

**Title: Asymptomatic and presymptomatic transmission of 2019 novel coronavirus (COVID-19) infection: An estimation from a cluster of confirmed cases in Ho Chi Minh City, Vietnam**

Article Type: Original Article

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**Keywords**

Novel coronavirus (COVID-19), asymptomatic, presymptomatic, transmission, contact tracing, Go.Data, Vietnam

# ABSTRACT

## *Background*

The rapid increase in the number of coronavirus disease 2019 (COVID-19) cases worldwide has raised concerns of viral transmission from individuals displaying no or delayed clinical symptoms. We quantified the transmission potential of asymptomatic, presymptomatic and symptomatic cases using surveillance data from a bar gathering in Ho Chi Minh City, Vietnam.

## *Methods*

Between March 14 and April 25, 2020, we collected demographic, clinical and laboratory information of all COVID-19 confirmed cases and contacts from a bar gathering. We applied a Bayesian framework to estimate the proportions of asymptomatic, presymptomatic and symptomatic cases and transmissions with posterior modes and 90% credible intervals (CrI). Using Go.Data, we mapped chains of transmission and estimated the basic reproduction number ( $R_0$ ).

## *Findings*

Of the 298 individuals attending the bar gathering on March 14, 2020, 13 tested positive for SARS-CoV-2. Another 6 tested positive from 4466 contacts further traced. The proportions asymptomatic, presymptomatic, and symptomatic were 0.43 (90% CrI 0.26–0.60), 0.35 (90% CrI 0.20–0.52) and 0.22 (90% CrI 0.09–0.37), respectively. The proportion of asymptomatic, presymptomatic and symptomatic transmissions were 0.45 (90% CrI 0.13–0.74), 0.24 (90% CrI 0.11–0.38), and 0.31 (90% CrI 0.15–0.49), respectively. The cluster-specific  $R_0$  was 2.64 (90% CrI 1.41–3.68). The bar constituted 68%, workplace 21%, and household 11% of transmissions.

## *Interpretations*

We demonstrated using statistical models on surveillance data that high asymptomatic and presymptomatic transmission of COVID-19 occurred in a Vietnam cluster. Detecting and isolating presymptomatic and asymptomatic cases will be an important control measure as movement restrictions are lifted.

## Introduction

On January 30, 2020, the World Health Organization (WHO) declared the epidemic of 2019 novel coronavirus disease (COVID-19) as a public health emergency of international concern.<sup>1</sup> Caused by the severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) which was first reported in Wuhan, China, in December 2019,<sup>2</sup> COVID-19 quickly developed into a pandemic that has led to an unprecedented health crisis worldwide. As of May 11, 2020, 3 917 336 confirmed cases and 274 361 deaths were reported globally,<sup>3</sup> and the estimated case fatality rates ranged from 0.3% to 15%.<sup>4-7</sup> The rapid increase in the number of cases, particularly in countries now experiencing widespread community transmission, has raised concerns of viral transmission from asymptomatic carriers who display no clinical symptoms but are known to be contagious.<sup>8,9</sup> Studies have reported that transmission occurs by close contact (within 1 meter) with respiratory droplets of symptomatic patients infected with SARS-CoV-2.<sup>10,11</sup> Nevertheless, there is emerging evidence that has shown transmissions occurring from cases that were either presymptomatic or asymptomatic.<sup>12-15</sup> This poses a serious challenge for epidemic control given documented large proportions of cases that were presymptomatic or asymptomatic at diagnosis.<sup>16,17</sup> Uncertainties around COVID-19 transmission dynamics have posed challenges in implementing control measures at the scale required to stop transmission.

Statistical models estimate that anywhere between one-third to two-thirds of transmissions occur from presymptomatic cases and a small fraction from asymptomatic cases.<sup>18,19</sup> Asymptomatic infections cannot be recognized if they are not confirmed by

reverse transcription polymerase reaction (RT-PCR) or other laboratory testing, and symptomatic cases may not be detected if they do not seek medical attention.<sup>20</sup> For these reasons, quantifying the transmission potential of asymptomatic cases could help inform the intensity and range of social distancing strategies required to control infection, particularly given the reported high rates (17.9% to 87.9%)<sup>21,22</sup> of asymptomatic infections.

Although investigators have described clinical features, case fatality rates, reproductive numbers and key time periods for COVID-19,<sup>4,5,6,10</sup> a detailed quantification of the asymptomatic proportion and routes of transmission is needed.

In this study, we estimated the proportion of asymptomatic and presymptomatic cases, quantified asymptomatic and presymptomatic transmission, map routes of transmission and estimated the reproductive number ( $R_0$ ) of COVID-19 using a cluster of cases from a bar gathering that took place in Ho Chi Minh City (HCMC), the largest case reporting province in the south region of Vietnam, as a case study.

## **Methods**

### *Study Design*

On January 29, 2020, Vietnam's Ministry of Health (MOH) issued the addition of acute respiratory infections by new strains of coronaviruses to the list of communicable diseases in Group A (extremely dangerous infectious diseases capable of being transmitted very quickly, widely dispersed and with high mortality rate) as stipulated in the Law on Prevention and Control of Infectious Diseases 2007.<sup>23,24</sup> Thereafter, on March 18, 2020, an interim guidance on surveillance, prevention and control of COVID-19<sup>26</sup>

was developed which mandates all health facilities including border health control units to notify cases of COVID-19 to the MOH.

