Since January 2020 Elsevier has created a COVID-19 resource centre with free information in English and Mandarin on the novel coronavirus COVID-19. The COVID-19 resource centre is hosted on Elsevier Connect, the company's public news and information website.

Elsevier hereby grants permission to make all its COVID-19-related research that is available on the COVID-19 resource centre - including this research content - immediately available in PubMed Central and other publicly funded repositories, such as the WHO COVID database with rights for unrestricted research re-use and analyses in any form or by any means with acknowledgement of the original source. These permissions are granted for free by Elsevier for as long as the COVID-19 resource centre remains active.
Research Paper

Spread of SARS-CoV-2 aerosols via two connected drainage stacks in a high-rise housing outbreak of COVID-19

Qun Wang a,1, Zhang Lin b,1, Jianlei Niu c,1, Garnet Kwan-Yue Choi d,1, Jimmy C.H. Fung e, Alexis K.H. Lau f, Peter Louie f, Kenneth K.M. Leung f, Jianxiang Huang g, Pan Cheng a, Pengcheng Zhao a, Wenzhao Chen a, Sheng Zhang b, Liye Fu c, PW Chan h, Ann Han Wong i, Herman Tse d, Sally Cheuk Ying Wong d, Raymond Wai Man Lai i, David SC Hui j, Kwok-Yung Yuen k, David Christopher Lung d,i,* , Yuguo Li a,**,1

a Department of Mechanical Engineering, The University of Hong Kong, Hong Kong, China
b Division of Building Science and Technology, City University of Hong Kong, Hong Kong, China
c Department of Building Environment and Energy Engineering, The Hong Kong Polytechnic University, Hong Kong, China
d Department of Pathology, Hong Kong Children’s Hospital, Hong Kong, China
e Division of Environment & Sustainability, Hong Kong University of Science and Technology, Hong Kong, China
f Environmental Protection Department, Hong Kong SAR Government, Hong Kong, China
g Department of Urban Planning and Design, Faculty of Architecture, The University of Hong Kong, Hong Kong, China
h Hong Kong Observatory, Kowloon, Hong Kong, China
i Department of Microbiology, Prince of Wales Hospital, Hong Kong, China
j Department of Medicine and Therapeutics, Chinese University of Hong Kong, Hong Kong, China
k Department of Microbiology, The University of Hong Kong, Hong Kong, China
l Department of Pathology, Queen Elizabeth Hospital, Hong Kong, China

HIGHLIGHTS

• The vertical cluster of the outbreak is probably associated with drainage stacks.
• Tracer gas measurement and phylogenetic analysis of SARS-CoV-2 genome sequences were applied.
• The results of tracer gas monitoring agreed with the observed distribution of infected cases.
• Leaked stack aerosols may have played the main role in the vertical cluster.
• The chimney effect was the probable primary cause for the vertical spreading.

ABSTRACT

Vertical transmission of severe acute respiratory syndrome coronavirus-2 (SARS-CoV-2) along a vertical column of flats has been documented in several outbreaks of coronavirus disease 2019 (COVID-19) in Guangdong and Hong Kong. We describe an outbreak in Luk Chuen House, involving two vertical columns of flats associated with an unusually connected two-stack drainage system, in which nine individuals from seven households were infected.

Keywords:
COVID-19
infected. The index case resided in Flat 812 (8th floor, Unit 12), two flats (813, 817) on its opposite side reported one case each (i.e., a horizontal sub-cluster). All other flats with infected residents were vertically aligned, forming a vertical sub-cluster. We injected tracer gas (SF$_6$) into drainage stacks via toilet or balcony of Flat 812, monitored gas concentrations in roof vent, toilet, façade, and living room in four of the seven flats with infected residents and four flats with no infected residents. The measured gas concentration distributions agreed with the observed distribution of infected flats. Aerosols leaking into drainage stacks may generate the vertical sub-cluster, whereas airflow across the corridor probably caused the horizontal sub-cluster. Sequencing and phylogenetic analyses also revealed a common point-source. The findings provided additional evidence of probable roles of drainage systems in SARS-CoV-2 transmission.

1. Introduction

Leading health authorities have recognised the potential for aerosol transmission of severe acute respiratory syndrome coronavirus-2 (SARS-CoV-2), the pathogen responsible for the ongoing coronavirus disease 2019 (COVID-19) pandemic (World Health Organization, 2020). Meanwhile, indirect transmission via fomites is considered insignificant ((US CDC, 2021). Aerosol transmission probably occurred in poorly ventilated indoor spaces (Qian et al., 2021), and expired infectious droplets from infected individuals are believed to be the major source of the virus. Two early studies documented unusual vertical outbreaks of COVID-19 in high-rise buildings in Guangzhou (Kang et al., 2020) and Hong Kong (Wang et al., 2022). In these vertical outbreaks, family members living in flats in the same column as the flat of the index case were infected. These flats with infected residents were vertically far apart but shared a vertical wastewater drainage stack. The infection risk was low or non-existent in flats that did not belong to the same column. The chimney effect of the vertical stack was suggested to be responsible for transporting the infectious aerosols mostly upward from a flat with an infected resident (Kang et al., 2020), and the leakage of infectious aerosols into the bathrooms of other flats led to secondary infections in residents of those flats. This mechanism explains why most flats with infected residents were above the flat where the index case resided (Wang et al., 2022). The leaked aerosols were small (most likely less than 5 μm in diameter; Gormley et al., 2021), and aerosol transmission within each bathroom or flat was suspected of having occurred after the leakage.

