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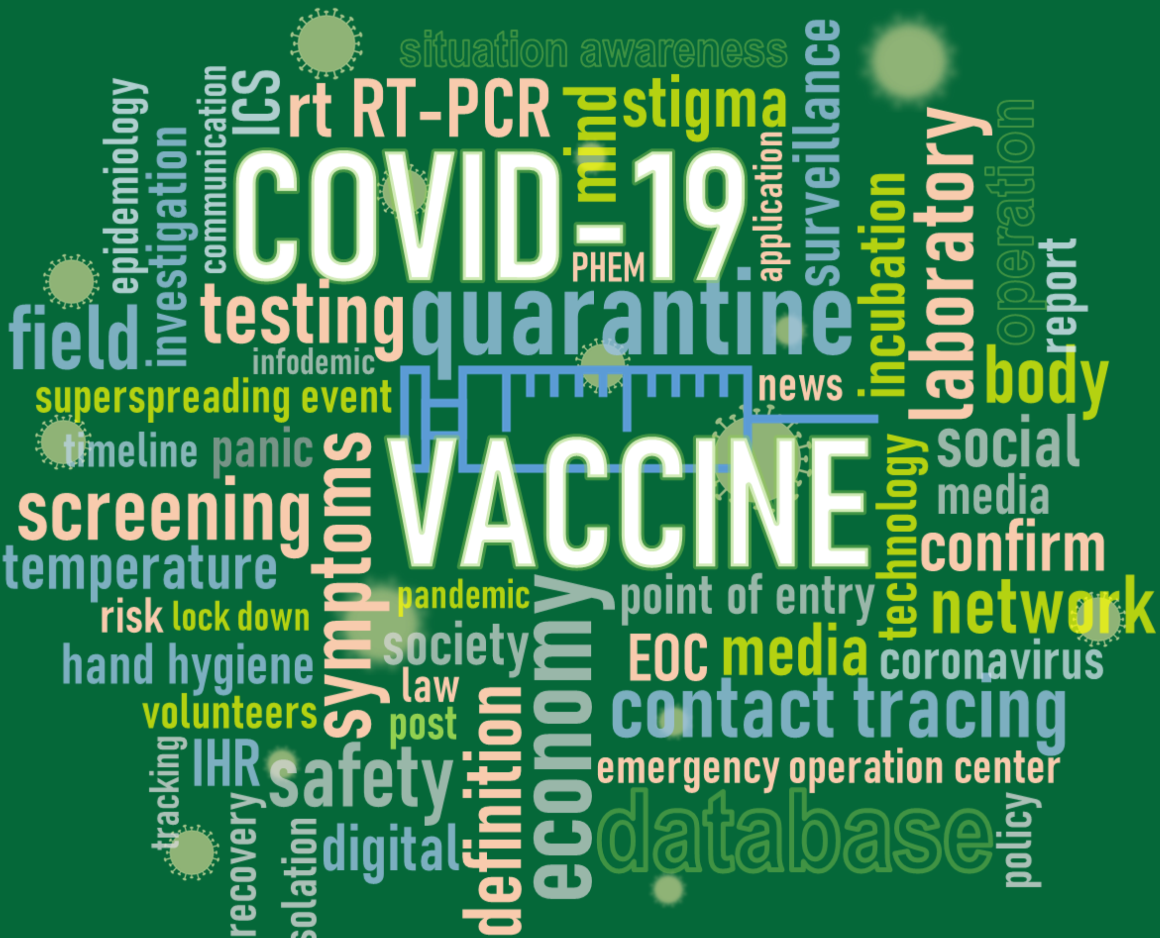

Volume 14, Issue 4

December 2021

www.osirjournal.net

ISSN: 2651-1061

The Outbreak, Surveillance and Investigation Reports (OSIR) Journal was established in 2008 as a free online publication in order to encourage and facilitate communication of health information and disease reporting across Asia and the Pacific. In September 2018, the journal is retitled as the "Outbreak, Surveillance, Investigation & Response" while maintaining the same abbreviation as OSIR.

Outbreak, Surveillance, Investigation & Response (OSIR) Journal

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Volume 14, Issue 4, December 2021

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Outbreak, Surveillance, Investigation & Response (OSIR) Journal
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Editorial

Living with COVID-19

Angela Song-En Huang, Chief Editor

No matter where you live, there have been restrictions in one form or another during the past two years, in response to the COVID-19 pandemic. These include restrictions that caused minor inconveniences in our lives, like wearing masks in public, and restrictions that heavily disrupted our daily routines, like having to work from home while watching kids attend online classes because in-person school had been suspended.[1] There are signs of people growing impatient with such restrictions, with people complaining about public health and social measures (PHSMs) and, in some countries, even violent protests.[2]

When COVID-19 was first identified at the end of 2019, few could have predicted that we would see multiple waves of the disease caused by different variants of the SARS-CoV-2 virus, and that the virus would continue to affect our lives two years on. While isolation, quarantine, and other public health and PHSMs have played important roles in slowing the transmission of the virus, pandemic fatigue is obvious, and not all PHSMs could be practiced long term.[3,4] We now have therapeutics and vaccines available that have shown to be effective in reducing hospitalizations and deaths.[5,6] Using a combination of these measures and tools at hand will help us move to end the pandemic, which is likely “living with COVID-19”, instead of eliminating the disease altogether.

To shift from disease elimination to disease mitigation strategies, much preparation is needed. In addition to having drugs, vaccines, and hospital beds ready, governments also need to communicate with the public and the healthcare sector on the objectives of mitigation strategies, and how each person could prepare for the eventuality of having widespread COVID-19 in our communities, because while the general public may welcome loosened restrictions which will afford them increased freedom to gather and travel, the healthcare sector may be angered by increases in patients with COVID-19.

In Taiwan, for example, people have grown used to not having locally-acquired cases of COVID-19, and every case without history of international travel cause anxiety for the general public. Much of the medical community have also expected to only see COVID-19 among international travelers. Changing these expectations take time and effort. The general public and the medical community must be made to understand that, to see an end to the COVID-19 pandemic, the implementation of mitigation strategies means that we will see an increase in COVID-19 cases, but we also have tools to protect ourselves and those around us. Practices that decrease the risk of infection should be done by everyone. These include, but are not limited to, becoming fully vaccinated, wearing masks when in the presence of other people, practicing good hand hygiene, and avoiding crowded, poorly ventilated places. Furthermore, the medical community may have to brace for an initial surge of COVID-19 patients. Empowering the public with knowledge and rationale for disease prevention and control measures will induce people to better adhere to our public health messaging.

Moreover, because different countries have used different COVID-19 control strategies, we have experienced COVID-19 pandemic differently. We must learn from each other’s experience to better plan for our own disease mitigation policies.

Pandemic fatigue is growing as we head into a third year of COVID-19 pandemic response. A shift in strategy is needed for us to see the end of the pandemic. Ultimately, as Gina Kolata wrote in The New York Times, “an end can occur not because a disease has been vanquished but because people grow tired of panic mode and learn to live with a disease”.[7]

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OSIR, December 2021, Volume 14, Issue 4, p.121-126

Outbreak, Surveillance, Investigation & Response (OSIR) Journal
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An Investigation of a Coronavirus Disease (COVID-19) Cluster from Saudi Arabia, in a State Quarantine, Chonburi, Thailand, 2020

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Abstract

On 7 Aug 2020, the Department of Disease Control, the Thai Ministry of Public Health, was notified of 14 COVID-19 cases from Saudi Arabia. The objectives of this study were to verify diagnosis, describe characteristics of the cases and identify possible causes of infection. A cross-sectional descriptive study was conducted by reviewing the cases' medical records, interviewing the cases and state quarantine staff, and surveying the environment. A confirmed COVID-19 case was defined as a passenger in a flight from Saudi Arabia on 25 Jul 2020 with positive RT-PCR. Out of 219, 14 were infected with SARS-CoV-2. Most of them were Thai students in Saudi Arabia. The median age of cases was 26 years and male to female ratio was 13:1. The median RT-PCR cycle thresholds for ORF1ab and N genes were 36 and 35. The state quarantine process mainly followed the national guidelines. These cases were likely to have contracted COVID-19 from Saudi Arabia. The risks of infection in Saudi Arabia included living together in the same dormitory and visiting crowded areas. The introduction of state quarantine and COVID-19 testing worked well in preventing new cases. The government should communicate with people planning to travel about the importance of physical distancing and avoiding any risk behaviors while being abroad.

Keywords: COVID-19, state quarantine, Thailand, Saudi Arabia

Introduction

On 22 Aug 2020, the World Health Organization reported almost 23 million confirmed cases of coronavirus disease 2019 (COVID-19) including approximately 800,000 deaths.[1] In Saudi Arabia, the COVID-19 situation was alarming as there were 305,186 confirmed cases and 3,580 deaths since the start of the pandemic in March 2020.[2] At time of writing, the number of total COVID-19 cases who departed from Saudi Arabia to visit Thailand was 43 (excluding the cases identified in this outbreak). Since March 2020, Saudi Arabia exercised a lockdown policy and a mandatory mask wearing policy in public areas.[3]

Since Thailand faced a cluster of COVID-19 in March 2020, a travel restriction policy was exercised. The number of daily cases started to subside in May 2020. The Thai government later relaxed its travel policies by allowing travelers and Thai returnees from abroad to enter the country. All inbound travelers are obliged to stay in a quarantine center (so-called, state quarantine [SQ]) for 14 days. Real-time polymerase chain reaction (RT-PCR) testing is done to detect SARS-CoV-2 twice while staying in the quarantine center (first test on day 3–5 and second test on day 11–13).[4-6] Cases with a positive result are referred to a designated hospital for further treatment.[7] International travelers need to have evidence of negative RT-PCR 72 hours before leaving (COVID-19 Free Certificate [CFC]) the country of departure. For Thai returnees, the requirement for getting on board is only a possession of Fit-to-Fly certificate, which requires only medical examination whereas CFC is optional.

On 7 Aug 2020, the COVID-19 Operation Team of the Department of Disease Control (DDC), the Thai Ministry of Public Health (MOPH), received a notification from the Office of Disease Prevention and Control Region 6 Chonburi (OPDC-6), that there was a cluster of confirmed COVID-19 patients (n=14) travelling from Saudi Arabia. These patients showed positive test results while staying in a quarantine center in Pattaya City (for convenience, we referred this to SQ-X). Therefore, the objectives of this study were to verify diagnosis, describe characteristics of the cases, identify possible causes of infection and provide recommendations for prevention and control.

Methods

We applied a descriptive cross-sectional study. Data collections consisted of in-depth interviews with the cases and SQ staff, reviewing medical records and flight history, and environmental survey on the SQ. The patients were asked about risk behaviors in Saudi Arabia and their travel history.

We performed contact tracing on travelers on the flight and in SQ, using 'Guideline for surveillance and case investigation for coronavirus disease 2019 (COVID-19)' version 15 May 2020, by the DDC.[7] We defined a confirmed case as a passenger on the same flight (EK0384, 25 Jul 2020) in the SQ that showed positive test for SARS-CoV-2 by RT-PCR during 25 Jul to 8 Aug 2020. A close contact was defined as any person interacting with a confirmed case of COVID-19 within a one-meter distance for at least five minutes, or being coughed or sneezed on, or being in an enclosed space without proper ventilation with a confirmed case for at least 15 minutes. A close contact was further categorized as high risk (without adequate personal protective equipment [PPE]) and low risk (with adequate PPE).

For the environmental study, we interviewed physicians at the SQ, the hotel manager, SQ commander, and infectious control nurse about the infection control processes. An environmental survey at the SQ was done by non-participant observation using 'Guidance for integrated management of state quarantine facilities' by the MOPH.[6]

Results

Descriptive Characteristics of the Cases

On 25 Jul 2020, there were 219 passengers on the flight. There were 199 passengers from Saudi Arabia; the rest were from Lebanon. Fourteen passengers from Saudi Arabia showed positive result for SARS-CoV-2 by RT-PCR while 20 passengers from Lebanon were tested negative. Only one case showed mild symptoms (having phlegm); and the other 13 cases were asymptomatic. All of them were Muslims. The overall attack rate from the flight was 6.4% (14/219). The attack rate among passengers from Saudi Arabia was 7.0% (14/199) and the median age of the cases was 26 years (Q1=24.25, Q3=26.75). Twelve out of all fourteen cases (85.7%) were students; the others were a religion volunteer and a housewife. All of them were Thai. About one fifth of the Islamic students were confirmed cases (12/56; 21.4%). Of these 219 passengers, 106 were taken to SQ-X. The attack rate among those staying in SQ-X was 13.2% (14/106). All confirmed cases were sent to nearby hospital to receive treatment for 14 days from date of sample collection. Brief characteristics of the cases and laboratory results are presented in Table 1.

