

A genomic and modelling approach to understanding the evolution, source and transmission of a recently emerged antimicrobial resistant lineage of *Campylobacter*

Nigel French, Sabrina Greening, Ji Zhang, Anne Midwinter, David Wilkinson, Ahmed Fayaz, Marti Anderson, Jonathan Marshall, Patrick Biggs, Lynn Rogers, Kristen Dyet, Brent Gilpin, Danielle Ingle, Glenn Carter, Kerry Mulqueen, Carolyn Gates, Debbie Williamson.

OHA 2020



Te Kunenga
ki Pārehuroa

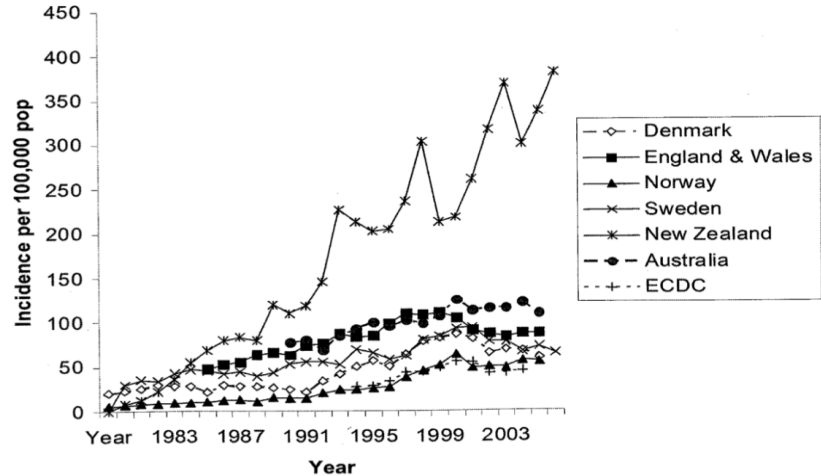
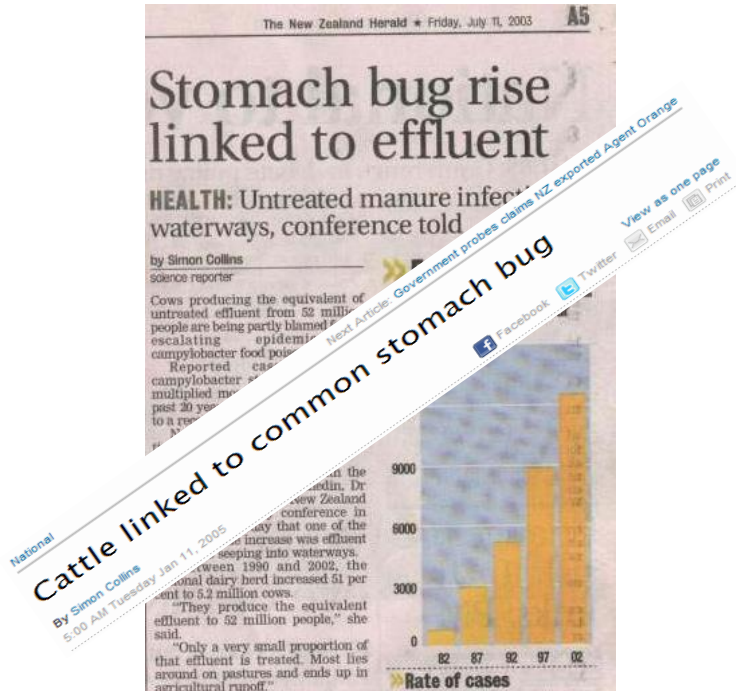


New Zealand: Food and waterborne diseases high on the list of notifiable diseases

<u>Number of notifications by disease, 2019</u>	
Disease	Total
Campylobacteriosis	6202
Measles	2213
Giardiasis	1749
Pertussis	1206
Salmonellosis	1188
Yersiniosis	1186
Shiga toxin-producing <i>Escherichia coli</i> infection	1101
Cryptosporidiosis	1035
Invasive pneumococcal disease	497
Acute gastroenteritis	489

Most zoonotic,
many food and
waterborne

Campylobacter in NZ: 1980-2006



THE NEW ZEALAND
MEDICAL JOURNAL

Vol 119 No 1243 ISSN 1175 8716

2006

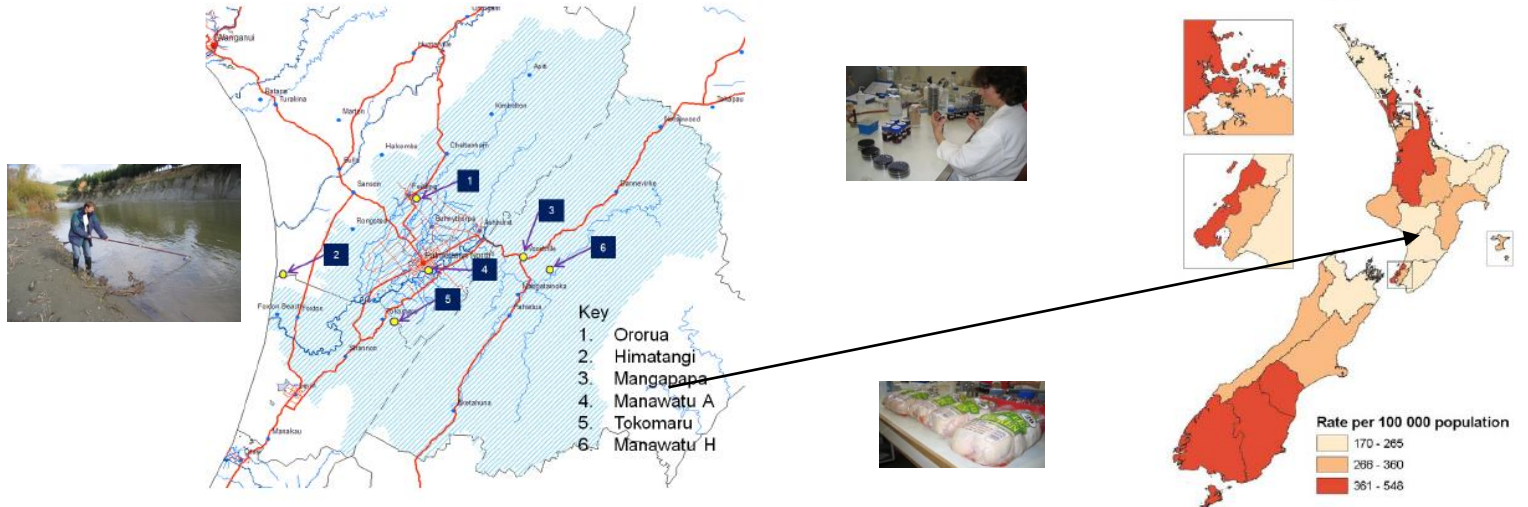


Regulation of chicken contamination urgently needed to control New Zealand's serious campylobacteriosis epidemic

