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Salmonella Bovismorbificans: EPIDEMIOLOGY AND ANTIBIOTIC SUSCEPTIBILITY IN NEW ZEALAND CATTLE

Introduction

In August 2021, MSD Animal Health NZ initiated a project whereby they funded the three commercial veterinary diagnostic laboratories; Gribbles Veterinary (now Awanui), SVS Veterinary Pathology and IDEXX, together with the Cognosco veterinary laboratory, to conduct antibiotic susceptibility testing on all bovine *Salmonella* isolates that were serotyped at the Institute of Environmental Science and Research (ESR) through the Ministry

for Primary Industries (MPI) Animal Health Surveillance programme. Because of the significant benefit this work could provide for animal health in New Zealand, MPI and MSD agreed the data from this project would be stored in MPI’s Surveillance & Incursion Investigation’s (S&II) Surveillance Information Management System (SIMS) and, in agreement with MSD, would complement the other animal health data already collected by S&II as part of their surveillance activities.

Figure 1: Predominant bovine *Salmonella* serotypes (left axis) and total cases (right axis) by year 2010–2023.

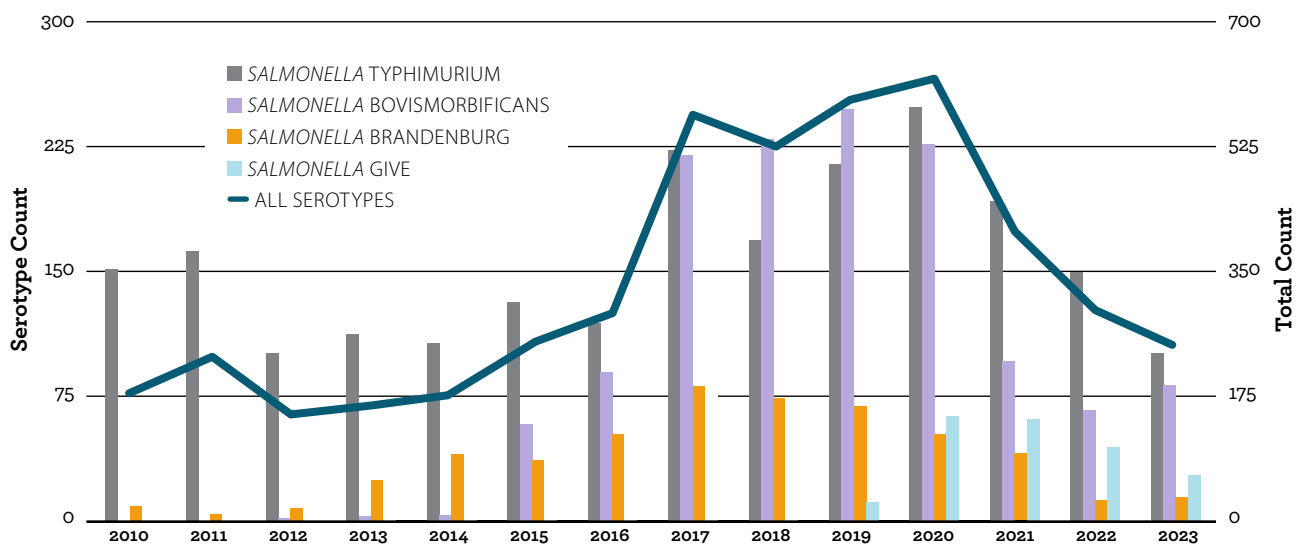


Figure 2: *Salmonella* cases diagnosed at Awanui Veterinary Laboratories in (A) calves/pre-production cattle (< 2 years of age) and (B) adult cows. The non-Bovismorbificans group includes all serotypes other than Bovismorbificans, excluding Brandenburg-associated abortions in A, which are presented separately in B for adult cows.



With the conclusion of this project in January 2024, MSD have agreed that MPI could publish the significant findings from this important piece of work.

In total 617 *Salmonella* isolates had antibiotic susceptibility testing undertaken using disc diffusion testing according to CLSI guidelines (CLSI Performance Standards for Antimicrobial Susceptibility Tests for Bacteria Isolated from Animals, 5th Edition). Of these isolates, 281 were *S. Typhimurium*, 164 were *S. Bovismorbificans*, 83 were *S. Give*, and 45 were *S. Brandenburg*. While the MSD

project has concluded, surveillance of antibiotic susceptibility in *Salmonella* spp. in the veterinary context (as well as other bacteria species) will continue via the Agricultural Compounds and Veterinary Medicines (ACVM) Antimicrobial Resistance (AMR) team's Animal Health AMR Surveillance programme. Data from this programme will continue to provide information that will augment this dataset allowing us to better understand trends over time.