The infectious aerosols in these vertical outbreaks were first suspected to be of faecal origin (Kang et al., 2020). Indeed, faecal aerosols may play a role in SARS-CoV-2 transmission (McDermott et al., 2020; Heller et al., 2020). A SARS outbreak in a high-rise estate in Hong Kong in 2003, leading to SARS-CoV-1 infections in more than 300 people, highlighted the probable role of faecal aerosols in viral transmission (Yu et al., 2004). In contrast, however, the number of secondary infections in each of the abovementioned vertical outbreaks of SARS-CoV-2 was less than 10 (Kang et al., 2020; Wang et al., 2022). Washbasin wastewater discharge, not faecal aerosols, was assumed to be responsible, based on SARS-CoV-2-positive washbasin samples in at least one of the reported outbreaks (Wang et al., 2022). Aerosols that are generated within the drainage stack during wastewater discharge are referred to as stack aerosols.

If confirmed, these findings regarding the possible role of washbasins or faecal aerosols and transmission via drainage stacks will have significant implications for public health (Dancer et al., 2021). Possible interventions to address the drainage transmission route differ from those for conventional aerosol transmission, in that the leakage of air from the drainage systems needs to be avoided. It is not yet known how much the drainage transmission route contributes to the overall infection dynamics. It is also unknown if this novel transmission route has contributed to infections in cities other than Guangzhou and Hong Kong. Kang et al. (2020) and Wang et al. (2022) used small samples and conducted a limited number of field tests. New data are important to provide additional evidence for this mode of transmission.

In this study, we investigated an outbreak of COVID-19 involving nine confirmed cases from seven flats from 31 May to 13 June 2020 in Luk Chuen House, a large public housing block in Lek Yuen Estate, Hong Kong. Four of the seven affected flats were vertically aligned with the flat where the index case resided, and two additional flats were on the same floor as the index case’s flat. In contrast with the outbreaks reported by Kang et al. (2020) and Wang et al. (2022), four of the flats with infected residents did not belong to the same vertical column of flats as the index case’s flat, but were in two neighbouring columns of flats. We measured the airflow through the drainage pipes and between flats using a tracer gas to investigate the role of stack aerosols and the potential involvement of multiple transmission routes.

2. Methods

We first obtained the dates of symptom onset (Fig. 1) and the locations of the flats of the nine confirmed cases infected with SARS-CoV-2 from the Centre for Health Protection (CHP), Department of Health. We also collected building-related data, including site plans and drainage system data. Hourly weather data during the infectious period were obtained from a weather station close to the site. Extensive contact tracing and environmental detection were conducted from 1 to 18 June 2020 by the CHP and the Environmental Protection Department (EPD). Deep-throat saliva samples were collected from 1399 residents and management staff of Luk Chuen House (Fig. 2a), which is one of the seven high-rise housing blocks in Lek Yuen Estate built in 1975 (Fig. S1). The estate has 3200 flats with approximately 8100 residents. During the expected infectious period (19–30 May 2020; He et al., 2020), the prevailing wind was mostly easterly or south-westerly, with an average speed of 2 m/s (Figs. S6 and S7). There are 40 flats each on the 2nd to 15th floors (Fig. 2b) and a total of 560 flats in the building. Even- and odd-numbered flats are separated by a long corridor. The index case (case no. LC01 in Table 2) resided in Flat 12 on the 8th floor (Flat 812). All flats with numbers ending in 12 are designated as −12 flats.

Tracer gas dispersion tests were performed on 16–17 June 2020, while the residents of −10 and −12 flats were quarantined. We used a tracer gas (SF$_6$) as a surrogate for stack aerosols containing virus-laden droplets. Cautions need to be taken when using any gaseous tracer surrogate for fine infectious aerosols in drainage stacks. Two key differences between a tracer gas and aerosol particles exist for related applications, i.e., their diffusivities differ, and their surface behaviour differs. For example, when being approached a surface; the tracer gas molecule might be absorbed onto the surfaces and the water film,

Fig. 1. The epidemic curve of the COVID-19 outbreak by symptom onset dates.
whereas the aerosol particle would deposit via an adhesive force, also affected by the water film. Several existing studies indicated the validity of using tracer gas as a surrogate for fine aerosols (less than 5 µm) for indoor dispersion (Ai et al., 2020; Bjørn and Nielsen, 2002; Bolashikov et al., 2012). Gormley et al. (2021) found that most aerosols (>99.5%) generated during wastewater discharge in the drainage pipes are < 5 µm. Zhang et al. (2009) made a direct comparison of the distribution of SF6 tracer gas and 0.7 µm particles in an air-conditioned full-scale airliner cabin mock-up. They found that the distribution of the two simulated substances was similar within the cabin. After gaining access permission, the tracer gas concentrations were monitored in four flats with infected residents (710, 810, 812, and 1012), four flats with no infected residents (712, 910, 912, and 1412), façades, and roof vents, for a total of 21 sampling points. A 24-channel multipoint sampler and a photoacoustic gas monitor (Innova 1412i and 1409; LumaSense Technologies, Ballerup, Denmark), a 6-channel multipoint sampler and a multi-gas monitor (type 1303 and 1302; Brüel & Kjær, Nærum, Denmark), and an SF6 leak detector (3434i; LumaSense Technologies) were used to monitor the tracer gas concentrations. Examples of the sampling points set up for Flats 810 and 812 are shown in Fig. 3a. An inter-comparison test of the analysers was performed offsite and onsite before measurements were taken. The experiments were conducted between 12:36 and 18:13 on 17 June, following the experimental set up on 16 June. Two sets of tracer gas experiments were performed. First, the tracer gas was released into the drainage stack passing through the

| Flats | No. of family members | No. of infected members |
|-------|------------------------|-------------------------|
| 812   | 3                      | 3                       |
| 710, 810, 1012, 1112 | 12                      | 4                       |
| Twenty-three other – 10 and – 12 flats | 58s                     | 0                       |
| Two cross-corridor flats: 813 and 817 | 6                       | 2                       |
| The remaining 530 flats | 1325s                   | 0                       |

* Based on the assumption of 2.5 residents per flat. For other flats listed in the table, the actual number of family members is shown.