Table 1. Brief characteristics and results of RT-PCR testing of COVID-19 cases

No.	Gender	Age (years)	Occupation	Symptoms	Positive for SARS-CoV-2 on June 2020	Sample collection date	RT-PCR Ct*	
							ORF1ab	N gene
1	Male	24	Student	No	Yes	28 Jul 2020	37.96	37.56
2	Male	24	Student	No	Yes	28 Jul 2020	36.78	37.04
3	Male	28	Student	No	-	5 Aug 2020	35.24	34.26
4	Male	24	Student	No	-	5 Aug 2020	36.85	36.00
5	Male	24	Student	No	-	5 Aug 2020	36.41	35.05
6	Male	25	Student	No	-	5 Aug 2020	33.97	34.82
7	Male	25	Student	Yes	-	5 Aug 2020	36.22	35.36
8	Male	25	Student	No	-	5 Aug 2020	34.53	35.60
9	Male	26	Student	No	-	5 Aug 2020	36.25	35.00
10	Male	27	Student	No	Yes	5 Aug 2020	37.65	35.58
11	Female	50	Housewife	No	-	5 Aug 2020	37.50	38.69
12	Male	43	Religion volunteer	No	-	5 Aug 2020	33.57	33.48
13	Male	26	Student	No	-	7 Aug 2020	38.86	37.07
14	Male	26	Student	No	-	7 Aug 2020	34.81	33.80

**Cycle threshold*

Laboratory Results

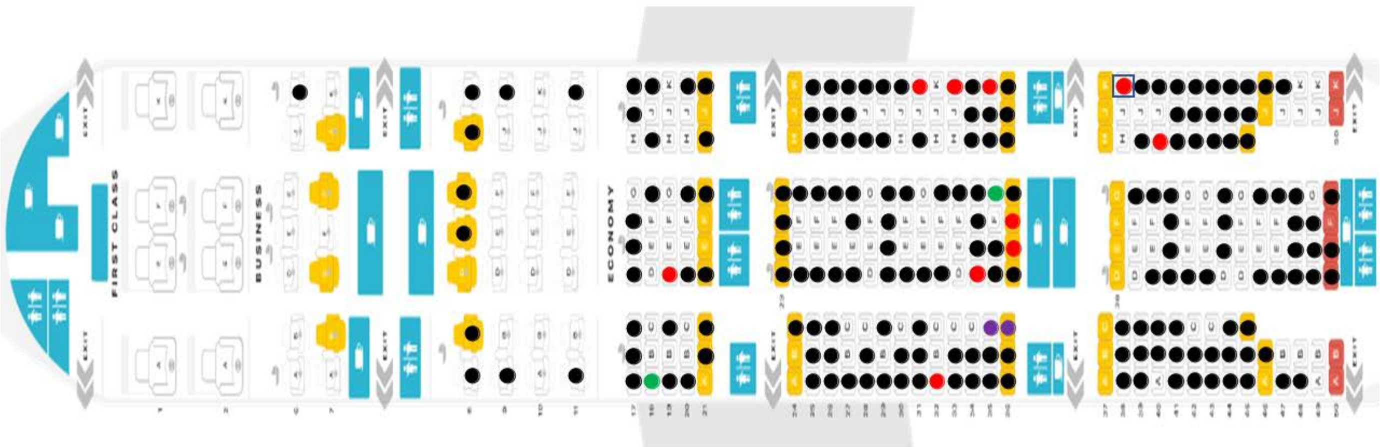
Three days prior to departure from Saudi Arabia, all of them undertook a RT-PCR test according to the regulation of the Minister of Foreign Affairs. The results showed negative before departure. Upon their stay in SQ-X, all 106 passengers were tested and two of them presented with positive SARS-CoV-2 detection on the first round of testing (on 28 Jul 2020; day 3 after arrival). The SQ officers performed nasopharyngeal swab again on 104 passengers on 5 Aug 2020 (Day 11 after arrival) and ten were found positive for SARS-CoV-2. On 7 Aug 2020 (Day 13 after arrival), the other two passengers, showing inconclusive results in the second test, were tested again and showed positive results. The median cycle threshold (Ct) of RT-PCR for ORF1ab and N genes were 36.33 (Q1=34.92, Q3=37.34) and 35.47 (Q1=34.87, Q3=36.78) respectively (Table 1).

Risk History

During March to May 2020, Saudi Arabia imposed city lockdown and curfew. Universities were closed and students were screened for SARS-CoV-2. Five students on this flight were found positive for SARS-CoV-2 by RT-PCR and were isolated in university dormitory. Three students who were cases in this event informed that they had taken a RT-PCR test for COVID-19 in June 2020 with positive results. At that time, they were not admitted to a hospital, but were advised to self-quarantine for 14 days, in which they still shared room, kitchen and toilet with the other students.

All of the cases informed that, while being in Saudi Arabia, they went to a department store twice a week. Four of them visited a mosque two weeks before travelling. All of the students lived in the same dormitory affiliated to the Islamic University in Saudi Arabia. The dormitory had ten rooms and shared two toilets on each floor, and a shared kitchen on the first floor. They mentioned that they did not perform frequent hand washing and did not wear a mask all the time. They rarely practiced physical distancing when staying in their private rooms as 2–4 people were living together in the same room. The room was air-conditioned.

On 24 Jul 2020, 56 students took a public bus while the others (religious volunteer and housewife) took a taxi to the airport. On 25 Jul 2020, they took a flight from Saudi Arabia that took two hours and had a transit in United Arab Emirates, then arrived in Thailand by another flight that took six hours with a meal served on the flight. On both flights, all passengers wore a mask all the time on the plane except during meal time. The patients mentioned that the seat positions on the flight were randomly assigned. There was no specific cluster of the flight seats related to the cases. The flight's seat plan of 196 passengers is presented in Figure 1. There were three infants that sat on mothers' lap and 20 tested-negative passengers did not declare their seat numbers. All cabin crew wore a mask during service and wore gloves while serving the meals. There was no distancing at the airport during the immigration process and while waiting for the luggage. The bus provided by the Department of Land Transport took them to SQ-X. On the bus, all passengers and the driver wore a mask and practiced physical distancing.



Passengers positive for SARS-CoV-2 on 28 Jul 2020 (Day 3) (n=2)
Passengers positive for SARS-CoV-2 on 5 Aug 2020 (Day 11) (n=10)
Passengers positive for SARS-CoV-2 on a repetition of RT-PCR on 7 Aug 2020 (Day 13) (n=2)
Passengers negative for SARS-CoV-2 on both tests (n=182)
Symptomatic patient (n=1)

Figure 1. Flight's seat plan by EK0384 from United Arab Emirate to Thailand on 25 Jul 2020

Environmental Survey

The SQ-X composed of three buildings with a total of 360 rooms. It was jointly managed by the Royal Thai Army and the Office of Disease Prevention and Control Region 6 Chonburi, and Chonburi Provincial Health Office. Upon arrival at the SQ, the name of the passengers and bus numbers were recorded by hotel staff. The passengers' luggage was initially cleaned at the airport. There were no luggage or shoe cleaning areas at the SQ. All passengers had to carry their own luggage to the room. A registration area was placed in front of the hotel building and was separated from the staff operation area. Hotel staff were responsible for registration and were required to wear gloves and face mask all the time. Guests always wore a face mask. There was a specific elevator for guests, separated from the staff. Trash removal was done in the elevator for staff. Each guest individual was assigned a single room, except for children under 12 years or disabled people. No one was allowed to leave the room without permission except for taking food. The food was served at the entrance to each room. Guests were able to leave the SQ once completing a 14-day stay, and only if the RT-PCR results showed negative for all rounds. Staff monitored the guests' behavior by closed-circuit television. When any guest left the room without permission, the hotel staff would warn them using loudspeaker. If anyone showed positive results for SARS-CoV-2, they would be recognized as a patient and referred to the designated public hospital.

Discussion

All of the confirmed cases in this event had a history of staying in Saudi Arabia. During the investigation period, Saudi Arabia was one of the countries which severely suffered from the COVID-19 pandemic at that time.[2] The potential risk of contracting SARS-CoV-2 in Saudi Arabia was the behavior of students in the university dormitory.[8] All students always shared kitchens and bathrooms with each other even after some students were positive for SARS-CoV-2. Based on the interviews, the preventive behaviors in the dormitory were quite relaxed. Other risk factors included the use of public transport and visiting crowded areas (such as department store or mosque).[9] This finding coincided with the report of prior literature that revealed COVID-19 outbreaks in venues for religious activities.[10]

Laboratory results also provided evidence to determine the timing of disease transmission. The Ct times of RT-PCR testing on both ORF1ab and N genes were more than 32 in all cases.[11] The median Ct times of ORF1ab and N genes were quite high. A high value of Ct time indicates that the infection is not recent. A study by Bullard et al found that the Ct time of the positive test after ten days of onset was more than 30 and had less infectivity.[12] Therefore, the likelihood of contracting the disease before arrival to Thailand was higher than being infected within Thailand.

The risk of transmission happened even though the patients were asymptomatic or pre-symptomatic.[13] This means that although almost all cases were asymptomatic, the risk of disease transmission among each other could not be ruled out. There was also a risk of transmission on the plane as the seats were almost all occupied, making it difficult to practice physical distancing. Although in this event, it is not conclusive that the cases contracted COVID-19 on the plane, the risk of infection on board is worth considering as there are studies that point to the risk of SARS-CoV-2 transmission on flights.[14,15]

On the way to state quarantine, the passengers practiced physical distancing measures. Every passenger wore a mask at all times. Thus, the risk of infection on the way to the SQ was low. There had been no local cases in Thailand since May 2020.[16] This state quarantine was evaluated on June 2020 and it appeared that SQ-X well met the SQ standards. From our observation of SQ-X and the interviews with the SQ officers, there were no incidences resulting from contact among the guests. The control measures at the SQ mainly met the standards stipulated by the Guidance for Integrated Management of State Quarantine Facilities of the MOPH.[6] The internal report of DDC (as of 25 Sep 2020) showed no incidence of infection among guests in the SQ.[17] However, there were some pitfalls regarding the hygiene in the SQ that might aggravate infection risk. For instance, the SQ did not provide specific cleaning areas for shoes and luggage from the airport. In addition, the process of trash removal used the same elevator as staff. This might increase the risk of disease spreading via direct contact.[18,19]

Limitations

This study faces some limitations. Firstly, the source of infection is not definitely explained as we did not have strong evidence (such as whole genome data) to prove that all cases were infected with the same clade of SARS-CoV-2. Secondly, memory bias might persist as some activities happened long before the diagnosis. We minimized this bias by triangulating the interview data from various sources. Thirdly, the lack of data about patients at the same university as the cases was considered another limitation. Fourthly, we also lacked data about the flight from Saudi Arabia to United Arab Emirates before transit. However, we interviewed the patients, and they informed us that the behaviors of cabin crew on both flights were similar. Fifthly, the state quarantine management during the environmental survey might be different from its daily practice. Lastly, we lacked the information about the Ct cut-off value for RT-PCR in the Saudi Arabia.

Public Health Actions and Recommendations

State quarantine prevented new cases from emerging in Thailand. Routine evaluation of the SQ management should be conducted to minimize the risk of infection in the SQ. Passengers who need to travel to Thailand, especially those from countries with currently active COVID-19, should avoid going to crowded areas, keep physical distancing and refrain from any risk behaviors (such as sharing kitchenware and not wearing masks while in public spaces). The Thai government should communicate with Thai citizens abroad and emphasize the importance of risk-minimizing behaviors (such as mask wearing and physical distancing) all the time, from being abroad, on the flight, and upon arrival in. Further studies on the correlation of laboratory results (Ct time) and time of contracting the disease are recommended. Data sharing between the airline and the investigation officers should be more timely and more comprehensive than at present.

