Reviewer’s report

Title: Population structure and transmission modes of indigenous typhoid in Taiwan

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Reviewer: Obul Bandapalli

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Wang et al in their manuscript titled "Population structure and transmission modes of indigenous typhoid in Taiwan" have analyzed the source and transmission by which the local patients acquired typhoid and the population structure of the indigenous typhoid strains by whole-genome sequencing (WGS) and determined for pulsotypes.

The authors have analyzed a total of 43 S. Typhi isolates from indigenous cases and showed that a majority (39, 90.7%) of them belonged to six WGS-defined genotypes prevailing mainly in Southeast Asia. Two strains namely Genotype 3.4.0 and a multidrug-resistant type 4.3.1 (also known as pandemic H58 haplotype) were associated respectively with two solitary small-scale outbreaks, implying a transmission mode of importation followed by outbreak.

Twelve isolates with nearly identical core genomes were belonged to genotype 3.2.1 but were categorized into three different pulsotypes.

The authors imply that indigenous typhoid in Taiwan occurred mainly with the forms of small-scale outbreaks or sporadic events likely by contracting imported strains which prevailed in Southeast Asia. They have also reported sustained local transmission of certain strain was by WGS analysis, which was not possible by conventional pulsotyping, highlighting the importance of continuing molecular surveillance of typhoid fever with adequate tools in the non-endemic region.

The strength of the manuscript is that the authors have nicely tracked the origin and spread of S.typhi in this non-endemic island and also identified risk prone strains origin. This information can be used to screen and control the spread of this fever by monitoring the people returning from these countered.

I have minor comments

The authors mentioned that they have assembled the draft genome of each isolate with the same SPAdes. Do they make this available to the readers here?

The authors wrote "The S. Typhi isolates used in the study were all clinical strains identified during 2001 and 2014 in Chang Gung Memorial Hospital (CGMH)". Does this mean they have already know the strains then what is the novelty of this study?
Isolation of the strains and WGS methods were not adequately described.

Is there any pic available for PFGE? If so that should be presented

**Are the methods appropriate and well described?**
If not, please specify what is required in your comments to the authors.

No

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

No

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

Yes

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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

**Quality of written English**
Please indicate the quality of language in the manuscript:

Acceptable

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