

# Yersiniosis – a One Health approach for a growing problem in New Zealand.

**Lucia Rivas**<sup>1</sup>, Jackie Wright<sup>1</sup>, Hugo Strydom<sup>1</sup>, Jing Wang<sup>1</sup>, Shevaun Paine<sup>1</sup>, Sarah Jefferies<sup>1</sup>, Brent Gilpin<sup>1</sup> and Anne-Marie Perchec Merien<sup>2</sup>

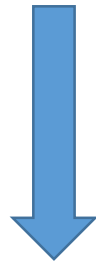
<sup>1</sup>Institute of Environmental Science and Research (ESR)

<sup>2</sup>Ministry for Primary Industries (MPI)

# Yersiniosis

- A disease in mammals that is caused by the bacteria *Yersinia*.

## *Y. pestis*



Plague "Black Death"

- 50 million deaths across Africa, Asia and Europe in the 14th Century. It wiped out up to half of Europe's population.
- Still exists today (not in NZ)

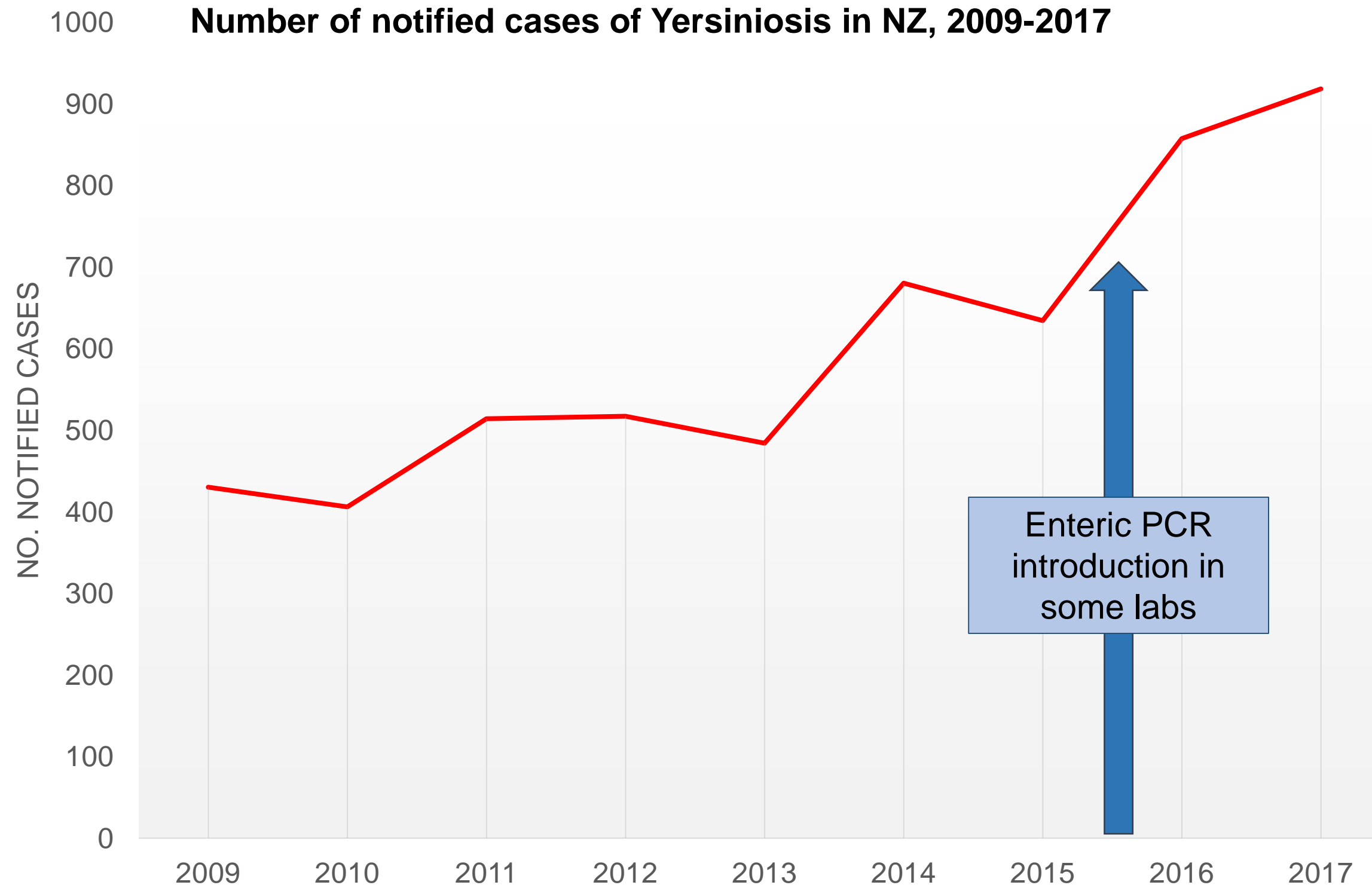


## *Y. enterocolitica* (YE) and *Y. pseudotuberculosis*

### Symptoms:

- Diarrhoea
- Stomach cramps (can be confused with appendicitis)
- Vomiting
- Fever
- Usually starts within a few days but generally <10 days after contact and usually lasts 2-3 days but can last as long as 3 weeks