Conclusion

Of 219 passengers travelling from Saudi Arabia, 14 tested positive for SARS-CoV-2. The overall attack rate among flight passengers was 6%. Only one patient showed mild symptoms; the others were asymptomatic. The majority of cases were male. The infection was most likely to have occurred when they were in Saudi Arabia as the cases had many risk behaviors, such as visiting crowded areas and sharing the same room in the dormitory. The risk of infection in Thailand was low because they were quarantined in the SQ with strict quarantining policies, though there were some minor pitfalls of the control measures in the SQ identified by the environmental survey. Maintaining the standards of SARS-CoV-2 preventive measures in the SQ with regular monitoring and evaluation is recommended. In addition, The Thai government should find ways to communicate with Thai people to emphasize the importance of mask wearing and practicing good social distancing when living abroad.

Acknowledgements

The investigation team thanks to mutual cooperation and support from the following organizations: Banglamung Hospital, Banbueng Hospital, Phanthong Hospital, Phanatnikhom Hospital, Kohchan Hospital, Watyan Hospital, Sattahip KM.10 Hospital, Chonburi Provincial Health Office, Office of Disease Prevention and Control Region 6 Chonburi, State Quarantine Commander and staff. We also thank Thaniya Saensri from Office of Disease Prevention and Control Region 6 Chonburi and Peeriya Watakulsin, Sahaphap Poonkesorn, Chanchanok Insri, Kawinna Kerdsalung from Operation Team of Thai DDC. Finally, the authors would like to thank all people involved in this study.

Suggested Citation

Jivaramonaikul T, Nittayasoot N, Suphanchaimat R. An investigation of a coronavirus disease (COVID-19) cluster from Saudi Arabia, in a state quarantine, Chonburi, Thailand, 2020. OSIR. 2021 Dec;14(4):121–6.

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Outbreak Investigation and Control of Coronavirus Disease 2019 in Entertainment Venues along Bangla Road, Phuket Province, Thailand, March–April 2020

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Abstract

On 22 Mar 2020, the investigation team was notified by the Phuket Provincial Health Office that there was an outbreak of coronavirus disease 2019 linked to entertainment venues on Bangla Road, Phuket Province. An outbreak investigation was conducted to verify, describe, and control the outbreak. A descriptive study was conducted by gathering epidemiological and clinical data from cases and an environmental study was conducted at the entertainment venues on Bangla Road. There were 63 confirmed cases linked to the entertainment venues. Most of the cases were Thai female employees. The median age was 32 years, and waitress and security staff were the most common occupations. The majority of cases were symptomatic with mild level of severity. The clinical manifestations were sore throat, cough and fever. Factors associated with being a case were occupational risk of infection, that is, having contact with a large number of tourists. The entertainment venues where cases were found were mostly air-conditioned closed indoor settings. This event might have originated from imported cases followed by local transmission. Therefore, employees and customers should be screened before working at or entering entertainment venues.

Keywords: outbreak, coronavirus disease 2019, entertainment venue

Introduction

Unknown cases of pneumonia were detected on 8 Dec 2019 from a group of people with respiratory symptoms in Wuhan City, People's Republic of China. The majority of patients worked and lived near the Huanan Seafood Wholesale Market.[1] On 7 Jan 2020, the causative agent, severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) was isolated from a patient's throat swab by the Chinese Center for Disease Control and Prevention.[2] On 30 Jan 2020, the World Health Organization (WHO) announced that this unknown pneumonia outbreak was a Public Health Emergency of International Concern, and was called coronavirus disease 2019 (COVID-19) on 11 Feb 2020.[3,4] The incubation period was reported to be 2 to 14 days with an average of 5 days.[5]

As of 13 Mar 2020, there were over 132,000 confirmed cases and 4,955 deaths of COVID-19 globally, most of which were found in WHO's Western Pacific region.[6] While in Thailand at that time, there were 75 cases and only one death.[7] On 22 Mar 2020, the investigation team was notified by the Phuket Provincial Health Office that they had detected a cluster of patients with COVID-19 epidemiologically linked to entertainment venues on Bangla Road, Patong Sub-district, Kathu District, Phuket Province, an attractive tourist destination which has a high volume of travelers per square mile.[8] The investigation was conducted by the Office of Disease Prevention and Control Region 11 Nakhon Si Thammarat and the Phuket Provincial Health Office. The objectives of this investigation were to: confirm the diagnosis and outbreak, describe the epidemiological characteristics and identify factors related to the outbreak, and control and prevent the spread of disease.

Methods

A descriptive study was conducted in Phuket Province from March to April 2020. The data was gathered from 63 confirmed cases who had a confirmed infection of SARS-CoV-2 by reverse transcription polymerase chain reaction (RT-PCR). We gathered epidemiological data via interviews from confirmed cases regarding general information, risk of infection, and travel history. Information from inpatient medical records was reviewed such as medical history, laboratory tests, diagnoses, symptoms, and clinical classification, and these were distinguished by Diagnosis and Treatment Protocol for Novel Coronavirus Pneumonia.[9] Patients in the community were identified by close contact tracing, and the surveillance of patient under investigation (PUI) in acute respiratory infection (ARI) clinics of both public and private hospitals in Phuket Province. The definitions for COVID-19 cases and close contacts are shown in Table 1.

Table 1. The definitions of COVID-19 cases and close contacts

Type	Definition
Patient under investigation (PUI)	Business owners, staff or tourists in the entertainment venues on Bangla Road, Kathu District, Phuket Province or contacts of a confirmed case who satisfied one of the following criteria between March and April 2020: (i) body temperature ≥37.5°C or history of fever, (ii) cough, (iii) runny nose, (iv) sore throat, (v) dyspnea, (vi) shortness of breath, (vii) pneumonia, or (viii) death with unknown cause
Confirmed case	
a. Symptomatic case	PUI with detected SARS-CoV-2 by RT-PCR from a reference laboratory between March and April 2020.
b. Asymptomatic case	Business owners, staff or tourists who frequented the entertainment venues on Bangla Road, Kathu District, Phuket Province or contacts of confirmed case who had no symptom according to the PUI criteria, with detected SARS-CoV-2 by RT-PCR from a reference laboratory between March and April 2020
Close contact	A person who had a close contact with a confirmed case
a. High-risk close contact	A person who satisfied at least one of the following criteria: (i) talked with a confirmed case within a distance of 1 meter for more than 5 minutes, (ii) exposed to bodily secretions of a confirmed case without wearing proper personal protective equipment (PPE), or (iii) stayed together with a confirmed case in a closed space for more than 15 minutes without wearing proper PPE.
b. Low-risk close contact	Spoke with a confirmed case within a distance of 1 meter for less than 5 minutes

Laboratory testing of PUI was performed in accordance with the guideline of the Thailand's Department of Disease Control as of 23 Mar 2020 by collecting nasopharyngeal and throat swab samples tested for SARS-CoV-2 by RT-PCR.[10] Symptomatic contacts, both low-risk and high-risk, were tested as soon as possible using the same methods, and the other high-risk close contacts were tested on day 5 after contacting confirmed cases.

Environmental surveys of the entertainment venues on Bangla Road were conducted by observing and interviewing staff or the owners of each entertainment place. The data collected consisted of the location, general environment, building characteristics and ventilation system, and the ability to accommodate customers.

Data were analyzed by descriptive statistics including mean and standard deviation (SD), frequency, and proportion.

Results

There were 197 PUIs in ARI clinics, of which 25 confirmed cases (12.7%) were found. From 1,070 people found through contact tracing, 38 confirmed cases (3.6%) were identified, including 30 symptomatic cases and eight asymptomatic cases. Overall, 63 people (5.0%; 63/1,267) were positive for SARS-CoV-2, including 55 symptomatic cases with one death and eight asymptomatic related to entertainment venues on Bangla Road from March to April 2020.

The dead case was a 25-year-old Hungarian male, with a history of traveling to the entertainment venue every day. He had an immunocompromised disease. His symptoms presented on 30 Mar 2020 with fever, sore throat, runny nose, and cough. He walked into a hospital on 8 Apr 2020 with chief complaints being dyspnea and exhaustion. Physical examination showed that blood pressure was 80/60 millimeter of mercury, pulse rate was 90 beats per minute, respiratory rate was 26 times per minute, oxygen saturation was 88% and chest radiography showed infiltration in both lungs. SARS-CoV-2 was detected the following day with progression of symptoms. Serial chest radiography was worse with ground-glass opacity being found. He died on 26 Apr 2020, 18 days after admission.

Most of the infected cases were females with ages ranging from 21–40 years. The median age of all cases was 32 years, and the age range was 21–63 years. The majority of cases were Thai nationality, followed by Russian and Italian, respectively. Most of the infected cases were staff of the entertainment venues, including waitresses and security officers, followed by household contacts of the staff, and tourists. Common underlying diseases of the cases were hypertension, chronic obstructive pulmonary disease, and diabetes (Table 2).

Table 2. Demographic characteristics of cases infected with SARS-CoV-2 (n=63)

Characteristic	Total	Percentage (%)
Gender		
Female	40	63.5
Male	23	36.5
Age (years)		
21-30	27	42.9
31-40	29	46.0
41-50	4	6.3
51-60	1	1.6
61+	2	3.2
Nationality		
Thai	44	69.8
Russian	5	7.9
Italian	4	6.3
French	3	4.8
Kazakhstan	2	3.2
Others	5	7.9
Occupation		
Waitress	14	22.2
Security personnel	8	12.7
Commercial sex worker	7	11.1
Unknown (tourist)	6	9.5
Freelance	4	6.3
Others	24	38.1
Relation to entertainment venue		
Staff	40	63.5
Household contact	9	14.3
Tourist	9	14.3
Business owner	4	6.3
Underlying disease		
Hypertension	16	29.1
Chronic obstructive pulmonary disease	7	12.7
Diabetes mellitus	6	10.9
Cardio vascular disease	4	7.3
Human immunodeficiency virus	4	7.3
Chronic kidney disease	3	5.5
Carcinoma	1	1.8

Among the 55 symptomatic cases, the most common clinical manifestations were sore throat (81.8%) followed by cough (72.7%), fever (67.3%), runny nose (43.6%), and difficult breathing (21.8). Anosmia and loss of taste were presented in 10.9% and 9.1% of the cases. The median clinical recovery time for people with mild symptoms was 12 days (range 6–18 days), for those with moderate symptoms was 18 days (range of 16–21 days), and among those with severe symptoms was 22 days (range of 20–26 days). One case with critical symptoms died 28 days after symptoms onset. Abnormal chest radiography was found in 18.2% of cases (Table 2).

Table 3. Clinical features of patients with COVID-19 (n=55)

Characteristic	Total	Percentage (%)
Clinical manifestations		
Sore throat	45	81.8
Cough	40	72.7
Fever	37	67.3
Runny nose	24	43.6
Difficulty breathing	12	21.8
Sputum production	10	18.2
Myalgia	9	16.4
Diarrhea	7	12.7
Headache	6	10.9
Anosmia	6	10.9
Loss of taste	5	9.1
Clinical classification		
Mild	40	72.7
Moderate	10	18.2
Severe	4	7.3
Critical	1	1.8
Chest radiography (CXR)		
Normal	45	81.8
Abnormal	10	18.2
- Infiltration	9	90.0
- Ground-glass opacity	5	50.0
- Consolidation	1	10.0
- Patchiness	1	10.0
- Reticular opacities	1	10.0

The initial laboratory results revealed eosinophilia (90.9%) and metabolic acidosis (61.8%) (Table 4). The majority of laboratory parameters were normal. Factors related to the outbreak were occupational risk, that is, contact with a large number of people, particularly tourists (81.1%), exposure to confirmed cases (50.8%), and traveling from the affected area (9.5%).

Table 4. Initial laboratory testing of COVID-19 cases (n=55)

Laboratory test result	Total	Percentage (%)
Complete blood count		
Platelet count		**239,000 (58,643)***
low (<12 x 10^4 cells/mm^3)	2	3.6
normal (12-38 x 10^4 cells/mm^3)	51	92.7
high (>38 x 10^4 cells/mm^3)	2	3.6
Hematocrit		**46.39 (8.1)***
low (<36%)	5	9.1
normal (36-56%)	42	76.4
high (>56%)	8	14.6
White blood cell count		**6,717.74 (1,926.4)***
low (<4 x 10^3 cells/cu.mm)	5	9.1
normal (4-9 x 10^3 cells/cu.mm)	48	87.3
high (>9 x 10^3 cells/cu.mm)	2	3.6
Neutrophil		**50.73 (13.9)***
low (<42%)	11	20.0
normal (42-85%)	39	70.9
high (>85%)	5	9.1

** Mean (standard deviation)*

Table 4. Initial laboratory testing of COVID-19 cases (n=55) (cont.)

