: comparing models

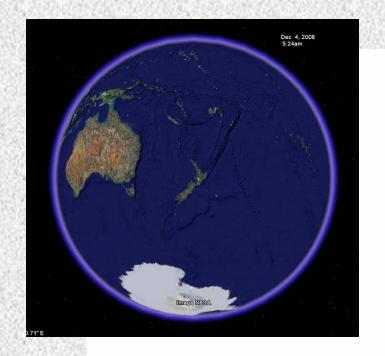




# Comparing models

- PS index and Dutch models easy to compute
- m. Hald and Island models include more of information from data - more complex
- m. Hald model captures food and pathogen factors
- · Island model can assign all human cases
- Therefore... recommend multiple, comparative approach...





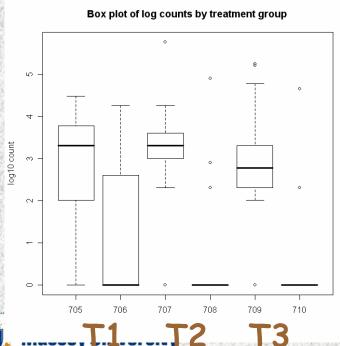


Campylobacter in Poultry – Risk Management Strategy 2007 - 2010



# Poultry industry intervention trials





#### Post spin-chill:

Tasker blue (Sulphuric acid and copper)

Sanova (ASC)

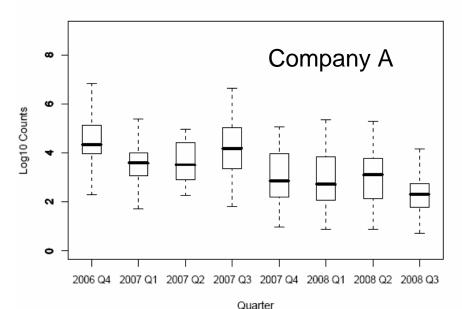
Pre spin chill:

Inspexx (hydrogen peroxide and peroxyactic acid)