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

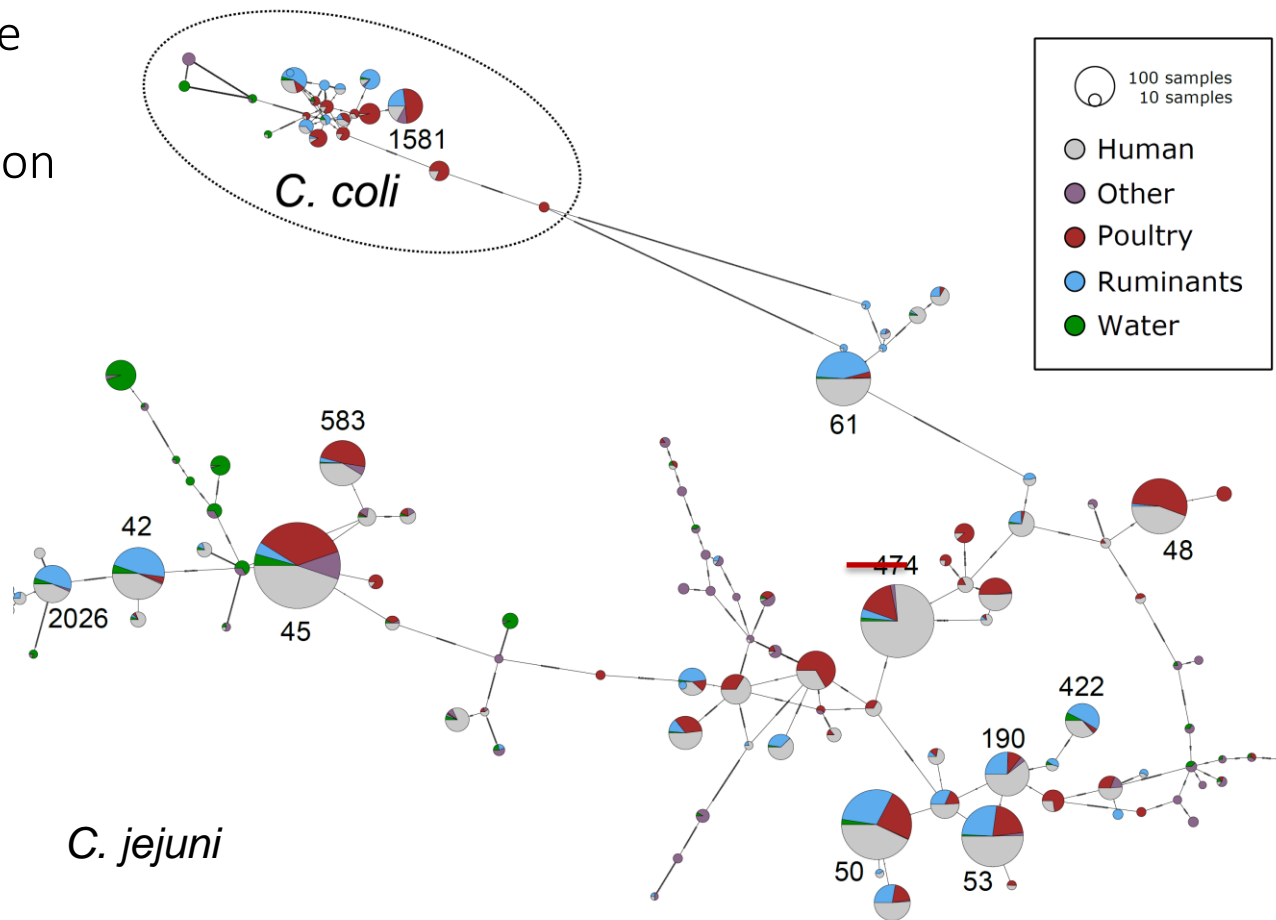
Manawatū sentinel site 2005-2018

- 'One health' approach: human, animal and environment
- Identify Multilocus Sequence Types common to particular sources
- Modelling (reservoir attribution)



Manawatu sentinel site
2005-18

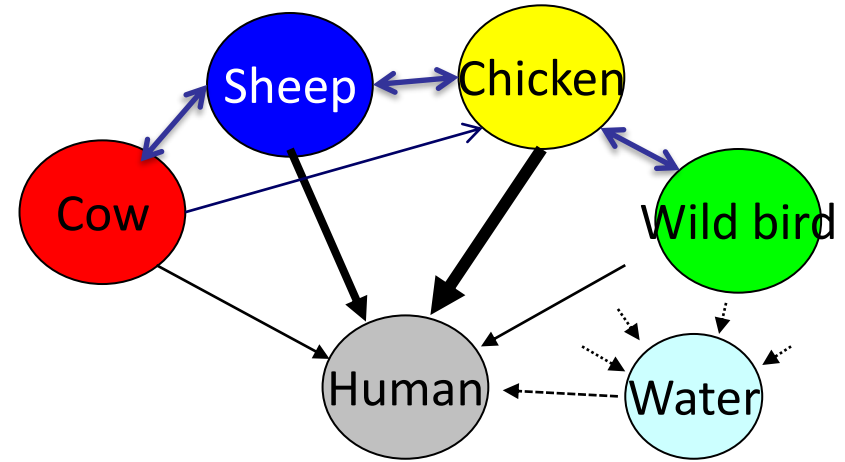
Campylobacter population
structure:
according to 7-genes



Reservoir attribution

‘Asymmetric Island model’ (AIM)

- Population genetics / evolutionary modelling approach
- Used to find out source of human infections
- Flow into the human “island” from animal “islands”



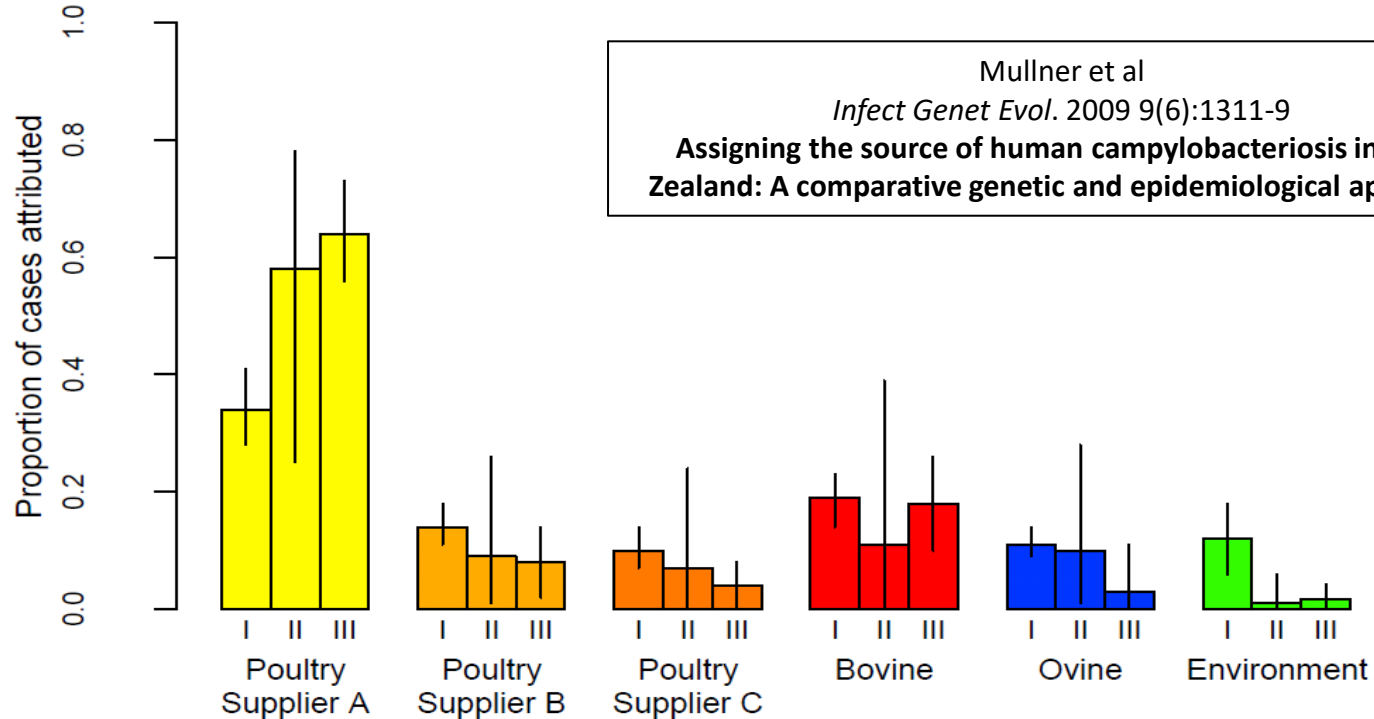
OPEN ACCESS Freely available online

PLoS GENETICS

Tracing the Source of Campylobacteriosis

Daniel J. Wilson^{1a*}, Edith Gabriel^{2ab}, Andrew J. H. Leatherbarrow³, John Cheesbrough⁴, Steven Gee⁴, Eric Bolton⁵, Andrew Fox^{4,5}, Paul Fearnhead¹, C. Anthony Hart^{6†}, Peter J. Diggle²