Laboratory test result	Total	Percentage (%)
Complete blood count (cont.)		
Lymphocytes		**37.71 (11.9)***
low (<11%)	4	7.3
normal (11-49%)	39	70.9
high (>49%)	12	21.8
Monocytes		**8.70 (2.6)***
normal (0-9%)	35	63.6
high (>9%)	20	36.4
Eosinophils		**2.22 (2.6)***
normal (0-6%)	5	9.1
high (>6%)	50	90.9
Renal function tests		
Blood urea nitrogen		**13.24 (5.6)**
low (<7 mg/dL)	3	5.5
normal (7-20 mg/dL)	45	81.8
high (>20 mg/dL)	7	12.7
Creatinine		**0.88 (0.3)**
low (<0.6 mg/dL)	4	7.3
normal (0.6-1.3 mg/dL)	49	89.1
high (>1.3 mg/dL)	2	3.6
Glomerular filtration rate		**124.74 (30.7)**
low (≤ 90 ml/min/1.73 mm^2)	3	5.5
normal (>90 ml/min/1.73 mm^2)	52	94.6
Liver function test		
Total protein		**7.61 (0.9)**
normal (6-7.8 g/dL)	34	61.8
high (>7.8 g/dL)	21	38.2
Albumin		**4.45 (0.9)**
normal (3.5-5.2 g/dL)	52	94.6
high (>5.2 g/dL)	3	5.5
Total bilirubin		**0.69 (0.2)**
normal (0.2-1.2 mg/dL)	51	92.7
high (> 1.2 mg/dL)	4	7.3
Globulin		**3.20 (0.5)***
Direct bilirubin		**0.25 (0.2)***
normal (0-0.5 mg/dL)	53	96.4
high (>0.5 mg/dL)	2	3.6
Aspartate transaminase		**31.11 (16.3)***
normal (5-34 U/L)	35	63.6
high (>34 U/L)	20	36.4
Alanine transaminase		**57.68 (20.6)***
normal (0-55 U/L)	47	85.5
high (>55 U/L)	8	14.6
Alkaline phosphatase		**76.96 (27.5)***
low (<40 U/L)	5	9.1
normal (40-150 U/L)	50	90.9

** Mean (standard deviation)*

Table 4. Initial laboratory testing of COVID-19 cases (n=55) (cont.)

Laboratory test result	Total	Percentage (%)
Electrolytes		
Sodium		**137.93 (5.4)***
low (<136 mmol/L)	9	16.4
normal (136-145 mmol/L)	45	81.8
Potassium		**4.15 (0.5)***
low (<3.5 mmol/L)	1	1.8
normal (3.5-5.1 mmol/L)	52	94.6
high (>5.1 mmol/L)	2	3.6
Chloride		**105.52 (16.4)***
low (<98 mmol/L)	3	5.5
normal (98-107 mmol/L)	43	78.2
high (>107 mmol/L)	9	16.4
Bicarbonate		**21.92 (2.0)***
low (<22 mmol/L)	34	61.8
normal (22-29 mmol/L)	18	32.7
high (>29 mmol/L)	2	3.6

** Mean (standard deviation)*

The primary case developed symptoms on 14 Mar 2020. The case was a 46-year-old Canadian who had a family living in Phuket Province. He was a business owner of an entertainment venue. The case did not have a travel history outside of the area in the 14 days prior to becoming ill, but gave a history of contacts with business partners traveling from China, Italy, and France, which were countries with ongoing epidemics at that time. Since then, more patients were detected as shown in Figure 1.

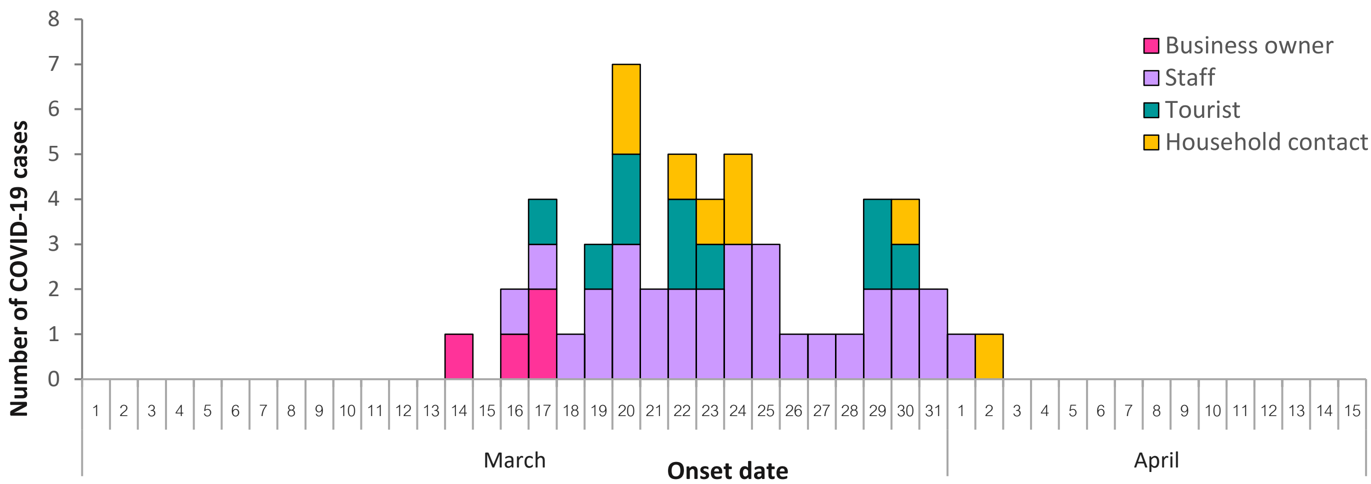

Figure 1. Epidemic curve of COVID-19 cases during the outbreak in entertainment venues, Bangla Road, Kathu District, Phuket Province, March–April 2020 (n=52)

From interviews with persons who had contact with confirmed cases, the outbreak spread to five generations of the COVID-19 epidemic, meaning a person who contracted disease from one source has infected a person, who infected another person, who then infected another person, who then infected another one, in entertainment venue that was divided by history of confirmed cases contact. The initial phase found cases among business owners who had contact with foreigners, customers or business partners who came from COVID-19 affected countries. After that, the next phase of cases consisted of staff and household contacts of staff members (Figure 2). Among 30 symptomatic close contacts, they presented with symptoms within 2–8 days (median of 5 days) after their first exposure (Figure 2).

There were 11 entertainment places where the patients worked or traveled to, most of which were closed settings and had integrated cooling systems. From the investigation, the first patient worked at entertainment venue number 38 (Figure 3). After identification of the first case, more cases were found widely distributed among staff working at venues along the Bangla Road.

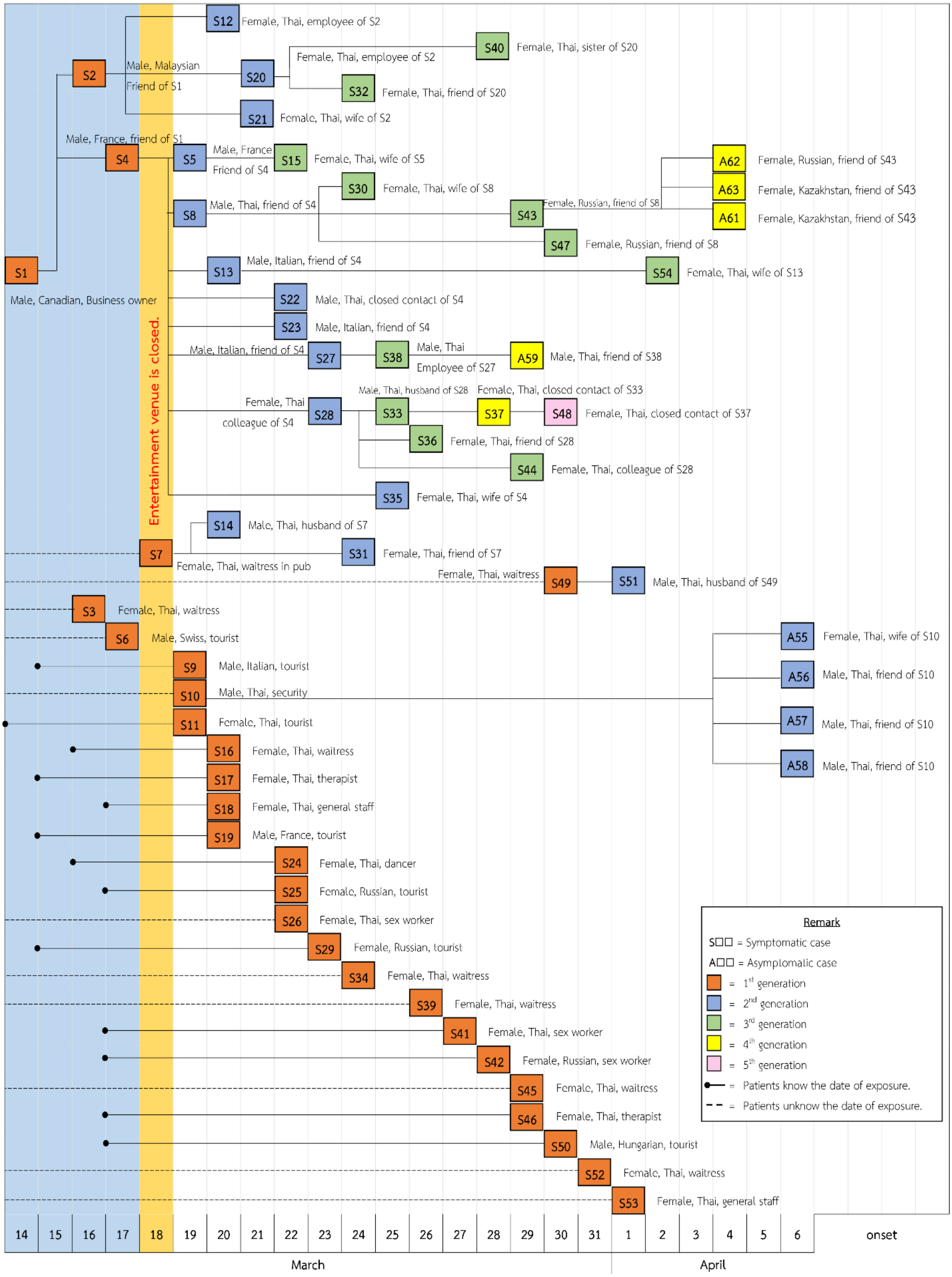

Figure 2. Linkage of symptomatic and asymptomatic cases during the COVID-19 outbreak in entertainment venues, Bangla Road, Kathu District, Phuket Province, March–April 2020 (n=62)

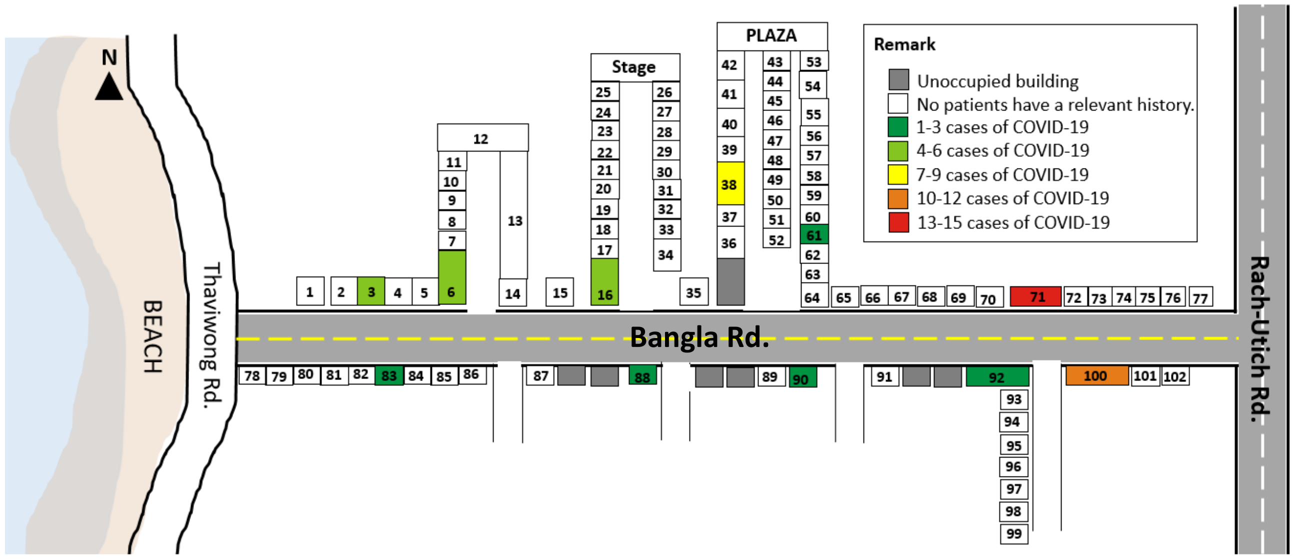

Figure 3. Map of Bangla Road and entertainment places where COVID-19 cases were found, Kathu District, Phuket Province, March–April 2020 (n=102 entertainment places)

Public Health Actions

The Provincial Communicable Disease Committee announced, on 18 Mar 2020, that the entertainment venues must be closed and prohibited citizens from entering and leaving Patong Sub-district on 4 Apr 2020, including ordering the entertainment venue owners or operators to disinfect their facilities.