Overseas, *S. Bovismorbificans* has caused human salmonellosis outbreaks in a number of countries, often associated with contaminated pork products, tahini, hummus, salad products and sprouted seeds. It is a relatively common isolate in both humans and cattle in Australia (Izzo and House, 2011; Stafford et al., 2002). Antimicrobial resistance including multiple drug resistance has been demonstrated in several studies (Izzo and House, 2011; Liesegang et al., 2002), the most recent detecting plasmid encoded resistance genes blaDHA-1 and qnrB4 in two *S. Bovismorbificans* isolates (Li et al., 2021).

Descriptive epidemiology

Before 2015, *Salmonella* Bovismorbificans was rarely isolated as a cause of salmonellosis in cattle. The predominant serotype was *S. Typhimurium* with cases of *S. Brandenburg* restricted predominantly to the South Island. However, in 2015 there was a sudden increase in cases of *S. Bovismorbificans*. This peaked in 2018 and 2019 when *S. Bovismorbificans* overtook *S. Typhimurium* as the most frequently detected serotype in bovine cases. Since 2020, cases numbers have gradually reduced to the point where detections in 2023 were slightly higher than those recorded in 2015, but significantly lower than the peak in 2019. Figure 1 shows this trend using data collected from the MPI Animal Health Surveillance programme; it therefore extends past the period during which the MSD project was being undertaken.

Cases of salmonellosis in cattle have predominantly occurred in adult dairy cows and calves on dairy farms or calf-rearing operations. Examination of the submissions through Awanui Veterinary's laboratories, which represent about two thirds of diagnosed bovine cases in New Zealand, indicates a similar number of cases occurring in adult dairy cows as in calves and preproduction animals (Figure 2). It should be noted that a single case may represent one animal or multiple animals on a farm.

continued

Table 1: *Salmonella* serotype by region of samples included in MSD project

| REGION | SALMONELLA GIVE | SALMONELLA BOVISMORBIFICANS | SALMONELLA TYPHIMURIUM | SALMONELLA BRANDENBURG | TOTAL |
|--------------------|-----------------|-----------------------------|------------------------|------------------------|------------|
| Gisborne | 0 | 1 | 0 | 0 | 1 |
| Marlborough | 0 | 0 | 0 | 1 | 1 |
| Tasman | 0 | 1 | 1 | 0 | 2 |
| Hawke's Bay | 1 | 1 | 1 | 0 | 3 |
| Wellington | 0 | 2 | 1 | 0 | 3 |
| West Coast | 0 | 0 | 2 | 2 | 4 |
| Auckland | 1 | 9 | 15 | 0 | 25 |
| Manawatu Whanganui | 0 | 13 | 13 | 0 | 26 |
| Bay of Plenty | 2 | 8 | 18 | 0 | 28 |
| Taranaki | 1 | 12 | 15 | 0 | 28 |
| Southland | 0 | 3 | 26 | 6 | 35 |
| Otago | 0 | 20 | 16 | 2 | 38 |
| Northland | 1 | 20 | 48 | 0 | 69 |
| Canterbury | 0 | 40 | 38 | 31 | 109 |
| Waikato | 77 | 34 | 87 | 3 | 201 |
| | 83 | 164 | 281 | 45 | 573 |

continued New Zealand human clinical cases of *S. Bovismorbificans* have followed a similar emergent pattern to cattle cases (Watts and Wright, 2021) and a number have been further characterised using whole genome sequencing analysis (manuscript in preparation, J Wright, pers. comm.).