# Yersiniosis is an emerging problem in NZ



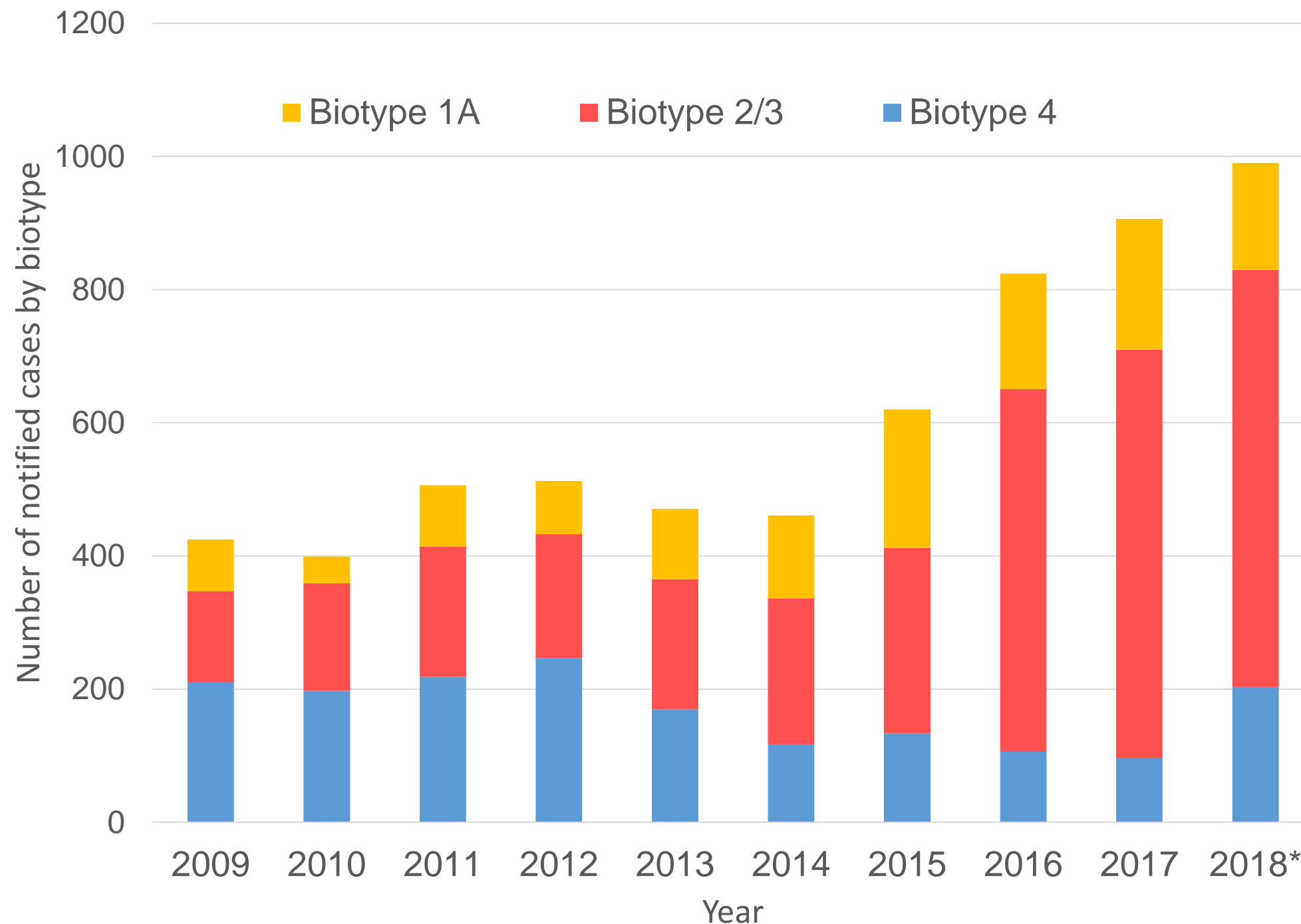
- The rate is higher in NZ than many other developed nations.
- E.g. In 2014, the European Union (EU; 25 countries) average rate was 1.8 per 100,000 population and Finland had the highest rate in the EU of 10.6 per 100,000\*.
- For NZ in 2014, the rate was **15.1** per 100,000.
- The introduction of Enteric PCR in some NZ regions began from 2015. Increase in notified cases was observed prior to introduction of the PCR.

Data from annual surveillance summaries: [https://surv.esr.cri.nz/surveillance/annual\\_surveillance.php](https://surv.esr.cri.nz/surveillance/annual_surveillance.php) and from Episurv Oct 2018

\*ECDC, 2017. <https://ecdc.europa.eu/en/publications-data/yersiniosis-annual-epidemiological-report-2016-2014-data>

# *Y. enterocolitica* - Biotyping

Number of notified cases of *Y. enterocolitica* by biotype, 2009 – Oct 2018



Data presented in the figure was extracted from EpiSurv (October 2018).

\*2018 only up to the end of October.

