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ORIGINAL PAPER

Infectious Diseases

Prevalence and transmission of COVID-19 in community and household levels of Bangladesh: Longini and Koopman epidemic modelling approach

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Abstract

Aim: To estimate the prevalence of COVID-19 pandemic and its transmission rates among people in both community and household levels of Bangladesh.

Methods: We use the cross-sectional online survey data of 2080 individuals, collected from 442 households during June to September 2020 in Bangladesh. The Longini and Koopman stochastic epidemic modelling approach was adapted for analysing the data. To validate the results, a simulation study was conducted using the Markov Chain Monte Carlo (MCMC) method via the Metropolis-Hastings algorithm in the context of the Bayesian framework.

Results: Overall, the prevalence of COVID-19 pandemic was 15.1% (315 out of 2080) among people in Bangladesh. This proportion was higher in smaller households (size one: 40.0%, two: 35.7% and three: 25.9%) than larger (four: 15.8%, five: 13.3%, six: 14.1%, seven: 12.5% eight: 8.7%, nine: 14.8% and ten or eleven: 5.7%). The transmission rate of COVID-19 in community people was higher (12.0%, 95% CI: 10.0% to 13.0%) than household members (9.0%, 95% CI: 6.0% to 11.0%).

Conclusion: The susceptible individuals have a higher risk of community infection than the household and the community transmission is more responsible than the household for COVID-19 pandemic in Bangladesh.

1 | INTRODUCTION

Coronavirus is an infectious disease popularly known as COVID-19, which was originated in Wuhan, China on 31 December 2019.[1] Currently, the COVID-19 pandemic affected people in more than 200 countries over the world.[2] The first three COVID-19 cases, two males and one female aged 20-35 years, were identified in Bangladesh on 8 March 2020.[3] The COVID-19 rapidly and widely spread throughout the Bangladesh and there were 223,453 confirmed cases, 123,882 recovered and 2,928 deaths by 26 July 2020.[4]

A rapid and effective response by different global scientific communities provided several main aspects of COVID-19 transmission and its natural history.[5-9] However, it is still unclear that how both community and household transmission probabilities characterize the COVID-19 pandemic. The household transmission became an important part of COVID-19 transmission and many confirmed cluster cases were found from family households.[7,10] It was estimated that the household transmission rate was 15% in China.[11] This study also reported that household contacts those travelling with COVID-19 cases were at higher risk of infection than others and children were more likely to be infected within households than adults. Another study on COVID-19 transmission reported that the households transmission rate was 12.4% in China and older people were the most susceptible to be infected among households than others.[12] Older age and marital relationship with COVID-19 positive case were reported as potential risk factors for household transmission.[13]

Some studies measured the effective reproduction numbers of COVID-19 using detailed case-level information in particular countries or regions that declined during lockdowns and other non-pharmaceutical interventions.[14-17] In Korea, a study estimated the transmission potential and severity of COVID-19, and reported that an early sustained transmission and the social distancing can control the pandemic.[18] Another study suggested that controlling the people movement and social gathering can significantly reduce the transmission of COVID-19 pandemic.[19]

In Bangladesh, major challenges of COVID-19 were investigated and it was suggested that mobile sanitisation services, temporary quarantine places and healthcare facilities may contribute to reduce the transmission of COVID-19 pandemic.[20] Another study suggested to maintain strongly the health preventive measures, avoiding social gathering and washing hands frequently, for controlling the transmission of COVID-19.[21] A study on transmission dynamics of COVID-19 used the secondary data collected from 8 March to 15 May 2020 and reported that the transmission rate was 4.5%.[22] Another study on forecasting COVID-19 infectious rate used the Susceptible Infectious Recovered (SIR) model and reported that the disease was transmitted among Bangladeshi people with a rate of 0.0014 over the period 7 March to 14 April 2020.[23]

People may be COVID-19 positive from the community first and then the infected persons spread this virus among household members. Thus, the community and household disease transmission parameters are correlated. Ignorance of such correlation in estimating model parameters may produce misleading inference and hence incorrect interpretation of results. The previous studies completely ignored this correlation and estimated the overall transmission rate of COVID-19 in Bangladesh.[22,23] In this study, we adapted the Longini and Koopman stochastic epidemic model[24] with correlation exists between the model parameters to jointly estimate the transmission rates of COVID-19 in both community and households levels that characterize the dynamics of disease transmission. Moreover, to validate the estimated model parameters we also considered the Markov Chain Monte Carlo (MCMC) method via Metropolis-Hastings algorithm in the context of the Bayesian framework.[25]