Figure 4: Distribution of dairy farms within New Zealand

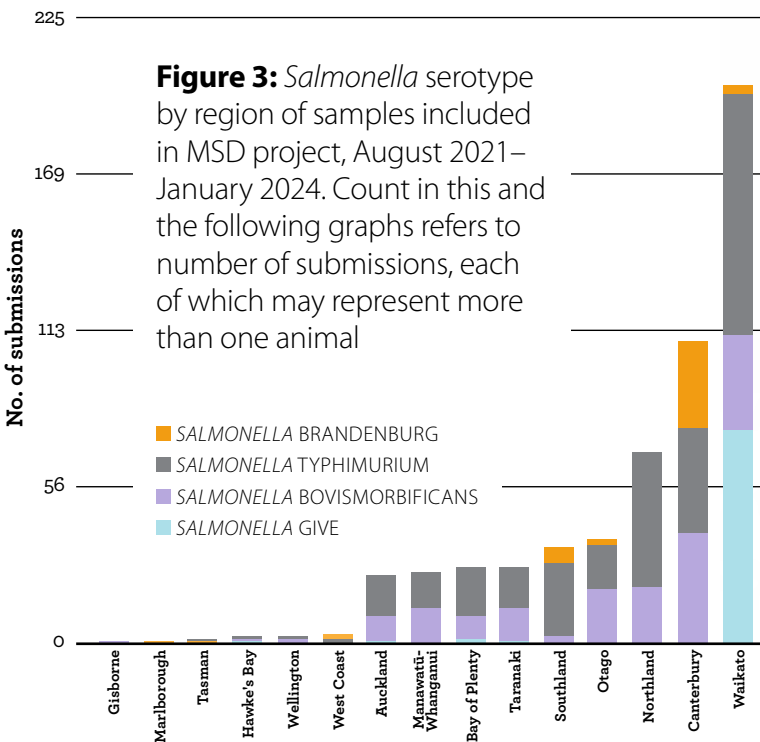
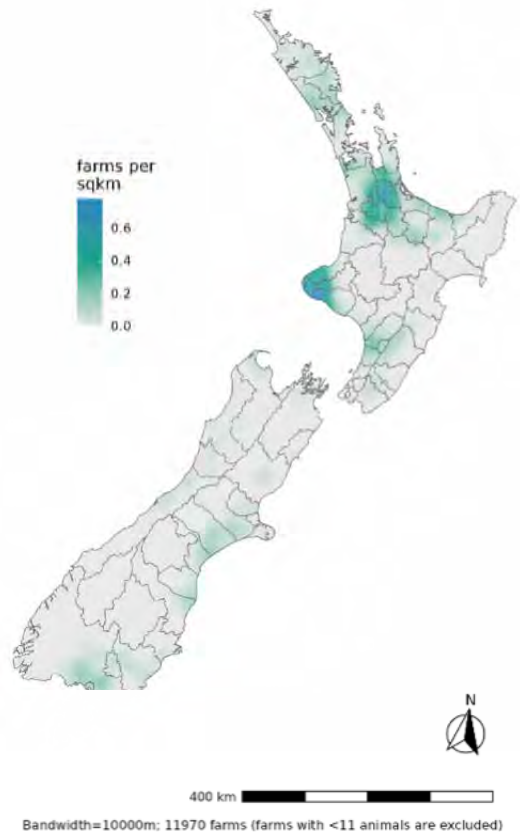


Figure 3: *Salmonella* serotype by region of samples included in MSD project, August 2021–January 2024. Count in this and the following graphs refers to number of submissions, each of which may represent more than one animal

Figure 5: *Salmonella* Bovismorbificans susceptibility to seven antibiotics (August 2021–January 2024).

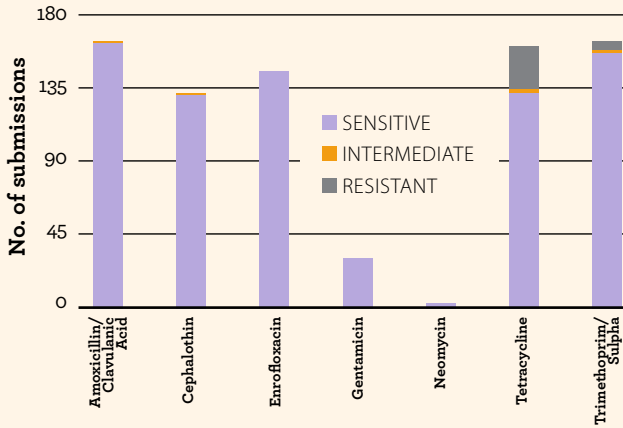


Figure 6: *Salmonella* Typhimurium susceptibility to seven antibiotics (August 2021–January 2024).

