Timeliness of *Salmonella* Typhimurium notifications after the introduction of routine MLVA typing in NSW

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**Abstract:** *Salmonella* Typhimurium is the most common bacterial cause of gastrointestinal disease in NSW. Regular review of surveillance procedures ensures system objectives are met and informs improvements in system utility and efficiency. This paper assesses the timeliness and data completeness of NSW *Salmonella* Typhimurium surveillance after the routine introduction of multilocus variable repeat analysis (MLVA), a rapid sub-typing technique. MLVA results were available significantly earlier than alternate sub-typing techniques over the 2 years of this review. Accordingly, from a timeliness perspective, MLVA offers a favourable *Salmonella* Typhimurium sub-typing option in NSW. Further opportunities to improve timeliness and data completeness are identified. This paper was produced as part of a review of *Salmonella* Typhimurium surveillance in NSW for the period 2008–2009 by members of OzFoodNet based at Hunter New England Population Health. OzFoodNet is a national network established by the then Commonwealth Department of Health and Ageing in 2000 to enhance foodborne disease surveillance in Australia.

*Salmonella* Typhimurium (STm) is the most common *Salmonella* serotype in New South Wales (NSW); in 2009 STm accounted for 54% of all NSW *Salmonella* notifications<sup>1</sup> and 77% of Australian foodborne outbreaks with an identified causative agent.<sup>2</sup> STm is a heterogeneous *Salmonella* serovar, requiring additional sub-typing to identify outbreak-specific strains. Research exploring sub-typing techniques proffers multilocus variable repeat analysis (MLVA) as a rapid alternative to phage typing,<sup>3,4</sup> the sub-typing technique historically used in Australia. MLVA typing has been shown to successfully differentiate strains within phage types 135a and 170 that comprise more than half the STm isolates in NSW.<sup>5</sup> In 2006 and 2007, routine STm MLVA sub-typing was implemented in Queensland and NSW, respectively.

Regular review of public health surveillance determines the success of system objectives and informs refinement of system utility and efficiency.<sup>6,7</sup> The NSW *Salmonella* surveillance system involves a complex network of local and interstate laboratories and notification processes. Local primary laboratories identify *Salmonella* species (spp.), while serovar confirmation and MLVA typing occur at the closest reference laboratory, and phage typing at one of the two national phage typing laboratories (Institute of Medical and Veterinary Science (IMVS), Adelaide and Medical Diagnostic Unit (MDU), Melbourne). The NSW Public Health Act 1991 (and its subsequent revision in 2010) mandates laboratories to notify all confirmed *Salmonella* cases. In 2008 and 2009 notifications were entered into the NSW Notifiable Diseases Database (NDD) by Public Health Units (PHUs) for data collation, timely outbreak detection and disease control, key objectives of the NSW surveillance system.<sup>8</sup>

This paper assesses the timeliness and completeness of NSW *Salmonella* Typhimurium surveillance data after the routine introduction of MLVA. Serovar and MLVA notifications received in 2008 and 2009 were reviewed to identify opportunities for minimising delays.

**Methods**

The Centers for Disease Control and Prevention’s Updated Guidelines for Evaluating Public Health Surveillance Systems<sup>6</sup> were used as an evaluation framework for this investigation.

**Data sources**

STm notifications of NSW residents with a specimen collection date from 1 January 2008 to 31 December 2009 were identified and extracted in August 2010. As a
A new data management system (Notifiable Conditions Information Management System (NCIMS)) was instituted in May 2010, notifications were entered into the NDD during 2008 and 2009, but data were extracted from NCIMS in 2010. Additional milestone dates were obtained from the Institute for Clinical Pathology and Medical Research (ICPMR) electronic notifications and Queensland Health Forensic and Scientific Services (QHFSS), the NSW and Queensland reference laboratories, respectively. Other state reference laboratories were excluded as MLVA typing was not routinely conducted during the period of interest. NDD data comprised primary laboratory name and the date of *Salmonella* spp. receipt at the relevant PHU. ICPMR data included the following dates: specimen collection, *Salmonella* spp. identification, isolate receipt at ICPMR, and the electronic notification of serovar, MLVA and phage typing. The QHFSS dataset provided specimen collection date and the electronic notification dates of serovar and MLVA typing.

### Data management and analysis

The relevant ICPMR and QHFSS dates were added to the NDD data extraction using SAS software (version 9.2, SAS Institute, Cary, NC, USA).