Following this guidance, HCMC, one of twenty provinces in the southern region of Vietnam, strengthened testing for SARS-CoV-2 at treatment facilities and enforced event-based surveillance for early detection and testing of suspected cases in health facilities and communities. As part of this, provincial Centers for Disease Control (CDC) coordinated case identification and management at commune level and reported daily case numbers to the Pasteur Institute Ho Chi Minh City (PI HCMC), the coordinating sub-national institution for southern Vietnam.

On March 20, 2020, the Ho Chi Minh City Centers for Disease Control (HCDC) reported a case from a cluster of COVID-19 cases linked to a bar gathering in HCMC. An epidemiological investigation was conducted following reports that one of the bar's customers, who attended the bar on March 14, tested positive for SARS-CoV-2 on March 20, 2020.

#### *Epidemiological and laboratory investigations*

Between March 14, 2020 and April 25, 2020 we used Go.Data<sup>26</sup>, a WHO outbreak investigation tool for field data collection, to collect demographic and clinical data from 14 days preceding symptom onset until hospital isolation of all confirmed cases and contacts who had attended the bar on March 14, 2020. The case definition issued by Vietnam's MoH<sup>25</sup> was applied for confirmed cases (supplementary material). We collected data on other reported symptoms, travel history, possible contact with confirmed cases reported overseas, context of exposure, and relationship to other cases. Confirmed cases were interviewed to document contacts with other known infected

individuals and other exposures. Information on close contacts (face-to-face contact within 1 meter for more than 15 minutes with a probable or confirmed case) were collected by contact tracing teams. These contacts were tested and placed under quarantine for 14 days at designated government quarantine facilities. Their health status was monitored daily; contacts who developed symptoms were conveyed in dedicated ambulances to hospital for isolation. Respiratory samples of suspect cases and contacts were taken and sent to one of the two COVID-19 designated laboratories in HCMC (National Influenza Center at PI HCMC and Hospital for Tropical Diseases) for testing. The presence of SARS-CoV-2 in nasopharyngeal and oropharyngeal swabs was detected by real-time RT-PCR methods<sup>27</sup>. Laboratory test results (both positive and negative) and dates samples were taken were extracted from the laboratory line lists, and matched with the respective Go.Data identification number.

*Definition of asymptomatic, presymptomatic and symptomatic cases*

We define an asymptomatic confirmed case as a person with laboratory confirmation of COVID-19 infection who reported to have not developed symptoms throughout a period of 14 days of follow-up from the time of diagnosis.<sup>27</sup> Asymptomatic transmission is defined as transmission of the virus from an asymptomatic case to a secondary case.<sup>27</sup>

We define a pre-symptomatic confirmed case as a person with laboratory confirmation of COVID-19 infection that was asymptomatic at time of testing and developed symptoms within 14-day follow-up period.<sup>27</sup> Pre-symptomatic transmission is defined as transmission of the virus from an infected person to a secondary patient before developing symptoms, as ascertained by symptom onset date.<sup>27</sup>

We define a symptomatic case as a person with laboratory confirmation of COVID-19 infection who developed signs and symptoms compatible with COVID-19 virus infection<sup>27</sup> and symptomatic transmission as transmission from a person while they were experiencing symptoms.<sup>27</sup>

### *Transmission chain*

We used the Go.Data visualization matrix to examine the chain of transmission for the bar cluster. We constructed a transmission tree using date of last contact with a confirmed case and date of symptom onset for each confirmed case. We used descriptive statistics to summarize characteristics of exposures. We used date of symptom onset (for those reporting symptoms) to calculate serial intervals (SI), defined as the interval between symptom onset in an index case and symptom onset in a secondary case infected by that index case and between consecutive cases. We characterized the transmission type (asymptomatic, presymptomatic, and symptomatic) and plot the timeline of occurrences. We mapped three contexts of transmission coming from field investigations (bar, household, workplace) for confirmed cases.

### *Estimation of asymptomatic, presymptomatic and symptomatic proportions*

Statistical models<sup>18</sup> were employed to estimate the proportion of asymptomatic, presymptomatic and symptomatic cases among those infected,  $p_{asy}$ ,  $p_{pre}$ , and  $p_{sym}$ , respectively, using the dataset described above. The asymptomatic/presymptomatic/symptomatic status of each person was modeled as independent with common probability. The prior distribution for the proportion of

asymptomatic statuses,  $(p_{pre}, p_{sym}, p_{asy})$ , was Dirichlet( $\alpha = (0 \cdot 875, 0 \cdot 875, 1 \cdot 5)$ ), based on the Diamond Princess outbreak.<sup>18</sup>

### *Estimation of the basic reproductive number ( $R_0$ )*

We let  $A$  indicate the asymptomatic/presymptomatic/symptomatic status of a person. We assumed that individuals have an infectivity profile given by a probability distribution  $p_{inf}^A(s)$ , dependent on time since infection,  $s$ , of an asymptomatic case and the time since onset of symptoms for a symptomatic case. The infectivity profile was assumed independent of calendar time,  $t$ . Let  $R_0^{asy} (R_0^{pre}, R_0^{sym})$  denote the basic reproductive numbers of asymptomatic, presymptomatic and symptomatic cases, respectively. We modeled transmission with a Poisson process in time, so that the instantaneous rate at which a case became infected or had symptom onset at time  $t - s$  is  $R_0^A p_{inf}^A(t - s)$ . Hence  $Y_i$ , the number of people infected by case  $i$ , is Poisson with mean  $R_0^A \int_s^{I_i} p_{inf}^{A_i}(t - s) dt$ , where  $I_i$  and  $A_i$  are the time of isolation and asymptomatic status of case  $i$ . The instantaneous reproduction number was assumed to be constant at  $R_0$ , the basic reproduction number through the study. We estimated  $R_0^{asy}, R_0^{pre}, R_0^{sym}$  separately and also  $R_0 = p_{asy} R_0^{asy} + p_{pre} R_0^{pre} + p_{sym} R_0^{sym}$ . The prior distribution for the  $R_0^{asy}, R_0^{pre}$  and  $R_0^{sym}$  was Gamma with mean 2.5 and standard deviation 2, expressing large uncertainty about the basic reproductive number in this context.<sup>28</sup> The infectivity profiles for asymptomatic, presymptomatic and symptomatic cases were those modeled from 77 transmission pairs obtained from publicly available sources within and outside mainland China,<sup>19</sup> and given in the supplementary material. The posterior distribution for



$R_0$  is Gamma and can be computed directly and for asymptomatic, presymptomatic and symptomatic cases separately.