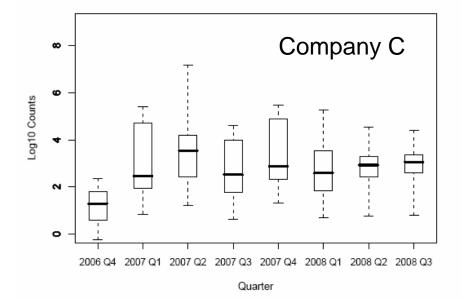


Poultry - count data at retail

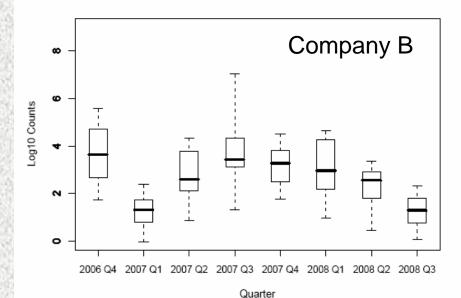


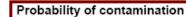


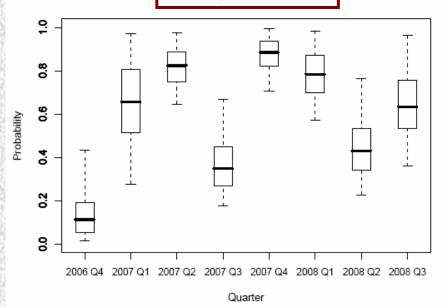
#### Level of contamination



#### Level of contamination















Up to 1000 people are hospitalised each year because of campulchacter

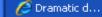






water use



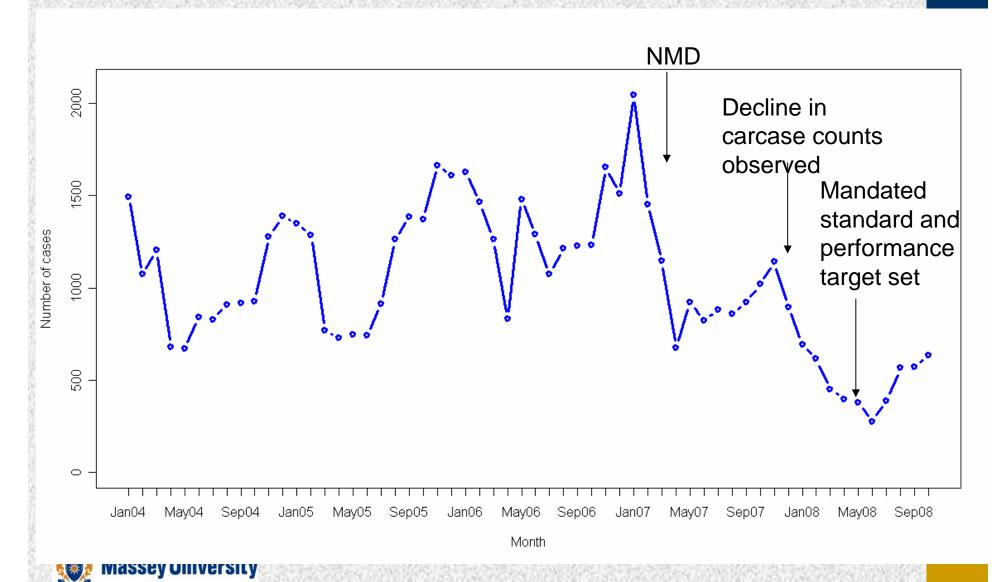


Internet





### Recent trends in NZ



#### Early Aberration Reporting System

#### **Salmonellosis**



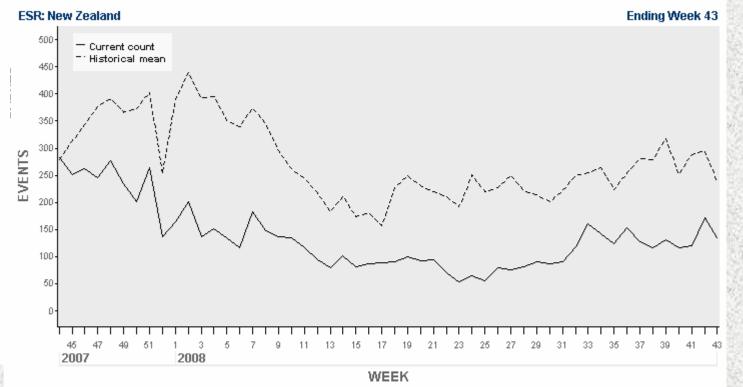
Early Aberration Reporting System

#### Cryptosporidiosis



Early Aberration Reporting System

#### Campylobacteriosis



50% reduction



**EVENTS** 

#### ABERRATION DETECTION FLAGS







### Conclusions

- NZ has unique epidemiology
  - Rural ruminant exposure in young children
  - Urban poultry across all ages
  - Dominant strain: ST474
- Source attribution modelling
  - Tools advanced in recent years
  - Applied to Campylobacter identified food, particularly poultry, most important source, cattle second
- · Focussing on poultry early signs of success
- · Environmental exposures less well defined
  - May become more important
  - Ruminants and wildlife



# Acknowledgements

- Staff lecturers
  - Dr Eve Pleydell, Dr Deb Prattley
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  - Dr Simon Spencer, Dr Jonathan Marshall, Dr Anne Midwinter, Dr Julie Collins-Emerson
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  - Rebecca Pattison, Rukhshana Akhter, Errol Kwan, Lynn Rogers, Isabel Li, Jim Learmonth, Anthony Pita, Sarah Vaughan,
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  - Petra Mullner, Vathsala Mohan,
- Masters students
  - Particularly Tui Shadbolt....
- ESR Phil Carter, Sharla McTavish
- AgResearch Grant Hotter
- CDRP team
  - NIWA Graham McBride
  - ESR Rob Lake
  - NZFSA Peter van de Logt
- Palmerston North Hospital / MedLab
- Massey IMBS, IFNHH, IFS
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- Universities of Liverpool, Lancaster, Oxford
- Industry



**NZFSA-funded** 