Information was publicized to business owners, staff, tourists, and contacts of the confirmed cases to avoid visiting crowded places and to seek medical treatment as soon as possible if they developed fever or respiratory symptoms. If this was not possible, they were advised to wear a face mask appropriately and perform sanitary hand washing with 70% alcohol gel or soap.

An active case finding was launched on any pharmacies in the area using Google Form to report PUI. Responsible hospitals were advised to contact these individuals to get the test in an ARI clinic at the nearest hospital. This active case finding was able to detect 109 PUI and found one confirmed case. All PUI were isolated and nasopharyngeal and throat swabs were collected to detect SARS-CoV-2, until the tests produced two negative results 24 hours apart. All close contacts were traced, especially among high-risk ones, and they were followed up and quarantined at a designated hotel. Samples were collected using the same method of collection for PUIs and the contacts were quarantined for 14 days. All 63 confirmed cases with severe chest radiographic findings and those with signs of pneumonia were treated with Favipiravir.

Discussion

We identified a cluster of COVID-19 cases in entertainment venues along a popular road for tourists, which might have started with an imported case and followed by local transmission. The primary cases had no history of traveling outside the area or traveling to other countries, similar to outbreaks found elsewhere such as Taiwan.[11] The initial phase of the outbreak consisted of an infection among staff and tourists; subsequently, cases among household contact were found. The outbreak reached five generations spreads of the COVID-19 epidemic that distinguished from contact history to confirmed case, as it did in the outbreak of religious evangelists at the Sri Petaling Mosque in Kuala Lumpur, Malaysia.[12]

The proportion of asymptomatic cases was lower than a study by Oran, and most clinical classifications were mild, similar to another study.[13,14] Therefore, there might be asymptomatic cases or cases with mild symptoms in the community who were not in isolation or the quarantine system and could have spread the virus in the area.

The most common clinical manifestations in this outbreak were sore throat and cough, unlike another study, which found that the majority of cases had fever, while some cases presented with anosmia and loss of taste, which suggests that national guidelines should include those symptoms in the PUI surveillance protocol.[15]

In this outbreak, the majority of infected cases were female, which was different from an outbreak among travelers in Germany.[16] This might be due to fact that the majority of cases were waitresses. Most of the cases in this outbreak worked in entertainment facilities where poor ventilation is usual condition. The majority of entertainment places were closed indoor settings that had air-conditioning systems. A study by the World Health Organization found that this type of setting has a high risk of infection.[17] Environmental factors such as high humidity, and poor ventilation has been shown to be significant risk factors of transmission of SARS-CoV-2.[18]

Recommendations

For the early detection of COVID-19 cases, Thailand should include anosmia and loss of taste in the national surveillance protocol and increase resources for screening at the points of entry such as setting up an RT-PCR laboratory testing unit to test SARS-CoV-2 infection on all international travelers or be strict about permitting people traveling from affected areas into the country. Patients should be advised to separate themselves from family immediately after feeling sick. At the workplace, staff should be screened each day and those with symptoms should be allowed to leave work and be tested.

The provincial health office needs to strengthen the surveillance system to detect outbreaks in the early stage by focusing on any clusters of people experiencing respiratory symptoms or fever. We recommend both measurement and verbal screening be used in staff and customers of entertainment venues. Notification of suspicious cases should be issued from the entertainment venue directly to the provincial health office and each venue must designate a responsible person for this matter. The situation awareness and the investigation teams should analyze the risk factors of each patient to find epidemiological connections.

Conclusion

We reported a COVID-19 cluster in entertainment venues of Bangla Road, Phuket from March to April 2020. There was a total of 63 infected persons including 55 symptomatic cases and 8 asymptomatic cases. Staff, comprising waitresses and security personnel, were considered at-risk during the outbreak. The outbreak investigation found five generations of human-to-human transmission. The outbreak was characterized by occupational risk and transmission to tourists and customers of entertainment venues. The median incubation period was 5 days. Among the symptomatic cases, most symptoms were mild, and we found that around 10% of cases had anosmia and loss of taste. Most of the entertainment places on Bangla Road that had confirmed cases were closed-door settings.

Acknowledgements

The authors are grateful for the patients and contacts for providing valuable information. In addition, we would like to express our deepest appreciation to both the public and private hospitals for their support and cooperation.

Suggested Citation

Naraart P, Wareewanit K, Choolue T, Leng-aee W, Kamsamarn S, Na Nakorn N, et al. Outbreak investigation and control of coronavirus disease 2019 in entertainment venues along Bangla Road, Phuket Province, Thailand, March–April 2020. OSIR. 2021 Dec;14(4):127–36.

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Outbreak, Surveillance, Investigation & Response (OSIR) Journal
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Investigation of an Unusual Crow Mortality Event in Jessore, Bangladesh, December 2018

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Abstract

After a report of an unusually high number of crow deaths in Jessore, Bangladesh, a multidisciplinary team investigated the event in December 2018 to identify the etiologic agent, and the source and extent of the outbreak. We interviewed students, teachers, live bird sellers, poultry farm owners and cleaners for fever and cough symptoms. We reviewed the hospital records for acute respiratory distress syndrome and chronic obstructive pulmonary disease. We observed live bird market practices, crow roosts and their feeding behavior, and collected cloacal and oropharyngeal swabs from moribund and dead crows, and pooled environmental samples from live bird markets (LBMs) and farms. All samples were tested for influenza A/H5, H7 and H9 by RT-PCR. The H5 prevalence was 77.4% in samples obtained from crow roosts. Among environmental samples from the LBMs, 11.1% were positive for H5 and 5.5% had co-infections with H5 and H9. Our results indicate that the H5 influenza virus is circulating in LBMs and was transmitted to crows through their feeding on the waste. We recommend that continuous surveillance in wild birds and LBMs is required to understand the virus's evolution, transmission pathways and potential source of infection. Improved waste management practices in LBMs and public awareness are needed to reduce the risk and stop spillover of avian influenza virus to humans in Bangladesh.

Keywords: Bangladesh, live bird market, crow, influenza, poultry

Introduction

Avian influenza is a highly contagious viral disease with a high fatality that affects poultry as well as wild and domesticated birds.[1] Bangladesh has reported H5N1 infections in domestic poultry since February 2007 and 64 Highly Pathogenic Avian Influenza (HPAI) outbreaks occurred in commercial poultry farms from February to December 2017.[2] Influenza A/H5 caused deaths in crows during 2012–2014 in Bangladesh.[3] The majority of the influenza A/H5-positive samples were from apparently healthy waterfowl in 2012. Multiple subtypes, including H1N1, H1N3, H3N2, H3N6, H3N8, H4N1, H4N2, H4N6, H5N1 H5N2, H6N1, H7N9, H9N2, H11N2, H11N3, and H11N6 were detected in waterfowl and environmental samples in Bangladesh.[4]

The World Health Organization has stated that animal influenza viruses are distinct from human seasonal influenza viruses and do not easily transmit from animals to human. However, influenza viruses from animals occasionally infect humans through direct or indirect contact and can cause disease in humans.[5] Generally, most human zoonotic influenza cases occurred due to exposure of the influenza A/H5 viruses through contact with infected poultry or contaminated environments, including live bird markets (LBMs).[6] From 2016–2020, only 14 human influenza A/H5 cases were reported and in 2018 no influenza A/H5 case was reported in the world.[1] Vaccine and hygienic measures can prevent transmission of human influenza and there is effective treatment with neuraminidase inhibitors.[7] Development of medium- and long-term capacities of the veterinary and public health systems are needed to strengthen the emergency response and "One Health" approach to ensure inter-sector coordination in control of HPAI outbreaks.[8]

During January to December 2011, the Forest Department and the Department of Livestock Services of Bangladesh received multiple reports of crow deaths from at least two administrative divisions (Rajshahi and Dhaka).[9] The Public Health Emergency Operation Centre (PHEOC) of Institute of Epidemiology Disease Control and Research (IEDCR) reported an unusually high number of crow deaths at Shankarpasha Secondary School, Abhaynagar, Jessore on 21 Dec 2018. PHEOC verified the event by telephone conversation with a news reporter, school teacher and Upazila Livestock Officer. A multidisciplinary investigation team included IEDCR, Department of Livestock Services (DLS) and Food and Agricultural Organization investigated the crow deaths to confirm and characterize the outbreak and to identify the etiologic agent and the source of the infection as well as possible associated human infections.

Methods

We used a mixed methods design and a One Health approach to determine the scope and magnitude of avian influenza outbreaks in humans and crows and to identify linkages between these occurrences. The outbreak occurred in Abhaynagar Upazila, Jessore District (population 262,434 in 2020) in the southwestern part of Bangladesh (Figure 1).

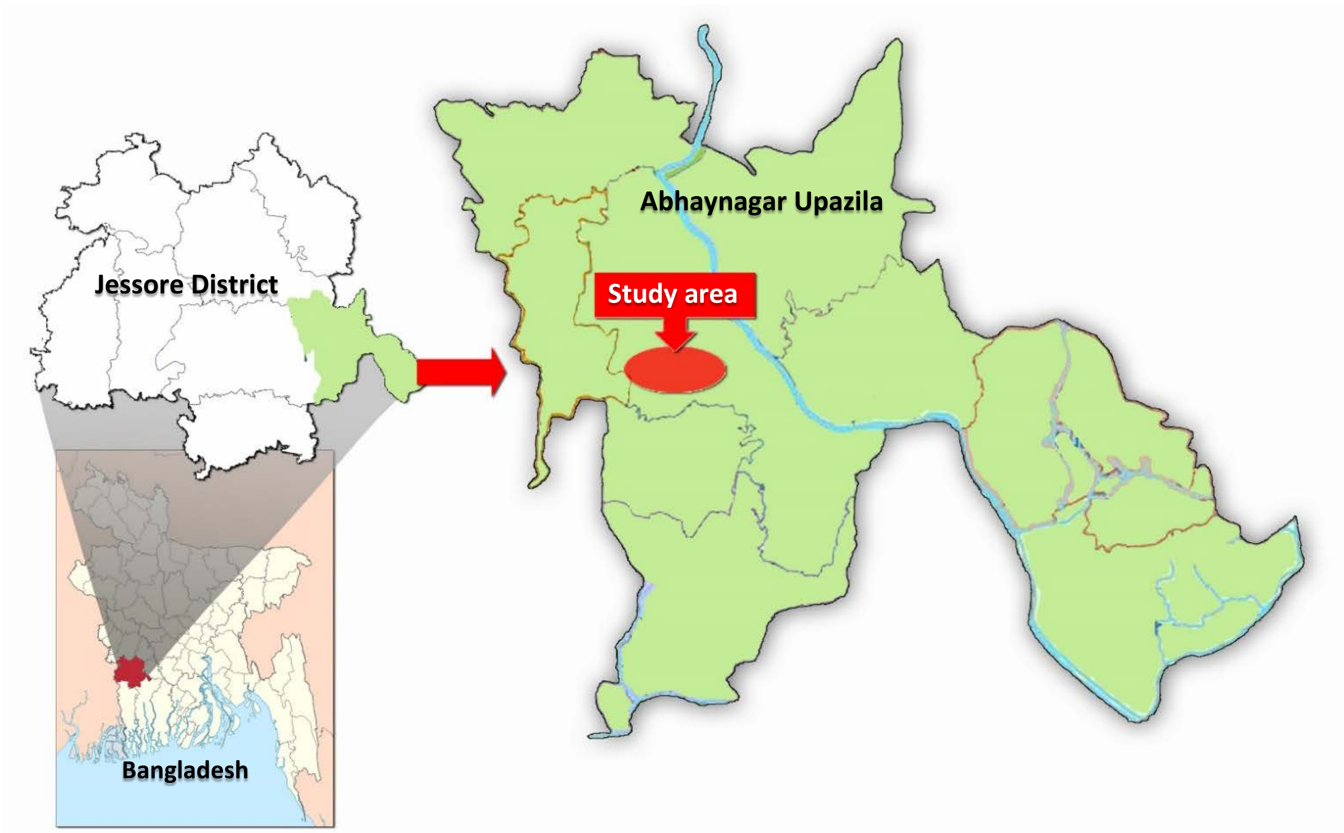

Figure 1. Map showing Abhaynagar Upazila in Jessore, Bangladesh

To verify a human outbreak, we reviewed the records of severe acute respiratory illness (SARI) and influenza like illness (ILI) patients in the 50 bed Upazila Health Complex. We reviewed medical records for acute respiratory distress syndrome and chronic obstructive pulmonary disease records for SARI and ILI patient with the help of medical officers for the last two months (October to December 2018).

