

Reducing spread of COVID-19 in closed environments: an outbreak investigation and modelling study in dormitory settings

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Abstract

Starting with a handful of SARS-CoV-2 infections in dormitory residents in late March 2020, rapid transmission in their dense living environments ensued and by October 2020, more than 50,000 acute infections were identified across various dormitories. Extensive epidemiological, serological and phylogenetic investigations, supported by simulation models, helped to reveal the factors of transmission and impact of control measures in a dormitory. We find that asymptomatic cases and symptomatic cases who did not seek medical attention were major drivers of the outbreak. Furthermore, each resident has about 30 close contacts and each infected resident spread to 4.4 (IQR 3.5–5.3) others at the start of the outbreak. The final attack rate of the current outbreak was 76.2% (IQR 70.6%–98.0%) and could be reduced by further 10% under a modified dormitory housing condition. These findings are important when designing living environments in a post COVID-19 future to reduce disease spread and facilitate rapid implementation of outbreak control measures.

Main

As countries reopen their society and economy after the first wave of the COVID-19 pandemic, control measures have to move from broad interventions such as widespread lockdowns and closures, to risk-based and targeted strategies in particular sub-populations or environments. Urban settings such as cities are vulnerable to COVID-19 spread as close-living environments (e.g. student or worker dormitories and hostels, senior living facilities, military camps, prison facilities) generally lead to higher degrees of social interactions which then contribute to communicable disease spread.¹

In Singapore, local community clusters involving imported cases and the largely naive local population were identified in late March, 2020.² Some clusters occurred at construction worksites and commercial areas frequented by foreign workers. In the same period, a surge of COVID-19 cases was identified across multiple foreign worker dormitories – the place of residence for about a quarter of the 1.4 million foreign workers in Singapore.^{3,4} These dormitories were built with features such as common recreational and shared facilities, such as gyms, outdoor game courts, minimarts, and cooking areas.⁵ Such facilities provide foreign workers with a good living environment and promote social interactions. However, with thousands of residents in each dormitory, the living density in a dormitory is about 4.5 square metre per resident (in-line with the International Labour Organization standards).^{6,7} Due to the dense contact networks in these closed living environments, infectious diseases introduced to a dormitory could result in high levels of transmission. Understanding the combination of factors that could result in the surge of COVID-19 cases in dormitories would shed light on transmission patterns, and guide future housing solutions and outbreak interventions in dormitories and other similar densely populated settings to curb communicable disease transmission.

In this study, we developed an individual-based model of a dormitory and incorporate the epidemiological and serological investigations findings to identify combinations of parameter that reproduced similar outbreak trajectory in the dormitory. We studied the temporal extent of missed infections and evaluate the

effectiveness of the outbreak control measures under the current dormitory outbreak and alternative scenarios: (i) baseline scenario: only case isolation and quarantine of roommates were implemented; (ii) enhanced response and physical distancing scenario: ground teams were deployed to expedite case isolation and enforce physical distancing measures but no strengthening of measures was applied to reduce probability of infections occurring outside a room in the lockdown phase of the outbreak; (iii) modified dormitory setting scenario: dormitory layout with reduced number of residents per room and, en suite bathroom, shower and cooking facilities to ensure that persons under quarantine did not leave their rooms and movement restrictions across different levels for the remaining residents when the dormitory was under lockdown. Details of the respective interventions in each scenario are described in the Supplementary Information.

Results

From March 23 to June 20, 2020, 2,787 COVID-19 all-male cases with a median age of 33 (IQR 28–38) were identified in a dormitory cluster; none had recent travel history 14 days prior to the onset of symptoms or notification date.

In the pre-lockdown phase (before April 6, 2020), 12 of the initial cases were tested based on doctor's clinical evaluation while one case was tested as part of pneumonia surveillance. An additional 68 cases were identified to fulfil the suspect case definition. Five of the cases were each identified to be associated with at least one other COVID-19 cluster occurring in three worksites and a commercial area frequented by foreign workers. Over the course of the outbreak, three dormitory operations personnel developed COVID-19.

