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Western Pacific Surveillance and Response

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COVID-19 and *Mycobacterium* coinfection in Brunei Darussalam: case series

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Coronavirus disease (COVID-19) and tuberculosis (TB) coinfection is expected to become more common in countries where TB is endemic, and coinfection has been reported to be associated with less favourable outcomes. Knowing about the manifestations and outcomes of coinfection is important as COVID-19 becomes endemic. During the second wave of the COVID-19 pandemic in Brunei Darussalam, we encountered seven patients with COVID-19 and *Mycobacterium* coinfection. Cases of coinfection included three patients with newly diagnosed pulmonary *Mycobacterium* infection (two cases of pulmonary TB [PTB] and one case of *Mycobacterium fortuitum* infection) and four patients who were already being treated for TB (three cases of PTB and one case of TB lymphadenitis). Among the new cases, one had previously tested negative for PTB during a pre-employment medical fitness evaluation and had defaulted from follow up and evaluation. One case died: a 42-year-old man with diabetes mellitus, chronic kidney disease and hypertension who had severe COVID-19 and needed urgent dialysis and supplemental oxygen. All other patients recovered from COVID-19 and completed their TB treatment.

Coinfection with severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) and other respiratory pathogens is not uncommon and has been reported to be associated with less favourable outcomes.[1] As a consequence of disruptions to health-care services due to the coronavirus disease (COVID-19) pandemic, there have been delays in patients presenting and being diagnosed with pulmonary tuberculosis (PTB) in areas where tuberculosis (TB) is endemic.[2,3] Diagnoses of TB infection declined in 2020, ranging from 16% to 41% reduction in the nine countries with the most TB cases documented previously.[3] Therefore, coinfections with COVID-19 and TB are expected, and patients with coinfection have been shown to do less favourably, including patients who have already recovered from PTB.[4,5] COVID-19 infection can also increase the risk of progression to TB disease or reactivation of previous TB, either due to the immunosuppressive effects of COVID-19 or from treatment, such as the use of steroids.[6,7] Therefore, timely diagnosis of TB and COVID-19 coinfection in TB-endemic countries is important.

Brunei Darussalam is a TB-endemic country and TB remains a public health problem despite rates declining from 106/100 000 population in 2000 to 64/100 000 in 2019. The rate increased in 2020 to 82/100 000 despite the disruption to health-care services caused by the COVID-19 pandemic. The rate dropped to a pre-pandemic level of 61/100 000 in 2021,[8] which was likely related to some services returning to normal. The COVID-19 outbreak in Brunei Darussalam started on 9 March 2020, and by 5 November 2021, the number of COVID-19 cases recorded was 13 673.[9] We report our experience with patients who were coinfected with COVID-19 and *Mycobacterium* during the second wave of COVID-19 that started on 7 August 2021.

CASE SERIES

COVID-19 and *Mycobacterium* coinfection

Of the 1490 adult patients admitted to the National Isolation Centre for COVID-19 infection between 7 August and 6 November 2021, during the second

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wave, seven were coinfected with TB, giving a coinfection rate of 4.7%. These included three new cases of *Mycobacterium* infection: two were diagnosed with PTB and COVID-19 coinfection, and one tested negative by sputum smear during admission but was later confirmed by culture to be infected with *Mycobacterium fortuitum*. The other four patients were already being treated for TB when they became infected with COVID-19: three had PTB and one had TB lymphadenitis (**Table 1**). The median age of patients with coinfection was 43.5 years (range: 15–71 years), with a male to female ratio of 4:3. Five patients had comorbidities: diabetes mellitus (n = 5), hypertension (n = 3), dyslipidaemia (n = 3), kidney disease (n = 2) and bladder cancer (n = 1). Four patients had not been vaccinated for COVID-19. Chest X-rays (CXRs) were abnormal in six patients. All patients tested negative for HIV.

Clinical information

New cases of pulmonary Mycobacterium *infection*

All three newly diagnosed cases with *Mycobacterium* infection had been vaccinated against COVID-19 (two doses) and were categorized as having moderate COVID-19 based on our criteria: mild – category 1 (asymptomatic) and category 2 (mild symptoms of COVID-19); moderate – category 3 (abnormal CXR); severe or critical – category 4 (needed supplemental oxygen) and category 5 (needed mechanical ventilation with or without other organ failure).[10]

Case 1 was a 53-year-old female with diabetes mellitus, chronic kidney disease, hypertension, dyslipidaemia and obesity who presented with chronic cough, weight loss, fever, rhinorrhoea, anorexia and dyspnoea on exertion. The admission CXR showed right upper lobe opacities (**Fig. 1a**). Sputum smear testing was negative for acid fast bacilli (AFB) but the Hain GenoType Line Probe assay (Hain Lifescience, Germany) was positive for *Mycobacterium tuberculosis*, which was confirmed by culture. This patient was treated with specific COVID-19 antibodies (casirivimab and imdevimab; Roche Pharmaceutical, Switzerland) and was also started on standard anti-TB treatment (2 months of rifampicin, isoniazid, ethambutol and pyrazinamide followed by 4 months of rifampicin and isoniazid). She reported no contact with anyone who had PTB, but she was positive for contact with COVID-19. She was categorized as having moderate COVID-19.

