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

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Yersiniosis

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

**Y. pestis**
- 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 and from Episurv Oct 2018
Y. *enterocolitica* - Biotyping

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

- Biotype 1A
- Biotype 2/3
- Biotype 4

- **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?**

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.mpi.govt.nz/dmsdocument/11030/loggedIn](https://www.mpi.govt.nz/dmsdocument/11030/loggedIn)
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?

Some species of animals can get Yersiniosis as well.

Does that contribute to human disease?
• Human cases are often sporadic.

• Case control studies and outbreaks have suggested the following as risk factors for Yersiniosis…. 
It would seem that there are many different sources.

Lacking baseline data in NZ.

The transmission routes are unclear.
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.
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*

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

\(^a\)MELAA = Middle Eastern/Latin American/African, \(^b\)Total rate includes cases where ethnicity was unknown.


• 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*.
- 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.

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

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