Model fitting

Following the lockdown, cases were observed to decline in mid-April 2020 (Fig. 1). The overall serology outcomes of the 7,367 workers who participated in the seroprevalence survey showed that 72.0% (95% CI 70.9–73.0) of the workers were seropositive and these workers were not identified previously as having acute infection.

From the 10,000 sampled parameter combinations, we observed that about 13 cases (range 6–19) were required for a continued outbreak to occur instead of an early outbreak extinction and 70.8% (95%CI 64.5–76.9%) of the infections were subclinical or asymptomatic cases with a relative infectiousness 17.5% (95%CI 11.3–23.7%) that of a symptomatic case (Table 2). We estimated that about 43.4% (95%CI 32.7–54.2%) of the symptomatic cases sought medical attention and were tested before isolated. The probability of infection upon contact with a susceptible roommate and others outside the room was 70.3% (95%CI 64.0–76.6%) and 54.9% (95%CI 41.9–67.9%) respectively before the strengthening of public health measures in the lockdown phase of the outbreak.

Table 2

Combination of factors that reproduced similar outbreak observations in the dormitory under study

Parameter category	Parameter set	Mean (95% Confidence Interval)
Disease transmission	Initial number of cases	13.9 (12.3–15.4)
	Proportion of asymptomatic cases (%)	70.8 (64.5–76.9)
	Relative infectiousness of an asymptomatic case (%)	17.5 (11.3–23.7)
	Probability of infection inside a room	0.70 (0.64–0.77)
	Probability of infection outside a room	0.55 (0.42–0.68)
Contact network	Mean number of random contacts form on the same level	9.9 (7.9–12.0)
	Mean number of random contacts form on different levels but same block	5.0 (3.9–6.1)
	Mean number of random contacts form in different blocks	2.6 (1.9–3.3)
Health seeking behaviour	Proportion of symptomatic cases seeking medical attention (%)	0.43 (0.33–0.54)
Effectiveness of public health measures	Probability that contacts with persons on the same level remains after social distancing	0.38 (0.29–0.48)
	Probability that contacts with persons on different levels of the same block remains after social distancing	0.42 (0.30–0.55)
	Probability that contacts with persons in different block remains after social distancing	0.51 (0.38–0.63)
	Reduction in probability of infection outside a household	0.22 (0.15–0.28)
	Days since deployment of ground officers when reduction in probability of infection outside a household occurred	3.9 (3.1–4.6)

For the outbreak to spread to other multiple blocks and levels of the dormitory by day 12, we observed from the sampled parameter combinations that the mean number of contacts formed by each individual (i) on the same level was 9.9 (95%CI 7.9–12.0), (ii) on the same block was 5.0 (95%CI 3.9–6.1), and (iii) in other blocks was 2.6 (95%CI 1.9–3.3).

Outbreak intervention scenarios

Based on the sampled parameter combinations, we estimated that the current outbreak peaked at 511 infections (IQR 407–732) on day 20 (IQR 19–21) with a final attack rate of 76.0% (IQR 70.6–98.0%) and

the outbreak ending on day 92 (IQR 65–109) (Table 3 and Fig. 2a). We estimated that 87.3% (IQR 80.8–86.7%) of the infections were not detected over the course of the outbreak prior to the use of serology testing.

Table 3
Outbreak characteristics by intervention scenarios

Outbreak outcomes	Current outbreak	Baseline	Enhance response and social distancing	Modified dormitory setting
Final attack rate (%)	76.0 (70.6–98.0)	97.9 (97.7–98.4)	93.1 (92.5–98.3)	66.4 (51.9–80.8)
Outbreak duration (days)	92 (65–109)	56 (52–60)	75 (63–83)	72 (59–100)
Peak outbreak size	511 (407–732)	905 (877–931)	602 (553–747)	415 (253–705)
Time to peak in outbreak (days)	20 (19–21)	22 (21–24)	23 (21–25)	22 (20–23)
Results reported as median (IQR)				

The maximum daily number of infections was 905 (IQR 877–931) in the baseline scenario (Fig. 2b), 602 cases (IQR 553–747) in the enhanced response and physical distancing scenario (Fig. 2c). The time to outbreak peak in both scenarios remained largely unchanged relative to the current outbreak scenario. The overall attack rate was 97.9% (IQR 97.7–98.4%) with the outbreak ending within 56 days (IQR 52–60) in the baseline scenario (Fig. 2b). Under the modified dormitory setting scenario, the final attack rate was 66.4% (IQR 51.9%–80.8%) (Fig. 2d).