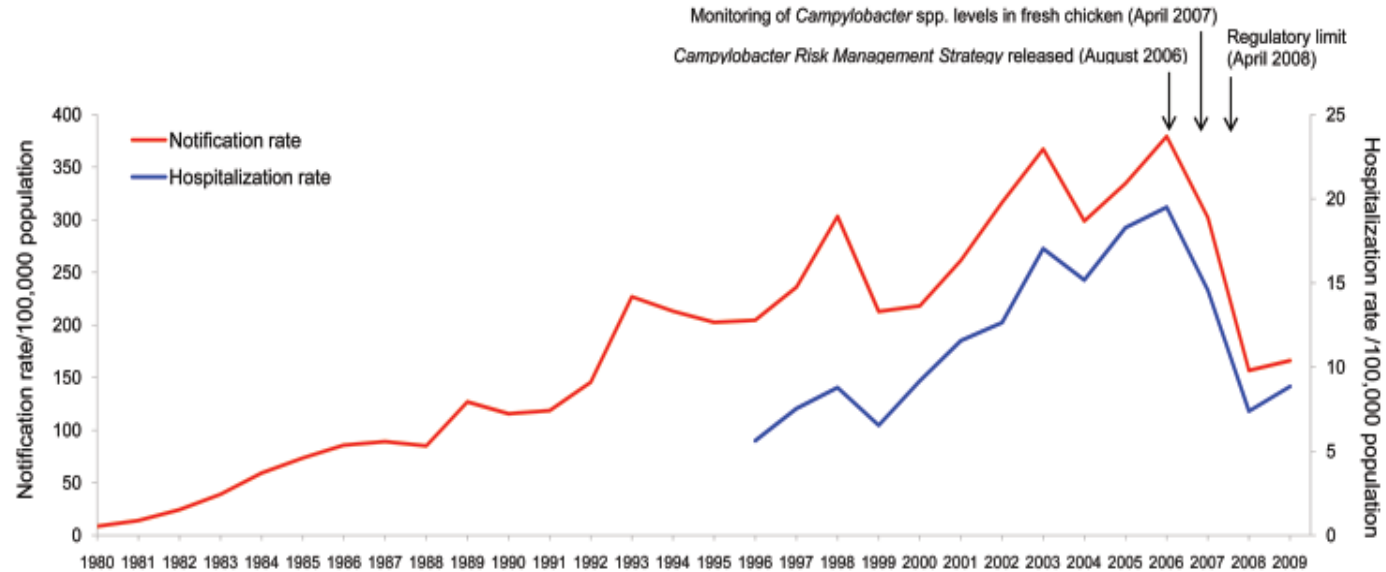
Reservoir attribution





Campylobacter in Poultry –
Risk Management Strategy
2007 - 2010

Relationship between campylobacteriosis notifications and hospitalisations

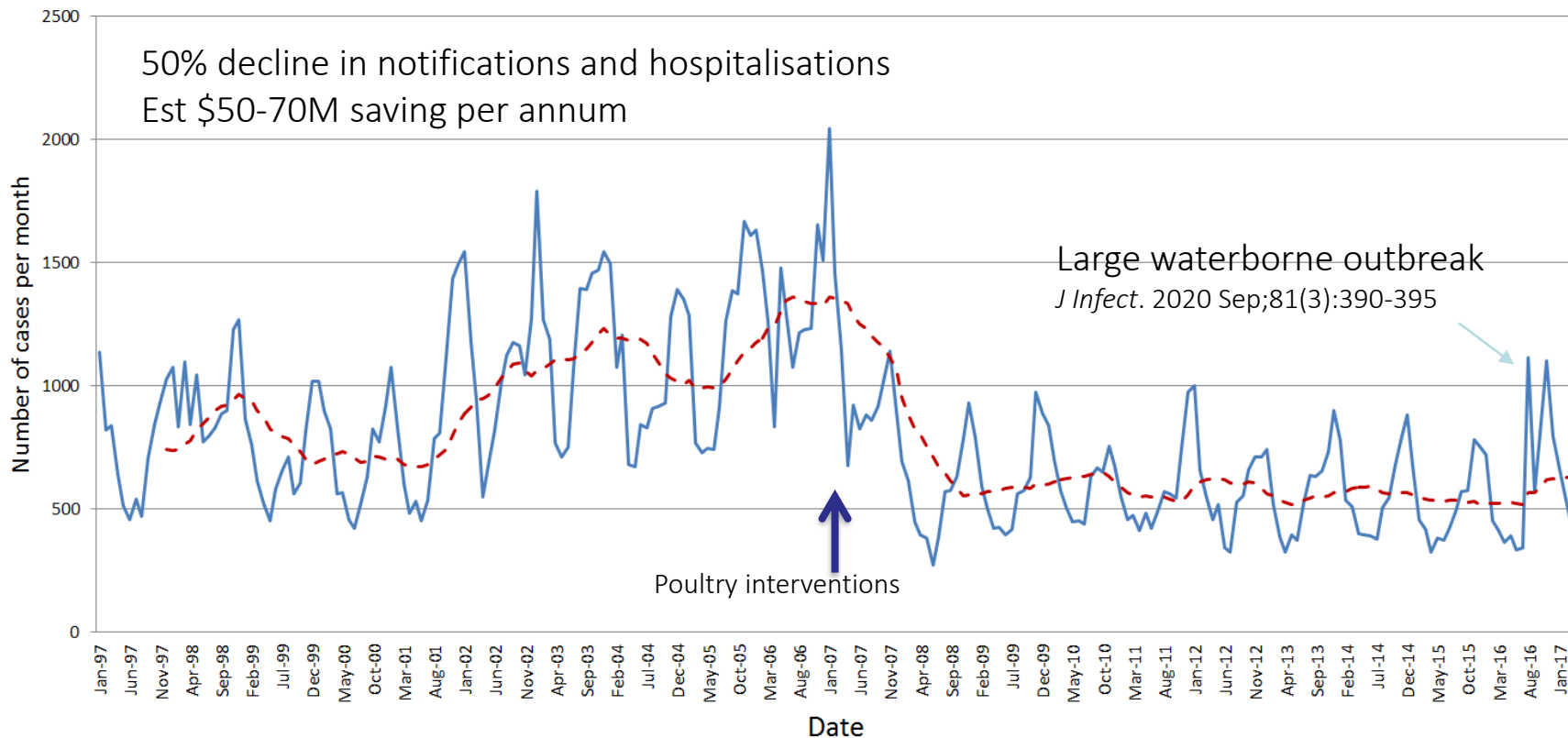


Data Sources: ESR Ltd notification data; NZHIS hospitalisation data (filtered)

Marked Campylobacteriosis Decline after Interventions Aimed at Poultry, New Zealand

Ann Sears, Michael G. Baker, Nick Wilson, Jonathan Marshall, Petra Muellner, Donald M. Campbell,
Robin J. Lake, and Nigel P. French

Sears et al 2011,
Emerging Infectious Diseases 17, 1007-15



Arrival of ST-6964 in 2014 and antibiotic resistance

SUNDAY STAR+TIMES
November 22, 2015
NEWS A3

Superbug found in chicken

Scientists are alarmed at the unprecedented discovery of a strain that resists drugs and has crossed into humans around NZ, writes Susan Edmunds.