- In NZ, >99% of cases are due to *Y. enterocolitica*.
- *Y. pseudotuberculosis* usually very few cases (2014 outbreak. 220 cases, 72 hospitalisations).
  - <https://www.esr.cri.nz/home/about-esr/our-science-in-action/esrs-response-to-the-yersinia-pseudotuberculosis-outbreak/>
  - <https://www.mpi.govt.nz/dmsdocument/11030/loggedIn>
- **Biotyping** based on biochemical characteristics.
- **Biotype 2/3 and 4** = pathogenic (presence of plasmid and chromosomal virulence genes).
- Shift from biotype 4 to biotype 2/3 over the years. NZ is different to other countries where biotype 4 predominates in clinical cases.
- **WHY THE SHIFT AND DIFFERENCE?**
- **Biotype 1A** are classically considered as non-pathogenic in many countries.
- **WHY IS IT APPEARING IN CLINICAL CASES?**

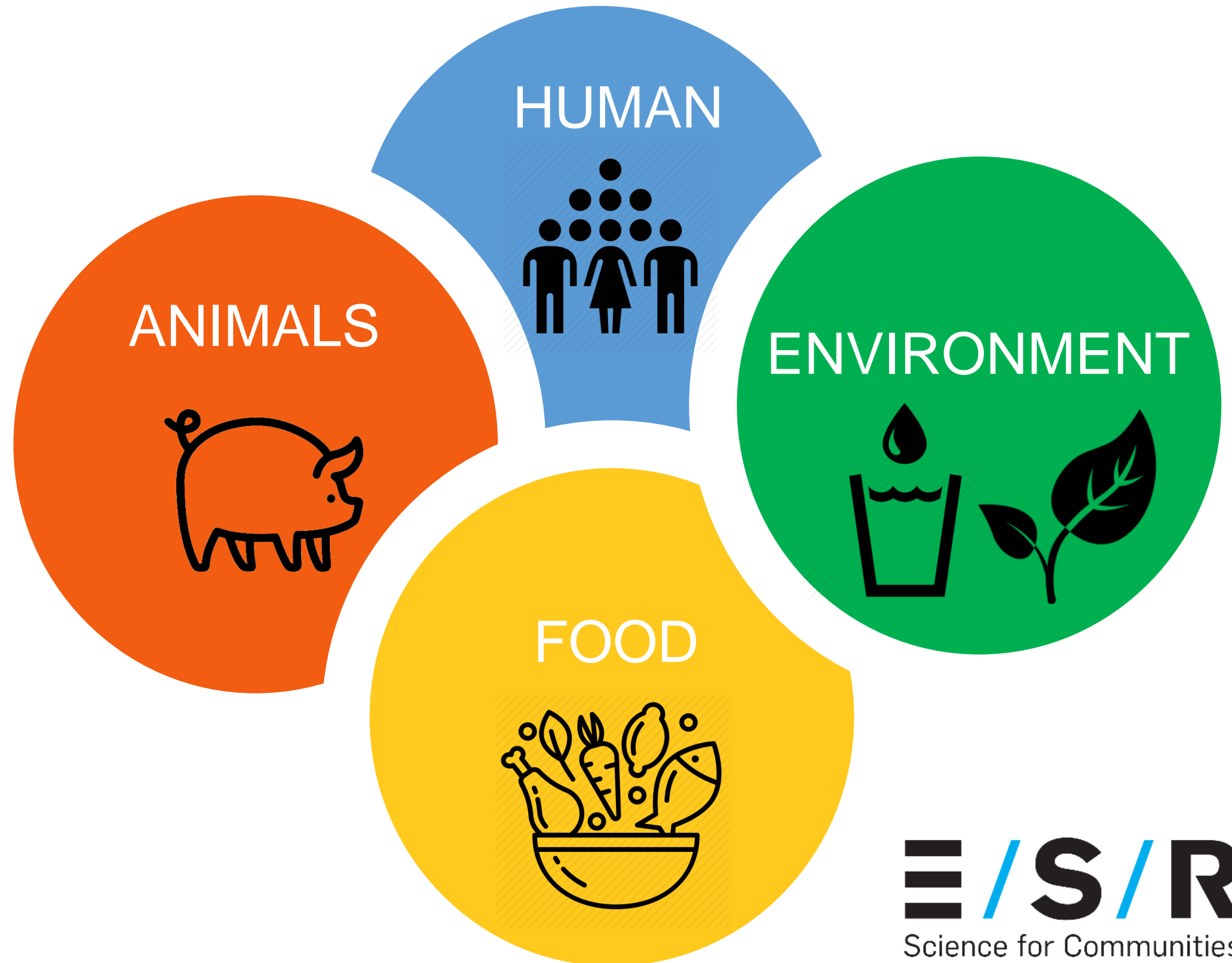


# What is the cause of all the yersiniosis?



## To discuss:

- The challenges that we are facing
- What information can we gain using a One Health approach?



- Estimated that the majority of cases of Yersiniosis is foodborne.
- *Y. enterocolitica*: Pigs are an important reservoir (YE biotype 4 predominates - also reported for NZ).
- Consumption of undercooked pork or cross contamination of other foods during handling and preparation of raw pork.
- Cross contamination of carcasses during slaughter.
- Interventions during slaughter can help.
- But YE has been isolated from cattle, deer, goats, dogs, cats, rodents and birds etc.
  - Are these sources contributing to human disease?

