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Short Communication

Superspreading potential of Nipah virus disease despite self-limited human-to-human transmission in community

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ABSTRACT

As of late January 2026, the World Health Organization (WHO) reported a small-scale Nipah virus (NiV) outbreak in West Bengal, India. Despite that NiV was primarily transmitted through animal sources, we assessed the transmission risks of NiV at human community level based on a total of 23 studies identified from literature of historical outbreaks that investigated human-to-human transmission of laboratory-confirmed NiV in Bangladesh and India. The data included transmission events containing 33 primary NiV cases and 152 secondary cases. We constructed a modelling framework for superspreading risk assessment, and found that 92.0% (95% CrI: 87.0, 95.4) of the NiV cases could not generate secondary cases via human-to-human transmission. With 5 seed cases imported to a community, there was a 1.1% (95% CrI: 0.3, 2.3) chance of observing an outbreak exceeding 50 NiV cases. Our findings may inform public health preparedness at community level and cross-border travel ban.

Introduction

Nipah virus disease is a zoonotic illness caused by the Nipah virus (NiV), characterized by high pathogenicity and a significant fatality rate, with mortality rates ranging from 40% to 75% [1]. As a pathogen primarily transmitted by bats [2], NiV was confirmed to possess human-to-human (H2H) transmission capabilities [3,4], which posed a persistent threat to public health. By the end of January 2026, the WHO reported a small-scale NiV outbreak in west Bengal, India [5]. Previous outbreaks in Bangladesh and India have predominantly been attributed to the NiV Bangladesh strains (NiV_B) [6]. Given the current absence of specific antiviral treatments and vaccines for NiV disease worldwide, a scientific assessment of its human-to-human transmission risk at the community level has become a critical foundation for developing effective intervention strategies. Therefore, we aim to utilize historical outbreak data to assess the risk of NiV_B human-to-human transmission at the community level.

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Methods

We collected the secondary epidemiological data compiled from 2 recent systematic analyses of historical NiV outbreaks [6,7]. A total of 23 studies were identified that investigated human-to-human transmission of laboratory-confirmed NiV_B in Bangladesh and India from 2001 to 2018. Among these, 33 primary NiV cases were associated with transmission events, including 152 secondary cases. Case clusters can be reconstructed based on epidemiological links, and aggregated into 32 observations (25 in Bangladesh, and 7 in India) of next-generation clusters with known numbers of primary and secondary cases (see Figure 1a), which were used for further modelling analysis.

The human-to-human transmission process of NiV was modelled as a branching process, with the number of secondary infections characterized by a negative binomial (NB) distribution [8]. Specifically, the next-generation cluster size ($y = x + i$) contained the primary (or seed) case numbers (i, $i \geq 1$, and i is an integer) and secondary case numbers (x, $x \geq 0$, and x is an integer), and can be modelled as an NB distribution with mean R and dispersion parameter k. The probability mass function is given as

$$f_{\mathrm{NB}}(X{=}x|R,k,i){=}\frac{\Gamma(ik{+}x)}{\Gamma(ik)\Gamma(x{+}1)}\cdot\left(\frac{k}{R{+}k}\right)^{ik}\cdot\left(\frac{R}{R{+}k}\right)^{x},$$

where $\Gamma(\cdot)$ is gamma function, and R could also be epidemiologically interpreted as reproduction number of NiV's human-to-human transmission. Considering the underdeveloped disease surveillance settings in the study area and the complexity of wild transmission routes of NiV, limited reporting accuracy was likely

(A)

seed cases	next-generation case cluster size	frequency
1	2	10
1	3	5
1	4	3
1	5	4
1	6	1
1	7	1
1	12	2
1	20	1
1	22	1
1	32	1
1	1.5	1
1	2.5	1
2	3	1