#### *Estimation of asymptomatic, presymptomatic and symptomatic transmission*

The proportion of asymptomatic, presymptomatic and symptomatic transmission was defined to be correspond expected number of infections divided by the total number (The formulas are in the Supplementary Material). The posterior distribution of these proportions were computed directly from those of the components.

All analyses were done using Go.Data<sup>26</sup> and R<sup>29</sup> software (version 3.6.3). All quantities were estimated in a Bayesian framework. Point estimates and the corresponding 90% credible intervals (CrI) were obtained from the posterior distributions. We undertook a sensitivity analysis that indicated robustness to the modeling assumptions (supplementary material).

#### *Ethics approval*

The study was undertaken as required by national legislation for outbreak investigation and response. All epidemiological investigations were conducted in accordance to the MOH's Decision Promulgating Interim guidance on COVID-19 surveillance, prevention and control. 963 / QD-BYT.<sup>25</sup>

#### *Role of funding source*

This was an exploratory study based on surveillance data, no funding was provided.

## Results

From March 14, 2020 to April 25, 2020 we identified 298 contacts that had attended the bar gathering on March 14. Of the 298 contacts, 13 (5%) tested positive for SARS-CoV-

2. From the 13 confirmed cases, 4466 contacts were traced of which 6 (<1%) tested positive. The 19 total confirmed cases (5 females and 14 males) were from the following 5 countries: 6 (32%) United Kingdom, 4 (21%) Vietnam, 6 (32%) Brazil, 2 (11%) South Africa and 1 Canada. The mean age of the cases was 33 (range 21–51) years.

Of the 19 confirmed cases, 4 (21%) reported either fever, cough, shortness of breath, sore throat at the time of testing, 7 (37%) reported no symptoms at the time of testing but either fever, cough, diarrhea, muscle pain, chest pain or conjunctivitis within the 14 day follow-up period, and 8(42%) reported no symptoms (Table 1). Two (11%) reported international travel to Brazil, Malaysia and Thailand within 14 days prior to the occurrence of the bar gathering.

The first confirmed case (C1) reported symptoms on March 17, 2020, and, was hospitalized on the same day, his sample was taken on March 18, 2020, and was confirmed positive on March 20, 2020. The last confirmed case from this cluster that reported symptoms was on April 14, 2020; one more case was reported after April 14, 2020, this case did not exhibit any symptoms. Although initial investigations indicated C1 as the index case given that he was the first case whose sample was taken and tested positive, the rise of symptomatic and presymptomatic secondary cases from an asymptomatic case (C2) made it possible for any of those who attended the bar on March 14, 2020, to be index cases (Figure 1).

### *Transmission chains*

We positioned all 19 confirmed cases for which exposure data was available in a transmission tree distributed between two generations (Figure 2). Within the first generation, 13 (68%) of the transmissions occurred during the bar gathering (with a mean SI of 8 days amongst those that reported symptoms), of which 1 (8%) reported symptoms at the time of testing, 1 (8%) reported symptoms the day before testing, 5 (38%) reported symptoms within the 14-day follow-up period and 6 (46%) reported no symptoms.

Within the second generation, 3 (50%) of the transmissions occurred within the household (with a mean SI amongst those that reported symptoms of 3 days) and 3 (50%) of the transmissions were workplace-related, of which 2 (67%) reported symptoms after being exposed to a case that did not report symptoms.

The transmission tree was well resolved, with 13 cases (68%) having a single possible exposure and 6 (32%) being exposed in only one context. The shortest chain had 1 case (excluding the index case since the index case cannot be ascertained) and the longest 3 cases (excluding the index case). Overall, SIs ranged from 3 days to 19 days amongst those that reported symptoms.

#### *Asymptomatic, presymptomatic and symptomatic transmission*

The posterior mode of the proportion of asymptomatic cases ( $p_{asy}$ ) is 0.43 (90% CrI 0.26–0.60). The estimates of the proportion of presymptomatic and symptomatic cases are 0.35 (90% CrI 0.20–0.52) and 0.22 (90% CrI 0.09–0.37), respectively. A plot of their posterior distributions is given in Figure 3. The posterior mode of the proportion of asymptomatic transmission is 0.45 (90% CrI 0.13–0.74). The estimates of the proportion of presymptomatic and symptomatic transmission are 0.24 (90% CrI 0.11–0.38) and

0.31 (90% CrI 0.15–0.49), respectively. A plot of their posterior distributions is given in Figure 4.

#### *Calculation of $R_0$*

The posterior mode of the basic reproduction number,  $R_0$ , is 2.64 (90% CrI 1.41–3.68).