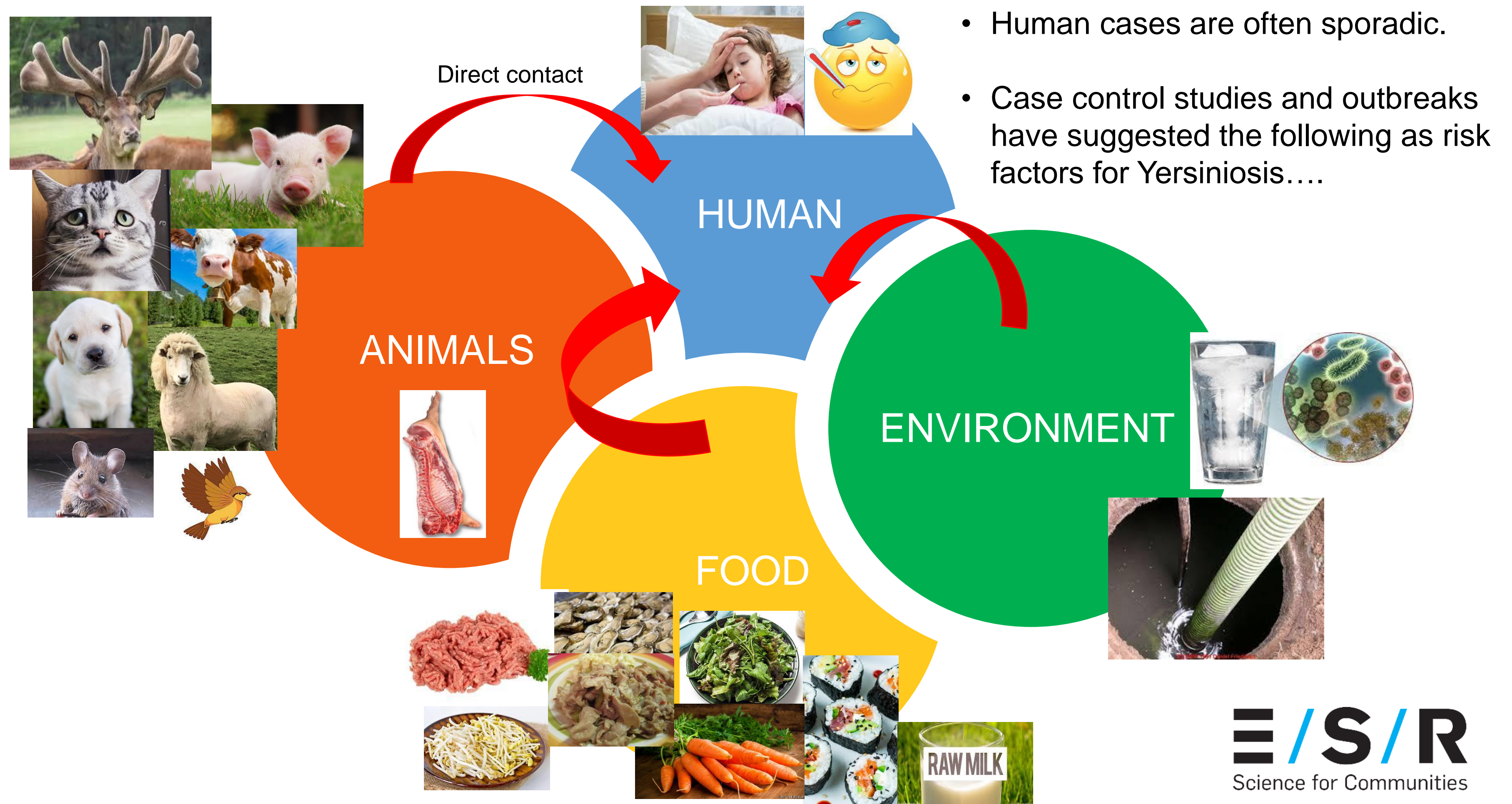
ANIMALS

FOOD

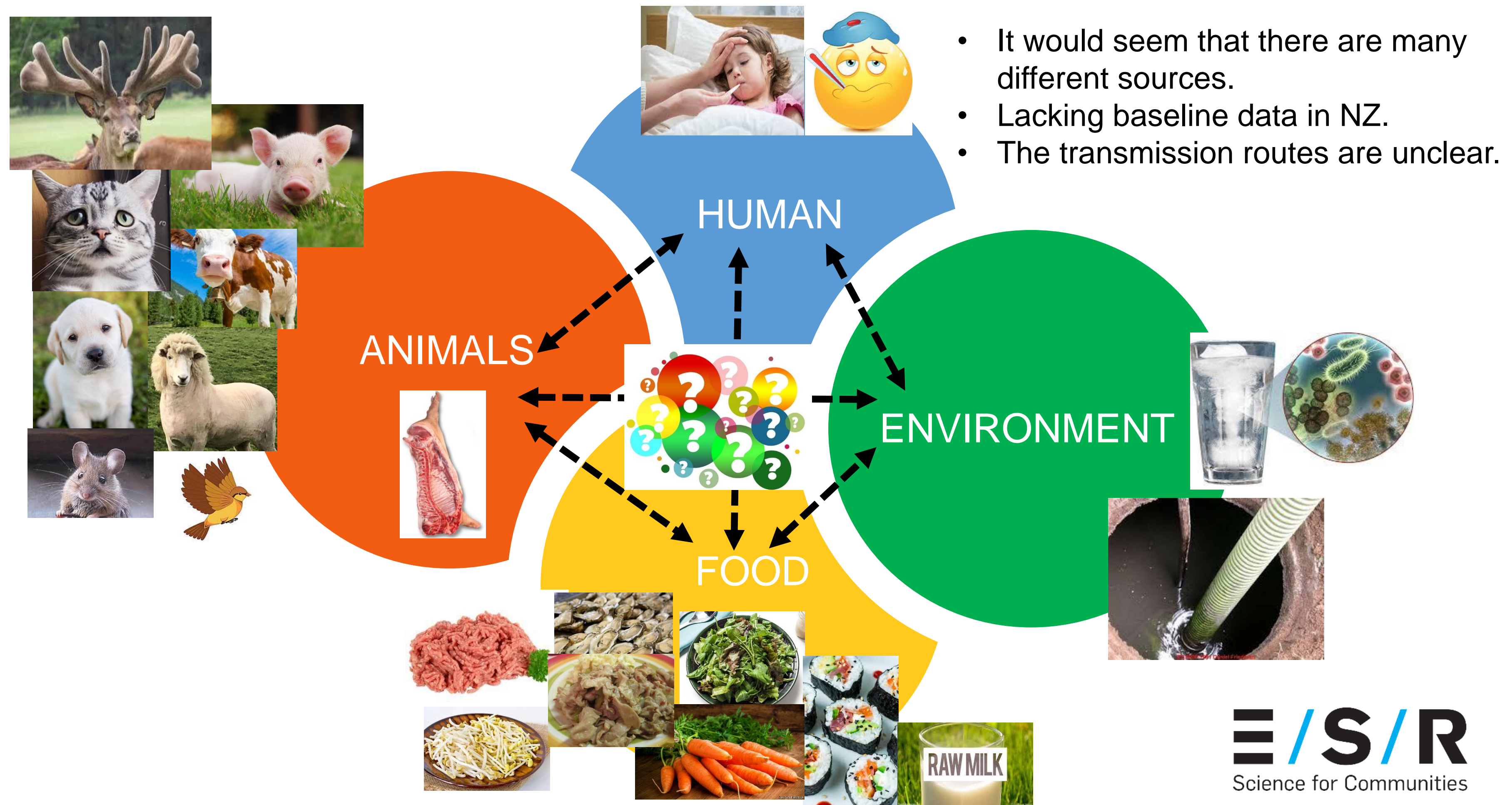
Some species of animals can get Yersiniosis as well.

Does that contribute to human disease?