A new superbug has been found in chicken from three of New Zealand's four major poultry suppliers. Groundbreaking research reveals the new antibiotic-resistant strain of campylobacter spreads to humans, which could make it hard to treat serious cases of infection.

Campylobacter occurs naturally in the gut of chickens but is the leading cause of food poisoning, with about 7000 cases reported in New Zealand each year.

The antibiotic-resistant strain was first found in 2014 and has now been identified in human cases in Manawatu, Auckland and Wellington.

The study, by Nigel French of Massey University and ESRR microbiologist Debbie Williamson, found three of the major poultry suppliers in the North Island tested positive for the strain. A fourth was still waiting for test results. The pair would not name the companies.

The resistance means two antibiotics – fluoroquinolones and tetracyclines – would fail in treating the infection. But erythromycin, which is more

Which comes first? The chicken or the campylobacter

Humans ingest the bacterium from surfaces or improperly cooked meat

Campylobacter spreads through handling, left in fridges

Consumers buy fresh chicken

Campylobacter develops in the gut

Photo: CHRIS MCKEEN / FAIRFAX NZ
Graphic: NEIL BOND

Antibiotic resistant Campylobacter in NZ

New Zealand Veterinary Journal 58(5), 229-236, 2010

229

Scientific Article

Low levels of antibacterial drug resistance expressed by Gram-negative bacteria isolated from poultry carcasses in New Zealand

EJ Pleydell^{*§}, L Rogers^{*}, E Kwan^{*} and NP French^{*}

Resistance in
humans
similarly low
~1-3% FQ

Drug	Disc ^a (µg)	Res (%) ^b	Zone size (mm)														
			≤6	7–15	16	17	18	19	20	21	22	23	24	25	26	27	≥28
Erythromycin	15	0.5	1				1			2	3	4	8	19	12	21	122
Ciprofloxacin	5	0											1	1	1	2	188
Enrofloxacin	5	0											1		3	4	185
Nalidixic acid	30	0			2	2	3	8	12	13	19	24	22	33	17	12	26
Chloramphenicol	30	0								1	1				9	10	172
Tetracycline	30	0													1		192

^a Concentration of drug within the disc

^b Percentage of isolates with zone sizes within the resistant category for that drug

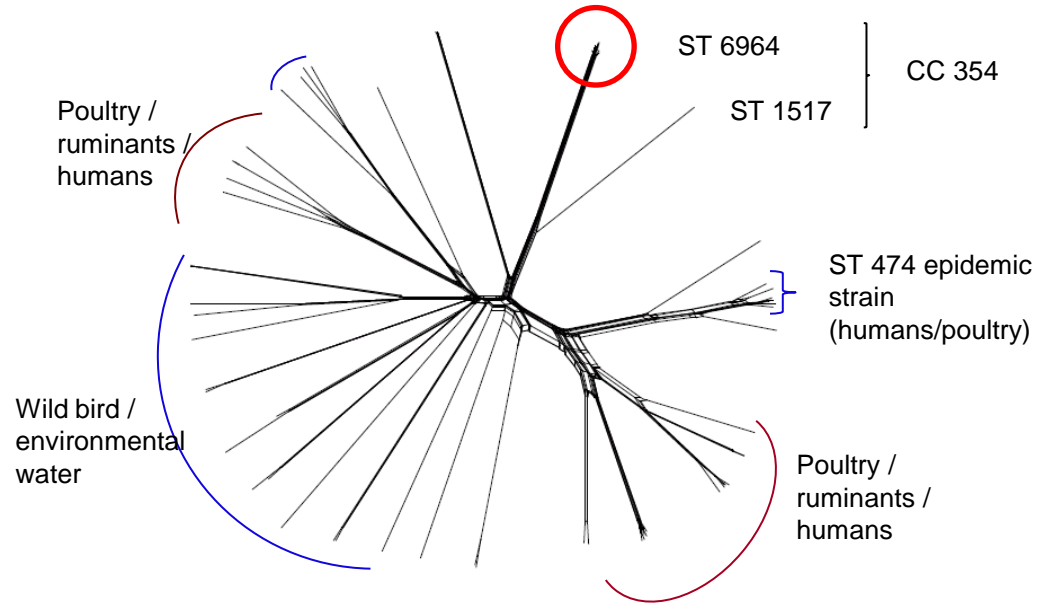
Very low by international standards
Low use of Abs in New Zealand poultry industry

Whole genome sequencing and Antimicrobial Resistance: Emergence of new strain: *Campylobacter jejuni* ST-6964

- August 2014: first two human cases of new *C. jejuni* ST-6964 detected in sentinel site
- Found in 4 poultry companies and 'breeder' (parent) flocks
- Resistant to tetracycline and fluoroquinolones
 - 0->37% in poultry
 - Sharp increase in AMR and ST 6964 in human cases across NZ (ESR study)
 - Chicken liver outbreak, Wellington



Whole genome sequencing showed AMR strain was new to New Zealand



Key questions?

- How long has it been in NZ?
- How has it been transmitted between poultry companies?
- What has driven the emergence?
- What is the main source of human infection?
- How is it evolving?
- Genetic basis for resistance?

These could only be addressed by Whole Genome Sequencing and a One Health approach