The posterior modes of the basic reproduction numbers of asymptomatic,  $R_0^{asy}$ , presymptomatic,  $R_0^{pre}$ , and symptomatic,  $R_0^{sym}$  cases are 2.36 (90% CrI 0.84–3.56), 1.97 (90% CrI 0.85–5.38), and 0.71 (90% CrI 0.28–5.50), respectively. The posterior mode of the basic reproduction number of secondary cases 1.58 (90% CrI 0.83–2.89).

This is the reproductive number for those infected by those infected at the bar on March 14. A plot of the posterior distributions is given in Figure 5.

## **Discussion**

This study provides an estimate of the proportion of asymptomatic and presymptomatic transmission of COVID-19 within the context of a specific cluster, demonstrating the extent to which such transmissions could impact the quantification of transmission dynamics of the COVID-19 pandemic, including the calculations of the basic reproductive number. Previous reports on the proportion of asymptomatic at time of testing have varied widely across different study designs, and our estimate of 69% combining both asymptomatic and presymptomatic proportions falls towards the high end of these estimates.<sup>16-22</sup> By using contact tracing data which ascertained symptomatic status for a 14-day follow-up period, we were able to distinguish between asymptomatic and presymptomatic cases, whereas in most other studies it was unclear whether the cases that were asymptomatic at testing went on to develop symptoms. We further found that 24% of the transmission was presymptomatic and 45% was asymptomatic. Our estimated

proportion of presymptomatic transmission is lower than other statistical modelling studies that have estimated anywhere between 33% and 62% ,<sup>18,19</sup> while the asymptomatic transmission proportion obtained from our cluster analysis is much higher than previously estimated using statistical modelling.<sup>18</sup>

The sequence of events in parallel with the serial intervals of some of the cases that attended the bar gathering suggests that COVID-19 may have been transmitted by either an asymptomatic or a presymptomatic case on the day of the event. Although any case at the bar gathering could have been the index case, a presymptomatic case has a higher probability than a symptomatic case to be the index case since a presymptomatic case is likely to be infectious for a longer period than a symptomatic case. C1 reported symptoms three days after attending the bar. According to the infectivity profile for symptomatic cases in which there is little infectivity two or more days before symptom onset,<sup>30</sup> his infectiousness while attending the bar was negligible. The other symptomatic case from the bar gathering reported symptom onset two days after the event and is therefore also unlikely to be the index case.

The absence of sequencing data, short incubation periods, and the international travel history of two confirmed cases (Brazil, Malaysia and Thailand within 14 days prior to the event) make it also difficult to ascertain and identify the index case.

Amongst the confirmed cases that reported symptoms, the estimated mean serial interval of 3 days is shorter than the reported average incubation time of 4.6 days.<sup>20</sup> This suggests that a significant proportion of secondary transmission can occur before the onset of illness, which is further substantiated with our estimated reproduction number based on secondary infections seen in Figure 6.

Taking into account that the calculation of our transmission rate includes the proportion of asymptomatic and presymptomatic transmission, our cluster estimated basic reproduction number  $R_0$  is higher than WHO estimates of 1.4 to 2.5<sup>27</sup> and higher than the 1.11 reported in Vietnam up until April 5, 2020.<sup>30</sup> A reason for the increase in the reported reproduction number could be that up until now, calculations of the reproduction number for COVID-19 have not included real estimates of the transmission rate given the uncertainty that existed amongst asymptomatic and presymptomatic cases and the effect they had on transmission. Although the estimates of the basic reproduction number depend on the estimation method used as well as the validity of the underlying assumptions, calculation of transmission rates should include the proportion of asymptomatic and presymptomatic transmission to be able to accurately report the reproduction number.

Knowledge of the proportion of infections that are asymptomatic and presymptomatic and their infectiousness relative to symptomatic infections have been important in optimizing public health control strategies in Vietnam. In parallel, novel data collection tools like Go.Data enabled us to visualize real-time data, detect and analyse patterns of transmission. Within our cluster, transmission varied across different settings; it remained predominant in areas with gatherings of more than 20 people such as bars, households and workplaces. Although infection prevention and control measures had been instituted at the time of data collection, they were not fully operational and constantly revised during the course of the outbreak. To further mitigate transmission of COVID-19 it will be necessary to continue to minimise the number of gatherings in confined settings and to enforce social distancing, including in common living spaces.

It is important to put our results into the wider context of the COVID-19 pandemic around the world. Our estimates of asymptomatic and presymptomatic transmission could aid estimation and prediction of incidence of infection from surveillance data. They can also guide the formulation of new public health guidelines and outbreak investigations as policies on infection control measures such as hand hygiene, temperature checks, contact tracing and quarantine of individuals. Given the growing body of evidence of presymptomatic and asymptomatic transmission, COVID-19 epidemic control will require aggressive contact tracing methods that reach contacts early during the presymptomatic period and testing strategies that test all contacts, not just those who are symptomatic. Large-scale community testing enabled by high quality rapid diagnostics will be needed as governments lift movement restrictions. Equally important are engaging the public to continue personal hygiene practices, physical distancing, and mask use in public spaces until vaccinations and therapeutics are available.

Our study was limited by the small sample size that was used for the analysis and comprised of a selective group of people attending a bar and therefore cannot be generalized to the overall population. Although including other clusters throughout the region was an option, complete and verified case data was only available in full for this specific cluster. Furthermore, estimates that were reported are context specific and pertain to a certain district within a province. This highlights the need for complete documentation of the symptomatic status of contacts and their linkages to confirmed cases in order for contact tracing data to be used for analyzing asymptomatic and presymptomatic transmission. Another limitation of the study is the potential for mild symptoms to not be recognized at the time of testing or during follow-up, which would have led to incorrect labeling of symptomatic cases as asymptomatic or presymptomatic

and therefore higher estimates than actual of transmission proportions from these cases. However, the public health importance from the findings is that onward transmission had occurred from individuals who were not aware of their infection status because they did not experience symptoms or did not have recognizable symptoms.