Fig. 2. Distribution of flats with infected residents (a) along the façade of – 10 and – 12 flats and (b) on the 8th floor of the building. Note that there is no 1st floor in the building. The – 10 and – 12 flats are located in the middle of the first half of this wide building. The building is 107.0 m long, 14.4–15.9 m wide, and 40.7 m high. The flat number is shown at the top (a) or in a circle (b). The suspected airflow direction is also shown with blue arrows in (b). The red flat is where the index case resided; the light red flats are where the secondary infections occurred, and the white flats are where no infections occurred.
List of confirmed COVID-19 cases during the outbreak, including three infected cases (LC03, LC04, and LC5) residing elsewhere but possibly linked to the same index case.

| Case no. | Date of symptom onset | Date of confirmation | Gender | Age | Flat | Note |
|----------|-----------------------|----------------------|--------|-----|------|------|
| LC01     | 22/5/2020             | 31/5/2020            | F      | 34  | 812  | Wife of case LC05 |
| LC02     | 26/5/2020             | 31/5/2020            | M      | 56  | 812  |                   |
| LC03     | 27/4/2020             | 1/6/2020             | F      | 40  | NA   |                   |
| LC04     | 25/4/2020             | 1/6/2020             | F      | 36  |      |                   |
| LC05     | 3/6/2020              | 1/6/2020             | M      | 27  |      | Paramedic<sup>a</sup> |
| LC06     | 29/5/2020             | 2/6/2020             | F      | 68  | 817  |                   |
| LC07     | 1/6/2020              | 2/6/2020             | F      | 57  | 710  |                   |
| LC08     | 30/5/2020             | 2/6/2020             | F      | 56  | 1012 |                   |
| LC09     | 1/6/2020              | 2/6/2020             | F      | 78  | 813  | Deceased          |
| LC10     | 3/6/2020              | 4/6/2020             | M      | 72  | 1112 | Deceased          |
| LC11     | 31/5/2020             | 12/6/2020            | F      | 58  | 812  |                   |
| LC12     | 4/6/2020              | 13/6/2020            | M      | 33  | 810  |                   |

<sup>a</sup> The flat where the infected person resided. Three associated infected individuals did not reside in the same building. The exact numbers of family members in each of the flats with infected residents are known (i.e., two in Flat 710, four in Flat 810, three in Flat 812, two in Flat 813, four in Flat 817, three in Flat 1012, and three in Flat 1112).

<sup>b</sup> On 30 May, a paramedic (LC05) provided high-flow oxygen therapy to the index case while wearing a surgical mask, goggles, and gloves. He was not wearing an N95 respirator at the time. He was confirmed to have COVID-19 on 1 June, but developed symptoms on 3 June. The association between LC05 and the index patient cannot be fully established, as LC05 had contacted other patients with confirmed COVID-19 on 29 May.

toilet in Flat 812 at a flow rate of 0.2–0.25 L/min under the following conditions: no flushing or one flushing of an individual toilet in Flats 912, 910, and 1412 in sequence and dual simultaneous flushing (Flats 712 and 912, 910 and 912, and 810 and 812 in sequence). The tracer gas tube was ensured to be behind the water trap (Fig. 3e). Second, the tracer gas was released on the balcony of Flat 812 at a flow rate of 0.4 L/min. This flow rate was much higher than the stack release rate, as we anticipated significant dilution in the air. The association between the spatial distribution of the flats with infected residents and the leaked tracer gas concentration under various flushing and non-flushing scenarios was examined.

All confirmed cases from this outbreak were admitted to a public hospital managed by the Hospital Authority in Hong Kong. Patients were isolated in an airborne infection isolation room. A real-time reverse transcription polymerase chain reaction (RT-PCR) assay was performed as described previously (Wong et al., 2020). SARS-CoV-2 genome sequencing and subsequent sequence analysis were also performed for laboratory-confirmed COVID-19 patient specimens archived at the Queen Elizabeth Hospital and the Prince of Wales Hospital. The study protocol was approved by the Research Ethics Committee of the Kowloon Central/Kowloon East Cluster (HA.KC/KE-20-0321/ER-2) and the Clinical Research Ethics Committee of the New Territories East Cluster (CREC Ref No. 2020.595).

To study the molecular epidemiology of the COVID-19 cases, complete genome sequencing of SARS-CoV-2 was performed using Nanopore (Oxford Nanopore Technologies, Oxford, UK) and Illumina (San Diego, CA, USA) sequencing platforms. Extracted RNA was first reverse transcribed to cDNA using SuperScript<sup>™</sup> IV reverse transcriptase (ThermoFisher Scientific, Waltham, MA, USA), followed by PCR amplification using the ARTIC network nCoV-2019 version 3 primer set (Integrated DNA Technologies, Coralville, IA, USA). For sequencing on the Nanopore platform, end preparation, barcoding, and sequencing adapter ligation were performed according to the COVID-19 virus PCR tiling protocol, as provided by the manufacturer (Oxford Nanopore Technologies). The prepared libraries were then sequenced on an R9.4.1 flow cell with the Flongle adaptor on a MinION device (Oxford Nanopore Technologies). For sequencing on the Illumina platform, library preparation and DNA sequencing were performed as described previously (Tse et al., 2021). DNA libraries were prepared using the Illumina DNA Prep kit (Illumina, USA) and IDT for Illumina DNA/RNA UD Index sets (Illumina). DNA fragments with indexed adaptors were generated by tagmentation and were then amplified and pooled according to the manufacturer’s instructions. The quality of the libraries was validated using a 2100 Bioanalyzer (Agilent Technologies, Santa Clara, CA, USA) and a Qubit 4 fluorometer (Thermo Fisher Scientific). Sequencing was performed on an iSeq 100 (Illumina) to generate paired-end 151-bp reads.

