Reviewer's report


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Reviewer: Laura Kuijpers

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The study "Investigation of Salmonella Enteritidis outbreaks in South Africa using multi-locus variable-number tandem-repeats analysis, 2013-2015" by Muvhali et al. describes three years of outbreak surveillance with analysis of isolates with MLVA.

Overall, the paper is well written and the method (MLVA technique containing five VNTR loci) used is appropriate.

Major comments:

1) The introduction contains a lot of information on invasive NTS disease. Although relevant to mention in the broader scope of things, the focus of the paper concerns non-invasive isolates (as far as information was available, only stool isolates were included according to table 2). The part on invasive disease could thus be a bit shorter. Throughout the text it should be clearly stated each time whether data or literature references concern invasive isolates, non-invasive isolates or both (see minor comments below).

2) Addition of phenotypic data could be interesting. Did all isolates of the dominant profile 28 share the same antibiotic susceptibility pattern? Was there a difference in susceptibility between the isolates of profile 28 and the other two profiles?

3) I'm not sure if you can state that isolates with closely related MLVA profiles share pathogenic traits. Don't you need more resolution for this? (And from the limited epi/clinical data available it seems that more people got infected (and hospitalized) during outbreaks with profile 28?)
4) Yes MLVA is an important tool for public health surveillance, but how did it concretely change the course of the outbreaks described in this paper? Was MLVA performed real time, and did it change public health interventions? This should be described more clearly. What changed, compared to if no MLVA typing had been done? In terms of One health, is there a plan to compare MLVA types of the human isolates in the CED database with those obtained from animals (e.g. as those isolated in other studies in South Africa, e.g. such as described by Magwedere et al, CID 2015?)

5) A limitations section in the discussion is missing and could state the following:

- Epidemiological and clinical data are not complete, and information is not available for all food items tested (e.g. chicken samples from outbreak 3)

- Only one isolate from food item (goat) was available

- MLVA was not supplemented with a second typing method, nor with whole genome sequencing which could have provided more information on phenotypic traits and more discrimination regarding isolates belonging to profile 28, but which were involved in separate outbreaks in different provinces (3-6).

Minor comments :

24: Upon first mentioning, also in the abstract, write 'Salmonella enterica serovar Enteritidis (Salmonella Enteritidis)'

57: Upon first mentioning, write 'Salmonella enterica serovar Typhimurium'

60/61: 'With fewer numbers of deaths in humans', compared to what? Humans in Africa, or adults vs. children?

62: Two times the word 'high burden' in one sentence, I would rephrase, e.g. 'However, in sub-Saharan Africa, NTS are commonly associated with invasive disease, which leads to a high burden or morbidity and mortality.'
71: Where is this centre based?

74: Upon first mentioning, write 'Salmonella enterica serovar Isangi'

78/79: More prevalent than Salmonella Typhimurium in terms of invasive or non-invasive infections or combined?

91: 'Number of Salmonella Enteritidis cases reported to the CED have increased' □ invasive, non-invasive, or combined? Important to differentiate throughout the text.

98: Received Salmonella Enteritidis isolates

113/114: 'in which NTS was the implicated pathogen', should read as 'in which Salmonella Enteritidis was the implicated pathogen?' Seven NTS outbreaks are mentioned, and seven Salmonella Enteritidis outbreaks. So there were no outbreaks associated with Salmonella Typhimurium or other NTS during the study period?

152: Font size 'Sint-Martens-Latem' is bigger compared to the rest of the text.

164: 'Were from human stool samples', you mention it in table 2 but also add it to the text. One sample per person was included in the analysis?

167: Double blank sentence

239: Double space between 'database' and 'In'

240/241: Human isolates (stool, blood or mix?)

252/253: More outbreaks need to be analyzed ◇ possibly supplemented with WGS for a selection of isolates, to compare between profiles and discriminate within profiles/clusters?
Are the methods appropriate and well described?
If not, please specify what is required in your comments to the authors.

Yes

Does the work include the necessary controls?
If not, please specify which controls are required in your comments to the authors.

Unable to assess

Are the conclusions drawn adequately supported by the data shown?
If not, please explain in your comments to the authors.

No

Are you able to assess any statistics in the manuscript or would you recommend an additional statistical review?
If an additional statistical review is recommended, please specify what aspects require further assessment in your comments to the editors.

Not relevant to this manuscript

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Please indicate the quality of language in the manuscript:

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