2 | MATERIALS AND METHODS

2.1 | Data

We conducted a cross-sectional online-based household survey on COVID-19 infectious disease during June to September 2020 among people in Bangladesh. The target group of the respondents consists of all members in the households. More precisely, the survey participants were those who had direct or indirect access to internet facilities with personal computers or laptops or smart mobile phones, etc. Those participants who did not have such facilities but they took part in the survey with assistance from others, for example students, son and daughter, etc The data were collected from 2080 people, who participated in the survey from 442 households in different administrative regions of Bangladesh.

What's known

- The transmission rate of COVID-19 was estimated ignoring the correlation effect between community and household levels.

What's new

- There are no studies on the transmission rate of COVID-19 considering the correlation effect between community and household parameters.
- We adapted optimal modelling for jointly estimating both community and household transmission rates in Bangladesh.

2.2 | Transmission model and estimation

We considered the Longini and Koopman stochastic epidemic model[24] for jointly estimating household and community transmission probabilities of COVID-19. The model assumes that a susceptible individual will be infected from the community where sources of infection are homogeneously distributed. The movement among household members is random and every individual can be infected from household or community independently.

Let B_c and Q_h denote the probabilities of avoiding infection from communities and households, respectively. Hence, $\left(1 - B_c\right)$ and $\left(1 - Q_h\right)$ represent the transmission probabilities of infectious disease (COVID-19) among community and household levels, respectively. The probability that exactly i of the s susceptible individuals in a given household are infected, denoted by $P(i/s)$, is given as

$$P(i/s) = \binom{s}{i} P(i/i) \left(B_c Q_h^i\right)^{s-i},$$

where $P(i/i), \quad i = 0, 1, \ldots, s-1$ is the probability of i individuals to be infected among i susceptible. It follows that the probability of infection of all s individuals among s susceptible individuals is

$$P(i/i) = 1 - \sum_{i=1}^{s-1} P(i/s).$$

Both community and household transmission model parameters are estimated by maximising the log-likelihood function, $l\left(B_c, Q_h\right)$[24]:

$$l\left(B_c, Q_h\right) = \sum_s \sum_i a_{is} \left(\ln \binom{s}{i} + \ln P(i/i) + (s-i)\ln B_c + i(s-i)\ln Q_h \right),$$

where a_{is} is the observed frequency of households with i infected from s susceptible so that $\sum_s \sum_i a_{is} = n$ for $s = 1, 2, \ldots, S$ and $i = 0, 1, \ldots, s$.

2.3 | Markov Chain Monte Carlo approach via Metropolis-Hastings algorithm

For the valid inference of parameters in the Longini and Koopman stochastic epidemic disease transmission model, results can be compared considering the MCMC method via Metropolis-Hastings algorithm.[25] The joint posterior density, $\pi\left(B_c, Q_h/a_{is}\right)$, considering the independent uniform prior distributions $U(0,1)$ for the parameters B_c and Q_h is used and can be written as[26]

$$\pi\left(B_c, Q_h/a_{is}\right) \propto L\left(B_c, Q_h\right),$$

where $L\left(B_c, Q_h\right)$ is the likelihood function. One then can construct a Markov chain, $\left\{Z_n\right\}$, and draw samples from $\pi\left(B_c, Q_h/a_{is}\right)$.[27] More precisely, the algorithm assumes a symmetric proposal density, $q(y/x)$, and draws a possible new point (y) from $q(y/x)$ as a candidate to be points of the Markov chain of interest. The symmetric distribution is introduced to make the algorithm more straightforward and speed up its convergence.[28] Suppose $Z_n = x$ is the current state of the Markov chain and the candidate (y) is accepted with probability

$$min\left(1, \frac{L(y)}{L(x)}\right) \tag{1}$$

and then set $Z_{n+1} = y$ otherwise set $Z_{n+1} = x$. Thus, the Markov chain of required samples is constructed with repeating this process until converged. One then can estimate the parameters of interest such as the posterior mean or median from the constructed Markov chain.

3 | RESULTS

3.1 | Prevalence of COVID-19 among individuals in households

The frequency and percentage distributions of COVID-19 pandemic among people in Bangladesh are summarized in Table 1.