Case 2 was a 45-year-old male expatriate worker from India who initially presented to another hospital with mild cough and abnormal CXR (**Fig. 1b**). He tested positive for COVID-19 and was transferred to the National Isolation Centre for treatment. He did not report haemoptysis, fever or weight loss and denied any history of PTB. He was also newly diagnosed with diabetes mellitus. Interestingly, a CXR done 7 months previously during a pre-employment medical fitness check was abnormal (showing a left lung nodule). Sputum smear and culture for PTB at that time were negative. He defaulted from follow up and did not have further evaluation. During the present hospitalization, sputum smear tests were positive for PTB. On repeated inquiry, it was revealed that he had been previously treated for PTB in India 2 years earlier. He was treated as a recurrent case of PTB with standard treatment. He reported no positive contact for COVID-19. He was categorized as having moderate COVID-19.

Case 3 was a 31-year-old male without any comorbidities who presented with sore throat, new onset cough and diarrhoea. CXR showed left-medial upper zone opacity (**Fig. 1c**). Sputum smear for AFB and line probe assay were both negative. His symptoms resolved and he was discharged. Follow-up review revealed that the sputum culture was positive for *M. fortuitum*, and he was started on treatment as a case of infection with nontuberculous mycobacteria (NTM), as per our guidelines. This patient had no risk factors for NTM but had a positive contact for COVID-19. He was categorized as having moderate COVID-19.

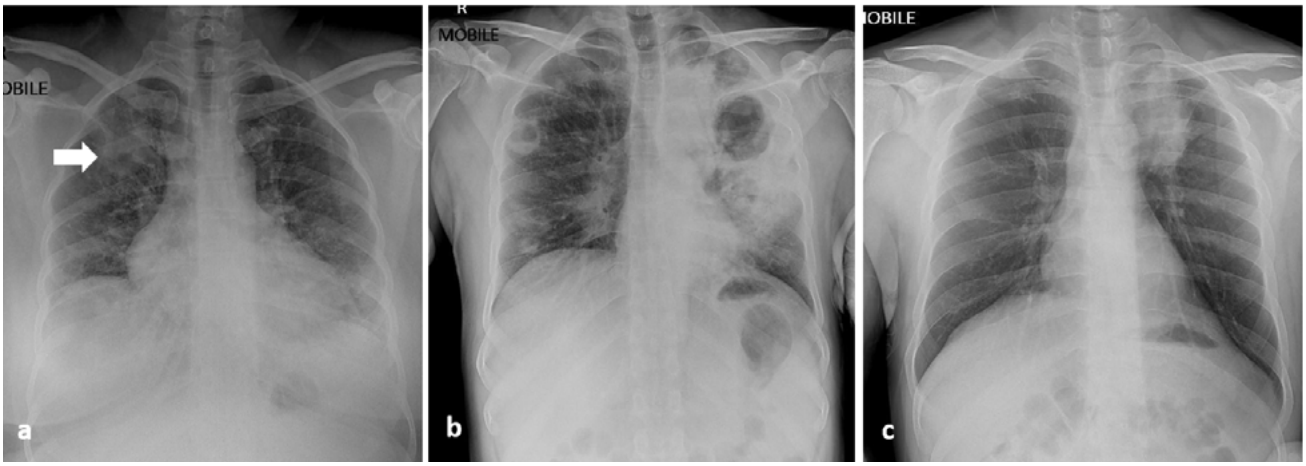
All three cases were discharged after testing negative for SARS-CoV-2 by polymerase chain reaction (PCR), after 5 to 11 days of hospitalization.

Cases with Mycobacterium *infection already being treated*

Four patients were undergoing treatment for TB infection when they became infected with SARS-CoV-2. Three were adults with PTB (cases 4–6) and one (case 7) was an adolescent with TB lymphadenitis. All patients continued their anti-TB treatment and sputum smear testing during hospitalization until sputum smear tests were negative for AFB.

Case 4 was a 50-year-old female with diabetes mellitus, hypertension and dyslipidaemia who was admitted to another hospital with cough, dyspnoea,

Fig. 1. **Admission chest X-ray for case 1 (a), case 2 (b) and case 3 (c)**



(a) Case 1 shows a soft shadowed mass (arrow) in the right upper lobe.

(b) Case 2 shows extensive consolidation of the left-upper and mid-zones, ill-defined ground glass opacities in the periphery of the right-upper, mid- and lower zones, and cavities in both upper zones and right lower zones, the largest one measuring about 5 cm in the left-upper zone.

(c) Case 3 shows a left-medial upper lung opacity.

lethargy and reduced appetite. She was transferred to the National Isolation Centre when she tested positive for SARS-CoV-2. Her risk factor for COVID-19 was a positive contact in the ward at the previous hospital. Her CXR was abnormal, but she did not require supplemental oxygen. She did not require any specific treatment for COVID-19. She was categorized as having moderate COVID-19.

Case 5 was a 42-year-old male with diabetes mellitus, hypertension, dyslipidaemia and predialysis chronic kidney disease who presented with cough and dyspnoea. His CXR was abnormal, showing consolidation in the right-middle and lower zones. He was started on high-flow nasal oxygen and commenced dialysis. He was categorized as having severe COVID-19. However, treatment for COVID-19 was contraindicated due to his end-stage kidney disease, so it was not started. His condition was stable, but he had a sudden cardiac arrest and died 4 days after hospitalization.

Case 6 was a 71-year-old male with diabetes mellitus and stage 4 urinary bladder cancer who was admitted with exertional dyspnoea and cough. His CXR was abnormal. He was started on supplemental oxygen, low-molecular-weight heparin and dexamethasone. He was also treated with a course of antibiotics for secondary pulmonary coinfection with *Klebsiella pneumoniae*. He was categorized as having severe COVID-19. His condition improved with treatment.