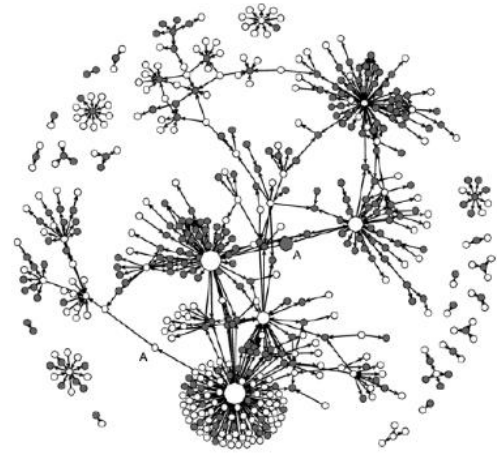
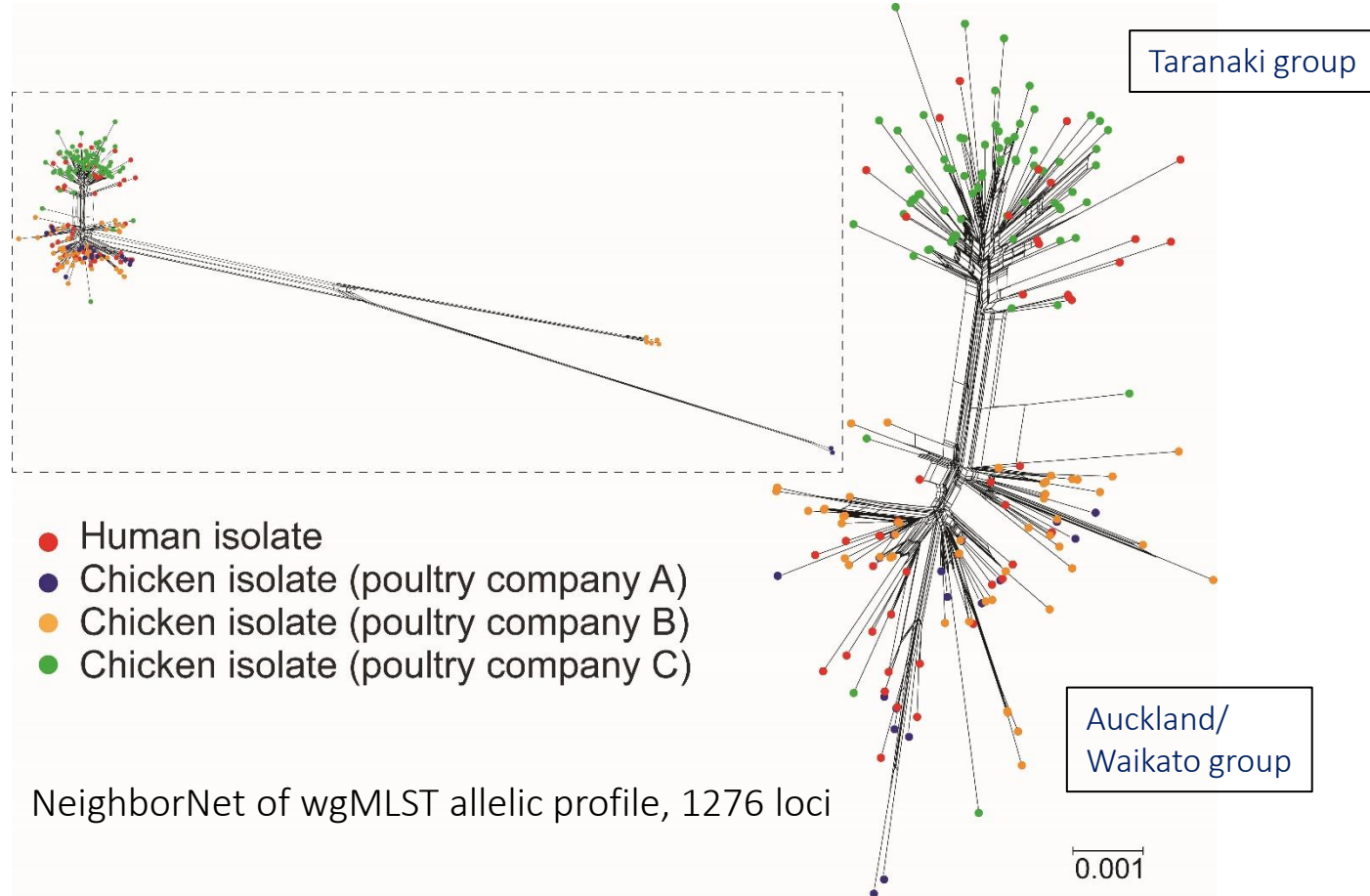
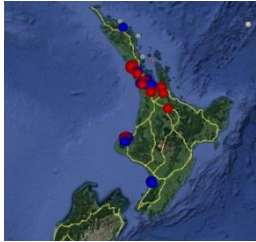
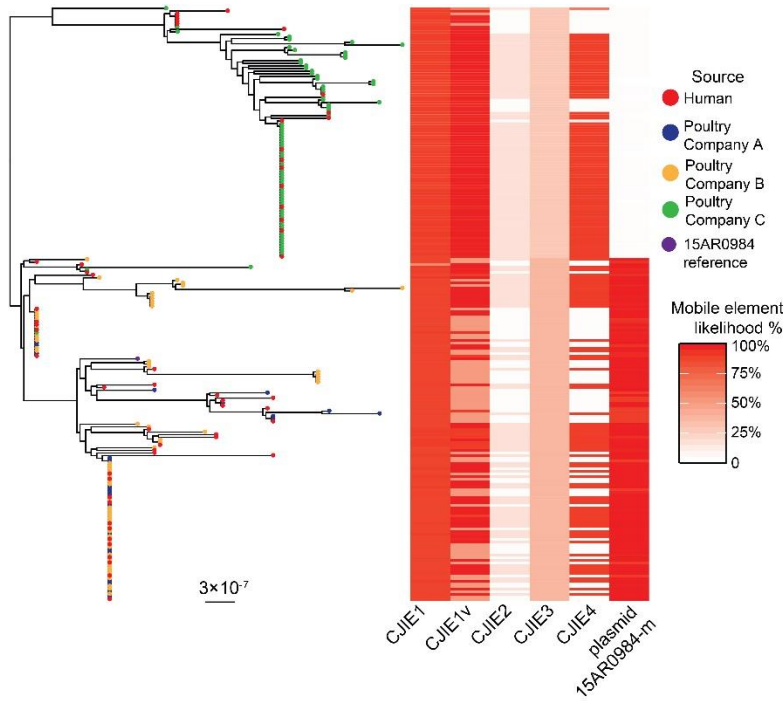


Fig.2. Social network analysis of feed-related contacts in the New Zealand

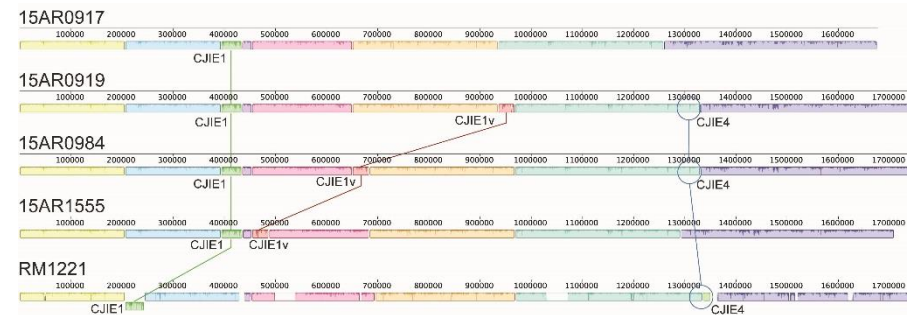
Pacbio and Illumina sequencing of 230 *C. jejuni* ST-6964 isolates from poultry farms and human cases



SNP-based phylogeny, plasmid and prophage integrated elements

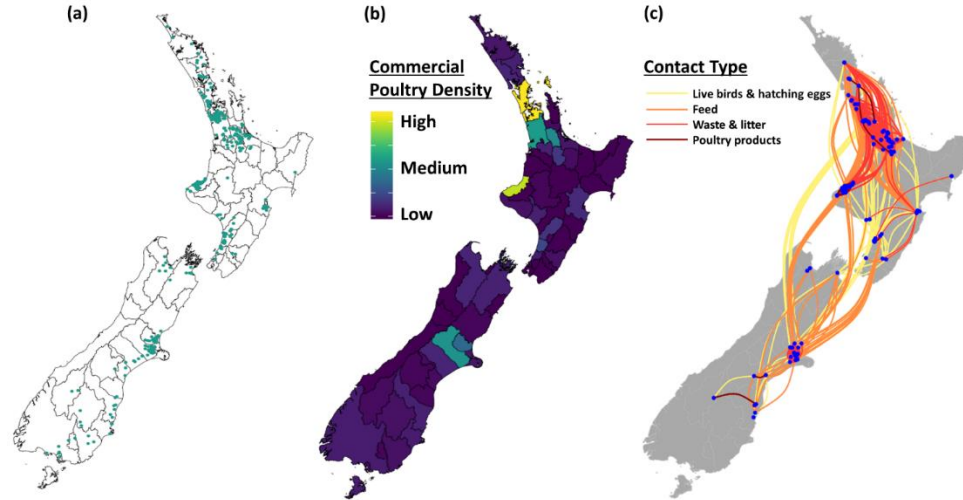


- Plasmid absent from company C
- Evidence of 3 prophage integrated elements
- CJIE1v identified in 3 locations in PacBio reference strains