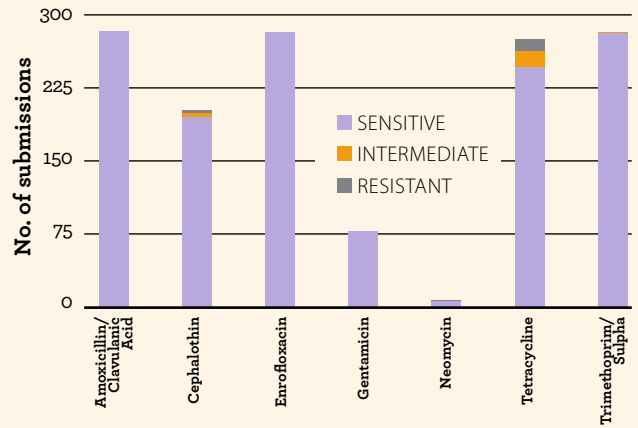


Figure 7: *Salmonella* Give susceptibility to seven antibiotics (August 2021–January 2024)

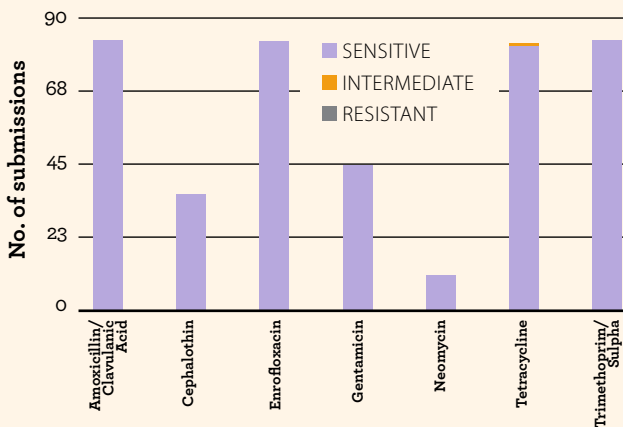


Figure 3 and Table 1 show the regional breakdown of serotypes that were tested as part of the MSD project. The majority of the serotypes came from Waikato, with 78/83 *S. Give* cases also coming from Waikato. *Salmonella* Brandenburg was mainly isolated from the South Island with only 3/45 cases reported from the North Island (Waikato). The spatial distribution of cases approximates the regions where dairy farm density is highest (Figure 4).

Note: In all tables and figures what is counted as a single submission may represent one or multiple animals.

While clinical information is often limited on submission forms accompanying samples, scouring was the most common clinical sign noted for Awanui

Figure 8: *Salmonella* Brandenburg susceptibility to seven antibiotics (August 2021–January 2024)

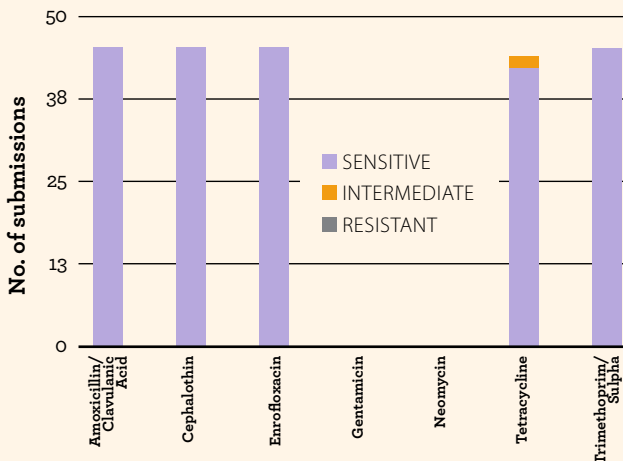
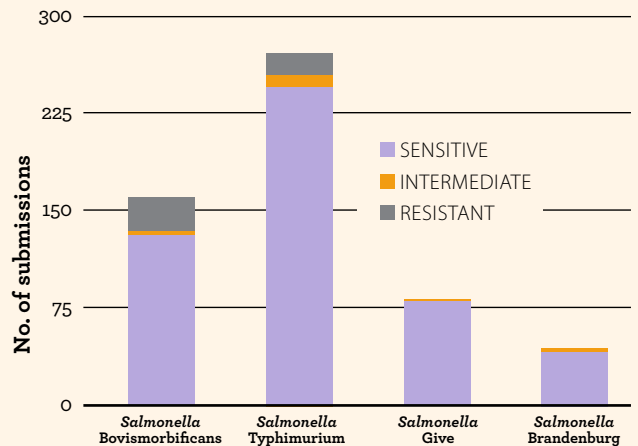