In the baseline scenario, we estimated that the reproduction number declined from 4.4 (IQR 3.4–5.4) to 2.1 (IQR 1.9–2.2) over 4 generations of transmission (Fig. 3b). In the current outbreak scenario, the reproduction number declined from 4.4 (IQR 3.5–5.3) to 1.9 (IQR 1.8–2.1) by the fourth generation (Fig. 3a). Under the modified dormitory setting, this was reduced to 1.8 (95%CI 1.6–1.9) by the fourth generation (Fig. 3d). The initial reproduction number of 4.4 was at least five times the observed reproduction number of 0.8 among cases in the community over the same time period (unpublished data). In all scenarios, the reproduction number falls below unity after seven generations of transmission.

Phylogenetic outcomes

Phylogenetic analyses showed that the genomes from dormitory under study (dormitory A) were highly similar and belonged to the pangolin lineage B.6 (GISAID clade O). As shown in the phylogenetic tree, viruses belonging to this lineage circulated with high frequency within several countries in the region such as India, Malaysia and Australia and were different from those circulating in Wuhan, China (Fig. 4).

Locally, the sequences were highly similar to other genomes from a cluster associated with a popular commercial area (commercial area M) frequented by foreign workers and travellers (Fig. 4). Documented index cases of commercial M cluster preceded dormitory A outbreak. Furthermore, worksite P where workers from different dormitories were intermixing with workers from dormitory A had seeded the virus into dormitory L, K, J, C.

Distinguishable clusters characterized by unique genetic markers were found for 3 dormitories (dormitory J, K and F) (Fig. 4). Interestingly, while most samples from the commercial area M were found basal to the outbreak, there was one sample (Singapore/556) that was part of a separate cluster unique to other sequences from India, suggesting the possibility of multiple introductions via similar routes.

Discussion

The spread of COVID-19 in densely populated residential areas has been documented in major cities and countries such as Australia⁸, South Korea⁹, India¹⁰ and Hong Kong¹¹. In Singapore, epidemiological investigation of the initial cases in the dormitory did not reveal a common source of infection. Some of the cases were associated with more than one COVID-19 clusters occurring at their worksites or social-recreational areas thereby increasing the chances of multiple introductions of COVID-19 infections into the dormitory from the foreign worker community. Furthermore, phylogenetic analysis of the genetic sequences showed close similarity with other circulating viruses in India and Malaysia, and hence, import-related transmission to the dormitory, directly or through other clusters, cannot be ruled out. Based on the epidemic trajectory, modelling outputs suggest that there were approximately 13 cases that seeded the outbreak.

Given the uncertainties of the contact network patterns and disease transmission dynamics in a dormitory, we explored and showed that varied parameter combinations could result in similar observations in the early and late phases of the outbreak. As such, multiple interventions are essential to successfully contain an outbreak in these settings. In the current outbreak scenario, with strengthened outbreak containment measures, the overall attack rate was about 22% lower than the baseline scenario. The strengthened measures help to flatten the epidemic curve with peak cases more than 40% lower as compared to the baseline scenario. However, the outbreak duration in the current scenario was lengthened by about 1–2 months compared to the baseline. The surge in cases into the hundreds per day further justified the need for ground healthcare and operations teams to assist in managing ill residents in situ, as most of the infections were mild in this group of mostly young and healthy individuals. Despite the large number of dormitory cases, strict infection control observed by these workers ensured that infections in dormitory operations personnel and spill over into the community were kept to a minimum (in this dormitory, three ground officers were infected).