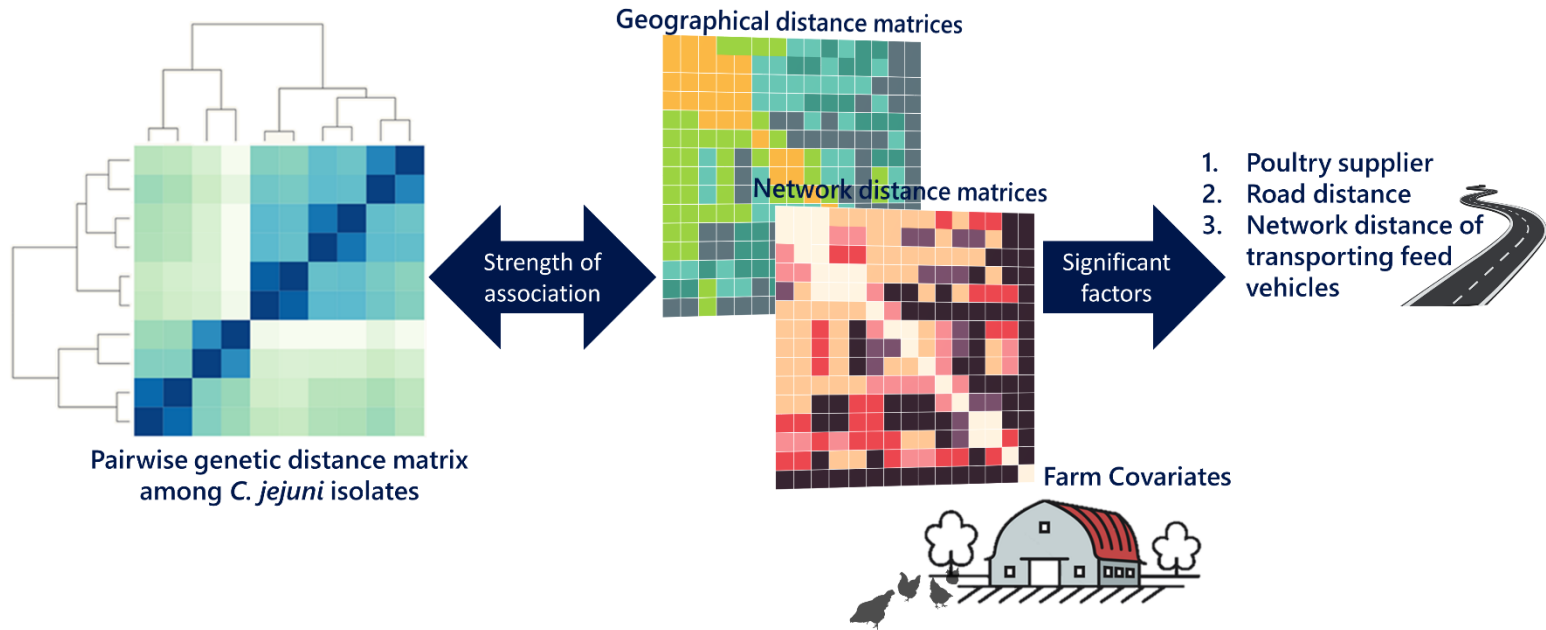


Transmission of *Campylobacter* in the poultry industry

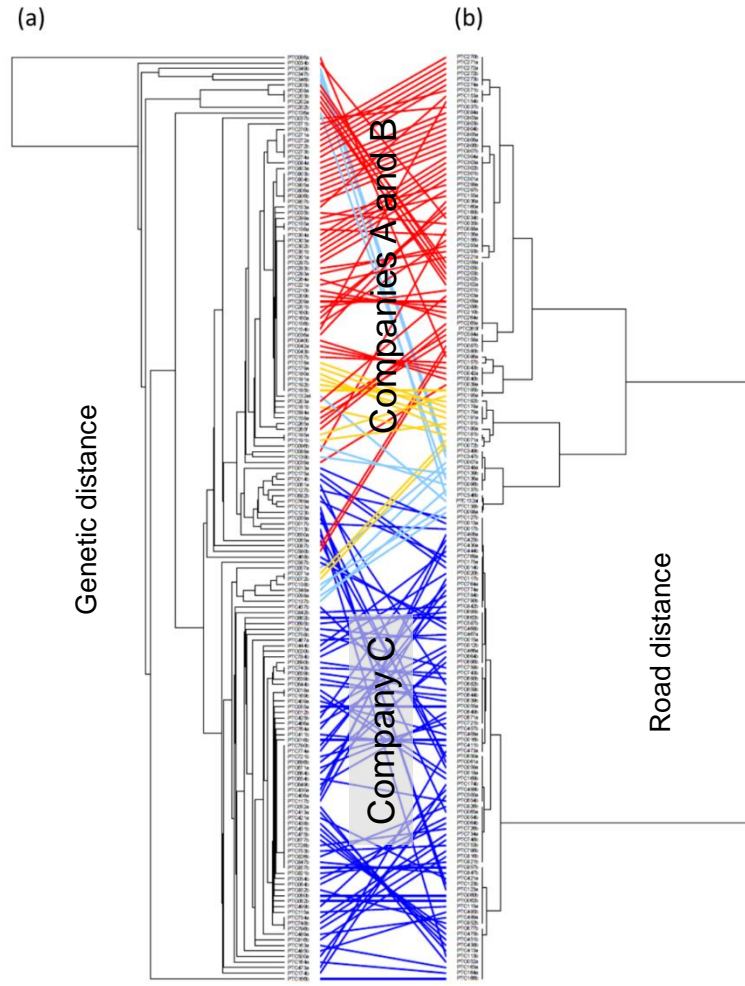
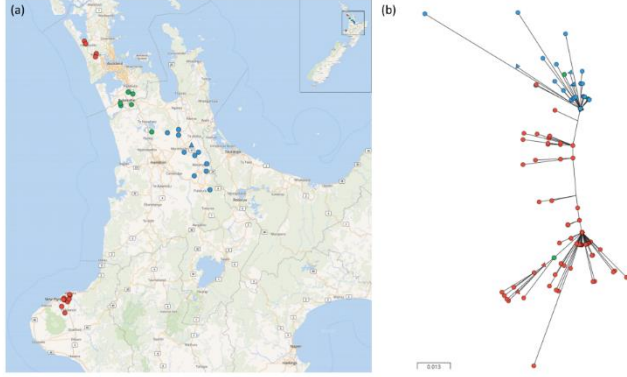
- Within company?
- Local spread?
- Spread through contact networks?
 - Feed
 - Chicks
 - Personnel