Eight milestones of public health importance were used in the analysis (Figure 1). Completeness and accuracy of milestones affected the number of cases available for timeliness evaluation; accordingly, a review of data completeness was conducted. Data cleaning verified the accuracy of extracted data and guided exclusion of duplicate cases and repeat specimens (specimens less than 14 days apart). Additional quality assurance checks involved scrutiny and possible exclusion of unexpected dates, established by negative time between sequential surveillance milestones. Time intervals greater than 365 days were reviewed to determine validity and excluded where appropriate. A total of 2458 cases (94.3% of all STm notifications) were included in the analysis (Figure 2).

SAS software and Microsoft Excel 2010 were used for quality assurance checks, calculation of time intervals between milestones, and significance testing, using Wilcoxon rank sum test methodology.
Results

Timeliness

The timeliness of all STm milestones, determined by the median interval in days, with the exception of receipt of phage typing, remained relatively consistent over time (Table 1). MLVA notification occurred 23 days earlier than phage typing in 2008 (p < 0.001) and 44 days earlier in 2009 (p < 0.001). The median time interval for MLVA notifications decreased significantly from 23 days in 2008 to 21 days in 2009 (2 days’ decrease, p < 0.001).

Data completeness

Missing or invalid data were infrequent for most milestones, with a few notable exceptions (Table 2). The receipt of the initial Salmonella spp. report at PHU level was missing in 16.5% of cases and invalid in 1.3% of cases. Serovar identification date was missing in 5.4% of cases.

Sub-typing was not recorded for a small number of STm cases, including 17 serovar, 33 MLVA and 88 phage type results.

Anomalies in sequential notification

Given the consecutive nature of STm typing, milestone notification for MLVA and phage typing are expected to occur after serovar availability. Time interval analysis indicated this was not always the case. Serovar and MLVA typing results were received simultaneously in 1% of cases in 2008 and 6% of cases in 2009.

Discussion

Regular evaluation of public health surveillance is important to confirm system utility and efficiency. To our knowledge, this is the first report of MLVA timeliness in

Table 1. Elapsed days from specimen collection to Salmonella Typhimurium surveillance milestones, NSW residents, 2008–2009

<table>
<thead>
<tr>
<th>Milestone</th>
<th>Available records (n)</th>
<th>Median days (range)</th>
<th>Available records (n)</th>
<th>Median days (range)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Salmonella spp. identified at primary laboratory</td>
<td>1047</td>
<td>3 (1–31)</td>
<td>1364</td>
<td>3 (1–13)</td>
</tr>
<tr>
<td>Salmonella spp. result received by PHU</td>
<td>812</td>
<td>7 (3–156)</td>
<td>1168</td>
<td>6 (3–69)</td>
</tr>
<tr>
<td>Specimen received by reference laboratory</td>
<td>1036</td>
<td>6 (3–13)</td>
<td>1358</td>
<td>6 (3–39)</td>
</tr>
<tr>
<td>Salmonella serovar identification</td>
<td>1039</td>
<td>8 (4–32)</td>
<td>1274</td>
<td>7 (4–41)</td>
</tr>
<tr>
<td>Salmonella serovar result received&lt;sup&gt;b&lt;/sup&gt;</td>
<td>1060&lt;sup&gt;c&lt;/sup&gt;</td>
<td>10 (4–377)</td>
<td>1380&lt;sup&gt;c&lt;/sup&gt;</td>
<td>9 (5–54)</td>
</tr>
<tr>
<td>MLVA result received&lt;sup&gt;b&lt;/sup&gt;</td>
<td>1047</td>
<td>23 (8–384)</td>
<td>1377</td>
<td>21 (7–376)</td>
</tr>
<tr>
<td>Phage type result received&lt;sup&gt;b&lt;/sup&gt;</td>
<td>1007</td>
<td>46 (21–786)</td>
<td>1362</td>
<td>65 (20–307)</td>
</tr>
</tbody>
</table>

MLVA: multilocus variable repeat analysis; PHU: Public Health Unit.
<sup>a</sup>Difference in 2008 and 2009 median (days), p < 0.001.
<sup>b</sup>Reference laboratory results are emailed to NSW Health; subsequent dissemination to the relevant PHU.
<sup>c</sup>Includes Queensland Health Forensic and Scientific Services (QHFSS) specimens where earlier milestone dates unavailable (QHFSS results notified on serovar identification).
Source: Notifiable Conditions Information Management System (SAPHaRI), NSW Ministry of Health.