Figure 9: Tetracycline susceptibility by serotype (August 2021– January 2024)



continued

Table 2: *Salmonella* Bovismorbificans tetracycline susceptibility by region (count = number of submissions)

| REGION | SENSITIVE | | INTERMEDIATE | | RESISTANT | |
|--------------------|-----------|------------|--------------|------------|-----------|------------|
| | COUNT | PROPORTION | COUNT | PROPORTION | COUNT | PROPORTION |
| Hawke's Bay | 0 | - | 1 | 1 | 0 | - |
| Gisborne | 1 | 1 | 0 | - | 0 | - |
| Tasman | 1 | 1 | 0 | - | 0 | - |
| Wellington | 2 | 1 | 0 | - | 0 | - |
| Southland | 3 | 1 | 0 | - | 0 | - |
| Manawatū-Whanganui | 6 | 0.46 | 0 | - | 7 | 0.54 |
| Auckland | 7 | 0.78 | 1 | 0.11 | 1 | 0.11 |
| Bay of Plenty | 8 | 1 | 0 | - | 0 | - |
| Taranaki | 9 | 0.9 | 0 | - | 1 | 0.1 |
| Northland | 17 | 0.89 | 0 | - | 2 | 0.11 |
| Otago | 18 | 0.9 | 0 | - | 2 | 0.1 |
| Waikato | 27 | 0.79 | 0 | - | 7 | 0.21 |
| Canterbury | 33 | 0.83 | 0 | - | 7 | 0.18 |

continued

isolates included in the MSD project (76.8 percent, n = 311/405). Abortion was listed for 8.7 percent of adult cow cases and death was recorded for 11.3 percent of adult cow and 23.6 percent of calf cases. Where mortality data were available in calf cases (n = 31), the mortality rate ranged from 0.2 to 50 percent, representing between 1 and 100 dead calves.

Antibiotic susceptibility

Here we compare the antibiotic susceptibility of *S. Bovismorbificans* with that of *S. Typhimurium*, *S. Give* and *S. Brandenburg* (Figures 5–8).

In Figure 9, it is apparent, for tetracycline, *S. Bovismorbificans* has a higher proportion of resistant isolates compared with *S. Typhimurium* (17 percent vs 4 percent, respectively). On a regional basis, Waikato and Canterbury have developed more resistance than other regions of the country (21 percent and 18 percent, respectively), other than Manawatū-Whanganui with 54 percent of its isolates demonstrating resistance to tetracyclines, although it should be noted that this is based on low case submission numbers (13 cases, 7 resistant) (Figure 10 and Table 2).

To better understand how tetracycline susceptibility of *S. Bovismorbificans* isolates

has changed over the course of the project (2021–2023), Figure 11 shows both the counts per month for the three-year period as well as the proportion of resistance isolates as a rolling average. As can be seen, there has been a significant increase in proportion of resistant isolates in 2023 when compared to 2021 and 2022.

Figure 10: *Salmonella* Bovismorbificans tetracycline susceptibility profile by region: number of submissions