Case 7 was a 15-year-old female who was being treated for lymphadenitis of the neck. She was admitted with cough, dyspnoea and chest pain. Her CXR was normal. *Pseudomonas aeruginosa* was isolated from her sputum. Because she was improving, no treatment was initiated. She was categorized as having mild COVID-19.

All surviving cases were discharged after testing negative for SARS-CoV-2 on PCR, after 12 to 23 days of hospitalization.

Outcomes and follow up

The length of hospitalization for all seven cases ranged from 4 to 23 days (median: 11). There was one death (case 5) due to severe COVID-19 and significant comorbidities, giving a mortality rate for COVID-19 and *Mycobacterium* coinfection of 14.3%. All other patients recovered from their COVID-19 infection and completed their TB treatment. However, case 6 died from advanced cancer of the bladder 271 days after recovering from COVID-19.

DISCUSSION

COVID-19 is a highly infectious disease and it is not surprising that patients with other infections become infected with it. One systematic review and meta-analysis reported a high prevalence of coinfection among

Table 1. **Details of patients coinfected with coronavirus disease (COVID-19) and *Mycobacterium* species, Brunei Darussalam, 7 August to 6 November 2022**

Case no.	Nationality	Sex/age (years)	Medical history	Chest X-ray	Tuberculosis				COVID-19					Other coinfection	Length of stay (days)	Outcome of co-infection
					TB status	Risk	Sputum smear for AFB during hospitalization	Culture for AFB	Vaccination status	Risk	Ctv at diagnosis	Disease severity[a]	Treatment			
1	Bruneian	F/53	DM, CKD, HT, DLD, obesity	Abnormal	New PTB	None	3 negative smears; positive on line probe assay	*M. tuberculosis*	Complete	Positive contact (son)	12.7	Moderate	Casirivimab and imdevimab	None	10	Alive
2	Indian	M/45	Newly diagnosed DM	Extensive consolidations and cavities	New PTB	Treated for PTB 2 years previously	Positive	*M. tuberculosis*	Complete	None	23.6	Moderate	None	None	11	Alive
3	Bruneian	M/31	None	Abnormal	New NTM	None	Negative	*M. fortuitum*	Complete	Positive contact (brother-in-law)	37.1	Moderate	None	None	5	Alive
4	Bruneian	F/50	DM, HT, DLD	Fibrosis and cavities; diffuse ground glass opacities in all zones	PTB and already on treatment	Mother >30 years ago	3 negative smears	*M. tuberculosis*	Unvaccinated	Positive contact (hospitalization)	17.3	Moderate	None	None	12	Alive
5	Bruneian	M/42	DM, HT, DLD, pre-ESRD	Right-middle and lower zone consolidation	PTB and already on treatment	None	2 negative smears	*M. tuberculosis*	Unvaccinated	Positive contact (hospitalization)	16.8	Severe	None; contraindicated by pre-ESRD	None	4	Started on haemodialysis; died of comorbidities and COVID-19
6	Bruneian	M/71	DM, stage 4 bladder cancer	Right apical fibrosis; left lower zone opacities	PTB and already on treatment	Relapse	3 negative smears	*M. tuberculosis*	Unvaccinated	Positive contact (family members)	13.5	Severe	Fondaparinux and dexamethasone	Secondary *Klebsiella pneumoniae* identified in sputum; chest infection was treated	23	Alive
7	Bruneian	F/15	None	Normal	EPTB and already on treatment	Grandfather and father	3 negative smears	*M. tuberculosis*	Ineligible	Positive contact (family member)	19.0	Mild	None	*Pseudomonas aeruginosa* (sputum): not treated	15	Alive

AFB: acid-fast bacilli; CKD: chronic kidney disease; Ctv: cycle threshold value; DLD: dyslipidaemia; DM: diabetes mellitus; EPTB: extrapulmonary tuberculosis; ESRD: end-stage renal disease; F: female; HT: hypertension; M: male; NTM: non-tuberculous mycobacteria; TB: tuberculosis.

[a] Disease severity was categorized as mild – category 1 (asymptomatic) and category 2 (mild symptoms of COVID-19); moderate – category 3 (abnormal CXR); and severe or critical – category 4 (needed supplemental oxygen) and category 5 (needed mechanical ventilation with or without other organ failure).

COVID-19 patients, with the most common coinfection being bacterial (pooled prevalence: 20.9%), followed by fungal (12.6%) and viral (12.6%).[11] The most common bacterial coinfections reported were primary or secondary bloodstream infections or lower respiratory tract infections.[12] COVID-19 and TB coinfection has been less commonly reported, and when reported it has been mainly as case reports or small case series. A systematic review of studies looking at COVID-19 and TB coinfection up to February 2021 identified 11 case series and 20 case reports with a total 146 patients, most from China and India, two of the most populous nations where TB remains endemic.[13] During the second wave of COVID-19 in Brunei Darussalam, we encountered seven cases of coinfection with COVID-19 and Mycobacterium, giving a coinfection rate of 4.7%.