### 3. Results

#### 3.1. Observed vertical and horizontal spread of infection

There were approximately 1400 residents in Luk Chuen House at the time of the study, assuming that each flat had 2.5 residents. This estimate is reasonable, as 1399 deep-throat saliva samples (excluding the index case and her husband) had been collected by 13 June. After all families had been contacted. Each flat has a living room, which may be subdivided by its resident(s) into a living room, a bedroom(s), a balcony with a small kitchen, and a toilet at one end. Most balconies are only partially enclosed; hence, the kitchens and toilets are open to the outside (Fig. 3a). However, each kitchen has an exhaust fan. There are separate public lifts for the even- and odd-numbered floors. Residents can use an overhead elevated walkway via the 3rd floor corridor to access a shopping centre.

All seven infected families (Table 1) were clustered around Flat 812, where the index case resided (Fig. 2). Two spatial clusters of infected flats were identified, i.e., a horizontal cluster involving Flats 813 and 817 across the corridor in the proximities of and opposite to Flat 812, respectively, and a vertical cluster involving Flats 710, 810, 1012, and 1112 connected by the drainage system below and above Flat 812 (Fig. 3b). The co-existence of the two spatial clusters proved challenging when adopting appropriate quarantine measures for residents as the outbreak unfolded from 31 May to 13 June.

The outbreak occurred when there was a low incidence of local SARS-CoV-2 infections in Hong Kong over a period of 3 weeks (Fig. S2) from 28 April. During this period, there were three local cases with symptom onset on 8, 11, and 12 May. On 31 May, a 34-year-old woman from Flat 812 (case no. LC01) was confirmed to have COVID-19. She developed a cough and fatigue on 22 May and was hospitalised on 30 May. Contact tracing identified two co-workers infected earlier, with symptom onset on 25 and 27 April. The index case worked in a warehouse where fruit and vegetables imported from the United Kingdom were handled. Her last day at work was 24 May.

By 2 June, five other cases, including the index case’s husband (case no. LC02), were confirmed in Luk Chuen House, with two infected residents on the 8th floor (Flats 813 and 817) and two more on floors 7 (Flat 710) and 10 (Flat 1012, Table 2). Eight environmental surface samples from the toilets of these flats were negative for SARS-CoV-2 (Table S1). At this time, transmission of COVID-19 through the shared use of building entrance gates, letterboxes, and lifts was suspected.

On 4 June, a 72-year-old man residing in Flat 1112 (case no. LC10) was confirmed to have COVID-19. The man had been home most of the time looking after his wife, who had a fall-related injury. The only time he left the flat was for a few minutes on 30 May, and during this time, he was wearing a mask. His deep-throat sample on 1 June was negative. As a vertical cluster pattern of flats with infected residents became clear, viral transmission through the drainage system was suspected. All other residents living in – 10 and – 12 flats were evacuated for quarantine on 4 June. Additionally, the index case’s sister (Flat 812, case no. LC11) developed a fever on 31 May, but her nasopharyngeal swabs and throat swabs on 31 May and 1 June were negative for SARS-CoV-2. Her fever subsequently subsided, and no additional symptoms were reported, but her deep-throat saliva sample tested positive for SARS-CoV-2 at the end...
of her quarantine period on 11 June. By 13 June, 1399 deep-throat saliva samples had been collected from residents in Luk Chuen House. None of these were positive for SARS-CoV-2, except those described above.

The last confirmed case in this outbreak revealed the diagnostic challenge of SARS-CoV-2 infections. A 33-year-old man (Flat 810, case no. LC12) developed a fever on 4 June. His nasopharyngeal and throat swabs, deep-throat saliva samples, and stool specimens collected during his entire hospital stay remained negative until he underwent a bronchoscopy on 12 June for persistent fever and pneumonia. His bronchoalveolar lavage specimen collected at that time tested positive for SARS-CoV-2. As the virus was only found in his lower respiratory tract specimens, very fine infectious particles were suspected of having infected his lungs, but not his upper respiratory tract, implying possible airborne transmission through droplet nuclei < 5 µm. It is known that most particles greater than 10 µm (aerodynamic diameter) are deposited in the nose or throat, and cannot penetrate the lower respiratory tract. But particles in size range between 2 nm and 6 µm can penetrate lower airways and deposit in the pulmonary regions (Cheng, 2014).

Subsequently, the second round of deep-throat sample tests for SARS-CoV-2 was arranged for all residents of the building on 14 June, and all 1258 samples collected by 18 June tested negative. All environmental samples in the toilet and kitchen of Flat 810 and the rooftop vent collected on 14 June were also negative. All residents of Flats 10 and 12 were tested again before returning from quarantine on 18 June, and no new cases were identified.

### 3.2. Measured vertical spread via the drainage system

A connected two-stack system is used for drainage in Luk Chuen House. Two neighbouring vertically aligned flats, such as – 10 and – 12 flats, share a connected two-drainage stack system. In such a system, the
two vertical stacks for two neighbouring flats, such as – 10 and – 12 flats, are connected by a horizontal vent pipe (Fig. 3 and S3). In this 14-story building (2nd to 15th floor), there are 14 horizontal vent pipes for each connected two-stack system, and the horizontal vent pipes serve to balance the air pressure during flushing and enable the second stack to act as a vent. The horizontal vent pipes remain in only four (5th, 6th, 9th, and 15th) of the 14 floors for the – 10 and – 12 flats, as the other vent pipes were removed during regular maintenance before the outbreak. The two stacks of the – 10 and – 12 flats are connected by these four horizontal vent pipes before they merge into one roof vent. In the building, there are 40 vertical columns of flats with 20 connected two-stack drainage roof vents.

In our tracer gas experiments (Fig. 4), 30.7 L of gas passed into the drainage stack and pipes over a duration of 2 h and 9 min, via the toilet in Flat 812, where the index patient resided. The total interior volume of the drainage system (both stacks and all pipes) was estimated to be 808.3 L. The continuously injected gas escaped through the roof vent and via leaks in the pipes due to gas expansion during discharge, even without the additional driving force of airflow within the stacks. Without flushing any toilets, we first saw a significant and immediate increase in gas concentration in the Flat 1012 toilet (bathroom) (~980 ppb), followed by the toilets in Flats 810 and 812 and Flats 910 and 912 (32, 58, 41, 104 ppb, respectively). We also detected an increase in gas concentration at the façade of Flats 710 and 712, suggesting probable leaks in the lower-floor toilets (e.g., Flats 610 and 612). Leaks in the drainage pipes were detected in Flats 810, 812, 910, 912, and 1012.