It was estimated that overall 15.1% (315 out of 2080) individuals were identified as COVID-19 positive patients in 442 households of different sizes considered in this study. More precisely, 40.0% (10 out of 25), 35.7% (20 out of 56), 25.9% (49 out of 189) people were found to be COVID-19 infected cases among households of size 1, 2 and 3, respectively. The prevalence of COVID-19 pandemic was observed to be lower for larger households (≥4 members) than smaller families (<4 members) in Bangladesh. The percentages of COVID-19 infected cases were 15.8% (58 out of 368), 13.3% (58 out of 435), 14.1% (67 out of 474), 12.5% (34 out of 273), 8.7% (9 out of 104), 14.8% (8 out of 54) and 5.7% (2 out of 102) for households with 4, 5, 6, 7, 8, 9 and 10+ family members. The household frequency distributions of COVID-19 pandemic with susceptible and infected individuals in Bangladesh are presented as a matrix form in Table 2.

Table 2 shows that 195 out of 442 households (44.12%) were found to be infected with COVID-19 patients. More precisely, 122, 40, 24, 5, 3 and 1 households were infected with 1, 2, 3, 4, 5 and 6 members, respectively. From Table 2, it is observed that there were 25 households of size 1, where 10 households were COVID-19 infected in Bangladesh. Out of 28 households with 2 members, 12 and 4 households were found to be infected with 1 and 2 persons, respectively. Among 63 households of size three, 25, 3 and 6 were infected each with 1, 2 and 3 persons, respectively. There were 92 households with 4 persons in which 16, 5, 8 and 2 were COVID-19 infected each with 1, 2, 3 and 4 persons, respectively. Out of 87 households with 5 members, it can be seen that 14, 8, 5, 2 and 1 households were infected each with 1, 2, 3, 4 and 5 members, respectively. In total, there were 79 households with size 6 in this study. Among these households 28, 10, 1, 2 and 1 were observed to be infected each with 1, 2, 3, 5 and 6 COVID-19 positive patients, respectively. Among 39 households with 7 family members, 13, 7, 1 and 1 were observed to be infected each with 1, 2, 3 and 4 COVID-19 positive cases, respectively.

3.2 | Estimating transmission parameters of COVID-19

The Longini and Koopman epidemic model was fitted for estimating the transmission probability of COVID-19 in both community and

TABLE 1 Frequency and percentage distributions of COVID-19 among individuals in different households of Bangladesh

		COVID-19 pandemic		
Household size	Number of households	Number of non-infected (%)	Number of infected (%)	Total
1	25	15 (60.0)	10 (40.0)	25
2	28	36 (64.3)	20 (35.7)	56
3	63	140 (74.1)	49 (25.9)	189
4	92	310 (84.2)	58 (15.8)	368
5	87	377 (86.7)	58 (13.3)	435
6	79	407 (85.9)	67 (14.1)	474
7	39	239 (87.5)	34 (12.5)	273
8	13	95 (91.3)	9 (8.7)	104
9	6	46 (85.2)	8 (14.8)	54
10	8	79 (98.8)	1 (1.2)	80
11	2	21 (95.5)	1 (4.5)	22
Total	442	1765 (84.9%)	315 (15.1%)	2080

TABLE 2 Household frequency matrix of COVID-19 with susceptible and infected individuals in Bangladesh

Number of infected individuals	Susceptible individuals in the household											
	1	2	3	4	5	6	7	8	9	10	11	Total
0	15	12	29	61	57	37	17	9	2	7	1	247
1	10	12	25	16	14	28	13	1	1	1	1	122
2		4	3	5	8	10	7	1	2	0	0	40
3			6	8	5	1	1	2	1	0	0	24
4				2	2	0	1	0	0	0	0	5
5					1	2	0	0	0	0	0	3
6						1	0	0	0	0	0	1
7							0	0	0	0	0	0
8								0	0	0	0	0
9									0	0	0	0
10										0	0	0
11											0	0
Total	25	28	63	92	87	79	39	13	6	8	2	442

TABLE 3 Maximum likelihood estimates (MLE) of COVID-19 transmission and non-transmission probabilities along with confidence intervals (CI) in both community and household levels