Among our patients with coinfection, three had recently detected pulmonary mycobacteria infections, two had PTB and one had pulmonary *M. fortuitum*. All new cases had changes on CXR reflecting coinfection with pulmonary *Mycobacterium* and COVID-19. The categorization of COVID-19 as moderate for these three patients was based on their CXR changes. If CXR had not been part of routine assessment, these diagnoses of pulmonary *Mycobacterium* would have been missed. Fortunately, our management protocol required selective follow up of patients with unresolved issues or pending investigations, and this prevented us from missing the case of NTM infection. Of major concern was that one patient (case 2), an expatriate labourer, had tested negative for PTB 7 months before his admission with COVID-19. Given his CXR findings, it is quite certain he already had active PTB at that time. Unfortunately, he defaulted from his scheduled follow-up appointment and did not have any further evaluation. If he had not been evaluated during his most recent admission, the diagnosis of PTB would have been missed again, posing a risk for continued community spread.

Hospitalizations were uncomplicated and all patients were discharged within 5 to 11 days, except for case 5 who died of comorbidities 4 days after admission. Importantly, all had received two doses of COVID-19 vaccine, and this may have mitigated the impact of COVID-19.

For cases known to have PTB and already on treatment, excluding the adolescent patient who was being treated for TB lymphadenitis (case 7), COVID-19 manifestations were more severe, with two cases needing supplemental oxygen. These three cases had pre-existing pulmonary damage from PTB in addition to other significant comorbidities. In addition to changes on CXR due to PTB, there were also changes due to COVID-19, such as ground glass opacities or consolidations. Severe manifestations are not unexpected in these patients, given their already compromised pulmonary function. Furthermore, none of the patients had been vaccinated for COVID-19. The adolescent patient being treated for TB lymphadenitis was not eligible for vaccination at that time because the COVID-19 vaccine had not yet been approved for people younger than 18 years. Patients in this group were hospitalized for longer compared with cases recently diagnosed with *Mycobacterium* infection.

There was one death in our series, giving a mortality rate of 14.3%, comparable to the 13.0% reported by Koupaei et al., and compared with the 6.6% rate of deaths from COVID-19 without coinfection.[13] A meta-analysis reported increased disease severity and mortality among those with coinfections compared with those without TB coinfection.[14] A study from the United States of America reported higher mortality among cases with TB–COVID-19 coinfection: it was two times higher compared with persons with TB before the pandemic and 20 times higher compared with persons with COVID-19 alone.[15] This may be due to the synergistic effects of coinfections and also because patients with PTB may have damaged lungs. Furthermore, COVID-19 can progress rapidly, leading to fulminant lung damage. Therefore, early diagnosis is important, especially now that treatment for SARS-CoV-2 is available.

As the pandemic continues, and even long after the pandemic is declared over, COVID-19 will persist as an endemic illness and eventually circulate as a common respiratory viral infection. The risk of coinfections occurring with COVID-19 will persist, especially for patients with chronic diseases such as PTB. Despite our findings of only a 4.7% coinfection rate, we continue to follow our protocol to screen

all PTB patients for COVID-19 and vice versa if the COVID-19 patients exhibit features on imaging or clinical features of TB, especially because treatments are available.

The main limitation of our study is the small sample size: we had only seven patients with coinfection, including a patient with NTM infection with *M. fortuitum*. However, as a result of the management strategy in the country, all patients with COVID-19 and *Mycobacterium* coinfection were isolated and treated during the study period. Therefore, our results are representative of the whole country.

CONCLUSIONS

Our case series showed that COVID-19 and *Mycobacterium* coinfection is uncommon, with only 4.7% of patients admitted during the second wave of the COVID-19 pandemic in Brunei Darussalam being affected. It is important to be aware that new cases of pulmonary *Mycobacterium* infection may present with COVID-19 as a coinfection, and similarities in clinical manifestations may result in missed diagnoses. Similarly, patients being treated for TB are susceptible to COVID-19. Almost all of our patients had moderate to severe COVID-19 disease and, fortunately, most recovered with or without specific COVID-19 treatment. There was one death (mortality rate: 14.3%) in a patient with significant comorbidities. Even though COVID-19 and TB coinfections were uncommon, we will continue to follow our protocol to screen for COVID-19 coinfection among patients admitted with PTB, either known or newly diagnosed. Similarly, we will also continue to screen for PTB in patients admitted for COVID-19 who exhibit features of PTB, especially if their CXR shows changes suggestive of PTB.

Conflicts of interest

The authors have no conflicts of interest to declare.

Ethics statement

This study was conducted in accordance with the Declaration of Helsinki.

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None.