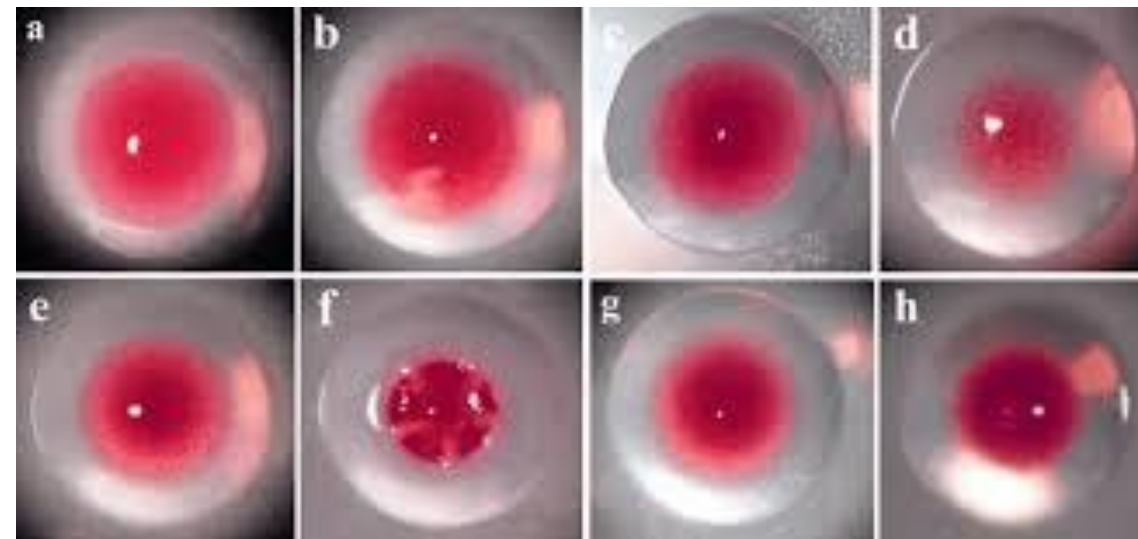


# The challenges...

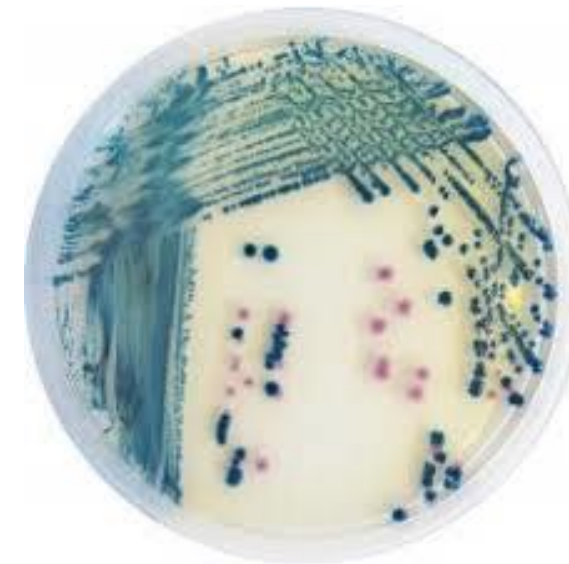
## Firstly....

Isolating *Y. enterocolitica* from foods is not easy.

- Standard international methods are insensitive and not very robust.
- Yersinia is present in foods in low numbers and it grows poorly amongst a high background flora.
- Cold enrichment usually needs a long time for incubation. Not practical for outbreaks.
- Recovery can depend on the biotype and matrix type (not one enrichment can be used)
- Molecular detection methods often do not detect YE biotype 1A (due to lack of common virulence genes used in these methods).
- ESR is working with MPI to make improvements in this area.



Different colony morphologies on CIN agar



ChromAgar Yersinia  
([www.chromagar.com](http://www.chromagar.com))

# The challenges...

## Secondly....

- Extended questionnaires administered by the District Health Board Public Health Units to notified cases are often by post, which results in a poor response rate (20%).
- In the few cases received, a potential source is rarely identified and the increasing number of cases, the turn-around-time and lack of sufficient resourcing prevents follow up and proper investigation.
- Can surveillance data help us?

**Notification rate per 100,000 population of selected enteric disease by ethnic group, 2017\***

Rate per 100,000	Māori	Pacific peoples	Asian	MELAA <sup>a</sup>	European or other	Total rate <sup>b</sup>
Campylobacteriosis	74.1	48	62.8	117.7	158.1	135.2
Yersiniosis	14.2	11.2	29.7	33.6	18	19.2
Cryptosporidiosis	19.3	15.6	8.5	22.4	28.2	24.9
Salmonellosis	15.6	16.7	16.5	24.3	25.9	23.3
VTEC/STEC infection	9.9	5.8	5.1	22.4	12.6	11.4

<sup>a</sup>MELAA = Middle Eastern/Latin American/African, <sup>b</sup>Total rate includes cases where ethnicity was unknown.

\*Pattis *et al.* (2018). Annual report concerning foodborne disease in New Zealand 2017. Draft report.

