E/S/R Science for Communities



Salmonella Bovismorbificans in NZ, human infection and genomic perspectives

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NZ Human cases of Salmonella Bovismorbificans as a percentage of national E/S/R salmonellosis cases



2019: Laboratory testing 1/6 of NZ's faeces samples ceased referral of isolates to ESR for > 6 months 2020: The "COVID effect" on Enteric transmission and testing (https://surv.esr.cri.nz/enteric reference/human salmonella.php?we objectID=5138) resulted in only 726 isolates being referred for typing (cf the usual 1100 -1200 per year) 2021: 10 months only – January - October



Epidemiology

Cumulative Salmonella Bovismorbificans case numbers per age in years at presentation 2015 - 2020



EpiSurv 1615 hours 11 November 2021 data range: 01 Jan 2015 to 31 October 2021



Salmonella Bovismorbificans case





EpiSurv 1615 hours 11 November 2021 data range: 01 Jan 2015 to 31 October 2021



Geographical distribution

Salmonella Bovismorbificans cases by DHB by year (2021 = 10 months)



District Health Board

EpiSurv 1615 hours 11 November 2021 data range: 01 Jan 2015 to 31 October 2021



Severity and locality

Percentage of Salmonella cases hospitalised each year

	2015	2016	2017	2018	201
Bovismorbificans	20.0	34.2	15.7	34.2	21.
All Salmonellae	19.1	21.9	21.1	22.6	25.

Percentage of Salmonella Bovismorbificans rural vs urban cases each year

	2015	2016	2017	2018	2019	2020	2021 Ja Octobe
% Rural	10.0	40.0	60.0	34.2	32.6	32.8	32.3
% Urban	90.0	60.0	40.0	65.8	67.4	67.2	67.7

EpiSurv 1615 hours 11 November 2021 data range: 01 Jan 2015 to 31 October 2021



The Conundrum

Hindmarsh 8, [20] r 1, 5

A long term mainly ovine pathogen in NZ with relatively infrequent human infections being noted

Bovismorbificans 1 6,8,[20] r,[i] 1,5

A predominantly cattle and human pathogen having emerged in significant numbers since 2015

BUT

Both serotypes type as *Salmonella* Bovismorbificans through genomic serotyping pipelines.

As both are associated with different animal hosts, we saw a need to establish the genomic relationship of NZ isolates to determine how we manage recognition and differentiation going forward on behalf of NZ zoonotic epidemiology.



Strategic Science Investment Fund Project E/S/R

107 NZ Bovismorbificans comprising

- 74 bovine (14 pre 2015 and 10 from each year 2015 & on)
- 26 Human
- 2 ovine
- 2 canine
- 3 food

45 NZ Hindmarsh comprising

- 38 Ovine
- 3 bovine \bullet
- 4 human

Analysed via whole genome sequencing (WGS)



SSIF PRELIMINARY results - MLST

Achtman 7-gene Multi Locus Sequence Type (ST): Based on seven housekeeping gene fragments (aroC, dnaN, hemD, hisD, purE, sucA, and thrA).

ST may be synonymous with serotype or a serotype may be differentiated into a number of ST types

All Hindmarsh tested are a single unique ST (ST 8346) and thus readily distinguishable from the Bovismorbificans isolates tested

Achtman M, Wain J, Weill F-X, Nair S, Zhou Z, Sangal V, et al. (2012) Multilocus Sequence Typing as a Replacement for Serotyping in Salmonella enterica. PLoS Pathog 8(6): e1002776. https://doi.org/10.1371/journal.ppat.1002776 pmid:22737074





S Bovismorbificans 7-gene MLST types



These six infections appear to have originated from outside of NZ (Malaysia, Vietnam and Thailand)

Preliminary conclusion: The now endemic NZ Bovismorbificans strain is ST 377 Looking to Enterobase we see this ST is widely distributed with submissions originating from the UK, US, South America, Asia and Australia

Microreact visualization of the Salmonella Bovismorbificans and Hindmarsh study isolates. The tree is a maximum likelihood tree using core single nucleotide polymorphic (SNP) differences identified using Snippy 4. IQ-TREE was used for tree construction with 2000 ultrafast bootstrap.





 \bullet ST 377 isolates)



The emergent NZ Bovismorbificans strain is genomically highly conserved over eight years

Salmonella Give

- Salmonella Give in NZ humans historically associated with SE Asian travel history
- Since 2019 locally acquired human cases of infection are gradually emerging
- A small subset of NZ bovine isolates have been sequenced
- All are ST654
- There are 720 ST654 isolates uploaded in Enterobase.warwick.ac.uk predominantly from animals, animal feed and the environment in the Americas, the majority being from the US; with occasional human isolations from this region and human and other isolations from Europe.
- Internationally there are more than six ST types associated with *Salmonella* Give including: ST516, ST524, ST654, ST2709, ST2876, ST2903.
- It is noted that the Enterobase dataset does not represent worldwide trends, but rather what individuals select to upload from their work (ESR only routinely uploads) isolates for which we are seeking conferment of a new ST type).

In summary

- As new Salmonella serotypes and subtypes emerge in our farmed animal populations, human infections will follow
- Anecdotally initial locally acquired human infections are those cases with direct contact with infected animals and their products
- Infection will also emerge in domestic pets
- Overtime transmission from animal to human occurs via complex pathways, including the food chain
- Understanding these pathways is paramount to limiting transmission
- Ongoing surveillance of both animal and human strains is essential for identifying emerging types
- WGS coupled with detailed and timely epidemiological information are together a powerful combination in increasing our knowledge and interrupting spread
- Working together across organisations improves timeliness of recognition and intervention



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