Contact tracing activities were limited at the beginning of the investigation due to the lack of self-reporting that followed the MOH mandate that asked all of those who had attended the bar or were in its vicinity (within a 1 km radius) on March 14, 2020, and March 15, 2020, to fill out health declaration forms. Although this mandate was further strengthened by HCMC broadcasters and social media, it became very difficult for contact tracing teams to know whether they had contacted and traced all those who had come into contact with the 298 bar attendees, or to investigate those who may have attended the bar but never reported.

In conclusion, our results emphasize the importance of quantifying asymptomatic and presymptomatic transmission and how these estimates have important implications for public health as it indicates that viral transmission cannot be completely prevented solely by isolating symptomatic patients. Currently, physical distancing strategies, which are not based on symptom onset, remain a cornerstone control measure and should continue to be practiced. Surveillance guidelines for COVID-19, however, need to be revised and adapted in order to ensure that identification, testing, isolation and daily monitoring of asymptomatic or presymptomatic cases is done routinely to prevent transmission. Contact tracing activities should expand to include those that have been in contact with asymptomatic and presymptomatic cases as well. Characterizing transmission dynamics using statistical models will be key in providing the necessary data to ascertain the high



proportion of asymptomatic and presymptomatic transmission of COVID-19 that is needed to be factored into containing this pandemic.

## **Contributors**

CV, LNL, QD, MSH conducted literature search. CV, MSH and LNL contributed to study design. HD, SO, LCQ, TL, PTL, TVN, QDP contributed to roll out of the study and implementation. DTN, NHL and TT collected the data. QD, CV, LCQ obtained the data and verified the linelists. CV and MSH analysed the data. CV, MSH and LNL wrote the first draft; and all authors reviewed and edited the manuscript.

## **Declaration of Interests:**

We declare no competing interests

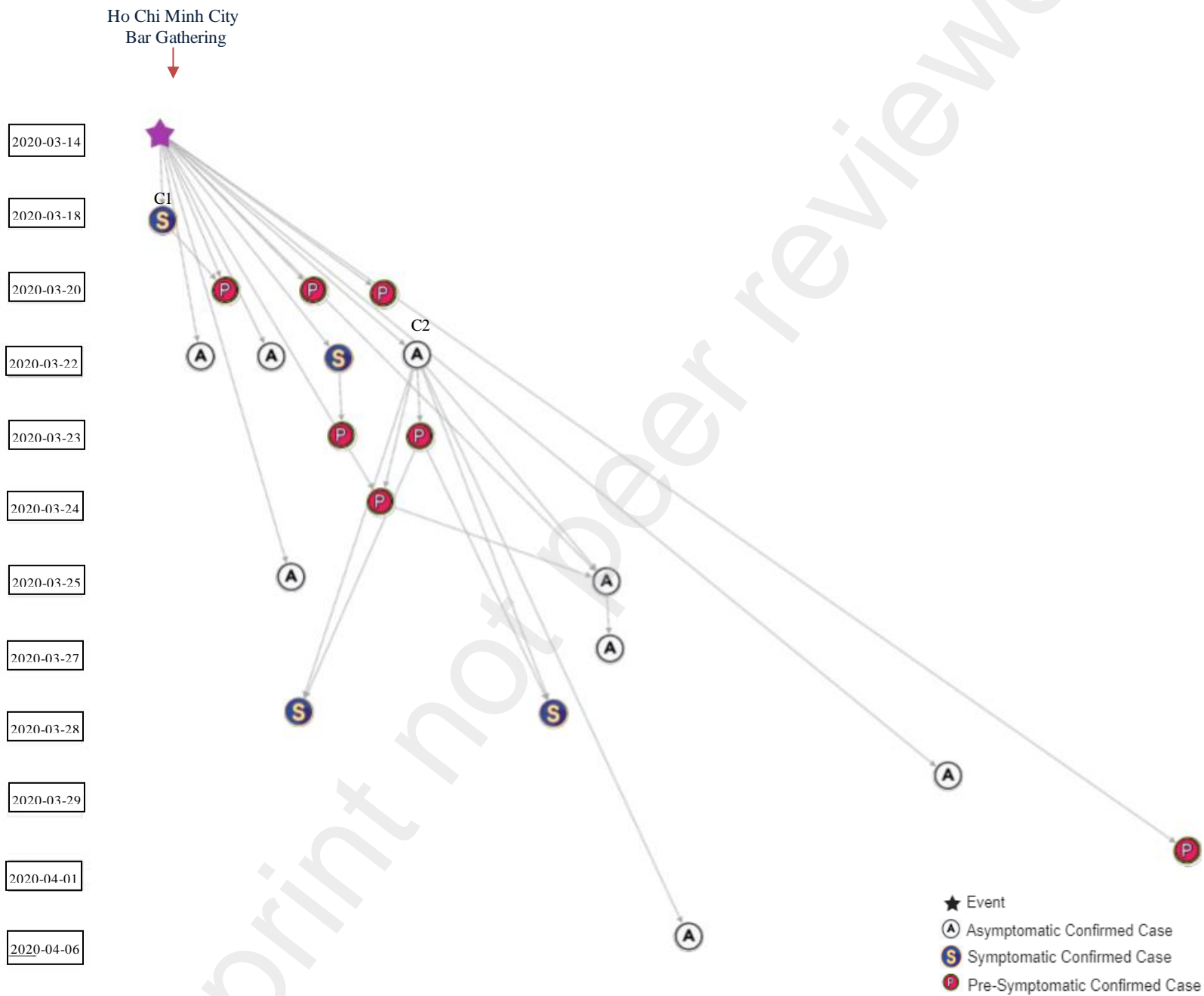
## Tables and figures

**Table 1: Characteristics of confirmed cases of COVID-19 from bar cluster, Ho Chi Minh City, Vietnam, March 14 to April 25, 2020**