COVID-19 antibodies were detected in 72.0% of the 7367 persons with no prior PCR confirmation of SARS-CoV-2 infection. Our model estimated that about 71% of the infections in the current outbreak were attributed to subclinical asymptomatic infections, and about 57% of the symptomatic cases did not seek

medical attention. Findings of the latter could be attributed to mildly symptomatic persons who did not report symptoms and the overall extent of missed infections corroborates with a WHO report where 80% of the infections were mild or asymptomatic.¹² More could be done to educate individuals on the symptoms of COVID-19 and to encourage testing.

Our model estimated that each worker had approximately 18 contacts outside the household with nearly 80% of the contacts formed within the same block and the remaining with persons in other blocks. The dense contact network facilitated disease transmission with the reproduction number in the dormitory exceeding 1 for six generations. This was several times higher than that observed in the community given the dense living conditions and because dormitories are specifically set up for social interactions among foreign workers. Hence, modified living environments for dormitories and similar living settings should be explored for the post-COVID-19 era to include increased living space, lowered occupancy per room and en suite facilities where possible.⁶ The modelled number of infections under a modified dormitory setting would be reduced by at least 10%, and more if we incorporate a reduced probability of infection within the room given the increase in living area per individual. Furthermore, our model suggested that the majority of the random contacts outside the room were made with persons within the same block for a dormitory with shared facilities. Given that these persons could be exposed prior to the isolation of their infector, future outbreak containment could consider the movement restrictions of all persons in a block when a case of COVID-19 is identified. This would be at odds with the design of such living environments to promote social interaction but is necessary in the post-COVID-19 era to reduce the spread of infectious diseases in a naïve population. As the modification of the built environment of these residential areas comes at higher capital and operational cost, cost-effectiveness studies will need to be performed to determine the optimal build strategy.

Our study has some limitations. While there was regular disinfection and housekeeping in the dormitories, environmental transmission¹³ could have occurred but were not modelled. We also assumed that symptomatic cases who sought medical attention will do so upon onset. This is pertinent to the lockdown phase of the outbreak with increased residents' awareness of the situation and delayed testing would reduce the effectiveness of the outbreak control measures. We did not stratify the model by age and COVID-19 infection in older individuals could result in increased severity of symptoms and likelihood of seeking medical treatment.

Conclusion

Our study found that having multiple interventions such as active case isolation and enforcement of safe distancing measures together with improved dormitory design are effective in flattening the epidemic curve. These findings can be used to guide in the planning and design of high-density living areas, while adequately balancing the social interaction and outbreak response needs.

Methods

Over the course of the pandemic, the Ministry of Health, Singapore (MOH) had over time fine-tuned and adjusted the local COVID-19 suspect case definitions along with the growth and evolution of global evidence base. Under the Infectious Diseases Act in Singapore, suspect COVID-19 cases are required to undergo medical investigation¹⁴ [Supplementary Table 1] while all pneumonia cases admitted in public hospitals will also be tested for SARS-CoV-2. Furthermore, doctors can conduct discretionary tests on patients based on clinical suspicion or epidemiological risk factors. A confirmed case of acute SARS-CoV-2 infection is defined as a person with respiratory sample positive for SARS-CoV-2 using a laboratory-based reverse transcription polymerase chain reaction (RT-PCR) test.¹⁵

On March 30, 2020, MOH identified a COVID-19 outbreak in a foreign worker dormitory in Singapore and all epidemiological investigations and outbreak containment measures were implemented under the Infectious Diseases Act, which grants the use of outbreak investigation data for analysis and evaluation.

Epidemiological investigation and public health measures

The outbreak response in the dormitory was divided into two phases based on the extent of transmission in the dormitory. In the pre-lockdown phase in the dormitory (before April 6, 2020), all laboratory-confirmed cases were interviewed to collect data on demographic characteristics, clinical symptoms, and activity patterns for the fourteen days preceding symptom onset or notification date until isolation in hospital.

Contact tracing was initiated to identify close contacts within the dormitory (persons who stay in the same room as a confirmed case) and in the work and social contexts (persons who spend at least 30 minutes within 2 metres of a confirmed case). These contacts were placed under quarantine for fourteen days from last exposure to the case at designated government quarantine facilities located outside the dormitory. The health status of all persons under quarantine was monitored daily and those who developed symptoms would undergo medical investigation as part of active case finding.