When we flushed the toilet in Flat 912, a high gas concentration was observed in the toilets (rooms) in Flats 910, 912, 1012, and 710 (1364, 804, 700 and 29,305 ppb, respectively). The same phenomenon was observed in a study by (Gormley et al., 2017), which showed that the turbulence caused by the flush led to more aerosolisation and changed the airflow characteristics inside the building. We then simultaneously flushed the toilets in Flats 712 and 912, which resulted in a high concentration of gas in the toilets (bathrooms) in Flats 1012 and 812 (11, 030 and 237 ppb, respectively). When we repeated the experiment, in addition to the same result in the toilet in Flat 1012, we also observed a sudden large increase in gas concentration in the toilet (bathroom) in Flat 1412 and a high gas concentration in the toilet (bathroom) in Flat 910 (Fig. S5b). We then simultaneously flushed the toilets in Flats 810 and 812, leading to a high gas concentration in Flats 710, 910, 812 and

---

Fig. 4. The registered peak concentration (ppb) under the four test conditions ((a) no flushing, (b) one flushing, (c) two flushing, and (d) balcony release). Detailed temporal profiles of the monitored concentrations are presented in Figs. S4 and S5. A red star indicates a flat with an infected resident due to a secondary infection. A mixed red-blue star indicates Flat 812, where the index case resided and where the tracer gas was released via the toilet. A red cross indicates where the originally designed horizontal vent pipe was removed. RV = roof vent, L = living room, F = façade below the flat window, and T = toilet.
1412. The toilets in Flats 710 and 1412 did not show any leaks during the no-flush test, but a significant increase in gas concentration was detected when the toilets in the other flats were flushed. The drainage system used in the building, which we refer to as a truncated connected two-stack system, may have led to complex variations in air pressure during the flushing process. Flushing may have introduced higher pressure than the no-flushing condition, leading to leaks through small cracks (Swaffield and Campbell, 1992). No anti-syphonage valves were installed, which might have led to the loss of water seals when flushing. However, there was no direct evidence to support this.

We detected significant gas leakage in Flats 710, 812, and 1012, where infections were reported. We did not detect significant gas leakage in Flat 810 (although some leaks were found during the no-flushing test), where infections were also reported. We detected no significant leaks in Flat 712, where no infections were reported. However, we also detected high gas concentrations in Flats 910, 912, and 1412, where no infections were reported. Additional host- and exposure-related factors may have played roles in the lack of infections in these flats.

3.3. Measured upward spread along the façade

When the tracer gas was released on the balcony of Flat 812 (close to the water basin), there was a noticeable increase in gas concentration in the façades of Flats 912 and 1012. The gas concentrations are 1281 ppb for Flat 912 and 2440 ppb for Flat 1012, respectively (Fig. 4d). These concentrations were higher than those detected when dosing within the drainage stack. But in addition to an increase on the balconies of Flats 912 and 1012 and in the living room in Flat 1012, there were no detectable changes in gas concentration in any of the – 10 flats. The vertical distribution of gas concentration could less likely explain the two-column vertical distribution of infected flats along flat-10 and – 12. These results probably reflect the fact that the balcony release rate (0.4 L/min) was twice as high as the release rate used in the no-flushing tests (0.2 L/min) and 60% higher than the release rate used in the flushing tests (0.25 L/min). Furthermore, the leakage of previously released gas in the drainage pipe continued during the gas release at the balcony, as shown in Figs. S4 and S5.

The prevailing wind at the time of measurement was south-westerly. This may have created an upward flow at the downstream façade (Zajic et al., 2011), leading to the observed upward spread. We cannot discount the possibility that virus-containing aerosols were generated due to respiratory activity in the balcony area of Flat 812 and were then dispersed by the wind to the upper and lower floors, as shown in the field experiments. However, significant dilution during this process and difficulties in explaining how the wind could bend and travel both upward (e.g., to Flat 1112) and downward (e.g., to Flat 710) make this route less likely.

3.4. Horizontal spread between flats on the 8th floor

Both faecal aerosols from the toilet in Flat 812 and respiratory aerosols from the balcony or the main room of Flat 812 may have spread across the corridor to Flats 813 and 817 when the wind was coming from the easterly direction. We used computational fluid dynamics to predict the wind pressure distribution over the building surfaces and a multi-zone airflow model to predict the airflow between rooms on the 8th floor at the time of infection. We demonstrated cross-corridor flow from Flat 812 to Flats 815 and 817 (Figs. S8 and S9). These circumstantial data may be useful for understanding the potential for cross-corridor spread. In Fig. S5-C, we demonstrate the detection of elevated tracer gas concentration in the 8th floor corridor after balcony release. The wind was weak during the test period and in an unfavourable direction for the transport of the tracer gas from Flat 812 to the corridor and Flat 817. Only limited horizontal spread was detected. Our research assistants occasionally accessed Flat 812 (e.g., during toilet flushing at 16:55), and some gas escape into the corridor was seen after 17:00 on 17 June. Subsequent increases in gas concentrations in the corridor and Flat 817 were observed. We also detected a high gas concentration in the living room in Flat 812 during most test periods, due to direct leakage from the gas cylinder at that location (Fig. S5-C). The gas concentration in the living room in Flat 812 was associated with the dosing period. This high gas concentration may also partly explain the high gas concentration detected in the toilet in Flat 812.

