

Cryptic sources of New Zealand yersiniosis

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Questions

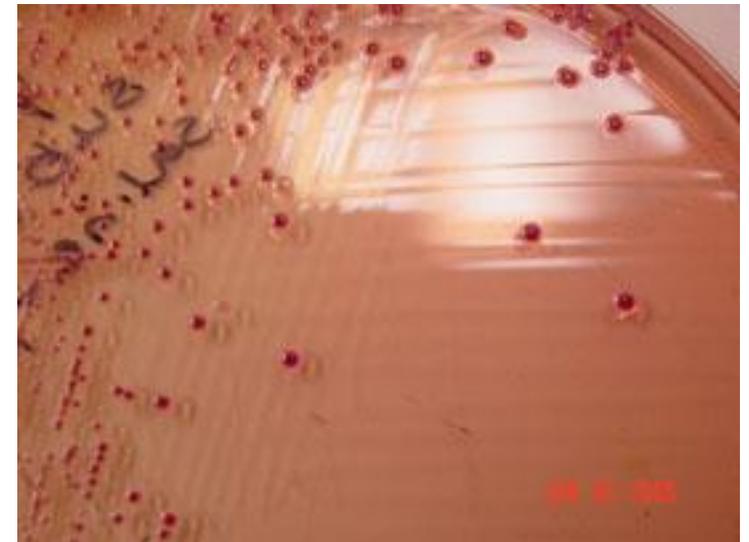
What are the sources of human yersiniosis in New Zealand?

- Contamination by ruminants?
- Other food-associated animals?

Using whole genome sequencing

Methods

- Samples from (healthy) animals, water, soil, sick animals
- Isolated *Yersinia*
- Identified by MALDI-TOF
- Genome sequenced



(FDA Bacteriological Analytical Manual)

Results: Detection and typing

host	# samples	# pooled samples	# Yersinia pos.	# <i>Y. enterocolitica</i> or <i>Y. pseudotuberculosis</i>	# genomes sequenced	comments
exotic animals	2	2	1	1	1	
calves/cows	526	145	21	6	10	
sick livestock	70	70	20	20	20	
sheep	518	135	20	11	13	(2 from the same sample)
mice	195	76	7	5	6	
rats	22	14	1	0	1	
hedgehogs	25	18	5	2	3	
rabbits	2	2	1	0	1	
mustelid	5	5	1	2	2	(both isolates from the same animal)
dog	1	1	1	0	0	
native birds	1	1	1	1	1	
nematodes	24	24	4	4	3	(from one packet of commercial nematodes)
water	26	26	5	0	1	

Negative samples: cats (n=4), possums (n=15), soil (n=17).

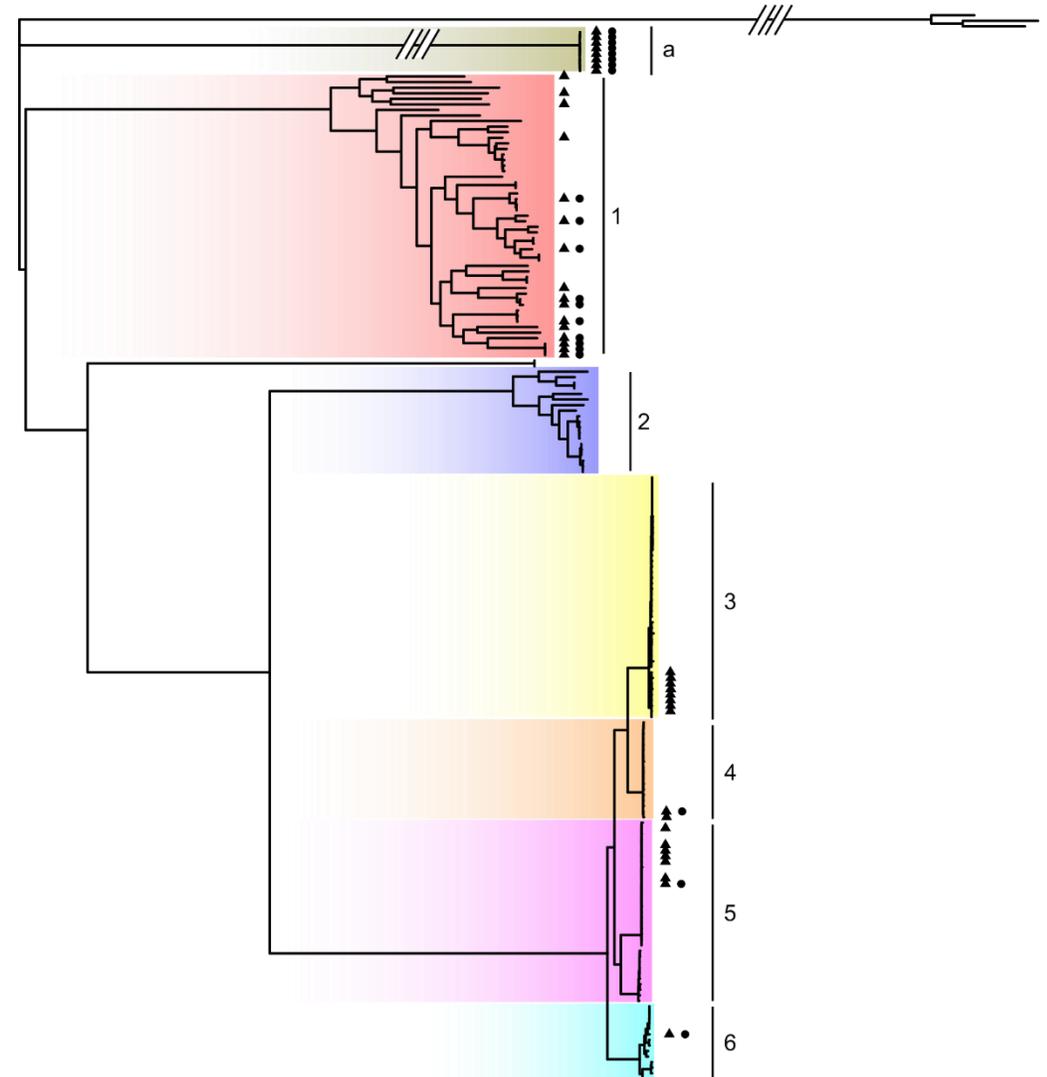
Samples obtained through microbiology labs as part of routine diagnostic practice (NZVP IDEXX)
Or through separate projects (relevant animal ethics code: MUAEC Protocol 16/92)

