Published in final edited form as:

Tuberculosis (Edinb). 2018 December ; 113: 122–124. doi:10.1016/j.tube.2018.09.003.

Response

Lauren A. Saag and

Division of Epidemiology, Vanderbilt University, Nashville, TN, USA

Peter F. Rebeiro

Division of Epidemiology, Vanderbilt University, Nashville, TN, USA

Division of Infectious Diseases, Vanderbilt University School of Medicine, Nashville, TN, USA

We appreciate the thorough explanation and presentation of additional data from Dr. Qi Jiang, Dr. Chongguang Yang, and Dr. Qian Gao in response to our letter regarding their recently published manuscript about tuberculosis (TB) contact investigation and case finding in Shanghai [1].

However, regarding their response on the inclusion of 15 incident cases *without* whole genome sequencing (WGS) alongside the 24 cases *with* WGS according to the proportional distribution of observed transmission links, we still believe the authors are implicitly making a strong assumption about the absence of selection bias. As they describe in their response, inclusion of these 15 cases in this manner would indeed result in statistical significance of their calculated odds ratio, though even rounding to the nearest whole person would make this finding precarious (Table). In fact, it is completely plausible that the 15 incident cases without WGS were characteristically different from those with WGS, rather than being equivalent to a random sample of the population with WGS, which essentially describes an assumption of no selection bias. Though it is not explicit, this is the assumption that the authors invoke in their response.

Additionally, we thank the authors for the clarification regarding the repeated and shared contacts depicted in Figure 1 of their original paper. It is helpful to know that both index cases of shared contacts would have been considered for strain genotyping if any of the contacts developed culture-positive TB, as this was not entirely clear in the original paper.

We agree with the authors that active case finding, though especially challenging among non-familial contacts and in resource-limited settings, is fundamental for decreasing TB transmission. We are grateful to the authors for their work in this area and for their careful and timely response to our queries.

References

- [1]. Jiang Q, Lu L, Wu J, et al. Assessment of tuberculosis contact investigation in Shanghai, China: an 8-year cohort study. *Tuberculosis* 2018;108(1052):10–5. [PubMed: 29523308]
- [2]. Glynn JR, Guerra-Assunção JA, Houben RMGJ, et al. Whole genome sequencing shows a low proportion of tuberculosis disease is attributable to known close contacts in rural Malawi. *PLoS One* 2015;10(7):1–12.

Distribution of 15 excluded incident cases according to proportions in original study, with cell counts rounded to the nearest whole person (as would be observed in an actual cohort)

Confirmed linkage to index case	Contact type		Odds Ratio (95% CI)
	Familial	Non-familial	
Yes	$9 + (12 \times 0.600) = 16.2 \rightarrow \mathbf{16}$	$2 + (3 \times 0.222) = 2.67 \rightarrow \mathbf{3}$	4.36 (0.96, 19.86)
No	$6 + (12 \times 0.400) = 10.8 \rightarrow \mathbf{11}$	$7 + (3 \times 0.778) = 9.33 \rightarrow \mathbf{9}$	Ref.