References

1. Feldman C, Anderson R. The role of co-infections and secondary infections in patients with COVID-19. Pneumonia (Nathan). 2021;13(1):5. doi:10.1186/s41479-021-00083-w pmid:33894790
2. McQuaid CF, Henrion MYR, Burke RM, MacPherson P, Nzawa-Soko R, Horton KC. Inequalities in the impact of COVID-19-associated disruptions on tuberculosis diagnosis by age and sex in 45 high TB burden countries. BMC Med. 2022;20(1):432. doi:10.1186/s12916-022-02624-6 pmid:36372899
3. 12 months of COVID-19 eliminated 12 years of progress in the global fight against tuberculosis. Geneva: Stop TB Partnership; 2021. Available from: https://www.stoptb.org/file/9099/download, accessed 24 February 2022.
4. Song WM, Zhao JY, Zhang QY, Liu SQ, Zhu XH, An QQ, et al. COVID-19 and tuberculosis coinfection: an overview of case reports/case series and meta-analysis. Front Med (Lausanne). 2021;8:657006. doi:10.3389/fmed.2021.657006 pmid:34504847
5. Sy KTL, Haw NJL, Uy J. Previous and active tuberculosis increases risk of death and prolongs recovery in patients with COVID-19. Infect Dis (Lond). 2020;52(12):902–7. doi:10.1080/23744235.2020.1806353 pmid:32808838
6. Tian W, Zhang N, Jin R, Feng Y, Wang S, Gao S, et al. Immune suppression in the early stage of COVID-19 disease. Nat Commun. 2020;11(1):5859. doi:10.1038/s41467-020-19706-9 pmid:33203833
7. Chen F, Hao L, Zhu S, Yang X, Shi W, Zheng K, et al. Potential adverse effects of dexamethasone therapy on COVID-19 patients: review and recommendations. Infect Dis Ther. 2021;10(4):1907–31. doi:10.1007/s40121-021-00500-z pmid:34296386
8. Tuberculosis profile: Brunei Darussalam. Geneva: World Health Organization; 2021. Available from: https://worldhealthorg.shinyapps.io/tb_profiles/?_inputs_&entity_type=%22country%22&lan=%22EN%22&iso2=%22BN%22, accessed 15 April 2023.
9. 128 cases COVID-19 reported today, 5 November 2021: media statement on the current situation of COVID-19 in Brunei Darussalam [website]. Bandar Seri Begawan: Ministry of Health, Brunei Darussalam; 2021. Available from: https://www.moh.gov.bn/Lists/Latest%20news/NewDispForm.aspx?ID=1089&ContentTypeId=0x0104009A3003A09F8D6E42981D262E322516A2, accessed 15 April 2023.
10. Rahman NA, Abdullah MS, Asli R, Chong PL, Mani BI, Chong VH. Challenges during the second wave of COVID-19 in Brunei Darussalam: National Isolation Centre to National COVID-19 Hospital. Western Pac Surveill Response J. 2022;13(3):1–7. doi:10.5365/wpsar.2022.13.3.913 pmid:36688181
11. Pakzad R, Malekifar P, Shateri Z, Zandi M, Akhavan Rezayat S, Soleymani M, et al. Worldwide prevalence of microbial agents' coinfection among COVID-19 patients: a comprehensive updated systematic review and meta-analysis. J Clin Lab Anal. 2022;36(1):e24151. doi:10.1002/jcla.24151 pmid:34851526

12. Ripa M, Galli L, Poli A, Oltolini C, Spagnuolo V, Mastrangelo A, et al. Secondary infections in patients hospitalized with COVID-19: incidence and predictive factors. Clin Microbiol Infect. 2021;27(3):451–7. doi:10.1016/j.cmi.2020.10.021 pmid:33223114

13. Koupaei M, Naimi A, Moafi N, Mohammadi P, Tabatabaei FS, Ghazizadeh S, et al. Clinical characteristics, diagnosis, treatment, and mortality rate of TB/COVID-19 coinfected patients: a systematic review. Front Med (Lausanne). 2021;8:740593. doi:10.3389/fmed.2021.740593 pmid:34926494

14. Nabity SA, Han E, Lowenthal P, Henry H, Okoye N, Chakrabarty M, et al. Sociodemographic characteristics, comorbidities, and mortality among persons diagnosed with tuberculosis and COVID-19 in close succession in California, 2020. JAMA Netw Open. 2021;4(12):e2136853. doi:10.1001/jamanetworkopen.2021.36853 pmid:34860244

15. Wang Y, Feng R, Xu J, Hou H, Feng H, Yang H. An updated meta-analysis on the association between tuberculosis and COVID-19 severity and mortality. J Med Virol. 2021;93(10):5682–6. doi:10.1002/jmv.27119 pmid:34061374

Creating "boots on the ground": addressing the shortage of field epidemiologists in the Philippines through intermediate-level training programmes

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Problem: As of 2022, only 49 graduates of the Philippines' Field Epidemiology Training Programme (FETP) were employed by the Philippine Government, emphasizing the urgent need to increase the number of practicing field epidemiologists to better equip the country for public health emergencies.

Context: The FETP–Intermediate Course (IC) curriculum is based mainly on the module of the United States Centers for Disease Control and Prevention that was incorporated into the Philippine context. It consists of five 1–2-week lecture series that provide participants with the knowledge and tools necessary to conduct job-relevant field projects. Individual projects are the centrepiece of the FETP–IC, requiring trainees to investigate outbreaks, design and develop protocols, conduct field data collection, manage data, analyse data, interpret data, write reports and deliver oral presentations.

Action: To address the shortage of practicing field epidemiologists in the Philippines, a subnational initiative in Northern Luzon was implemented.

Outcome: Within 3 years, the two FETP–IC subnational training programmes have produced 42 applied epidemiologists who will strengthen epidemiology and surveillance in their respective localities. As of February 2023, 92 studies have been conducted, including 39 outbreak investigations, 37 data quality analysis/process improvement projects, 10 epidemiological studies and six surveillance evaluations.

Discussion: By training and deploying skilled epidemiologists to local health offices and hospitals, the programme is helping to improve the capacity of the health system to respond to public health threats and protect the health of the population. The programme's emphasis on practical training and real-world experience is an effective way to build a strong and sustainable epidemiological workforce.