Results: Genomics

- Part 1 (*Y. enterocolitica*):
 - *Y. enterocolitica* isolates belonged to seven separate genetic groups.
 - One of these groups was only observed in New Zealand mammals (sheep and mice), is atypical and previously undescribed (a).

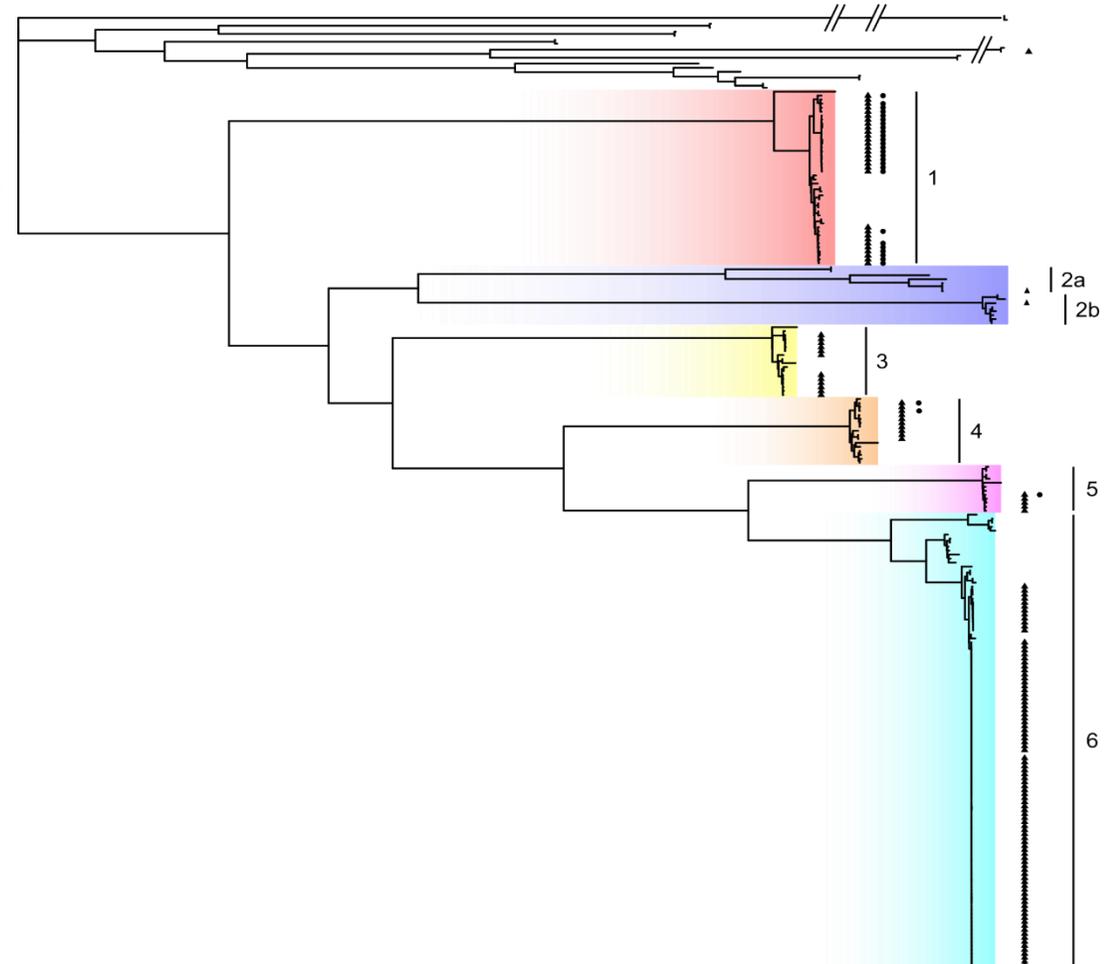
• = this study

▲ = NZ genome



Results: Genomics

- Part 2 (*Y. pseudotuberculosis*):
 - NZ *Y. pseudotuberculosis* isolates belonged to six separate genetic groups.
 - The outbreak was due to Clade 6
- = this study
- ▲ = NZ genome



Conclusions

- *Yersinia* are carried by a wide variety of hosts and host-specificity is not tightly linked to genomic clade
- *Y. enterocolitica* may have virulence-related genomic associations
- Human *Y. pseudotuberculosis* may be associated with livestock strains

Acknowledgements



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