3.5. SARS-CoV-2 genome sequencing and phylogenetic analysis

Eight nearly full-length SARS-CoV-2 genome sequences were obtained from the clinical samples of cases LC01, LC02, LC05, LC06, LC07, LC08, LC10, and LC12. Viral genome sequencing from the other cases was not successful due to the low viral loads in the associated samples. PANGOLIN sequence analysis (https://pangolin.cog-uk.io/) supported the assignment of all eight viral genomes to PANGO lineage B.1. The following common single nucleotide variants (SNVs) were detected in all sequenced genomes: C241T, C1059T, C3037T, C6807T, C9474T, C14408T, A22007G, A23403G, G24368T, and G25563T. Up to three additional SNVs were also detected in these viral genome sequences. The maximum-likelihood phylogenetic tree of the cluster was constructed using IQ-TREE and is shown in Fig. 5. Overall, the results of the sequencing and phylogenetic analyses were consistent with a common point-source for this outbreak.

4. Discussion

Our epidemiological and environmental investigations suggested that the outbreak probably originated in Flat 812 (where the index case resided), as the subsequently affected flats were clustered around it. There were at least two possible sources of the virus-containing aerosols: faecal aerosols and washbasin aerosols. Toilet flushing can generate aerosols within drainage stacks (Gormley et al., 2021). Yu et al. (2004) also found that large amounts of bio-aerosols were generated in similar high-rise vertical drainage stacks due to hydraulic interactions after the index case flushed the toilet in the 2003 Amoy Garden outbreak. Solid wastewater discharged from a toilet may contain faeces, urine, and exhaled mucus from infected persons. The presence of SARS-CoV-2 in anal swabs was also reported by Zhang et al. (2020), who found that there were more positive tests from anal swabs than from oral swabs in the later stage of the infection. Kang et al. (2020) also hypothesised that stack faecal aerosols were responsible for the spread of SARS-CoV-2 in a high-rise building outbreak. However, stack faecal aerosols should not be confused with toilet flushing-generated aerosols that spread directly into a bathroom. Thus far, viable SARS-CoV-2 has not been detected in wastewater. The infectivity of faecal aerosols in building drainage systems has not been definitively determined (Wang et al., 2022). Based on the common knowledge that nasal mucus, saliva, and sputum from infected individuals contain viable SARS-CoV-2 and that washbasins in bathrooms may be contaminated with nasal mucus and/or saliva, wastewater discharged from washbasins may also be contaminated, which may generate washbasin aerosols within the stack (Wang et al., 2022).

However, the question remains how these stack aerosols were transported from the index case’s flat into the other flats. The drainage stack transport of faecal and/or washbasin aerosols may provide an explanation for the vertical infection cluster. The significant leaks of the tracer gas associated with the communal drainage stacks observed in these flats provided strong evidence for this hypothesis. These results demonstrated that the two connected drainage stacks for – 10 and – 12 flats served as the transport route for bio-aerosols between flats. The variation in the monitored concentrations was likely due to differences in the leakage areas, driving pressures, and complex interactions during flushing.
Wang et al. (2022) reported a vertical outbreak of COVID-19, in which the transmission of SARS-CoV-2 occurred between one-column vertical flats. Differently, two vertical columns of infected flats are involved in the outbreak being studied here. The two vertical columns of infected flats are associated with a connected two-stack drainage system. Additionally, flushing by the index case probably provides the infectious stack aerosols. Using a test rig of a plumbing system, Gormley et al. (2021) found that a 6 L toilet flush can generate 280–400 aerosols per second at a concentration of 9–12 numbers per cm$^3$ and a total count of 3000–4000 aerosols. Our data show that different scenarios of toilet flushing (i.e., when the index case flushed alone and when the index case flushed at the same time when another resident also flushed in a separate flat) could alter the leaks of infectious aerosols into indoors. For example, the toilets in Flats 710 and 1412 did not show any leaks during the no-flush test, but a significant increase in tracer gas concentration was detected when the toilets in the two flats were flushed.

Unlike the toilets in the flats associated with the Amoy Gardens outbreak (Yu et al., 2004), the toilets in Luk Chuen House are in semi-open balconies (Fig. 3b); therefore, no significant negative pressure (relative to that of the outdoor) can be established in the toilet cubicle. The upward chimney effect in the drainage pipe may have also played a role in transmission, which would explain why the flats with infected residents were mostly in the upper stories (Figs. 3 and 6). Sufficiently small bio-aerosols are likely to be airborne in drainage pipes and vent pipes for several hours, and they may be continuously sucked into a bathroom when the conditions are favorable. The transient movement of bio-aerosols in drainage stacks and vent pipes may be due to stack and wind effects during non-flushing periods or the downward movement of wastewater during flushing periods.

Fig. 5. Maximum-likelihood phylogenetic tree of SARS-CoV-2 genome sequences from the outbreak. The genome sequence of the reference strain, Wuhan-Hu-1, was included as an outgroup.

Fig. 6. Illustration of the cut-off horizontal vent pipes on the 7th and 8th floors. The 6th and 9th floors remain connected. (a) When the toilet is flushed in Flat 812, a complex air pressure field is created. (b) Chimney effect. The horizontal vent pipes remain on the 5th, 6th, 9th, and 15th floors, while those on all other floors were removed.
wastewater is discharged into the drainage stack, e.g., during a shower.

Our measurements revealed that a reasonable amount of tracer gas stayed in the stack air for at least 1 h during the post-dosing period (Fig. S5). Van Doremalen et al. (2020) detected a 1-hour half-life of viruses in aerosols. However, the survival characteristics of the stack aerosols may be different from those of respiratory aerosols, as the ambient impurities differ. The spread of bio-aerosols via drainage stacks and vents is characterised by minimum dilution. This behaviour differs from window plumes, in which the concentration of virus-containing droplets rapidly decreases along the length of the plume. The concentration of virus-containing aerosols may remain high in tall vertical stacks, as they are not well ventilated. Once these aerosols enter a toilet cubicle, they may be deposited on surfaces within the room; they may be directly inhaled by the occupants of the toilet cubicle; or they may be directly deposited on surfaces within the room; they may be directly inhaled by the occupants of the toilet cubicle; or they may penetrate into other spaces and cause further contamination. However, no environmental surface samples were positive during this outbreak, directly inhaled by the occupants of the toilet cubicle; or they may penetrate into other spaces and cause further contamination. However, no environmental surface samples were positive during this outbreak.
in healthcare settings (Ong et al., 2020; Ding et al., 2020) and on a cruise ship (Yamashita et al., 2020).