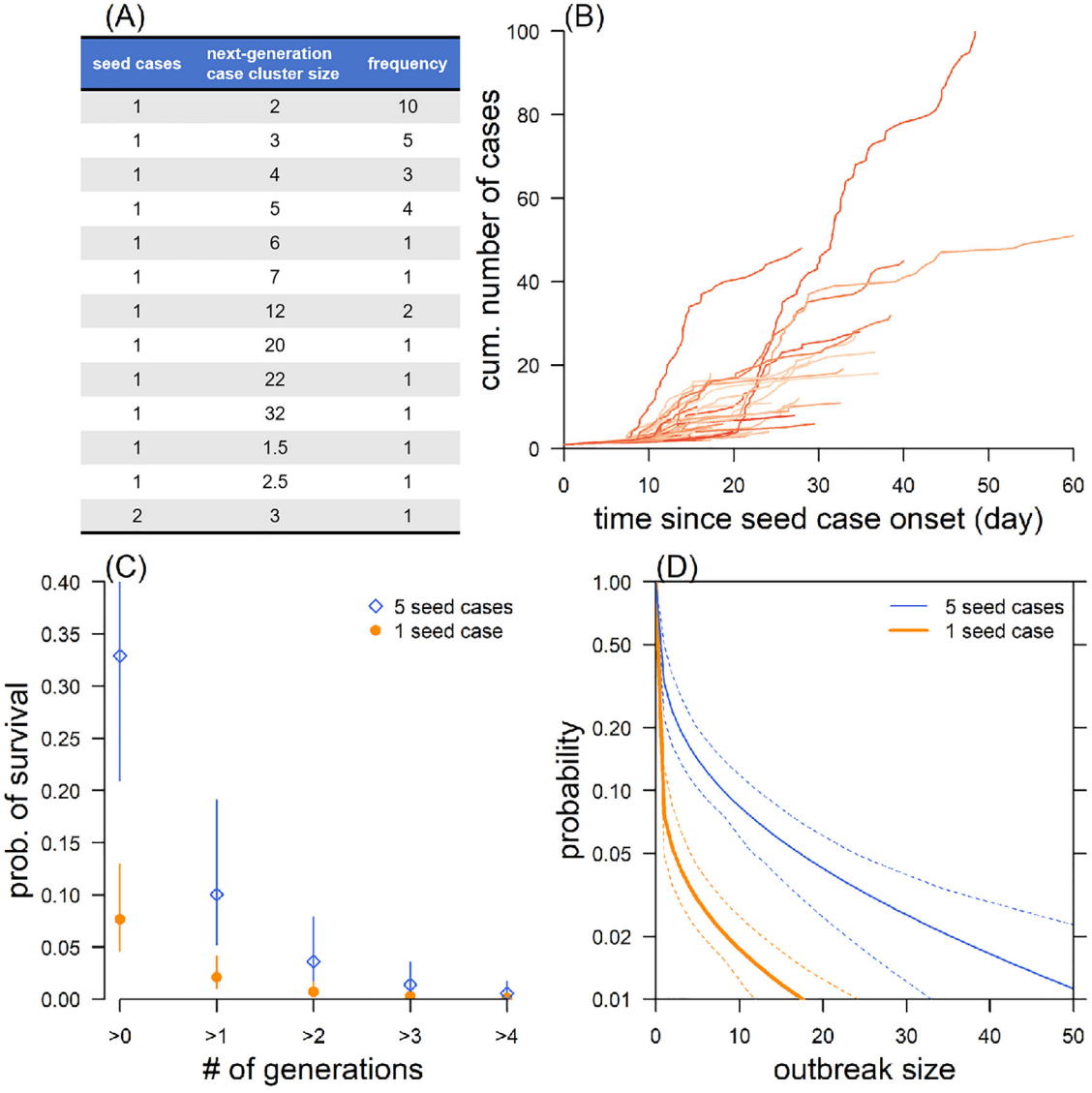

Figure 1. The case cluster data and superspreading risks of Nipah virus (NiV). Panel (a) showed a table summarizing the frequency distribution of next-generation case cluster sizes (denoted as $y = x + i$ in NB model) with known seed case numbers (denoted as i). Panel (b) showed 100 stochastic simulations (curves in different colors) of NiV outbreak trajectories (i.e., cumulative number of cases over the first 60 days), following the introduction of 1 seed case into a susceptible community. Panel (c) showed the probability of a NiV outbreak persisting for over a given number of transmission generations (on the horizontal axis) seeded by 1 (in orange) or 5 (in blue) seed cases in community, respectively. Panel (d) showed the probability of observing at least 1 NiV outbreak with a final size larger than a given size when 1 (in orange) or 5 (in blue) seed cases were separately introduced into community, respectively. *Note*: In panel (a), the observations for 1 seed case and next-generation case cluster sizes of 1.5 and 2.5 were summarized from the epidemiological situation in which cases a and b jointly infected case c (i.e., co-primary cases), while case A solely infected case d, as reported in Figure 1A of [7].

to occur among zero-offspring cases, and thus they were excluded from analysis by using zero-truncated negative binomial model (ZTNB) [9].

$$f_{\mathrm{ZTNB}}\left(X=x|R,k,i\right)=\frac{f_{\mathrm{NB}}\left(X=x|R,k,i\right)}{1-f_{\mathrm{NB}}\left(X=0|R,k,i\right)},$$

where $x \geq 1$ for ZTNB distribution.

To link observations of case clusters with ZTNB model, we derived the following likelihood function for each observation, which accounted for a few complex situation that multiple primary cases were associated with a secondary case (see the footnote of Figure 1).

$$l\left(R,k|X=z,i\right)=\frac{f_{\mathrm{ZTNB}}\left(X=\lfloor z\rfloor|R,k,i\right)+f_{\mathrm{ZTNB}}\left(X=\lceil z\rceil|R,k,i\right)}{2},$$

where z (z is not necessarily an integer) is the average number of secondary cases seeded by i primary cases.

Likelihood-based statistical inference for model parameters was performed by using Markov chain Monte Carlo (MCMC) approach with informative prior ranging from 0.30 to 0.50 for R [7], and non-informative prior distribution for k. A gamma-distributed serial interval with mean (standard deviation) 12.7 (3.0) days [7], and posterior samples of parameters would be used for stochastic simulation of outbreak size under the transmission chain size modelling framework as per [10], to assess NiV superspreading risks. To further assess the robustness of model estimates, we performed a sensitivity analysis regarding the setting of prior distribution of reproduction number R of NiV's human-to human transmission.