Table 2. Missing and invalid Salmonella Typhimurium surveillance milestones, NSW residents, 2008–2009

<table>
<thead>
<tr>
<th>Milestone</th>
<th>Missing dates (n) (%)</th>
<th>Invalid entries&lt;sup&gt;a&lt;/sup&gt; (n) (%)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Specimen collection date</td>
<td>0 (0.0)</td>
<td>0 (0.0)</td>
</tr>
<tr>
<td>Salmonella spp. identified at primary laboratory</td>
<td>41 (1.7)</td>
<td>6 (0.2)</td>
</tr>
<tr>
<td>Salmonella spp. result received by PHU</td>
<td>405 (16.5)</td>
<td>32 (1.3)</td>
</tr>
<tr>
<td>Specimen received by reference laboratory</td>
<td>0 (0.0)</td>
<td>17 (0.7)</td>
</tr>
<tr>
<td>Salmonella serovar identification</td>
<td>133 (5.4)</td>
<td>12 (0.5)</td>
</tr>
<tr>
<td>Salmonella serovar result received&lt;sup&gt;b&lt;/sup&gt;</td>
<td>17 (0.7)</td>
<td>1 (0.0)</td>
</tr>
<tr>
<td>MLVA result received&lt;sup&gt;b&lt;/sup&gt;</td>
<td>33 (1.3)</td>
<td>1 (0.0)</td>
</tr>
<tr>
<td>Phage type result received&lt;sup&gt;b&lt;/sup&gt;</td>
<td>88 (3.6)</td>
<td>1 (0.0)</td>
</tr>
</tbody>
</table>

MLVA: multilocus variable repeat analysis; PHU: Public Health Unit.
<sup>a</sup>Data determined to be impossible values and excluded from analysis.
<sup>b</sup>Reference laboratory results are emailed to NSW Health, with subsequent dissemination to the relevant PHU.
Source: Notifiable Conditions Information Management System (SAPHaRI), NSW Ministry of Health.
Notably, median time to yet we found that the data capture system with enhanced foodborne disease opportunity to reduce notification delays. Salmonella spp. identification to PHU receipt provides an median 4- (2008) or 3- (2009) day time interval from neck’ in the surveillance system, identified in urgency for phage typing results. A previous study production of routine MLVA and an accompanying reduction have become more commonplace in NSW after the intro-
sufficient number of isolates are collated. Batching may also be impacted by isolate ‘batching’, where isolate service all Australian states. Phage type result timeliness affected as two reference laboratories (IMVS and MDU) resourcing impacts the time interval from specimen col-
collation and transmission between organisations are chal-
ance anomalies indicated notification lapses by pri-
mary laboratories. These data quality issues impact the day-to-day operational processes of outbreak identifi-
cation, investigation and control. However, due to the complex nature of NDD data entry and extraction from NCIMS, further exploration of this issue was not possible.

Occasionally, laboratories did not notify sub-typing results at the earliest opportunity, as indicated by simultaneous or non-sequential notification of serovar, MLVA or phage typing results. While electronic notification via email is undoubtedly faster than postal mail, human errors in data collation and transmission between organisations are chal-
genious outbreak linking during the study period, we cannot assess the impact of outbreak resolution on missing results.

Resourcing impacts the time interval from specimen collec-
tion to result availability. Phage typing is particularly affected as two reference laboratories (IMVS and MDU) service all Australian states. Phage type result timeliness may also be impacted by isolate ‘batching’, where isolate dispatch to the reference laboratory is delayed until a sufficient number of isolates are collated. Batching may have become more commonplace in NSW after the intro-
duction of routine MLVA and an accompanying reduction in urgency for phage typing results. A previous study identified Salmonella spp. identification as the ‘bottle neck’ in the surveillance system, yet we found that the majority of Salmonella spp. identification occurred within 3 days. Also, the time interval from specimen collection to Salmonella spp. PHU notification was similar to a previous international timeliness study. Nonetheless, the additional median 4- (2008) or 3- (2009) day time interval from Salmonella spp. identification to PHU receipt provides an opportunity to reduce notification delays.

In 2010, the NDD was replaced with NCIMS, an updated data capture system with enhanced foodborne disease surveillance capacities. NCIMS capabilities include date stamping (identifying the date and time of data entry), outbreak case linking, and recording MLVA and phage typing results. NCIMS performance enhancements are expected to improve outbreak identification, establish historical sub-typing data banks, and advance future surve-
ccession and control. However, due to the importance of rapid typing in outbreak res-

1. Dissemination of ELR across all laboratories, thereby reducing duplication of data entry and expediting data delivery.
2. Development of NCIMS capability for efficient data extraction and reporting relevant to future data completeness and timeliness evaluations. This would enable evaluation of NCIMS capacity to enhance the NSW STm surveillance system.

Acknowledgments
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Health and Ageing to enhance foodborne disease surveillance in Australia. We wish to acknowledge the contribution of Tracey Findlay for her role in data collation and cleaning. We would also like to thank our public health reference laboratory colleagues at ICPMR and QHFSS for their enthusiasm for MLVA typing and the provision of additional milestone data, as well as our colleagues at MDU and IMVS for phage typing.

References