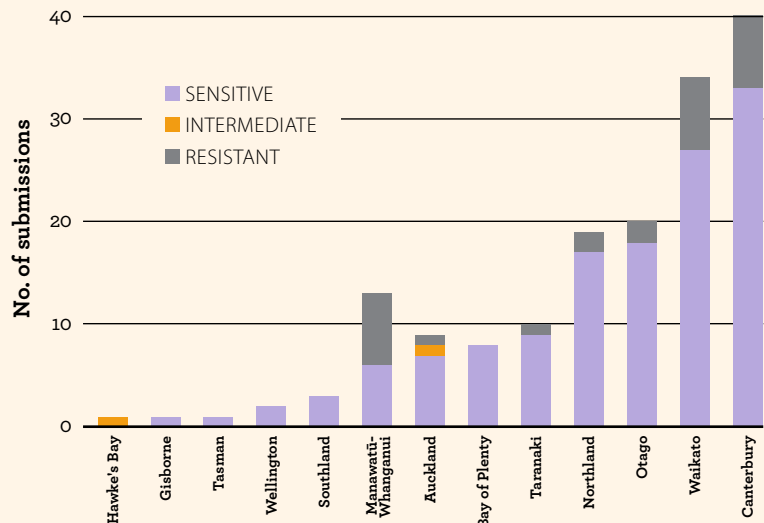
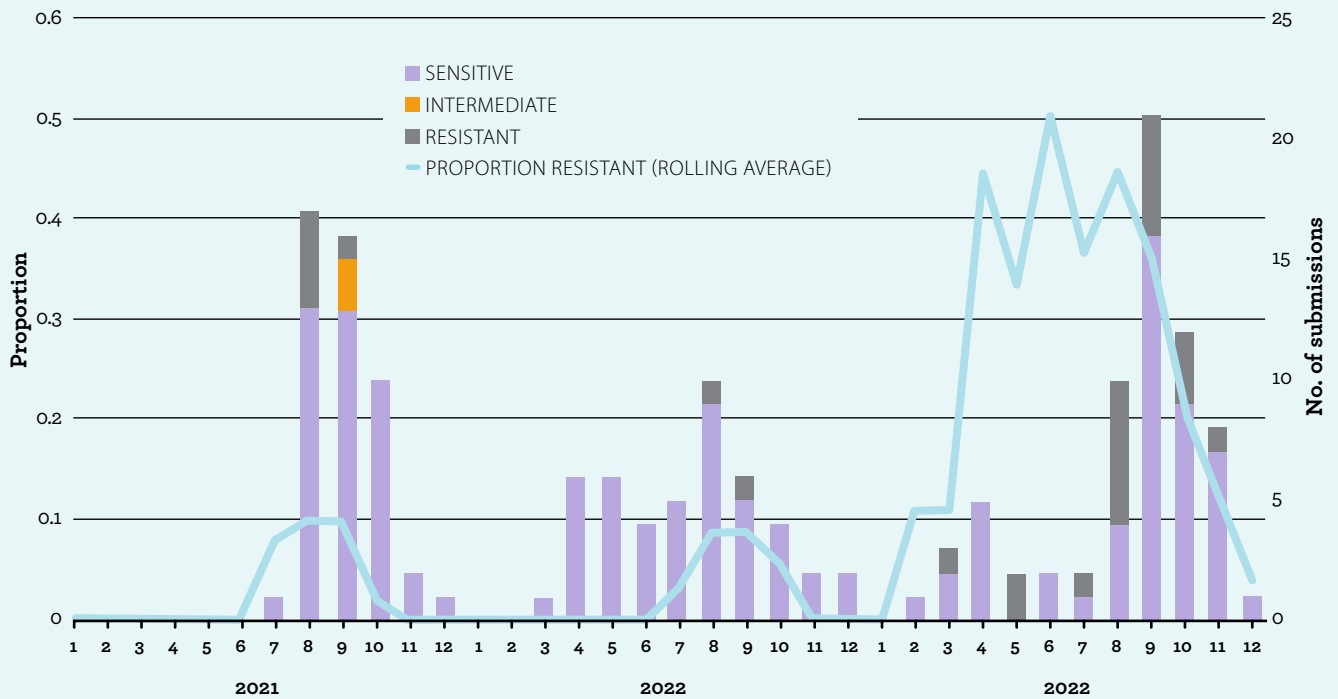


Figure 11: *Salmonella* Bovismorbificans tetracycline resistance time series (blue line is proportion rolling average)



Conclusion

As demonstrated in this report, based on the information collected over the three years of this project, resistance to tetracycline antibiotics in *S. Bovismorbificans* appears to be increasing.

Trends in tetracycline sales (indicative of usage) increased between 2018 and 2020 with most sales attributed to oxytetracycline. However, since 2020 oxytetracycline sales have steadily declined annually.

Antibiotic use data would provide more granularity and may help identify any links between tetracycline use and tetracycline resistance in *S. Bovismorbificans*. Currently no links can be identified but MPI’s AMR Team is developing a use-data collection system to support its AMR surveillance programme.

Acknowledgement

The authors would like to thank MSD Animal Health NZ for sharing this important dataset with them. Particular thanks go to Andrew MacPherson and Jo Holter for their management of the programme.

The AMR Team will continue to monitor and report tetracycline resistance trends in *S. Bovismorbificans*, *S. Typhimurium*, *S. Give* and *S. Brandenburg* in cattle as part of their antimicrobial resistance (AMR) surveillance reporting programme.

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