	Community		Household	
	Non-transmission $\left(\widehat{B}_c\right)$	Transmission $\left(1-\widehat{B}_c\right)$	Non-transmission $\left(\widehat{Q}_h\right)$	Transmission $\left(1-\widehat{Q}_h\right)$
MLE	0.88	0.12	0.91	0.09
95% CI	(0.87, 0.90)	(0.10, 0.13)	(0.90, 0.94)	(0.06, 0.10)

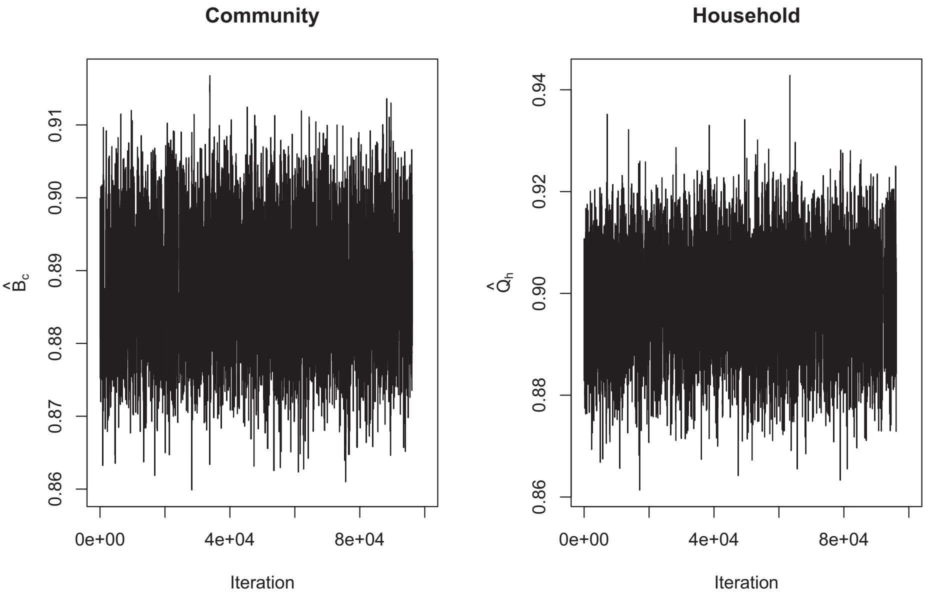

FIGURE 1 Posterior trace plots of estimated model parameters for community $\left(\widehat{B}_c\right)$ and household $\left(\widehat{Q}_h\right)$ levels

households levels of Bangladesh. Table 3 shows that the probability of COVID-19 transmission among the community people (0.12, 95% CI: 0.10 to 0.13) was higher than the household individuals (0.09, 95% CI: 0.06 to 0.10). Therefore, the susceptible individuals have a higher risk of the community infection compared with the infection among household members.

3.3 | Simulation study

A simulation study was conducted adapting the MCMC method via Metropolis-Hastings algorithm in the context of Bayesian framework to validate the maximum likelihood estimators (MLEs) of model parameters (Table 3). We simulated data from both the posterior and

TABLE 4 Posterior estimates along with 95% Bayesian credible interval (BCI) obtained from the Markov Chain Monte Carlo (MCMC) via Metropolis-Hastings algorithm

	Community		**Household**	
Posterior estimates	**Non-transmission** $\left(\hat{B}_c\right)$	**Transmission** $\left(1-\hat{B}_c\right)$	**Non-transmission** $\left(\hat{Q}_h\right)$	**Transmission** $\left(1-\hat{Q}_h\right)$
Mean	0.88	0.12	0.90	0.10
95% BCI	(0.87, 0.90)	(0.10, 0.13)	(0.89, 0.92)	(0.08, 0.11)

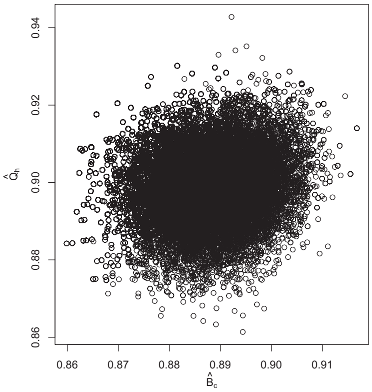

FIGURE 2 Scatter plot of estimated model parameters $\left(B_c, Q_h\right)$ obtained from Markov Chain Monte Carlo (MCMC) through Metropolis-Hastings algorithm

proposal distributions to construct a Markov chain of 100 000 values satisfying the condition (1). In this chain, the "burn-in" period was the first 300 simulation runs.