Based on clinical features and review of the literature, we defined a suspected SARI and ILI case as any resident of Abhaynagar, Jessore, with fever, sore throat, or cough and/or sneezing with the onset of illness from 15 to 31 Dec 2018. We performed active case search among the students and teachers of Shankarpasha Secondary School of which there were 304 students and 20 teachers. Because of the winter vacation, only a limited number of students and teachers were present. We also interviewed live bird sellers, poultry farm owners and farm cleaners.

To verify the avian influenza outbreak in birds, we reviewed the mortality records, with a focus on crows, from the Upazila Livestock Office (ULO). The population of birds in Abhaynagar Upazila was 127,842 poultry, 841,520 ducks and 95,845 pigeons (source: ULO Abhaynagar). We actively searched for dead or moribund crows, poultry and pigeons among farms within five kilometers radius of the Shankarpasha Secondary School. We interviewed all commercial poultry and backyard farm owners and pigeon farmers. We interviewed the temporary workers who handled the dead crows (note: paid by school). We also interviewed sellers at the live bird market. A live bird market is a temporary non-structured market in the district, sub-district or village level with between 6-10 vendors and 200–1000 birds. The market is open every day. Most of the shops have no municipal water supply and waste is discharged into open sewers. The bird sellers wear no personal protective equipment and do not have access to first aid for emergencies.

Laboratory investigation was conducted by collecting pooled environmental samples from the poultry cages in the LBMs, fecal and offal samples from poultry in LBMs, oropharyngeal and cloacal samples from dead and moribund crows in secondary school playgrounds, fecal samples beneath crow roosts, and oropharyngeal and cloacal swabs from poultry and pigeons from commercial and backyard farms.

The collected samples were stored in a dry shipper and transported in a viral transport media to the National Reference Laboratory for Avian Influenza at Bangladesh Livestock Research Institute. In addition, all samples were tested for influenza A/H5, H7 and H9 viruses by RT-PCR and Matrix gene (M-gene). M-gene is the influenza A genome consisting of eight segments of single-stranded, negative-sense RNA. The matrix (M), non-structural (NS), and PB-1 genes, each of which encodes two proteins encoded by the matrix gene. M1 is important in initiating progeny virus assembly, while M2, an integral membrane protein.[10] Therefore, the evolution of the M-gene may reflect host-specific adaptation. Despite the association of the two genes, influenza viruses in wild waterfowl contain distinguishable lineages of M-genes.[11]

Results

Human Cases

In our investigation, we identified 178 patients suffering from acute respiratory distress syndrome and 290 patients from chronic obstructive pulmonary disease at the Upazila Health Complex. There was no SARI and ILI patients. Next, we interviewed 45 students, 15 teachers, 26 bird sellers, 12 poultry farm owners and two cleaners. None reported that they had SARI or ILI symptoms during the past 15 days (Table 1).

Table 1. Descriptive epidemiology of the participants, Jessore, Bangladesh, 2018

Sl No	Source of participant	Number interviewed or reviewed	Male (%)	Average age (range) in years	Remarks
1	Medical records of patients with acute respiratory distress syndrome	178	47.8	38.0 (3-72)	No one met case definition
2	Medical records of patients with chronic obstructive pulmonary disease	290	62.1	35.5 (4-75)	
3	Students (class 9 and class 10)	45	47.0	15.8 (14-19)	
4	School teachers	15	86.7	46.2 (31-54)	
5	School cleaners	2	50.0	45.0 (42-48)	
6	Live bird market, bird sellers	26	100.0	41.0 (23-51)	
7	Commercial and backyard poultry farm owners	12	16.7	36.5 (35-61)	
	Total	**568**			

Table 2. Sample collected from different types of birds in Jessore and results of laboratory tests, Bangladesh, 2018

Sample site	Type of sample	Number of samples	M-gene reaction[a]	H5 (%)	H9 (%)
Live bird market	Fecal and offal sample of poultry	18	2	11.0	5.5
Crow roost	Swab sample (oropharyngeal and cloacal)	31	24	77.0	0.0
	Fecal and urine sample	17	1[b]	0.0	0.0
Poultry farm	Commercial farm (oropharyngeal and cloacal)	2	0	0.0	0.0
	Backyard poultry (oropharyngeal and cloacal)	1	0	0.0	0.0
Pigeon farm	Pigeon (oropharyngeal and cloacal)	3	0	0.0	0.0
	Total	**72**	**27**	**37.5**	**0.01**

Note: [a] M-gene Reaction: Matrix gene responsible for influenza A virus, [b] Influenza A/untypable.

Bird Mortality

The team found 31 dead and moribund crows during the investigation period. The crow mortality increased from 19 to 25 December and reached a peak on 24 December (Figure 2). The investigation team assumed that the approximate number of crows was 1,000 at Shankarpasha Secondary School crow roost and 1,500 at Pirbary roost, the two nearest crow roosts to Shankarpasha Secondary School.

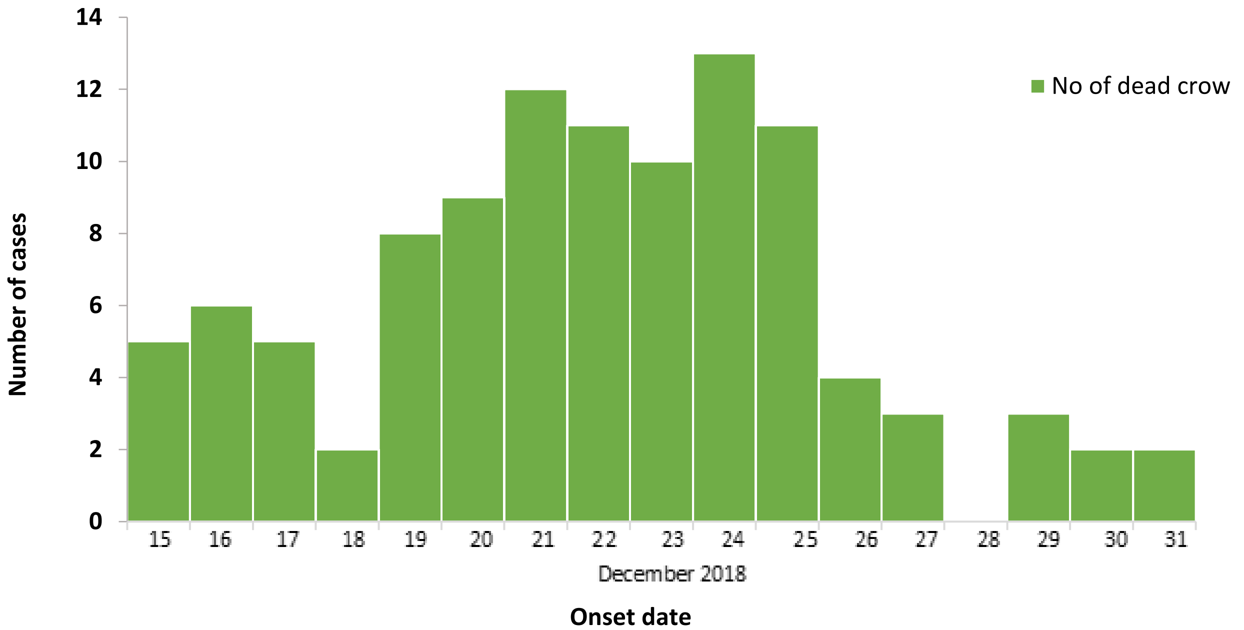

Figure 2. Epidemic curve of crow mortality at reported site premises, Jessore, Bangladesh, 2018 (n=106)

Laboratory Investigation

All crow, poultry and pigeon samples were tested by RT-PCR for influenza A (M-gene) and for H5, H7, H9, and N1. Among all tested crows and poultry from the live bird markets, 77.4% (24/31; 95% confidence interval (CI): 58.9-90.4) of crow and 11.1% (2/18; 95% CI:1.4-34.7) of poultry samples were positive for the influenza A/H5 virus, respectively; all pigeons were negative and 5.5% (1/18; 95% CI: 0.1-27.3) of the poultry had co-infection with influenza A/H5 and H9.

Among fecal samples obtained from the crow roosts, 5.8% (1/17; 95% CI: 0.2-28.7) were positive for influenza A/untypable. All the environmental samples of pigeon and poultry farms were negative for influenza.

Walk Through Survey

Most of the shops in the LBMs have no supply of water from the municipality. Waste is discharged into open sewers. The team observed that the birds sellers threw offal and poultry wastage into nearby rivers and ponds. More importantly, we noticed crows eating the poultry offal and waste materials in the LBMs and areas along the river. We observed that crows shared their roosts with other wild birds.

Discussion

This investigation confirmed that the influenza A/H5 virus was found in sick and dead crows at Jessore, Bangladesh. No transmission to humans occurred. Avian influenza in crows has previously been reported in Bangladesh, Russia, and South Korea. In January

2017, influenza A/H5 infection was found in dead and moribund crows in Rajshahi Medical College Hospital, Bangladesh.[12] In Russia 2007, RT-PCR revealed influenza virus A/H5 in more than half of pigeons and crows and in around 20% of starlings.[13] In South Korea, the prevalence of avian influenza was 0.6% in wild birds from 2003–2008.[14] The World Organization for Animal Health reported that an outbreak occurred in domestic birds in Bangladesh from January to June 2018, where 385 domestic birds and 600 wild birds died.[15] Globally, avian influenza surveillance has identified many subtypes of influenza A in LBMs, duck farms, and wild birds.[16] The small seller sells poultry to larger LBMs in the city, due to fear of financial loss, so sometimes clinically diseased poultry is sold. Diseased poultry is cheaper, which encourages other villagers to buy these birds. People purchase live poultry and slaughter them at home. The inedible portions from poultry are usually disposed in an unsafe way or are fed to other birds, which grossly enhances incursion risks.[17]

No transmission to humans occurred based on clinical observation because there is no direct food chain connectivity from crow to human. Muslims do not eat crows due to religious beliefs. Therefore, it is difficult to transmit the avian influenza virus from crows to human.[18] Humans may be infected with influenza A/H5 from LBMs but there are no reports of transmission of influenza A/H5 from crows. Therefore, we assumed influenza A/H5 can be transmitted to crows but not from crows to humans.

The unprecedented epizootic of influenza A (H5N1) viruses among birds continues to cause human disease with high mortality and poses a threat to future pandemics.[19] According to the World Health Organization there were 456 deaths from H5N1 out of 860 human avian influenza cases (2003 to 2018) in 16 countries.[20] The influenza A (H5N1) viruses that have infected humans have been entirely avian in origin, and they reflect strains circulating locally among poultry and wild birds.[21] If HPAI Asian H5N1 viruses gain the ability for efficient and sustained transmission among humans, an influenza pandemic could result, with potential high rates of illness and deaths worldwide. Therefore, the HPAI epizootic continues to pose an important public health threat.[22]

Bangladesh Livestock Research Institute isolated influenza A/H5N1 viruses from crows that ingested the internal organs of infected poultry sold at live bird markets.[23] In Bangladesh, the majority of isolated subtype was non-pathogenic H9N2, but virulent subtypes H1N2, H1N3, H3N6, H4N2, H5N1, H5N6 and H10N7 were also found in LBMs in 2011.[24,25] The presence of influenza A/H5 in the samples collected from LBMs suggested that the crows share the viruses with the chickens. The crows, as carrion eaters, could be infected from the offal or wastage of infected poultry. Live bird sellers throw offal and wastage into the river where the crows frequently feed, which might be a source of infection. The crow is the closest wild bird to the human habitat and sometimes it also moves to urban kitchen. House crow deaths appeared to be an indicator of the presence of HPAI viruses in poultry at live bird markets.[26] Despite numerous efforts at containment from the World Health Organization, H5N1 influenza viruses and their precursors still circulate among poultry and wild birds in Asia and remain a threat to both veterinary and human public health.[27]

Limitations

Human cases may have been underreported because the study protocol tested only symptomatic cases while asymptomatic people can be tested positive for avian influenza. Ideally, necropsy should be done soon after the animal has died. However, for these dead crows, necropsy was not feasible because we arrived at the site too late and all of the crows were too decomposed. Generalization of the study is limited because the affected school was on winter vacation and we could only interview the students and teachers that remained.