Results and discussion

We estimated k at 0.03 (95% credible interval [CrI]: 0.02, 0.06), which suggested a high degree of heterogeneity in human-to-human transmission of NiV, and 80% of transmission events were contributed by only 3.1% (95% CrI: 1.9%, 5.2%) of the 'most infectious' cases. Although 92.0% (95% CrI: 87.0, 95.4) of the NiV cases could not generate secondary cases, which was in line with 91% reported in [7], a low but non-negligible risk may persist for large-scale and sustained NiV epidemic at community level (see Figure 1b). Merely 2.1% (95% CrI: 1.1, 4.1) of single-case introductions and 10.0% (95% CrI: 5.2, 19.1) of five-case introductions of NiV were estimated to sustain for more than 1 transmission generation (see Figure 1c). Thus, quarantine would be recommended for primary contacts, not necessarily for secondary contacts. When 5 seed cases were introduced into a susceptible community, there was a 1.1% (95% CrI: 0.3, 2.3) likelihood of observing an outbreak exceeding 50 NiV cases (see Figure 1d), which was contributed by superspreading potential of NiV. In sensitivity analysis, when the prior value of R ranged from 0.3 to 0.5, the log-likelihood profiles of k showed differences in maximal values of less than one unit (Figure 2a), and the estimates of k merely varied within a small range (Figure 2b).

This study has several limitations. First, the number of collected cases was relatively small. Second, limited epidemiological investigation and diagnostic resources in underdeveloped setting may have led to the underreporting or misreporting of cases. Third, constrained by the contact tracing capacity, the transmission chain data collected may have included not only single-generation transmission but also multi-generation transmission.

Given the current lack of licensed pharmaceutical interventions against NiV, continuous surveillance and timely risk assessment of human-to-human transmission were therefore essential for understanding the risk of NiV disease, informing public health preparedness at community level, and guiding cross-border travel ban at regional level.

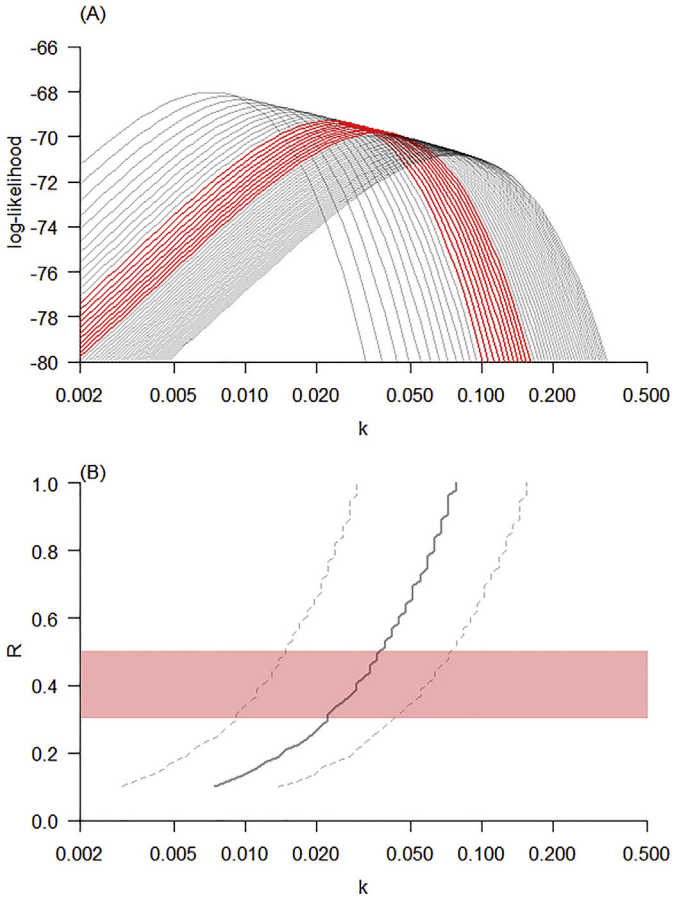

Figure 2. Log-likelihood profiles and estimates of dispersion parameter k, with reproduction number R varying from 0.1 to 1.0. Panel (a) showed the log-likelihood profiles (i.e., curves) for k, with R fixed at a value from 0.1 to 1.0, where red curves were those with R fixed at a value from 0.3 to 0.5. Panel (b) showed maximum log-likelihood estimates (bold line) and 95% confidence intervals (dashed lines) of k for each fixed value of R on the vertical axis, where the red shading region marked the range of R from 0.3 to 0.5.

Ethical approval and consent to participate

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

Availability of materials

All data used in this study were publicly available.

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Disclaimer

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Author contributions

SZ conceived the study. KP and SZ collected and processed the data, and carried out the analysis. KP, ZY, and SZ drafted the first manuscript. All authors discussed the results, critically read and revised the manuscript, and gave final approval for publication.

Declaration of competing interest

The authors have no competing interests to declare.

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