This study has limitations that should be noted. To perform the measurements for this study, we only had access to eight of the twenty-eight flats along with the two columns of flats, and we did not have access to Flat 813 or 817 (Fig. 2b). Leakages into other flats could not be quantified. We only had two days of access for field measurements, due to the constraints of the quarantine periods and the need for full disinfection before access by the field test team. There was also a lack of data on the usage of toilets by the residents. As in studies of other vertical outbreaks of COVID-19 (Kang et al., 2020; Wang et al., 2022), the number of flats with infected residents was too small to perform meaningful statistical analyses of the vertical cluster of infections.

Additionally, genome sequencing was not performed for all the cases; therefore, we could not objectively demonstrate that the index patient was responsible for all of the observed transmission. However, the outbreak occurred during a 3-week period in which there were no other local cases of infection in Hong Kong (Fig. S2), with the exception of three isolated local cases with symptom onset on 8, 11, and 12 May.

Authors’ contributions

Concept and experimental design: Y Li, KY Yuen. Design and coordination of field measurements and reporting: Z Lin, J Niu, J Fung, A Lau, P Louie, K Leung. Analysis and interpretation of data: Z Lin, J Niu, G Choi. Drafting of article: Q Wang, G Choi, L Lau, P Louie, K Leung. Provision of study materials or patients: G Choi, A Wong, H Tse, S Wong, R Lai, D Hui. Provision of study resources: G Choi, A Wong, H Tse, S Wong, R Lai, D Hui, KY Yuen, DC Lung. Administrative, technical, or logistic support: K Leung, Z Lin, J Niu, J Fung, A Lau, P Louie. Obtaining funding: Y Li. All of the authors contributed to the revision of the manuscript. All of the authors have approved the submitted version of the manuscript and have agreed to be personally accountable for their own contributions.

Declaration of Competing Interest

The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

Data availability statement

The authors are willing to share the study protocol and the data sets from which the results were derived, if requested.

Acknowledgements

We thank Pak-To Jack Chan, Shenglan Xiao, Nan Zhang, and Maosu Li of the University of Hong Kong; Jian Liu, Yanlin Lu, and Yafeng Gao of the City University of Hong Kong; Kit Hung and Michael Fung of The Hong Kong Polytechnic University; and Kwong Hoi Tsui, Ka Wing Shek, Ngai Ting Lau, Kwok Pong Ho, Weiwei Chan, Billy Wong, and Hao Liu of the Hong Kong University of Science and Technology for participating in the field measurements. We thank Professor Wilson Lu, Dr Fan Xue, Dr Ruoyu You, Dr Charles Wong, and Dr Chao Ren for their support and Dr Vincent Cheung for coordinating the field measurements. We are also grateful to many individuals at CHP, EPD, and the Housing Department for their coordination and support during the course of this research. This study was partially supported by the Research Grants Council of Hong Kong with a Collaborative Research Fund (grant number C7025-16G) and a General Research Fund (grant number 17203321) grant.

Appendix A. Supporting information

Supplementary data associated with this article can be found in the online version at doi:10.1016/j.jhazmat.2022.128475.

