Reviewer’s report

**Title:** Improving public health surveillance for human Salmonella enterica serovar Typhimurium infection: 3-years of prospective multiple-locus variable-number tandem-repeat analysis (MLVA)

**Version:** 1 **Date:** 15 November 2011

**Reviewer:** Eva Moller Nielsen

**Reviewer’s report:**

This manuscript describes 3 years of surveillance of all Salmonella Typhimurium (STM) infections in one Australian state. Isolates were MLVA typed and clusters were prospectively detected and investigated.

Overall, an interesting paper that contributes to the understanding of the dynamic of STM infections and suggests parameters that can be used for the surveillance and as cluster indicators for public health intervention.

**Major Compulsory Revisions**

1) **MLVA typing:** It is now well known that there can be a considerable discrepancy between the fragment size measured by capillary electrophoresis and the actual length of a fragment as determined by sequencing. This discrepancy depends on factors like the instrument/polymer, size marker, locus, etc. Since the MLVA profile in this study is presented as the actual number of repeats in each locus (+1) calculated on basis of the measured fragment sizes, it would be relevant to describe how it was ensured that the correct number of repeats was obtained.

2) **Clusters:** it is noteworthy that 30% of all isolates in the study belong to 3 closely related MLVA profiles, and 1 MLVA profile represents 79% of the PT170 isolates (1536 isolates). No details are given on the distribution of this MLVA profile over the 3 years, but from Figure 1 it is clear that PT170 is mainly found in 2008-9. It seems that the 1536 isolates with one specific MLVA type must influence the study considerable. How many clusters were defined with this MLVA profile and how large were these clusters? Were the 2 closely related MLVA profiles found concurrently with the most prevalent type?

3) **This is a prospective study and some of the detected clusters were investigated further. However, it is not clear how the cluster definition and the indicators such as “cluster case density” and the ratio between novel and persistent types were used in the active surveillance. On what basis and how fast was a cluster defined and selected for public health actions?**

**Minor Essential Revisions**

4) **Background:** Reference 10 (Grimont 2007) does not seem to be the correct
one for the number of phage types in the phage typing scheme (ref 10 concerns the serotyping scheme). Usually, the definitive phage types of STM are designated DT, not PT.

5) The figure numbers should be checked in the text.

Results, discriminatory power…. Three closely related patterns included 30% of all isolates (Figure 1B and 1C) – cannot see this in Figure 1B and 1C or in any other figure.

Results, Diversity: reference to Figure 1-B and 1-C should be shifted around (or changed in the figure). No significant change in number of clusters… Reference to Figure 1-D should be Figure 2.

6) Figure 5 and 6: very difficult to read these.

Discretionary Revisions

7) Were monophasic variants of STM included in the study – and how prevalent are these in NSW, Australia?

8) Methods:

Sequence analysis: Cannot find anything about which strains/loci were sequenced and what were the results?

**Level of interest:** An article whose findings are important to those with closely related research interests

**Quality of written English:** Acceptable

**Statistical review:** No, the manuscript does not need to be seen by a statistician.

**Declaration of competing interests:**

I declare that I have no competing interests.