PROBLEM

The Philippines' 2-year Field Epidemiology Training Programme (FETP) was established in 1987 to train professional epidemiologists and develop a self-sustaining capacity for this training within the Department of Health (DOH). Over 35 years, the programme has produced 128 graduates (an average of three graduates per year). However, due to various circumstances, such as retirement, death and transfer to other positions, only 49 FETP graduates are currently employed in government service in the field of epidemiology. Among these, the distribution of epidemiologists is uneven, with only 22 graduates employed in local government units, 11 in the DOH Center for Health Development (CHD), seven in the DOH's Central Office and Epidemiology Bureau, and six in hospitals, while the remaining three are employed in other government agencies. Moreover, the median age of practicing field epidemiologists in the country is 52, with 17 expected to retire in the next 5 years.

In a 2017 assessment carried out by the Training Program in Epidemiology and Public Health Interventions Network (TEPHINET), evaluators identified the need to expand the programme. The Joint External Evaluation of the implementation of the International Health Regulations (IHR 2005) in the Philippines in 2018 also recommended articulating three levels of FETP and

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ensuring adequate numbers are trained and available at the local, regional and national levels. Therefore, there was an urgent need to take proactive steps to increase the number of practicing field epidemiologists in the Philippines to ensure that the country is better equipped to handle public health emergencies in the future.

CONTEXT

The FETP is a specialized training programme aimed at enhancing the skills of public health professionals, specifically epidemiologists, to respond effectively to public health threats. The programme offers hands-on training in applied epidemiology, outbreak investigation, surveillance and programme evaluation. Originally established in 1975 by the United States Centers for Disease Control and Prevention (CDC), the FETP has been adopted by many countries worldwide, including the Philippines, to develop a cadre of field epidemiologists who serve as a key component of the country's public health system.[1] The FETP has been credited with facilitating early detection and response to outbreaks of infectious and noncommunicable diseases such as Ebola, SARS and COVID-19.

Globally, the FETP has evolved into a tiered programme, with an intermediate level added between the front-line and advanced levels, providing more structured career progression for field epidemiologists.[2] The intermediate level offers specialized training in topics such as outbreak investigation, data management and surveillance system design, building upon the core competencies learned at the front-line level.

A subnational initiative was implemented in Northern Luzon (**Fig. 1**) to address the shortage of practicing field epidemiologists. The Joint External Evaluation of IHR (2005) set the standard of one field epidemiologist per 200 000 population,[3] which the Philippines has not met.

The FETP in the Philippines is hosted by the DOH CHD with support from partners such as the DOH Epidemiology Bureau, the World Health Organization, the Field Epidemiology Training Program Alumni Foundation, Inc. (FETPAFI) and the South Asia Field Epidemiology and Technology Network (SAFETYNET).

ACTION

The FETP–Intermediate Course (IC) aims to:

1. enhance the competencies of public health workers in data collection, analysis, interpretation and communication to support effective decision-making;
2. build the capacity at the subnational level to respond to outbreaks and other public health threats; and
3. foster a network of skilled field epidemiologists with a shared sense of purpose, working to common standards.

Curriculum and competency domain

The FETP–IC curriculum is a 9-month modular training course that is based mainly on the CDC module and has been adapted to the Philippine context. It consists of five 1–2-week lecture series that provide participants with the knowledge and tools necessary to conduct job-relevant field projects. Individual projects are the centrepiece of the FETP–IC, requiring trainees to design and develop protocols, conduct field data collection, manage data, analyse data, interpret data, write reports and deliver oral presentations. Other on-the-job field projects include summarizing surveillance data, evaluating and making recommendations to improve a surveillance system, and investigating outbreaks. The field intervals between lecture series are 5–6 weeks, and participants are expected to complete field assignments while performing their usual job responsibilities.

Upon completion of the programme, participants should be able to summarize, identify and describe trends and patterns; interpret data from a surveillance system; conduct an outbreak investigation using descriptive epidemiology; design, conduct, analyse and interpret data from a descriptive epidemiological study; produce epidemiological reports; write an abstract; and deliver an oral presentation.

Recruitment

Once the decision was taken to implement the FETP–IC, the recruitment and selection of trainees commenced.

Fig. 1. **Map indicating Northern Luzon provinces, Philippines**

The first step involved interested applicants and local government units submitting a letter of intent to participate in the programme. After receiving the letters, the second step was a panel interview. The panellists were selected from FETP–Advance Course graduates, ensuring that the interviewers had the necessary experience and knowledge to determine the best candidates for the programme. A structured rating tool was used to maintain fairness and objectivity. Selection criteria were adapted from FETP Philippines to guide the panellists' decision-making process.

The programme emphasizes the importance of teamwork among trainees, and participants are required to sign contracts with their local government units and the DOH to serve as epidemiologists after completing the programme.

Master Trainer and mentors

In the programme, each cohort is assigned a Master Trainer, an experienced professional who has completed the FETP-Advance Course and is responsible for overseeing the progress of the trainees in their cohort. The Master Trainer provides guidance, feedback and support to the trainees throughout the duration of the programme.

In addition to the Master Trainer, coaching and mentoring are provided to the trainees by FETP graduates. These mentors are professionals who have successfully completed the FETP and have been trained to provide support and guidance to new trainees. Each mentor is responsible for supporting and coaching two trainees.

Through this coaching and mentoring system, the trainees receive personalized support and guidance as they go through the programme. The mentors provide feedback on the trainees' performance, help them identify areas for improvement and provide guidance on how to address challenges that may arise during the programme. This system ensures that the trainees receive the necessary support and guidance to succeed in the programme and develop the skills needed to become effective epidemiologists.