Public Health Actions and Recommendations

We recommend surveillance of influenza A/H5 in birds to further understand the influenza evolution, transmission pathways and potential source of infection in crows and poultry. This investigation also demonstrated the value of following the One Health strategy to respond and mitigate the zoonotic transmission risk. Live bird market waste management should be improved to reduce the potential risk of transmission of avian influenza. There is a need to strengthen outbreak investigation considering co-infection, toxicity and bacterial infection, and histo-pathological test to identify the etiologic agent and the source of infection in future investigations. Moreover, awareness building and community engagement is important for obtaining accurate information in the shortest possible time.

The investigation findings were shared with all stakeholders to increase awareness and ensure use of personal protective equipment by workers related to disposal of dead birds and to improve bio-security measures in LBMs to reduce the spread of influenza A/H5. Local authorities should improve public awareness to reduce the risk of influenza virus spillover to humans in Bangladesh. These findings indicate that improvements in hygiene and biosecurity measures are needed in LBMs to reduce exposure to the avian influenza virus.

Acknowledgements

We acknowledge IEDCR and DLS, Bangladesh and Training Programs in Epidemiology and Public Health Interventions Network for their financial support. We cordially thank ECTAD-Food and Agricultural Organization for rapid kit support. We also thank the US Centers for Disease Control and Prevention (CDC) country director and Dr. Alden Henderson for their technical support. We extend our heartfelt thanks to the sellers who worked at the live bird markets and other participants for their cooperation.

Conflict of Interest

The authors declare no conflict of interests.

Suggested Citation

Khokon MSI, Billah MM, Fakir MAU, Shirin T, Ali MZ, Islam S, et al. Investigation of an unusual crow mortality event in Jessore, Bangladesh, December 2018. OSIR. 2021 Dec;14(4):137–43.

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Outbreak, Surveillance, Investigation & Response (OSIR) Journal
Field Epidemiology Training Program, Division of Epidemiology
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Risk Factors of an Influenza A(H1N1)pdm09 Outbreak in a Nursing Institute, Noagaon, Bangladesh, 2015

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Abstract

An H1N1 outbreak in the Noagaon Nursing Institute in Bangladesh allowed examination of risk factors for influenza transmission and a return-to-work policy. We conducted a retrospective cohort study of 119 nursing students residing in the nursing institute's dormitory. The attack rate of influenza was 51% (61/119) and 28% (5/18) of suspected influenza cases tested positive for influenza A(H1N1)pdm09. Eighty percent of the students returned to their training in the hospital and the classroom three days after the first onset of symptoms. Living in overcrowded dormitories (risk ratios (RR) 1.7, 95% confidence interval (CI) 1.2-2.4), contacting with students with influenza-like illness (RR 2.7, 95% CI 1.6-4.6) placed students at greater risk for receiving and for transmitting influenza. To prevent transmission, we recommended isolating students with influenza during the viral shedding period and annual influenza vaccination.

Keywords: H1N1, influenza, nursing student, Bangladesh

Introduction

In 2007, a hospital-based influenza surveillance was established in twelve sentinel hospitals in Bangladesh. This surveillance system reports the burden and trends of influenza infection in Bangladesh. On 18 Jun 2009, through event-based surveillance system at the Institute of Epidemiology, Disease Control and Research (IEDCR), the first human case of influenza A(H1N1)pdm09 was detected in Bangladesh. In 2010, another surveillance system, the National Influenza Surveillance Platform, Bangladesh (NISB), was established to strengthen influenza surveillance activity in Bangladesh.[1] From January to December 2015, NISB identified 201 cases of influenza A and among them 70% (142) were laboratory confirmed H1N1 cases.[2]

In 2012 and in 2015, the outbreak investigation teams of IEDCR investigated five outbreaks of influenza-like illness (ILI) across the country.[3] Of the five events, two were ILI and three were suspected to be caused by influenza A(H1N1)pdm09. Overcrowding and contact with positive cases were risk factors of the spread of influenza virus. In 2012, the outbreak of H1N1 occurred among students in the Kurigram Nursing Institute in the west-northern part of Bangladesh. The study concluded that crowded living conditions facilitated transmission of influenza infection among the dormitory students.[4]

On 2 Jul 2015, the local health authority in Noagaon District reported an increase of ILI cases in the nursing students to IEDCR. A team from IEDCR investigated this outbreak with the following objectives: to identify the causative and risk factors associated with the outbreak, to provide evidence-based recommendations to stop viral transmission under this setting, and to prevent future influenza outbreaks.

Methods

From 3 to 20 Jul 2015, the outbreak team conducted an initial field investigation in the Noagaon Nursing Institute. There were 126 students enrolled in the nursing institute. All students were female and 119 lived in dormitory. There were six teachers, three females, and one male supervisor. The school has a three-year curriculum with the first year in classroom and the second and third year in classroom and hospital.

The institute has a two-story dormitory with 27 rooms for the students and one room for the teachers. We restricted our analysis to 119 students who lived in the dormitory.

We collected information on the number of students affected, the cases' symptoms, the status of hospitalized students, and the steps taken by local health authorities. To verify the diagnosis, we reviewed medical records in Noagaon Hospital where the affected students sought treatment. We also reviewed the medical records of inpatients and outpatients in the same hospital during 20 to 25 Jun 2015 to identify other ILI cases. To identify potential risk factors, we interviewed all the students, the supervisor, the teachers, and other staffs using a semi-structured questionnaire.

Study Design

We conducted a retrospective cohort study to identify the cause and possible risk factors for this outbreak. The definition for a suspected influenza case was a person in the Noagaon Nursing Institute suffering from fever with or without cough, headache, runny nose and sneeze from 20 Jun 2015 to the date of their interview.

Laboratory Testing

Nasal and throat swabs were collected from study subjects using viral transport media and the samples were transported to the National Influenza Center at IEDCR in cold boxes. Nasal and throat swabs were first tested for influenza A and B viruses by reverse transcription polymerase chain reaction (RT-PCR) (ABI 7500 Fast Dx, Thermo Fisher, Waltham, MA). All influenza A positive samples were then tested for other influenza viruses (e.g., H1N1pdm09).

Statistical Analysis

Crowding in the dormitory was calculated by the area per person with more crowding having an area of approximately 1.6 m^2/person and less crowding having an area of approximately 2 m^2/person. We calculated the risk ratio (RR) for contacting influenza with overcrowding, contact history, and years of education. To determine whether the students returned to the regular academic or practical sessions during the infectious period, we calculated the number of days of absenteeism by subtracting between the date of isolation to the date they returned to their training hospital. We entered the data into Microsoft Excel (Office Professional Plus 2013) and used STATA (Version 13, College Station, TX) to calculate attack rates, RR and 95% confidence intervals (CI).

Results

The outbreak team traveled to Noagaon on 3 Jul 2015 to investigate and control the outbreak and returned to Dhaka on 20 Jul 2015. All 119 students in the dormitory participated in this study. Seven students, all teachers and the supervisor were not included in the study because they resided outside the dormitory.

Among the 119 students in the dormitory, 61 met the suspected case definition. We collected swab samples from 18 students and 5 were positive for influenza A by RT-PCR. Further testing showed that all of the Influenza A cases were found positive for influenza A(H1N1)pdm09.

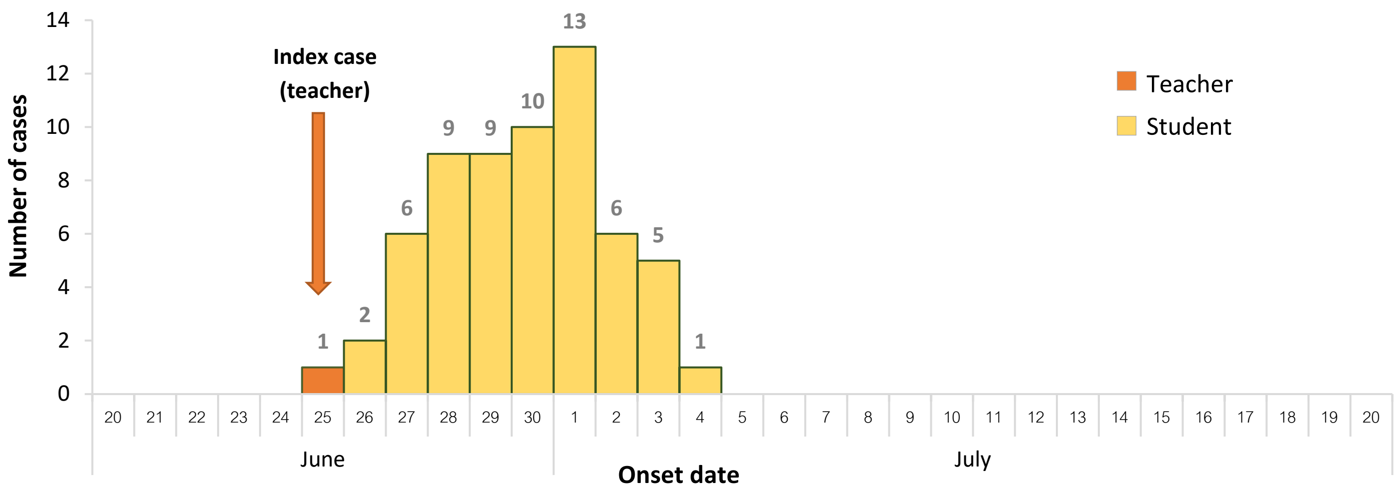

Figure 1. Epidemic curve of suspected influenza cases at Noagaon Nursing Institute, Bangladesh, 2015 (n=62, including the index case)

The onset date of the students' illness ranged from 26 Jun and 4 Jul 2015 with the highest number of cases on 1 July (Figure 1). The epidemic curve showed a single peak followed by a gradual decline of the suspected influenza cases. The shape of the curve followed a pattern of point source outbreak. The index case for this outbreak was "teacher X" as indicated in Figure 1. Teacher X developed ILI symptoms on 25 June.

She attended scheduled classes and official meetings while being ill. On 28 June, teacher Y of the institute became ill and remained in the teacher's room. Another "teacher Z", who is the sibling of teacher Y, provided care to teacher Y. Teacher Z did not wear a mask or other protective equipment during that time. Teacher Z developed symptoms on 30 June. All teachers reported neither history of exposure to poultry nor travel history during the last seven days before their illness. All three teachers taught students in the classroom and did not live on the school premises.

The attack rate among the students was 51.3% (61/119). The mean age and standard deviation of the affected students was 19.3±1.2 years (Table 1). Students affected most were in the first year of schooling. The risk of developing influenza was higher in the crowded rooms (1.6 m^2/person) compared with the less crowded rooms (2.0 m^2/person), RR 1.7, 95% CI 1.2-2.4. Moreover, the risk among those who had a history of contact with positive cases was 2.7 (95% CI, 1.6-4.6) times as large as the risk in students with no contact history. The first-year students faced higher risk of developing the disease compared with the students in the second and third years (RR 1.7, 95% CI 1.2-2.4) (Table 2). The mean absence period of students equaling three days (Table 1) and about 80% (33/41) of students returned to their regular classroom work and attended practical sessions at the hospital, three days after the symptom onset. However, the surveillance for ILI in the hospital showed no new cases after the nursing students returned to their training in the hospital.