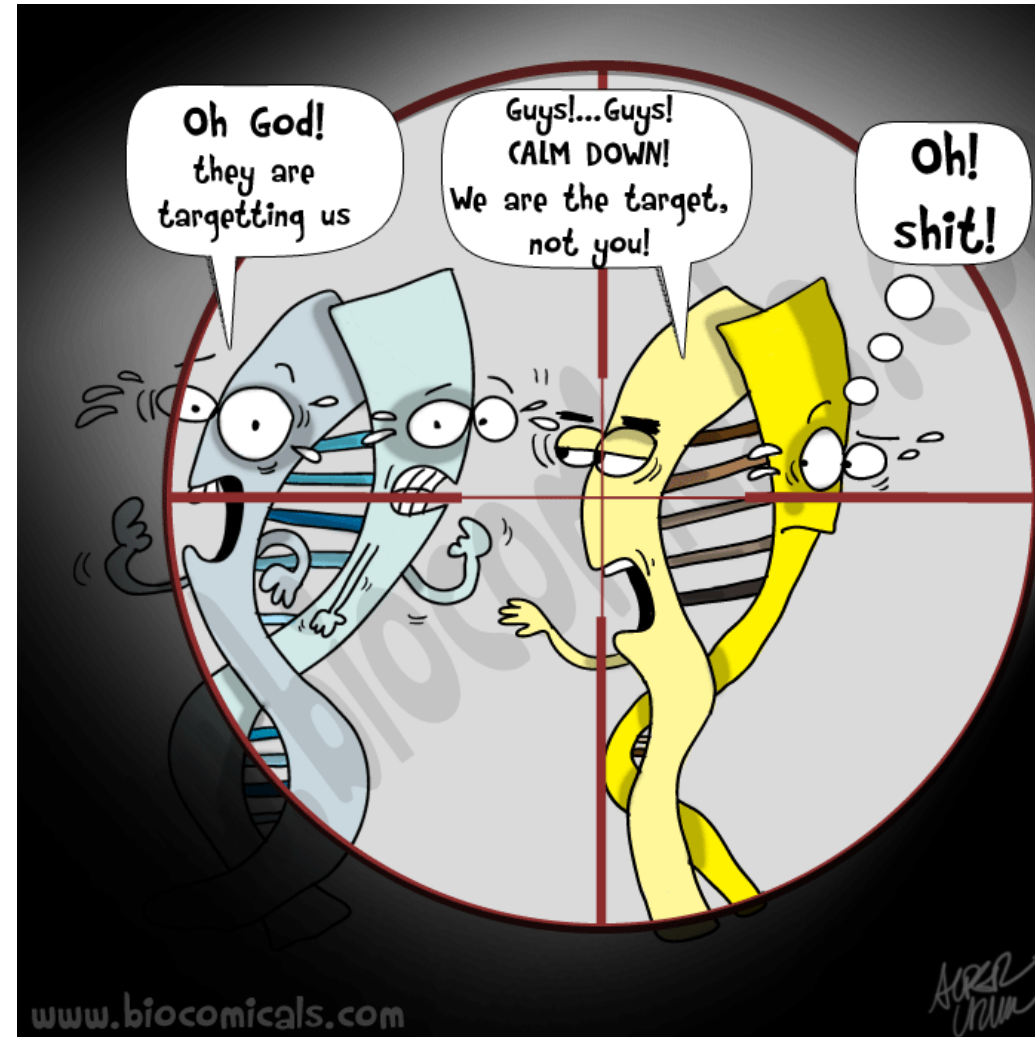
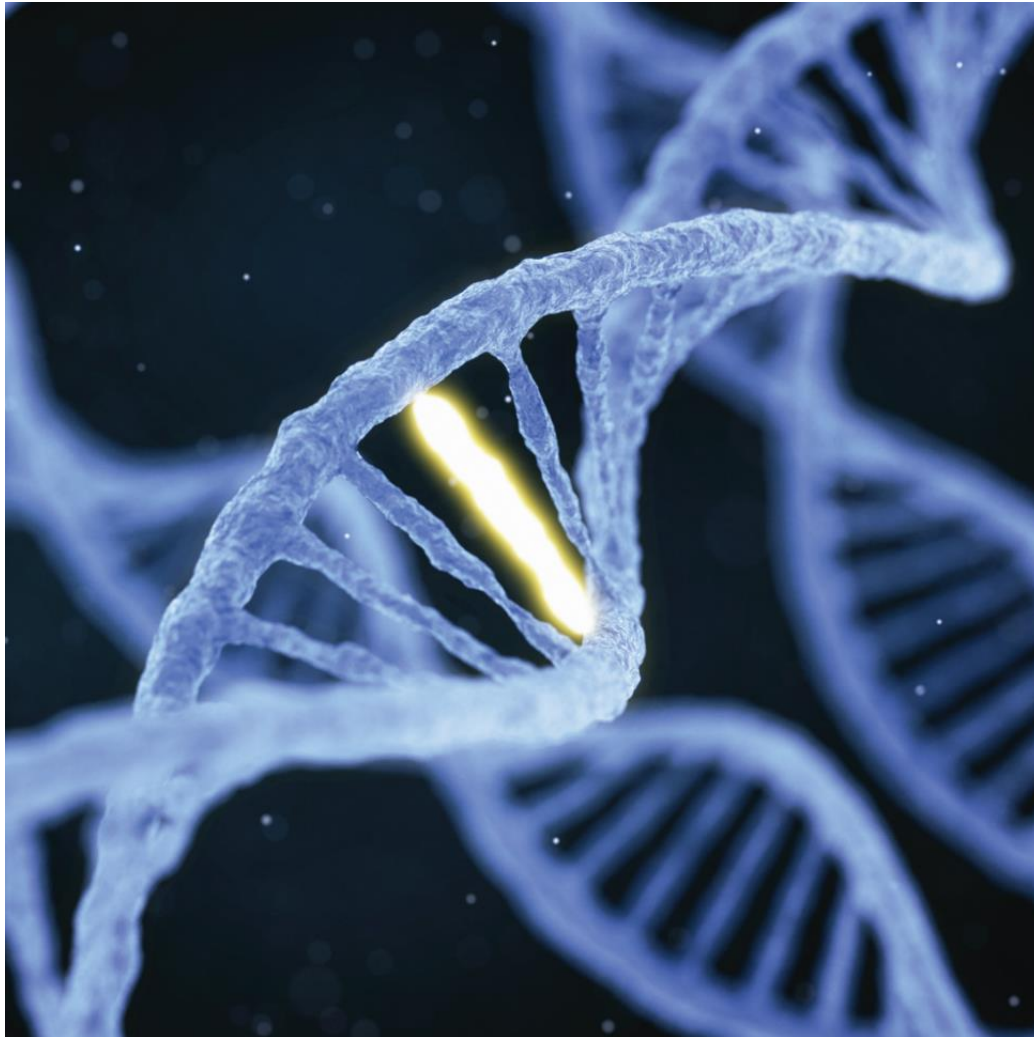
- People of Asian and MELAA ethnicity had higher notification rates for yersiniosis compared to other ethnic groups.
- Food sources that are more popular in these groups, food/cultural practices and preparation?