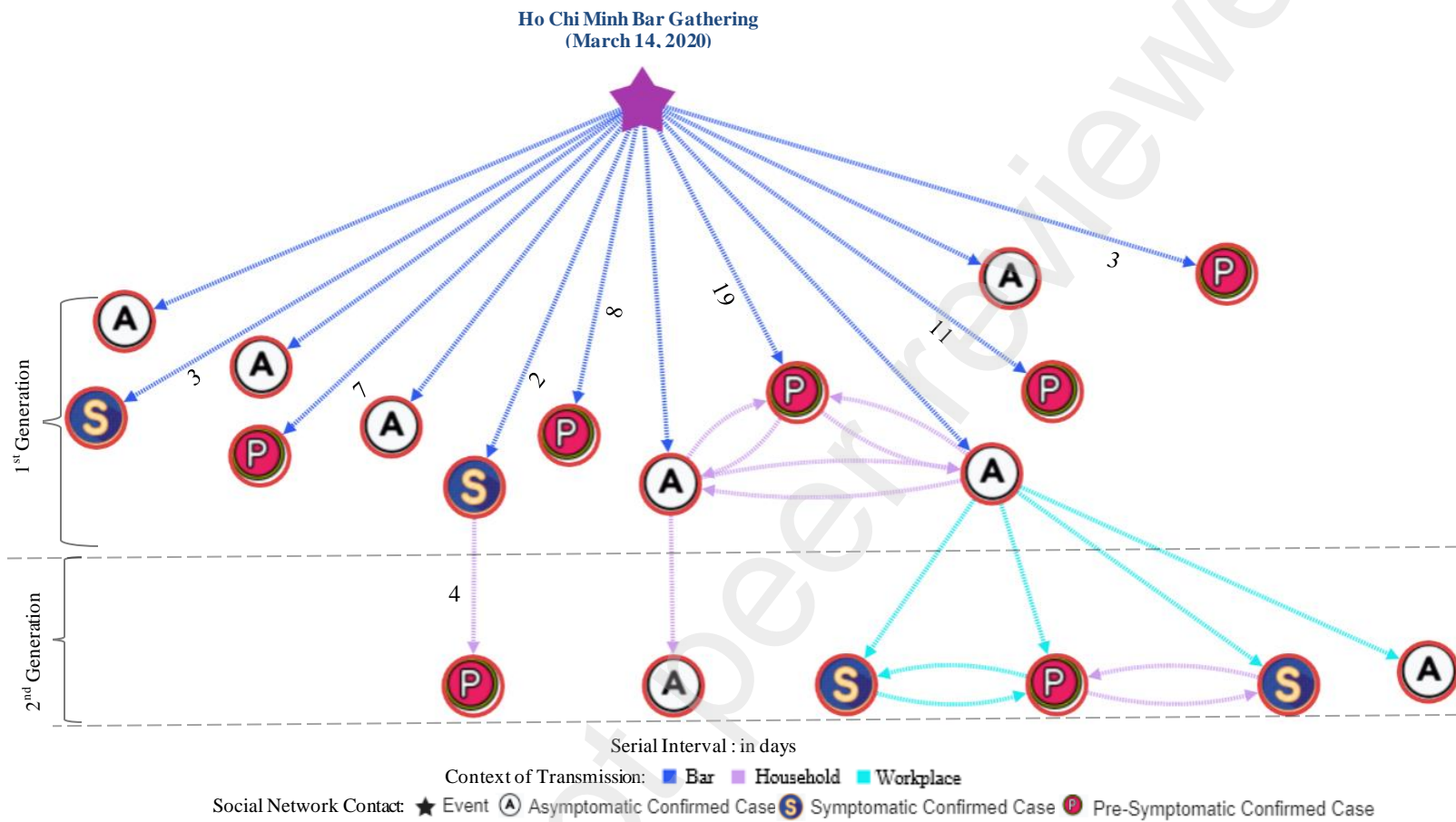
		Confirmed Cases (n=19)
Mean age (years)		33 (21-51)
Gender		
	Male	14 (74%)
	Female	5 (26%)
Province of residence		
	Ho Chi Minh	18 (94%)
	Dong Nai	1 (6%)
Nationality		
	United Kingdom	6 (32%)
	Brazil	6 (32%)
	Vietnam	4 (21%)
	South Africa	2 (11%)
	Canada	1 (5%)
Symptoms		
	Cough	4 (21%)
	Fever	3 (16%)
	Sore Throat	2 (11%)
	Muscle Pain	2 (11%)
	Shortness of Breath	1 (5%)
	Diarrhea	1 (5%)
	Chest Pain	1 (5%)
	Conjunctivitis	1 (5%)
Asymptomatic		8 (42%)
Symptoms after sample taken		7 (37%)
International travel in past 14 days		
	No	17 (89%)
	Yes	2 (11%)
Attended bar gathering on March 14, 2020		
	Yes	13 (68%)
	No	6 (32%)
In contact with a confirmed case that had attended bar gathering		
	No	13 (68%)
	Yes	6 (32%)
Context of exposure		
	Bar	13 (68%)
	Workplace	4 (21%)
	Household	2 (11%)
Interval between symptom onset* and hospitalization (days)		2.6 (0-4)