Training coordinator and staff

A dedicated training coordinator and training staff are responsible for ensuring the effective implementation of the training programme. They play a critical role in managing the logistics and administrative tasks associated with the programme, such as scheduling and organizing training sessions, coordinating with trainers and mentors, preparing training materials and tracking trainee progress.

Sustainability

The programme's graduates are awarded the title of Certified Applied Epidemiologist (CAE) through a CHD Regional Order, and the lecture series has been accredited by the Philippine Professional Regulation Commission, providing a maximum of 135 continuing professional development units. Moreover, a memorandum of agreement has been signed between the graduates' hospital or local government unit and the CHD, signifying their commitment to collaborate continuously in enhancing epidemiology and surveillance in their respective areas.

OUTCOME

Establishment

In 2021, the DOH CHD of Cagayan Valley launched the first FETP–IC in the country, with 12 graduates deployed in the regional and local health offices of Cagayan Valley. In 2022, the CHD conducted their second batch with 12 trainees who graduated in March 2023.

On 16 May 2022, the DOH CHD of Cordillera Administrative Region, in partnership with Region I, launched the FETP–IC Northern Luzon Cluster with 18 trainees. This group comprised six trainees from the CHD, six from the provincial health offices, six from the municipal and city health offices, and two from hospitals.

The training team consisted of FETP–Advance Course graduates in partnership with SAFETYNET and FETPAFI.

Accomplishments

Within 3 years, the two FETP–IC subnational training programmes produced 42 applied epidemiologists. As of February 2023, 92 studies had been conducted by the FETP–IC trainees, including 39 outbreak investigations, 37 data quality analysis/process improvement projects, 10 epidemiological studies and six surveillance evaluations. One of these studies has been published,[4] while three more are undergoing the peer review process. Six papers were accepted for presentation at the Bi-regional TEPHINET Scientific Conference to be held in September 2023, and another was accepted for presentation at the European Scientific Conference on Applied Infectious Disease Epidemiology in November 2023.

Trainees also conducted 37 trainings with a total of 700 participants in basic epidemiology, data management and analysis, disease surveillance, and the establishment of epidemiology and surveillance units (**Table 1**).

Notable studies conducted by trainees

A 2022 outbreak investigation in the municipality of Buiguias, Mountain Province, Philippines, found that only 15 out of 220 suspected cases of typhoid fever reported to the surveillance system corresponded to the case definition used in this study, indicating that the majority of reported cases did not meet the case definition.[5] The study highlighted the importance of improved surveillance and response systems for infectious diseases, as well as the need for control and preventive measures, including safe water and food handling practices, to prevent the spread of the disease in the municipality.

A 2021 study in Isabela on the mental health status of health-care workers involved in the COVID-19 response found that they faced stigma related to COVID-19, which affected their psychological well-being (unpublished). Health-care workers have reported symptoms of depression, anxiety and insomnia. The study recommended that policies be implemented to support mental health programmes at all levels and that changes be instituted, especially at the facility level, to address the growing problem of mental illness among health-care workers.

A 2021 evaluation of the dengue surveillance system in Cagayan Valley Region identified several challenges in terms of data quality, timeliness and sensitivity (unpublished). The study found that data quality needed improvement at all levels, as did timeliness and sensitivity ratings. The majority of cases were identified in hospitals, with most being dengue with warning signs. Although the study focused on a specific region, the challenges highlighted are not unique to this area.

A 2022 case study from a regional hospital showed the significance of effective surveillance and reporting systems for timely and accurate health data (unpublished). Consequently, the hospital made changes to improve their reporting, such as by creating an automated weekly surveillance report and by training link nurses. In 2022, the hospital achieved 100% reporting through the weekly surveillance reports from morbidity weeks 24 to 52. They also created a monitoring sheet, provided a laptop for surveillance activities, and reorganized their Hospital Epidemiology and Surveillance Unit.

DISCUSSION

The FETP–IC in the Philippines is an important effort to improve the country's public health response capacity by building a skilled epidemiological workforce. The programme has produced 42 graduates from its first two subnational training programmes who will be deployed to strengthen epidemiology and surveillance in their respective localities.

Table 1. **Type and number of accomplishments of FETP–IC trainees, 2021–2023, Philippines**

Accomplishment	No.
Outbreak investigations	39
Data quality analysis/process improvement projects	37
Epidemiological studies	10
Surveillance system evaluations	6
Case investigations	4
Trainings conducted by trainees	37[a]

FETP–IC: Field Epidemiology Training Programme–Intermediate Course.

[a] Total of 700 participants.

Although not a formal evaluation of the FETP–IC, the outcomes reported in this study present convincing evidence of the immediate impact of the training. These outcomes demonstrate how the participants have used their newly acquired skills in data collection, analysis, interpretation and communication. Moreover, the training has aided effective decision-making at the subnational level, building the capacity to respond to outbreaks and address other public health hazards.

The programme's impact can be seen in the number and variety of studies conducted by the trainees, including outbreak investigations, data quality analysis and process improvement projects, epidemiological studies and surveillance evaluations. These studies have helped to identify and respond to public health threats and have contributed to a better understanding of disease patterns and risk factors in the country.

Overall, the FETP–IC is an important investment in the country's public health infrastructure.[6] By training and deploying skilled epidemiologists to local health offices and hospitals, the programme is helping to improve the capacity of the health system to respond to public health threats and protect the health of the population. The programme's emphasis on practical training and real-world experience, as evidenced by the variety of studies conducted by trainees, is an effective way to build a strong and sustainable epidemiological workforce.