To facilitate outbreak investigations and management, details of the dormitory layout and all dormitory residents were requested from the dormitory operator. Employers of a confirmed case and the dormitory operators were also advised to monitor the health condition of all other workers and dormitory residents respectively daily and to advise any person who was unwell to seek medical attention immediately.

The dormitory was locked down on April 6, 2020. During the lockdown phase, healthcare and other workers were deployed to set up medical posts and perform active case finding via swabbing exercises, case isolation and quarantine of close contacts in situ, implementation of safe distancing measures while ensuring the welfare of the dormitory residents. All personnel involved in the dormitory operations were required to observe proper infection control measures at all times and to monitor their health. Residents who were unwell were advised to seek medical attention immediately and were investigated for SARS-CoV-2 infection.

Sequencing and phylogenetic analysis

All primary samples or residual extracted nucleic acid tested positive for SARS-CoV-2 by RT-PCR at diagnostic laboratories were forwarded to Singapore's National Public Health Laboratory. Available samples from the dormitory cases and other samples linked to the dormitory outbreak (e.g. from the workplaces or social interactions) between April 1 and June 6, 2020 were randomly selected for next generation sequencing.

Selected residual diagnostic RNA were subjected to tiled amplicon PCR using ARTIC nCoV-2019 version 3 panel,¹⁶ where One-Step RT-PCR was performed using the SuperScript™ III One-Step RT-PCR System with Platinum™ *Taq* DNA Polymerase (ThermoFisher Scientific). Sequencing libraries were prepared using the Nextera XT and sequenced on MiSeq (Illumina) to generate 300 bp paired-end reads. The reads were subjected to a hard-trim of 50 bp on each side to remove primer artifacts using BMap¹⁷ prior to consensus sequence generation by Burrows-Wheeler Aligner-MEM v0.7.17, with default settings. Only sequences with $\geq 98\%$ genome coverage and supported by an average depth of 100x were included for phylogenetic analysis. The generated consensus sequences were shared via GISAID.¹⁸ To place these sequences into global context, we searched for closely related strains using BLASTN¹⁹ against all genomes in the GISAID database and retained representative hits with 99.99% identity and matching the time window of our sequences [Acknowledgements in Supplementary Information]. The sequences were merged with hCoV-19/Wuhan/WIV04/2019 (accession: EPI_ISL_402124) as reference and root for the tree and aligned using MAFFT (v7.427)²⁰. The alignment was manually inspected and trimmed at the 5' and 3' ends using Jalview.²¹ A maximum likelihood phylogenetic tree was created with IQ-TREE v1.6.1²² using ModelFinder²³ for estimating the best fit model (TN + F in this case) and 1,000 steps of ultrafast bootstrapping²⁴ with zero length branches collapsed in the final tree, visualized with Figtree.²⁵

Seroprevalence survey to determine extent of undetected infections

To determine the extent of undetected infections within the dormitory, we undertook a prospective cross-sectional seroprevalence survey in a convenience sample of 7,367 dormitory residents who had no travel history 14 days prior to the onset of the first dormitory case and were not previously identified as a confirmed case of acute SARS-CoV-2 infection. Blood samples were collected between May 13 to June 1, 2020 (52 to 79 days since the onset of the first case; 37 to 70 days since the lockdown of the dormitory) were tested for SARS-CoV-2 Immunoglobulin G (IgG) using either Abbott Architect SARS-CoV-2 IgG assay or Roche Anti-SARS-CoV-2 assay. For the overall seroprevalence, we computed the 95% confidence intervals (CI) for binomial proportions using Wilson's method.²⁶

Transmission model

Despite the strengthening of public health measures during the lockdown phase, cases continued to rise. This could be attributed to the dense contact networks and living conditions resulting in rapid transmission, the presence of pre- or asymptomatic transmissions, and variable health seeking behaviour

of symptomatic persons that could have resulted in a delay or failure to isolate cases who went on to transmit the virus to others. Hence, to estimate the outbreak trajectory within the dormitory and to evaluate the effectiveness of the outbreak control measures, we used an individual-based model of COVID-19 transmission in a simulated population of 12,091 individuals (scaled based on number of individuals in a room) residing in a dormitory with a similar number of blocks, levels and rooms as the dormitory under study [Supplementary Table 2]. We assumed that the entire dormitory population was naïve to SARS-CoV-2 infection and disease transmission parameters such as the infectiousness over time and incubation period were modelled based on assumed distributions as elaborated upon in the Supplementary Information.