\* For confirmed cases where date of onset of symptoms was available

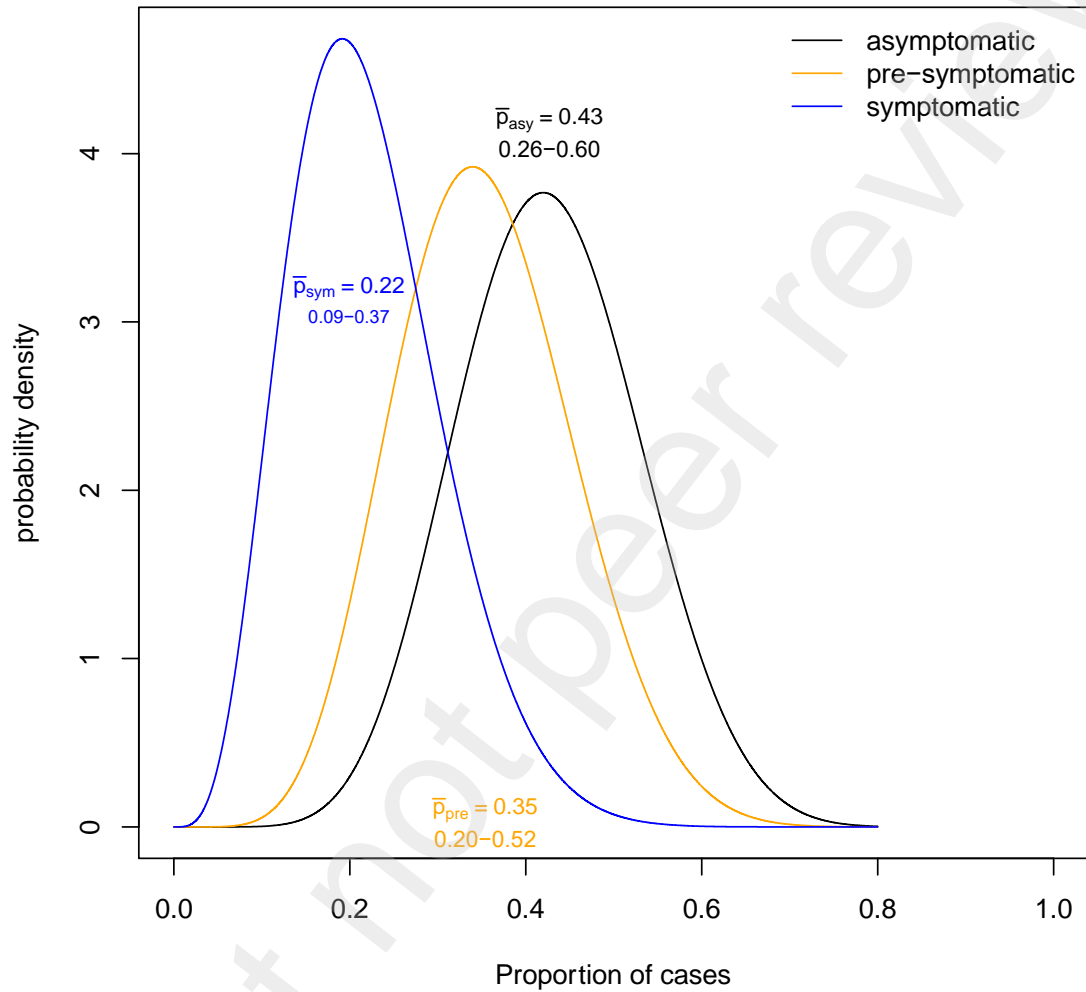
**Figure 1. Timing of events and confirmed COVID-19 cases from bar cluster, by day of sample taken and transmission type (symptomatic, presymptomatic, asymptomatic), Ho Chi Minh City, Vietnam, March 14, 2020-April 25,2020**