Table 1. Characteristics and attack rates during an influenza A(H1N1)pdm09 outbreak in students at Noagaon Nursing Institute, Bangladesh, June to July 2015 (n=119)

Total number of suspected cases	**61**
Age of the student cases in years (Mean±SD)	**19.3±1.2**
Clinical features (n=61, (%))	
Fever	61 (100.0)
Cough	39 (63.9)
Headache	43 (70.5)
Body ache	35 (57.4)
Runny nose	26 (42.6)
Vomiting	15 (24.6)
Sneeze	13 (21.3)
Sore throat	12 (19.7)
Attack rate by student years	
First year (n=45)	31 (68.9)
Second year (n=45)	18 (40.0)
Third year (n=29)	12 (41.4)
Attack rate by room occupancy	
Five persons per room (n=55)	36 (65.5)
Four persons per room (n=64)	25 (39.1)
Days of absenteeism of the students (n=41) (Mean±SD)	**3.0±0.6**

Table 2. Risk ratio among the affected students, Noagaon Nursing Institute, Bangladesh, June to July 2015 (n=119)

Exposure	Suspected cases n (%)	Not suspected cases n (%)	RR (95% CI)
Crowding status			
Relatively more crowding (1.6 m^2/person)	38 (64.4)	21 (35.6)	1.68 (1.16-2.44)
Relatively less crowding (2.0 m^2/person)	23 (38.3)	37 (61.7)	Reference
Contact with infected patients			
History of contact with infected patients	50 (66.7)	25 (33.3)	2.67 (1.56-4.56)
No contact history with infected patients	11 (25.0)	33 (75.0)	Reference
Years of education			
First year	31 (68.9)	14 (31.1)	1.70 (1.21-2.38)
Second and third years combined	30 (40.5)	44 (59.5)	Reference

Discussion

Clinical evidence and epidemiological and laboratory results verify that an outbreak of influenza A(H1N1)pdm09 occurred in the Noagaon Nursing Institute. In Bangladesh, the influenza season lasts from April to September with a peak in July and August and this outbreak occurred during the peak time of influenza season.[5] Bangladesh recorded 1,408 cases of influenza A(H1N1)pdm09 and eight deaths from 2009-2010.[7,8]

Overcrowded living conditions and contact history with a case were associated with developing influenza. The students of Noagaon Nursing Institute lived in overcrowded rooms. The 2012 Kurigram outbreak reported a significantly higher risk of developing influenza among the students with five roommates or more.[6] In this outbreak, the higher risk of developing influenza occurred in the crowded rooms than the less crowded rooms and among those with history of contact with the cases. The Bangladesh Government increased the number of seats at the nursing institutes from 1,590 to 2,580 but the classroom size and student accommodations did not change in tandem; this resulted in more overcrowding.[9]

The outbreak in Kurigram and Noagaon Nursing Institutes had a much higher attack rate compared with the World Health Organization global attack rate.[9] In 2012 an outbreak of influenza A(H1N1)pdm09 was detected among the students of Kurigram Nursing Institute. The attack rate was 42% among the students.[5] The 2015 outbreak among students in Noagaon Nursing Institute was similar to the 2012 outbreak in Kurigram. Both events demonstrated similar risk factors and both showed a high attack rate. The high attack rate also occurred in a residential school in Panchgani, Maharastra, India, with an attack rate of more than 70%.[8] According to World Health Organization, the estimated annual global attack rate for influenza is 5-10% for adults.[9]

The index case for this outbreak was “teacher X” who was suspected of spreading the disease to the other teachers and students. Teacher Y and Z had a close relationship with each other, so the virus was spreading among all three teachers. By tracing back to the index patient’s infection source, we found that the most probable source was the exposure to a tuberculosis patient four days before the index patient’s symptom onset. Unfortunately, this tuberculosis patient lived far away and we were not able to reach the person by phone. The first-year students had more theoretical classes and spent more time in the classroom and had more contact with teachers compared with students in other years.

There were five students with laboratory tests positive for H1N1pdm09 and thirteen with negative results. The influenza virus can be detected from throat and nasopharyngeal swabs obtained within three days of onset of illness. In this outbreak, the samples were collected from the students during the recovery stage because we were notified five days after the symptom onset of the index case which explained the low proportion of virus detection.

An influenza case can be infectious from one day before the onset of symptoms to five days after the illness onset.[10] From a study of Praekunatham, median duration from onset of symptoms to the last day of viral shedding detected was five days (range 3-9 days).[11] We found that the students with influenza infection returned to the training hospital while they were still able to shed the virus. Fortunately, no new cases were reported in the hospital after the students returned to the institute. Most of the affected students were in the first year and did not go to the hospital. This can be a reason why no influenza cases occurred in the hospital after students returned to the institute. If the second- and third-year students were affected more than the first-year students, they might serve as the source of influenza virus transmission to the high-risk hospitalized patients, such as the elderly or children and infants.

Public Health Actions and Recommendations

All of the training institutes and the affiliated hospitals should have an annual influenza vaccination plan for students and healthcare workers to protect themselves and prevent high-risk groups from contracting the disease and spreading the viruses. The accommodation arrangement in the dormitory of the institute should provide enough space to minimize person-to-person viral transmission. The institute should require workers and nurses not to go for working and to remain in the dorms up to seven days after the onset of ILI.[10] The training sessions with regular refreshing should be given to all hospital staff and students at the institute to emphasize the importance of prevention and control measures and to maintain good personal hygiene.

Acknowledgements

We would like to thank Dr. Alden Henderson for his contribution in preparing the manuscript.

Biographical Sketch

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Financial support provided by IEDCR, Bangladesh Ministry of Health and Family Welfare. No authors had financial interest in the subject matter and have no conflicts of interest.

Suggested Citation

Khan SR, Billah MM, Monalisa, Billah SB, Shirin T, Rahman M. Risk factors of an influenza A(H1N1)pdm09 outbreak in a nursing institute, Noagaon, Bangladesh, 2015. OSIR. 2021 Dec;14(4):144–8.

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OSIR, December 2021, Volume 14, Issue 4, p.149-151

Outbreak, Surveillance, Investigation & Response (OSIR) Journal
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Epidemiological Workforce for Current and Future Pandemic Control

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Abstract

Epidemiology is the frontline combatant discipline against COVID-19. Human's knowledge and technology evolve in parallel with the emergence of this and other coming pandemics. Modern epidemiologists must have a glimpse at various relevant scientific fields and employ them to tackle the problems. In order to shape up such competence for the new generation epidemiologists, the educational institutes must critically review the training curricula.

Introduction

Interacting with the current coronavirus disease 2019 or COVID-19 has been continuingly giving us new lessons all the time. The highly contagious agent, SARS-CoV-2 virus keeps on spreading as well as evolving. Human beings, the target host, keep on gathering data, developing new technology and doing large-scale experiments. While the host cannot evolve quickly enough to escape the catastrophe, the complex immune system would have change susceptibility level to the infection.

Epidemiology is the frontier discipline to get information about the pandemic, gain insight in transmission patterns, identifying risk factors for infection, severe illness and death. Finally, the discipline evaluates all the measures to contain, control and get rid of the problems through vaccination, therapeutics and non-pharmacologic interventions. In response to the unprecedented swiftly rising and large scale of damage to the global population, we need a larger number and better (new) quality of epidemiologists to tackle the problems.

Rapidity of the Spreading

The frightening characteristics of COVID-19 include its highly effective air-borne-cum-droplet transmission, and high case-fatality rate. It also has short latency period of only a few days.[1] With current rate of transportation, the disease has become pandemic in a short period and started killing all walks of lives just a few weeks after. Learning from SARS outbreak, the only effective main measure in the early phase was social distancing, or 'lockdown' on a larger scale. This solution has however disrupted the global economy and livelihood. The rapid increase of burden has also paralyzed health services in many countries, causing massive excess deaths among those who were sick from non-COVID diseases. SARS-CoV-2 is extra virulence for the elderly and those with chronic non-communicable diseases. The pandemic thus seems to target the global weaknesses resulted from demographic and epidemiological transition.

HIV/AIDS–the Unnoticed and Unfinished Pandemic

HIV is another on-going pandemic. It has been indirectly de-emphasized by the emergence of COVID-19. HIV has been less alarming because of the fact that its transmission is not airborne, which is somewhat avoidable by the upper class. However, the incubation period of HIV is much longer making it impossible for the transmission to be controlled by quarantine or isolation. For the past four decades, HIV/AIDS has killed over 36 million people (nearly seven times of that from COVID-19). A slightly higher number of people (37.7 million) are living with HIV.[2] The damage from HIV is longer lasting than that from COVID-19, which has killed five some million.[3] Another worse part of HIV/AIDS is that there has no effective vaccine and therapeutic cure is still limited.

Opportunity for Improvement of Prevention and Control Measures

Sciences and technology in the COVID-19 period have been developed very far from that in 1918, the period of the Spanish flu. From the turning of this century, bio-technology on '-omics', such as genomics, transcriptomics, microbiomics has made advancement in an exponential speed. During the SARS (much smaller) pandemic in 2002, it took weeks for scientists to identify the causative agent and months to get the coronavirus genetic sequence. For the COVID-19, it took only a few days to get the whole genetic sequence of this SARS-CoV-2 openly published.[4] Within a few days after, the diagnostic tests were developed. Having the proper diagnostic tools has helped the health system to identify and stop the infected persons who, otherwise, would be spreading the disease.

Knowledge on genetic sequence also led to quick designs on nucleic acid vaccine, which was later shown to be effective within around one year after the first case was diagnosed.

The other promising technology that helps contact tracing, a routine epidemiological work, is the advanced data science. A number of East Asian countries such as South Korea, Singapore, Taiwan of China have employed this technology to trace and track suspects who were potentially infected.[5-7] This linked with notification to the person and the systems, which could stop further disease spread. However, the evolution of the coronavirus is smarter than the development of this technology. The new variant (delta) spread too fast for the intelligent system to stop them. Detection of the cases was always some steps behind the successful spread of infection, especially among the majority asymptomatic and pre-symptomatic persons.

What have We Learned from COVID-19 Pandemic regarding Human Resources for Disease Control

This pandemic has been telling us that we need multi-disciplines to help tackling the problems. To coordinate the team, epidemiologists, the core members of the control team, must be equipped with broader knowledge than before. They must have some good ideas about how the experts in other disciplines can contribute in the disease control. While people from other disciplines must get acquainted with epidemiological concepts and jargons, the epidemiologists must reciprocally counter-learn from them.

Revision of Existing Curriculum and Designing a Refresher Course

COVID-19 pandemic has taught us a lot of lessons. When the level of burden has decreased to some extent, we need a mindful retreat to reflect what we have learned and how we should go further. This will help us to handle the current and the future pandemic more properly.

Based on the results of the retreat to come, a training program or a training institution should do at least two related things: revision of the training course for the trainees and create a refresher course for the practitioner of epidemiology. One of them is Data Sciences.

Suggested Contents on Data Sciences to be Included

Data Sciences is a part of computational sciences, which make use of robust quantitative reasoning, analysis and development. It grows steadily both in theory and in technological development. Many theories are testable only when suitable Big Data and computing power are available.

In the past, field epidemiological data are mainly from a survey or an outbreak investigation. Currently, epidemiological data are routinely generated by registration and follow up of the mass population under the control measures. As mentioned above, contact tracing can be enhanced by the information technology that can trace and track individuals' activities. In Thailand, in the active vaccination period, there are at least one hundred thousand vaccinations entered into the vaccination data set per day. The same individuals need to be re-immunized or booster with the same or different kinds of vaccines. They need to be followed up and linked to the registry of case records to evaluate vaccine protective effectiveness.

Epidemiologists who are involved with these data, which are just small examples, are playing the role of data stewards. Their duties include to ensure that the data are properly designed and collected in an analyzable fashion. Then, another or the same group of epidemiologists must be involved in data analytics. Epidemiological researchers should direct the objectives of the analysis, interpret the results and present and discuss with the policy makers. On the way, they should grasp the principle of data visualization, which is important in design of dashboard to the policy makers and people to follow up the situation of the subgroups of interest. Basic epidemiological training that they already have, should enable them to be aware of the limitation of the results either from bias or confounding and etc.

Modern epidemiologist should also have a glimpse at the other fashionable part of data sciences such as the '-omics', machine learning and artificial intelligence. Unlike the above mentioned parts on epidemiological Big Data, it is not essential to dip most of the new batch of epidemiologists profoundly into these trendy subsets of data sciences. It is however essential to know when to employ these technologies under what conditions.

Conclusion

COVID-19 has taught us a lot of lessons. The way to learn the lessons together is to have a retreat at a proper point of time. New generations of epidemiologists need novel ideas and state-of-the art sciences and technology to support their work to tackle new problems. This must be organized by the training institutions.

Suggested Citation

Chongsuvivatwong V. Epidemiological workforce for current and future pandemic control. OSIR. 2021 Dec;14(4):149–51.

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