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Rapid Communication

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# Estimating the serial interval of Marburg virus human-to-human transmission from a case cluster seeded by a cross-border traveller

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The Marburg virus disease (MVD) is a zoonotic disease caused by the Marburg virus, which belongs to the filoviridae family. The MVD is highly virulent with a case fatality ratio (amongst reported cases) higher than 70% in recent outbreaks occurred in African countries, with human-to-human (H2H) transmission.[1] As a key epidemiological parameter for describing the transmission characteristics of an infectious agent, the serial interval (SI) is defined as the duration between the illness onset dates of the primary case and the secondary case. Herein, we estimated the SI of MVD patients infected by H2H transmission during an outbreak that seeded by a cross-border traveller in the United Republic of Tanzania in 2023.

From March to April 2023, Tanzania reported its first local MVD outbreak, which involved a total of nine individuals linked to a single household cluster (Figure 1A).[1] The cluster was initiated by an index case who had a history of travelling and became sick upon returning. Six out of eight secondary cases were family members of the index case, and the rest two were healthcare workers, who had direct contact with the confirmed cases.[1]

Similar to the Ebola virus, which also belongs to the filoviridae family, pre-symptomatic transmission amongst MVD patients is highly unlikely and we assumed the SI of MVD followed a gamma distribution. To deal with the two healthcare workers whose source cases were unknown, we considered cases with earlier symptom onset as their source cases. Then, by adjusting the likelihood function, all possible observations of SI were accounted for in the statistical inference of SI distribution (Supplementary Appendix 1). Model parameters were estimated by using the Markov chain Monte Carlo method with informative prior based on SI of Ebola with mean of 15.3 and standard deviation (SD) of 9.3 days.[2]

We estimated the SI of this MVD outbreak at a mean of 11.3 days [95% Credible Interval (CrI): 8.1, 15.4] and an SD of 9.3 days (95% CrI: 6.1, 13.2). The estimated cumulative distribution was shown in Figure 1B. A previous study calculated the SI using pooled historical MVD outbreak data obtained a median of 11 days (Interquartile range: 8, 15),[3] which is comparable to ours (8.3 days, 95% CrI: 5.5, 12.6). Currently, no published data is available on the SI distribution of MVD, which is crucial for guiding control measures, especially in the

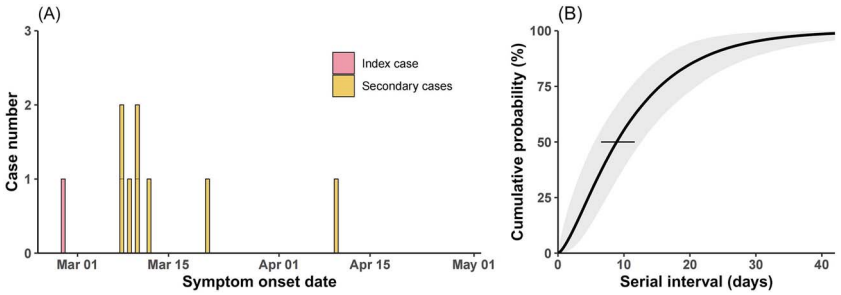


**Figure 1.** (A) The epidemic curve of MVD outbreak in the United Republic of Tanzania in 2023. (B) The estimated cumulative probability distribution of SI for the MVD. In panel (B), the grey shaded area represented 95% credible interval (95% CrI), and the black horizontal line represented the median estimates of SI.

absence of approved vaccine for MVD. SI is indispensable in the estimation of the reproduction number, an important metric determining whether an outbreak will continuously be spreading or going extinct. Previous data showed the basic reproduction number of MVD is 1.59,[4] falls within the range of Ebola (1.38–2.01) and Lassa fever (1.1–1.8),[2,5] which is another zoonotic disease that can cause haemorrhagic fever. It should be noted that the statistical adjustment we used to estimate SI can be relaxed if future study with a larger sample size becomes available. Despite the low occurrence of MVD, imported cases may occur in developed countries in future due to exploratory travel to endemic regions.

## Supplementary data

Supplementary data are available at *JTM* online.

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## Authors' contributions

SZ and ZG designed the study. ZG collected the data and carried out the analysis. ZG write the original draft. SZ, SS, KW, JR, DH, YW, HW, JS and KCC gave critical revisions of the manuscript with important intellectual contents. KCC and EKY supervised this study. All authors read and approved the final manuscript.

**Conflict of interest.** The authors have declared no conflicts of interest.

## Data availability

All data used in this study were publicly available, and the computer codes used for statistical analysis may be available based on request to the authors.

## Ethics approval and consent to participate

The data used in this study were publicly available, and thus neither ethical approval nor individual consent was applicable.

## References

1. Who.int. [cited 2023 Jul 3]. Available from: https://www.who.int/emergencies/disease-outbreak-news/item/2023-DON471
2. WHO Ebola Response Team. Ebola virus disease in West Africa–the first 9 months of the epidemic and forward projections. *N Engl J Med* 2014; **371**:1481–95.
3. Pavlin BI. Calculation of incubation period and serial interval from multiple outbreaks of Marburg virus disease. *BMC Res Notes* 2014; **7**:906.
4. Ajelli M, Merler S. Transmission potential and design of adequate control measures for Marburg hemorrhagic fever. *PloS One* 2012; **7**:e50948.
5. Wang J, Zhao S, Chen X *et al.* The reproductive number of Lassa fever: a systematic review. *J Travel Med* 2021; **28**:taab029.