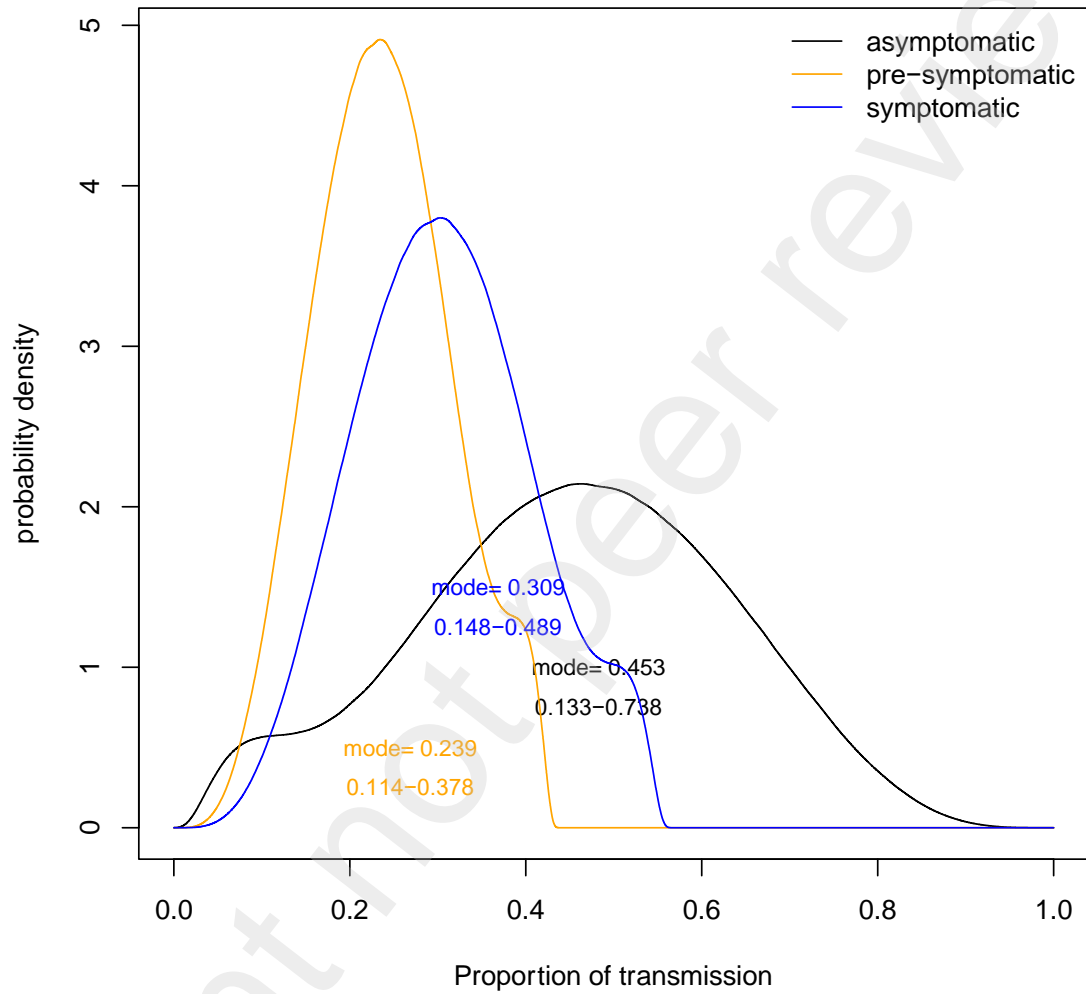
**Figure 2. Transmission tree of four identified COVID-19 transmission chains within the bar cluster with un-weighted serial intervals (in days), by context of exposure and transmission type (symptomatic, presymptomatic, asymptomatic), Ho Chi Minh City, Vietnam, March 14, 2020-April 25, 2020**



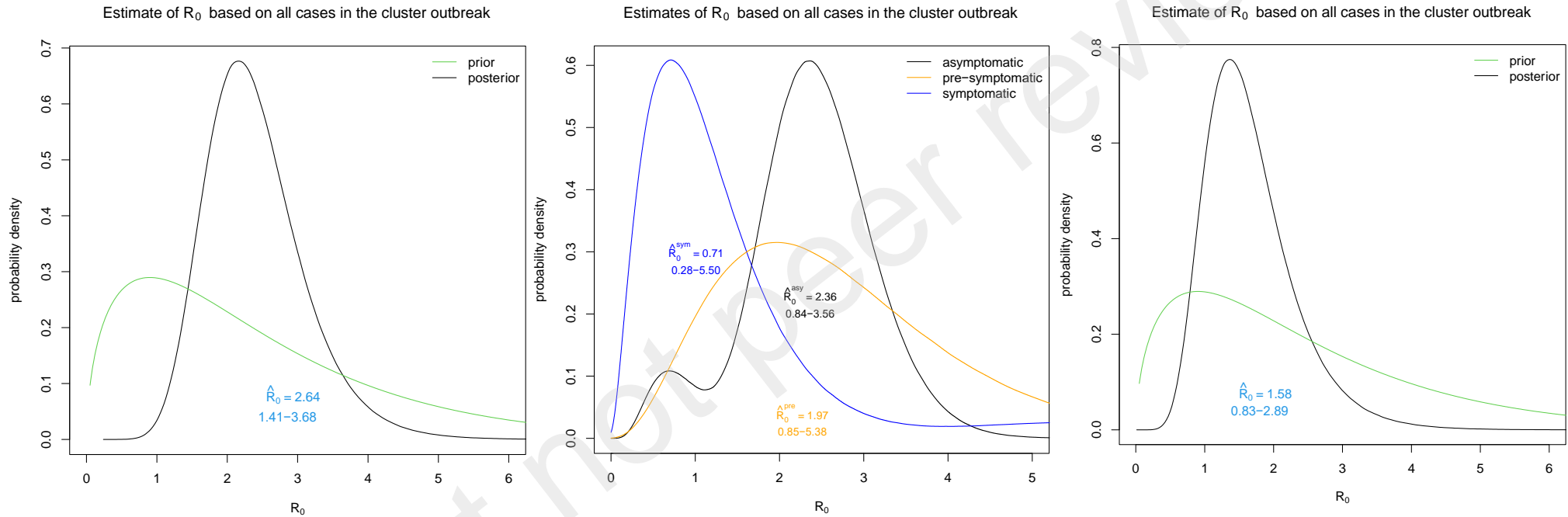
**Figure 3. Posterior distribution of the proportion of COVID-19 asymptomatic, presymptomatic and symptomatic, Ho Chi Minh City, Vietnam, March 14, 2020- April 25, 2020**



**Figure 4. Posterior distributions of the proportion of COVID-19 asymptomatic, presymptomatic and symptomatic transmission in the bar cluster, Ho Chi Minh City, Vietnam, March 14, 2020-April 25, 2020**



**Figure 5. Posterior distribution of the basic reproductive number in the bar cluster, by COVID-19 confirmed cases, asymptomatic, presymptomatic and symptomatic transmission and secondary infections, Ho Chi Minh City, Vietnam, March 14, 2020-April 25, 2020**



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