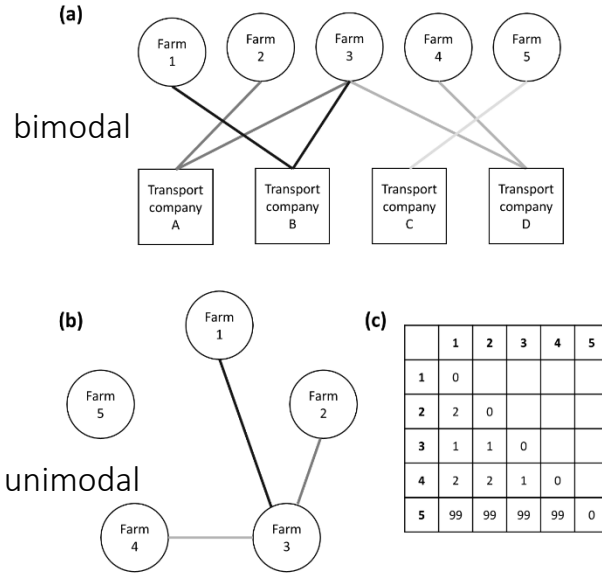
Transmission in the poultry industry



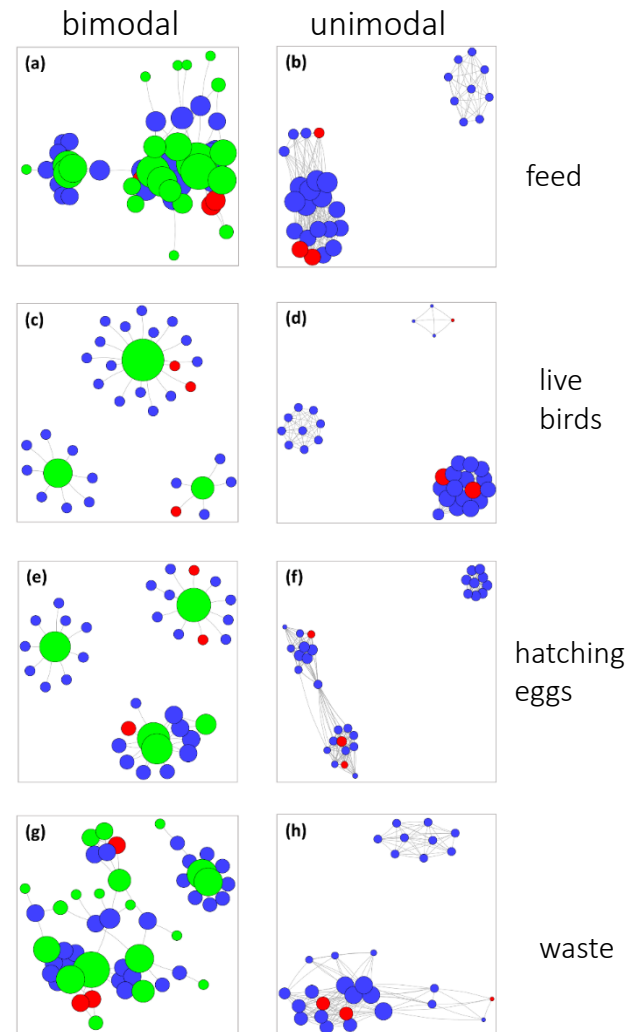
Comparing genetic relatedness of isolates revealed association with parent company and geographical location (evidence of local spread)



Modelling genetic distance and potential transmission networks

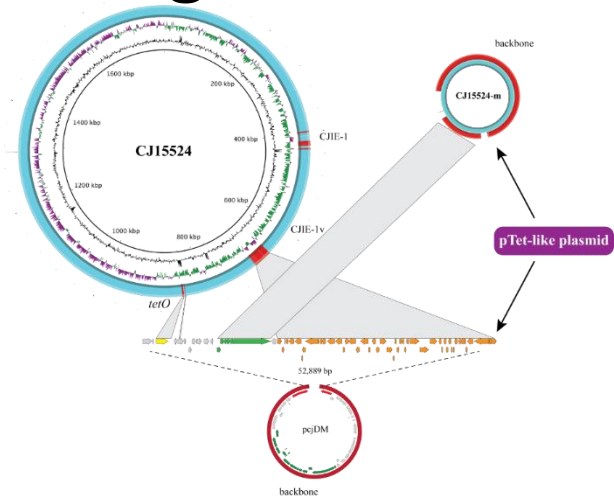


Multivariable model (Distance-based redundancy analysis):
 Parent company, farm and road and feed networks associated with genetic distance



Key questions addressed by whole genome sequencing

- How long has it been in NZ?
 - ~mid-late 2013.
- How has it been transmitted between poultry companies?
 - Within company
 - Local spread – road/feed network
- What is the main source of infection?
 - All companies contributing to human infection
- Genetic basis for resistance?
 - megaplasmid and mutation



Genomic Analysis of Fluoroquinolone- and Tetracycline-Resistant *Campylobacter jejuni* Sequence Type 6964 in Humans and Poultry, New Zealand, 2014–2016

Nigel P. French, Ji Zhang, Glen P. Carter, Anne C. Midwinter, Patrick J. Biggs, Kristin Dyet, Brent J. Gilpin, Danielle J. Ingle, Kerry Mulqueen, Lynn E. Rogers, David A. Wilkinson, Sabrina S. Greening, Petra Muellner, Ahmed Fayaz, Deborah A. Williamson



genomeA[®]nnouncements



Whole-Genome Sequencing of a *Campylobacter jejuni* Strain Isolated from Retail Chicken Meat Reveals the Presence of a Megaplasmid with Mu-Like Prophage and Multidrug Resistance Genes

Daya Marasini, Mohamed K. Fakhr

Department of Biological Science, The University of Tulsa, Tulsa, Oklahoma, USA

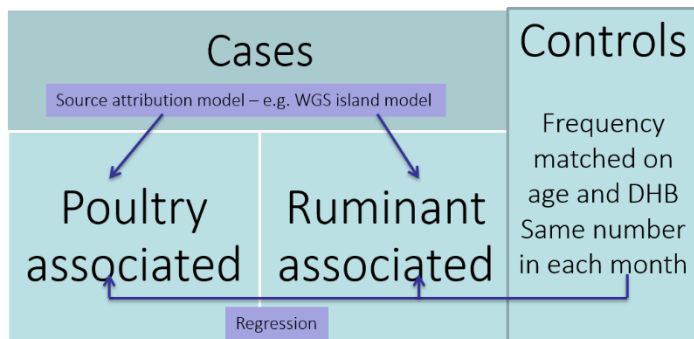
Genome sequencing of *Campylobacter jejuni* strain T1-21 isolated from retail chicken meat revealed the presence of a chromosome of 1,565,978 bp and a megaplasmid of 82,732 bp that contains Mu-like prophage and multidrug resistance genes. This is the first reported sequence of a *Campylobacter* megaplasmid >55 kb.

Public health significance?

- Resistant to two classes
 - Unless invasive, antibiotics not recommended
 - Sensitive to GP drug of choice, erythromycin
 - ...but others still given by some GPs
- New strain hasn't caused increase in notifications
- But potential for spread of other, more virulent pathogens

Symptom/treatment	Auckland (%)	Manawatu (%)
Hospital admission	59/445 (13.3)	36/220 (16.4)
Antibiotics	159/442 (36.0)	94/217 (43.3)
Type of antibiotics		
Cipflox	2/147 (1.4)	0/87 (0.0)
Ciprofloxacin	28/147 (19.1)	11/87 (12.6)
Ciproxin	2/147 (1.4)	2/87 (2.3)
E-Mycin	10/147 (6.8)	6/87 (6.9)
ERA	1/147 (0.7)	0/87 (0.0)
Erythromycin	53/147 (36.1)	36/87 (41.4)
Norfloxacin	3/147 (2.0)	2/87 (2.3)
Other	48/14 (32.7)7	30/87 (34.5)

Source Assigned – case control study design using WGS



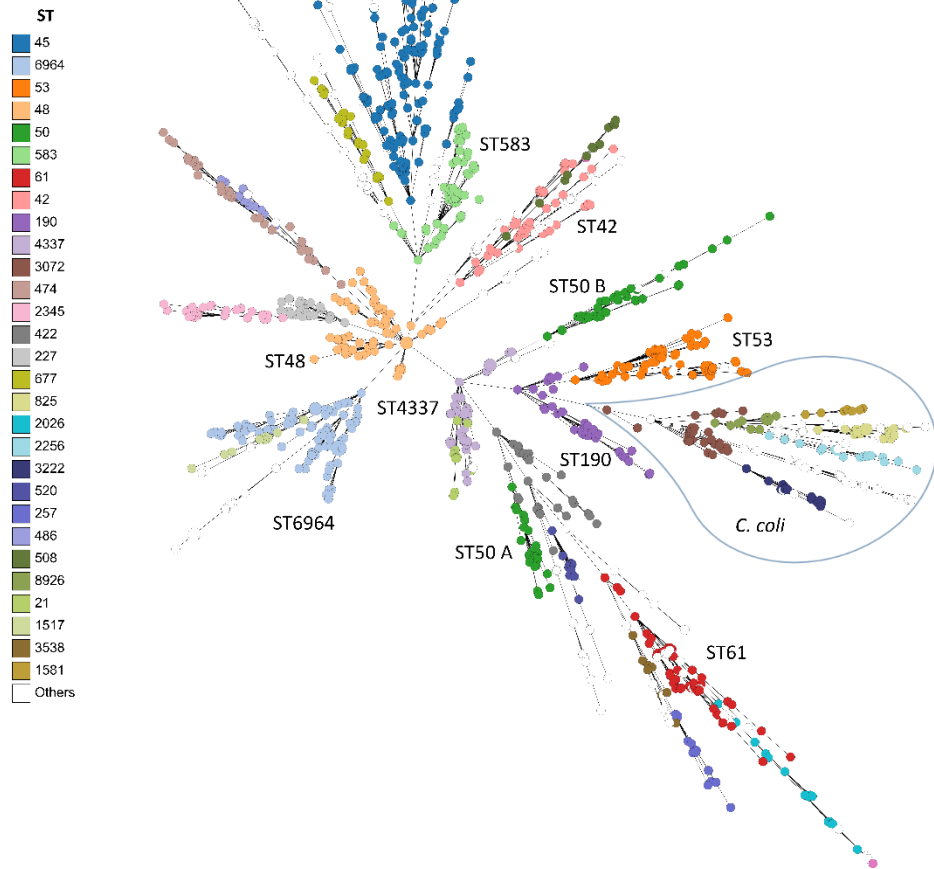
> [Int J Infect Dis.](#) 2020 Nov 19;S1201-9712(20)32479-6. doi: 10.1016/j.ijid.2020.11.167.
Online ahead of print.