Model fitting

We hypothesized that a diverse range of parameters could drive similar outbreak trajectory in the dormitory. We generated 50,000 random parameter combinations containing parameters related to disease transmission, contact network of the residents within the dormitory, health seeking behaviour or the effectiveness of public health measures (Table 1).

Table 1
Range of values for each parameter in a parameter set

Parameter category	Parameter	Minimum	Maximum
Disease transmission	Initial number of cases	3	20
	Proportion of asymptomatic cases (%)	30	90
	Relative infectiousness of an asymptomatic case (%)	0	50
	Probability of infection inside a room	0.5	1
	Probability of infection outside a room	0	1
Contact network	Mean number of random contacts form on the same level	0	20
	Mean number of random contacts form on different levels but same block	0	10
	Mean number of random contacts form in different blocks	0	5
Health seeking behaviour	Proportion of symptomatic cases seeking medical attention (%)	0	100
Effectiveness of public health measures	Probability that contacts with persons on the same level remains after social distancing	0	1
	Probability that contacts with persons on different levels of the same block remains after social distancing	0	1
	Probability that contacts with persons in different block remains after social distancing	0	1
	Reduction in probability of infection outside a household	0	0.5
	Days since deployment of ground officers when reduction in probability of infection outside a household occurred	1	7

The outbreak trajectory in each iteration of a parameter combination was fitted against (i) the number of cases and number of affected locations since the earliest observed onset date (day 1) till day 12 of the outbreak (prior to the lockdown of the dormitory) and (ii) the overall serology outcomes in persons with no recent travel history and no laboratory confirmation of SARS-CoV-2 infection tested by day 79 of the outbreak. For each parameter combination, the full outbreak was simulated ten times to generate 500,000 outputs. The fit of the model against the observed data in the early and late phases of the outbreak was determined by computing the likelihood [Supplementary Information]. Observed case counts in the lockdown phase were not used for model fitting as symptom onset dates were not routinely collected.

Outbreak interventions scenarios

Parameter combinations were assigned a weight based on the corresponding likelihood and weighted sampling of the parameter combinations with replacement was performed 10,000 times. We simulated the current outbreak scenario with interventions including the deployment of ground teams to expedite case isolation, quarantine of roommates, enforcement of social distancing and reduction in probability of infection outside the room in the lockdown phase of the outbreak [Supplementary Information]. Using the same disease transmission and contact network parameters, we also simulated alternative scenarios of the dormitory outbreak: (i) baseline scenario: only case isolation and quarantine of roommates were implemented; (ii) enhanced response and physical distancing scenario: ground teams were deployed to expedite case isolation and enforce physical distancing measures but no strengthening of measures was applied to reduce probability of infections occurring outside a room in the lockdown phase of the outbreak; (iii) modified dormitory setting scenario: dormitory layout with reduced number of residents per room and, en suite bathroom, shower and cooking facilities to ensure that persons under quarantine did not leave their rooms and movement restrictions across different levels for the remaining residents when the dormitory was under lockdown.⁶ Details of the respective interventions in each scenario are described in the Supplementary Information.

For each parameter combination, disease progression was tracked over time and generations (g_x where the subscript x indicates the respective generation). The reproduction number of the x^{th} generation—i.e. the ratio of cases in consecutive generations (i.e. $\frac{g_{x+1}}{g_x}$) which provides an indication of the growth of an outbreak—was determined. All analyses were done using R version 3.5.1.²⁷ A full description of the model is available in the supplementary information.

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