Figure 1 shows that the Markov chain was converged to the stationary points $\hat{B}_c = 0.89$ (left panel) and $\hat{Q}_h = 0.90$ (right panel). These points were very close to the corresponding MLEs $\hat{B}_c = 0.88$ and $\hat{Q}_h = 0.91$ (Table 3). Posterior mean and corresponding 95% Bayesian credible interval (BCI) of both transmission and non-transmission model parameters are given in Table 4. The posterior mean estimate of community transmission probability $\left(1-\hat{B}_c = 0.12,\ 95\%\ \text{BCI}: 0.10\ \text{to}\ 0.13\right)$ was the same as the estimate obtained from the maximum likelihood estimation algorithm. This estimate for household transmission parameter $\left(1-\hat{Q}_h = 0.10,\ 95\%\ \text{BCI}: 0.08\ \text{to}\ 0.11\right)$ was also very close to the corresponding MLE (Table 3). These findings validate the estimated transmission probabilities of COVID-19 for both community (0.12) and household (0.09) levels in Bangladesh.

3.4 | Correlation between community and household parameters

The correlation coefficient between model parameters $\left(B_c, Q_h\right)$ was estimated as $r = 0.56$, which shows that there was a positive association between the community and household transmission rates of COVID-19. The scatter plot of estimated values of B_c and Q_h (Figure 2), obtained from the MCMC approach, revealed such positive relationship between model parameters. The positive correlation between community and households transmission rates of COVID-19 indicates that there exists a chain of transmission among both community and household individuals. Therefore, the transmission parameters of the epidemic model cannot be estimated separately. As a result, we jointly estimated both community and household transmission probability parameters of COVID-19 adapting the Longini and Koopman stochastic epidemic modelling approach.

4 | DISCUSSION AND CONCLUSION

The novel corona virus is currently a pandemic disease throughout the world including Bangladesh. Bangladesh is a densely populated country where every day majority of people go outside the household for their daily necessities. The COVID-19 spreads from the community in a number of ways from person to person and then within households. For example, one can be infected from the community first and then the infected person spreads this virus within the household members. Our findings revealed that the prevalence of COVID-19 was 15.1% in Bangladesh with a higher proportion among members in smaller households than larger. As community and household transmission parameters of COVID-19 cannot be estimated separately because of correlation exists, we adapted the Longini and Koopman stochastic disease transmission modelling approach for jointly estimating the transmission rates of COVID-19 among people in both community and household levels of Bangladesh. The results were validated via simulation using the MCMC approach through Metropolis-Hastings algorithm in Bayesian framework. It was estimated that the transmission rate of COVID-19 was higher among the community people (12%) than household members (9%) in Bangladesh during the study period June to September 2020. However, another study estimated the substantially lower transmission rate of COVID-19 (4.5%) during March 8 to May 15, 2020 in Bangladesh.[22] In China, the household transmission rate was estimated to be 16.3% during January to February 2020[13] and this rate was 9% in two south Indian states.[29]

This study suggests that the government and relevant authorities need to control the community transmission first with high importance taking necessary measures such as temporarily lock-down, social distancing, stay at home, wear a face mask with the aim of breaking the chain of COVID-19 transmission.

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DISCLOSURES

Authors have declared that no conflicts of interest exist.

AUTHOR CONTRIBUTIONS

AR and ZH conceptualized the idea and designed the study; NM, NA and NA involved with conducting the survey and also contributed in the data collection and management; AR analysed the data; AR and ZH wrote the draft manuscript; ZH provided critical comments on important intellectual contents and jointly contributed in revising the manuscript with AR. All authors approved the final version of manuscript.

ETHICS APPROVAL

Primary data were collected and participants were given no economic benefit, and anonymity was maintained to make sure the confidentiality and reliability of data. This study was conducted through online in full conformity with the provisions of the Helsinki Declaration on human participant research.

CONSENT TO PARTICIPATE AND PUBLICATION

All participants gave informed consent before taking part in the survey. They also provide their consent for publishing the analytical results from this survey without their identifiable information.

CODE AVAILABILITY

Programming codes are available upon request.

DATA AVAILABILITY STATEMENT

All data are available upon request.

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