Source attributed case-control study of campylobacteriosis in New Zealand

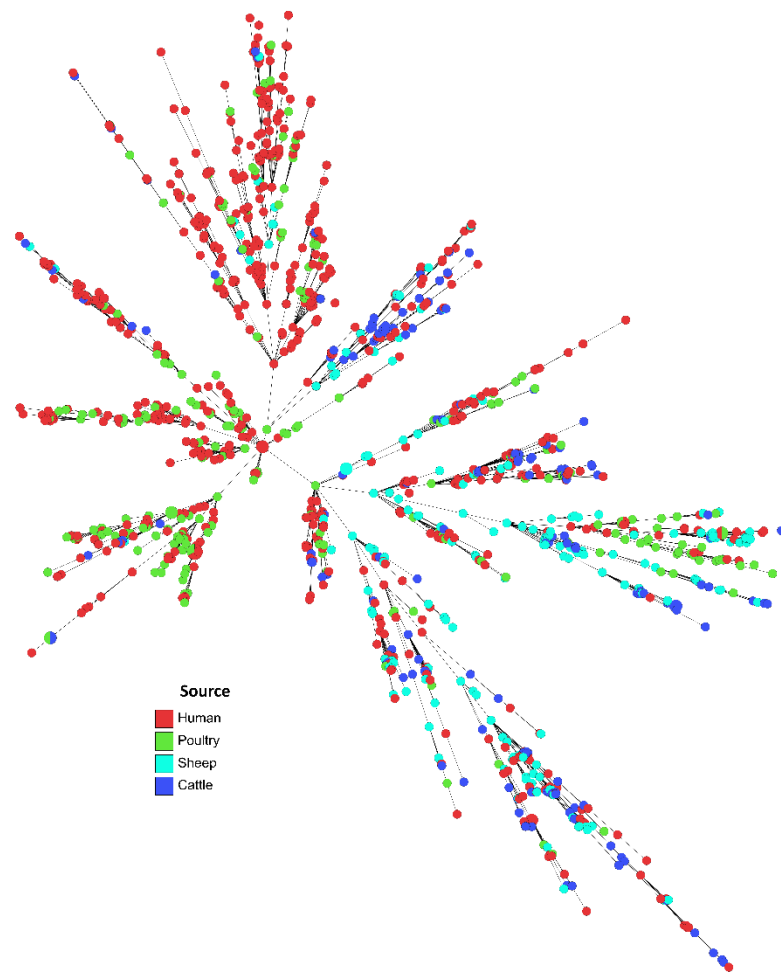
R J Lake ¹, D M Campbell ², S C Hathaway ³, E Ashmore ⁴, P J Cressey ⁵, B J Horn ⁵, S Pirikahu ⁶,
J M Sherwood ⁷, M G Baker ⁸, P Shoemack ⁹, J Benschop ¹⁰, J C Marshall ¹¹, A C Midwinter ¹⁰,
D A Wilkinson ¹⁰, N P French ¹²

- Conducted 2018-19
- >600 cases, 600 controls
- Over 150 isolates each from poultry, cattle, sheep
- >1200 isolates sequenced
- Risk factors associated with poultry and cattle

A



B



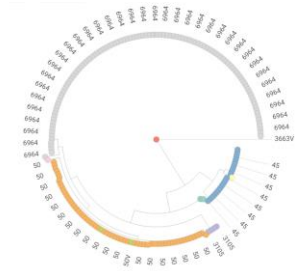
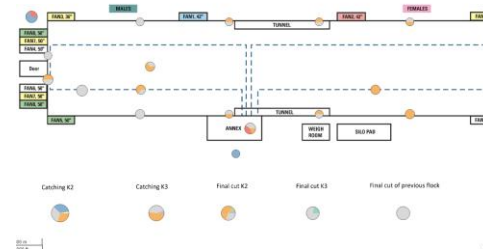
Current situation

Sequence type	Number of isolates by source				
	Human	Cattle	Sheep	Poultry	Total
45	119	2	9	24	154
48	46	-	-	24	70
583	42	2	-	8	52
6964	41	-	-	44	85
53	40	22	6	11	79
50	31	7	17	9	64
677	25	-	-	1	26

- ST-6964 was 4th most prevalent in human cases in 2018/19
- Most prevalent in poultry
- Recent work with industry indicates carry-over between flocks important for ST6964 transmission

Source SACNZ study

<https://microreact.org/project/ds4r5sfegYQaHg4mzttZCo>



<https://www.mpi.govt.nz/dmsdocument/39896-source-assigned-campylobacteriosis-in-new-zealand-study-sacnzs-report>

Conclusions

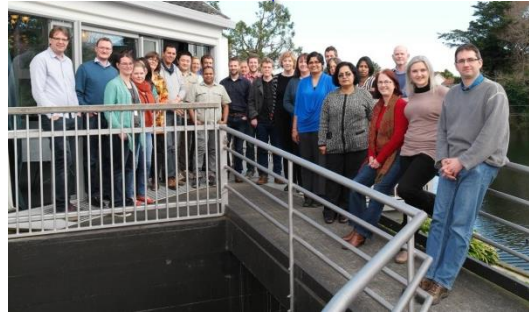
- Campylobacteriosis still concerning for New Zealanders despite significant gains in 2006/7
 - Sporadic food-associated cases
 - Large waterborne outbreak in 2016
 - Emergence of AMR linked to poultry consumption
- Poultry industry, government and research providers working together to achieve targets and further drive down contamination and notification rates
- AMR situation can change very rapidly
- MPI new strategy
- Advances in genome sequencing and modelling playing increasingly important roles in determining origin, evolution, transmission and prevention



Requires a One Health approach

Acknowledgements

- ^mEpiLab team: particularly David Wilkinson, Ji Zhang, Jonathan Marshall, Patrick Biggs, Lynn Rogers and Anne Midwinter
- Carolyn Gates, Sabrina Greening, Jing Liao, Marti Anderson, Petra Mullner and Martin Hazelton
- ESR: Rob Lake, Phil Carter, Brent Gilpin, Kristen Dyet
- University of Melbourne: Debbie Williamson, Ben Howden, Dieter Bulach, Glen Carter, Sarah Baines, Anders Gonçalves da Silva, Danielle Ingle
- University of Otago: Michael Baker
- MidCentral Public Health, MedLab Central
- Ministry for Primary Industries team: Donald Campbell, Steve Hathaway
- Poultry Industry Association



Funding