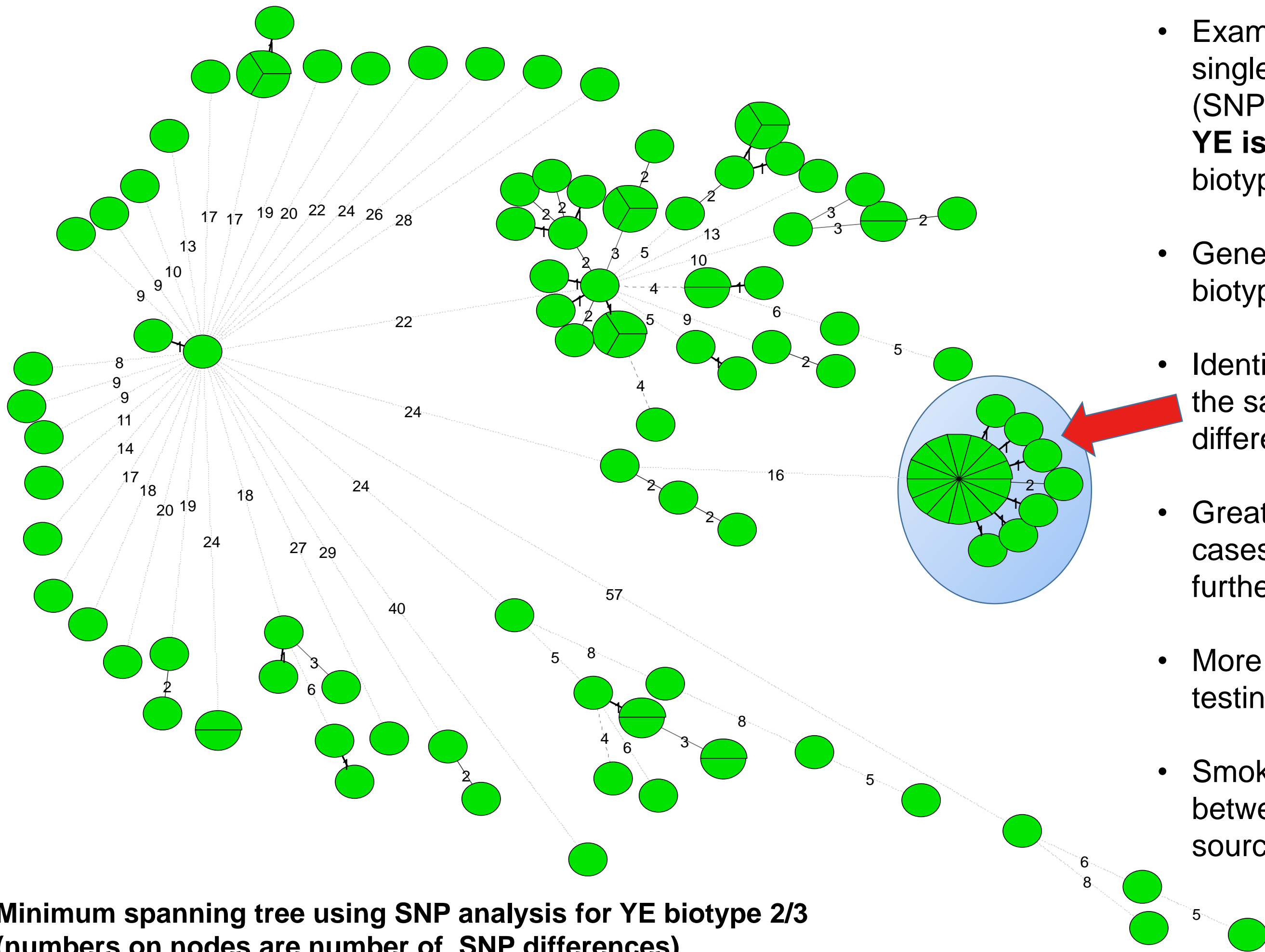


# The challenges...

## Thirdly...

- Traditional typing for *Y. enterocolitica* including biotyping lacks discriminatory power.
- Whole genome sequencing now offers sufficient resolution for more detailed and targeted characterisation of *Y. enterocolitica*.





**Minimum spanning tree using SNP analysis for YE biotype 2/3  
(numbers on nodes are number of SNP differences)**

- Example of using whole genome single nucleotide polymorphism (SNP) analysis on a **selection of YE isolates** (2014-2017, clinical, biotype 2/3)
- Genetic diversity within the same biotype(s)
- Identify outbreak isolates that are the same genotype (0-2 SNP differences between them).
- Greater potential to link human cases that can be investigated further.
- More animal/food/environmental testing.
- Smoking gun: same genotypes between human cases and other sources.



# Conclusions

- Increasing number of human yersiniosis in NZ.
- Epidemiology for *Yersinia* remains unclear in NZ.
- Lots of challenges in finding the sources and transmission routes.
- BUT there is a lot of potential to improve isolation methods and use better technologies to compare isolates from many sources.
- Collaboration helps!
- Are you working on *Yersinia*?
  - Workshop to be held as a part of the NZ Food Safety and Science Centre (March 2019).

Lucia (Lucy) Rivas  
[Lucia.Rivas@esr.cri.nz](mailto:Lucia.Rivas@esr.cri.nz)



# Acknowledgements

- ESR manages the national notifiable disease database, EpiSurv, on behalf of the New Zealand Ministry of Health.
- The Ministry for Primary Industries