References

Ai, Z., Mak, C.M., Gao, N., Niu, J., 2020. Tracer gas is a suitable surrogate of exhaled droplet nuclei for studying airborne transmission in the built environment. Build. Simul. 13, 489–496.
Bjorn, E., Nielsen, P.V., 2002. Dispersal of exhaled air and personal exposure in small displacement ventilated rooms. Indoor Air 12 (3), 147–164.
Bolshakov, Z.D., Melikov, A.K., Kierat, W., Popiolek, Z., Brand, M., 2012. Exposure of health care workers and occupants to coughed airborne pathogens in a double-bed hospital patient room with overhead mixing ventilation. HVAC&R Res. 18 (4), 602–615.
Cheng, Y.S., 2014. Mechanisms of pharmaceutical aerosol deposition in the respiratory tract. AAPS PharmSciTech 15 (3), 630–640.
Dancer, S.J., Li, Y., Hart, A., Tang, J.W., Jones, D.L., 2021. What is the risk of acquiring SARS-CoV-2 from the use of public toilets? Sci. Total Environ. 792, 148341.
Ding, Z., Qian, H., Xu, B., Huang, Y., Miao, T., Yin, H.L., Xiao, S., Cui, L., Wu, X., Shao, W., Song, Y., Sha, L., Zhou, L., Xu, Y., Zhu, B., Li, Y., 2020. Toilets dominate environmental detection of severe acute respiratory syndrome coronavirus 2 in a hospital. Sci. Total Environ. 753, 141710.
Gerba, C.P., Wallis, C., Melnick, J.L., 1975. Microbiological hazards of household toilets: droplet production and the fate of residual organisms. Appl. Environ. Microbiol. 30 (2), 229–237.
Gorny, M., Aspray, T.J., Kelly, D.A., Rodriguez-Gil, C., 2017. Pathogen crosstransmission via building sanitation systems in a full scale pilot test-rig. PLoS One 12 (2), e0171556.
Gorny, M., Aspray, T.J., Kelly, D.A., 2020. Aerosol and bioaerosol particle size and concentrations from defective sanitary plumbing systems. Indoor Air 31, 1427–1440.
He, X., Lau, E.H., Wu, P., Deng, X., Wang, J., Hao, X., Lau, Y.C., Wong, J.Y., Guan, Y., Tan, X., Mo, X., 2020. Temporal dynamics in viral shedding and transmissibility of COVID-19. Nat. Med. 26 (5), 672–675.
Heller, L., Mota, C.R., Greco, D.B., 2020. COVID-19 faecal-oral transmission: are we asking the right questions? Sci. Total Environ. 729, 138919.
Kang, M., Wei, J., Yuan, J., Guo, J., Zhang, Y., Hang, J., Qu, Y., Qian, H., Zhang, Y., Chen, X., Peng, X., Shi, T., Wang, J., Wu, J., Song, T., He, J., Li, Y., Zhang, N., 2020. Probable evidence of faecal aerosol transmission of SARS-CoV-2 in a high-rise building. Ann. Intern. Med. 173 (12), 974–980.
Li, Y., Duan, S., Yu, I.T., Wong, T.W., 2005. Multi-zone modeling of probable SARS virus transmission by airflow between flats in block E, Amoy Gardens. Indoor Air 15 (3), 294–321.
McDermott, C.V., Alicic, R.Z., Harden, N., Cox, E.J., Scanlan, J.M., 2020. Put a lid on it: faecal bio-aerosols a route of transmission for SARS-CoV-2? J. Hosp. Infect. 105 (3), 397–399.
Niu, J., Tung, T.C., 2007. On-site quantification of re-entry ratio of ventilation exhausts in multi-family residential buildings and implications. Indoor Air 18 (1), 12–26.
Ong, S.W.X., Tan, Y.K., Chia, P.Y.E., Lee, T.H., Ng, O.T., Wong, M.S.Y., Marimuthu, K., 2020. Air, surface environmental, and personal protective equipment contamination by severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) from a symptomatic patient. J. Am. Med. Assoc. 323 (16), 1610–1612.
Qian, H., Miao, T., Liu, L., Zheng, X., Luo, D., Li, Y., 2021. Indoor transmission of SARS-CoV-2. Indoor Air 31 (3), 439–445.
Sawfield, J.A., Campbell, D.P., 1992. Air pressure transient propagation in building drainage vent systems, an application of unsteady flow analysis. Build. Environ. 27 (3), 357–365.
Tse, H., Wong, S.C.Y., Ip, K.F., Cheng, V.C.C., Lung, K.K.W., Choi, D.C., Y, G.K., 2021. Genome sequences of three SARS-CoV-2 ORF7a deletion variants obtained from patients in Hong Kong. Microbiol. Resour. Announc. 10 (15), e00251–21.
US CDC (2021). Science brief: SARS-CoV-2 and surface (fomite) transmission for indoor community environments. Updated 5 April 2021. https://www.cdc.gov/coronavirus/2019-ncov/more/science-and-research/surface-transmission.html. Last accessed 19 September 2021.
Van Doremalen, N., Bushmaker, T., Morris, D.H., Holbrook, M.G., Gamble, A., Williamson, B.N., Tamin, A., Harcourt, J., Thornburg, N., Gerber, S., Lloyd-Smith, J., de Wit, E., Munster, V.J., 2020. Aerosol and surface stability of SARS-CoV-2 as compared with SARS-CoV-1. N. Engl. J. Med. 382 (16), 1564–1567.
Wang, Q., Li, Y., Lung, D.C., Chan, P.T., Dung, C.H., Jia, W., Miao, T., Huang, J., Chen, W., Wang, Z., Leung, K., Liu, Z., Wong, D., Tse, H., Wong, S., Choi, K.Y., Lam, J., Cheng, K., Yuen, K. Y, 2022. Aerosol transmission of SARS-CoV-2 due to the chimney effect in two high-rise housing drainage stacks. J. Hazard. Mater. 418, 128894.
Wong, S.C.Y., Tse, H., Shi, H., Ku, H.K., Kwong, T.S., Chu, M.Y., Lung, D.C., 2020. Posterior oropharyngeal saliva for the detection of severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2). Clin. Infect. Dis. 71 (11), 2939–2946.
World Health Organization. (2021). Transmission of SARS-CoV-2: implications for infection prevention precautions: scientific briefing, 09 July 2020. World Health Organization. https://apps.who.int/iris/handle/10665/333114. Last accessed 9 October 2021.
Wu, Y., Tang, T.C., Niu, J.L., 2016. On-site measurement of tracer gas transmission between horizontal adjacent flats in residential building and cross-infection risk assessment. Build. Environ. 99, 13–21.
Wu, Y., Tung, T.C., Niu, J., 2019. Experimental analysis of driving forces and impact factors of horizontal inter-unit airborne dispersion in a residential building. Build. Environ. 151, 88–96.

Yamagishi, T., Ohnishi, M., Matsunaga, N., Kakimoto, K., Kamiya, H., Okamoto, K., Suzuki, M., Gu, Y., Sakaguchi, M., Tajima, T., Takaya, S., 2020. Environmental sampling for severe acute respiratory syndrome coronavirus 2 during COVID-19 outbreak in the Diamond Princess cruise ship. J. Infect. Dis. 222 (7), 1098–1102.

Yu, I.T., Li, Y., Wong, T.W., Tam, W., Chan, A.T., Lee, J.H., Leung, D.Y., Ho, T., 2004. Evidence of airborne transmission of the severe acute respiratory syndrome virus. N. Engl. J. Med. 350 (17), 1731–1739.

Zajic, D., Fernando, H.J.S., Calhoun, R., Princevac, M., Brown, M.J., Pardyjak, E.R., 2011. Flow and turbulence in an urban canyon. J. Appl. Meteorol. Climatol. 50 (1), 203–223.

Zhang, W., Du, R.H., Li, B., Zheng, X.S., Yang, X.L., Hu, B., Wang, Y., Xiao, G., Yan, B., Shi, Z., Zhou, P., 2020. Molecular and serological investigation of 2019-nCoV infected patients: implication of multiple shedding routes. Emerg. Microbes Infect. 9 (1), 386–389.

Zhang, Z., Chen, X., Mazumdar, S., Zhang, T., Chen, Q., 2009. Experimental and numerical investigation of airflow and contaminant transport in an airliner cabin mockup. Build. Environ. 44 (1), 85–94.