Acknowledgements

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Conflicts of interest

The authors have no conflicts of interest to declare.

Ethics statement

This study did not use information from human or animal subjects, and the ethics of the study were taken into consideration. Consequently, ethics approval for this study was deemed unnecessary.

Funding

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References

1. White ME, McDonnell SM, Werker DH, Cardenas VM, Thacker SB. Partnerships in international applied epidemiology training and service, 1975-2001. Am J Epidemiol. 2001;154(11):993–9. doi:10.1093/aje/154.11.993 pmid:11724714
2. Traicoff DA, Walke HT, Jones DS, Gogstad EK, Imtiaz R, White ME. Replicating success: developing a standard FETP curriculum. Public Health Rep. 2008;123(Suppl 1) Suppl 1:28–34. doi:10.1177/00333549081230S109 pmid:18497016
3. Ijaz K, Kasowski E, Arthur RR, Angulo FJ, Dowell SF. International Health Regulations–what gets measured gets done. Emerg Infect Dis. 2012;18(7):1054–7. doi:10.3201/eid1807.120487 pmid:22709593
4. Victori EC, Ventura RJC, Blanco MZC, Pamintuan RP, Magpantay RL, Lonogan KB. School outbreak of hand, foot and mouth disease in Balungao, Pangasinan Province, Philippines, October 2022. Western Pac Surveill Response J. 2023;14(2):1–5. doi:10.5365/wpsar.2023.14.2.1001 pmid:37181824
5. Guzman JMC, Ventura RJC, Blanco MZC, Lonogan KB, Magpantay RL. Typhoid fever: the challenging diagnosis of a pseudo-outbreak in Benguet, Philippines. Western Pac Surveill Response J. 2023;14(4). [In press.] doi:10.5365/wpsar.2023.14.4.1047
6. Wilson K, Juya A, Abade A, Sembuche S, Leonard D, Harris J, et al. Evaluation of a new Field Epidemiology Training Program Intermediate Course to strengthen public health workforce capacity in Tanzania. Public Health Rep. 2021;136(5):575–83. doi:10.1177/0033354920974663 pmid:33541215

Circulation of influenza and other respiratory viruses during the COVID-19 pandemic in Australia and New Zealand, 2020–2021

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Objective: Circulation patterns of influenza and other respiratory viruses have been globally disrupted since the emergence of coronavirus disease (COVID-19) and the introduction of public health and social measures (PHSMs) aimed at reducing severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) transmission.

Methods: We reviewed respiratory virus laboratory data, Google mobility data and PHSMs in five geographically diverse regions in Australia and New Zealand. We also described respiratory virus activity from January 2017 to August 2021.

Results: We observed a change in the prevalence of circulating respiratory viruses following the emergence of SARS-CoV-2 in early 2020. Influenza activity levels were very low in all regions, lower than those recorded in 2017–2019, with less than 1% of laboratory samples testing positive for influenza virus. In contrast, rates of human rhinovirus infection were increased. Respiratory syncytial virus (RSV) activity was delayed; however, once it returned, most regions experienced activity levels well above those seen in 2017–2019. The timing of the resurgence in the circulation of both rhinovirus and RSV differed within and between the two countries.

Discussion: The findings of this study suggest that as domestic and international borders are opened up and other COVID-19 PHSMs are lifted, clinicians and public health professionals should be prepared for resurgences in influenza and other respiratory viruses. Recent patterns in RSV activity suggest that these resurgences in non-COVID-19 viruses have the potential to occur out of season and with increased impact.

The Australian and New Zealand governments' response to the coronavirus disease (COVID-19) pandemic has been described as "hard and fast", with the initial aim of elimination.[1] Both countries swiftly introduced a range of public health and social measures (PHSMs), such as physical distancing, mask use, school closures, border closures and travel restrictions. The stringency of these PHSMs fluctuated in both countries throughout 2020–2021, in response to local COVID-19 outbreaks. During this time, circulating patterns of influenza and other respiratory viruses changed dramatically.[2]

Respiratory viruses cause significant morbidity and mortality.[3,4] Influenza is known to cause severe illness in elderly adults,[3] while human parainfluenza virus types 1–3 (PIV-1–3) have the potential to cause severe disease in infants and children.[5] However, human

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PIV type 4 usually only causes mild or asymptomatic infections. Respiratory syncytial virus (RSV) and human metapneumovirus (hMPV) can cause severe disease in infants, children, elderly adults and immunocompromised patients.[6] Human rhinoviruses, one of the most commonly reported viruses in childcare centres where it is not uncommon for children to experience multiple infections in the same season, are almost invariably associated with mild disease.[7] Likewise, human adenoviruses usually only cause mild symptoms, but they have occasionally been associated with severe nosocomial outbreaks.[8]

In the temperate zones, most of these common respiratory viruses have tended to exhibit predictable seasonal patterns, with activity levels peaking in the winter months. Respiratory virus surveillance systems are designed to correspond to this seasonality and may be activated only during the winter months; however, most systems retain the capacity to be reactivated out of season in order to detect and monitor unexpected outbreaks.[2] The emergence of severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2), currently characterized as an endemic respiratory virus without a clearly defined seasonality, has highlighted the importance of having systems capable of detecting and monitoring any variations in seasonal respiratory virus activity in order to inform clinical management, public health planning and resource allocation. Here we describe respiratory virus activity from January 2020 to August 2021 in selected regions of Australia and New Zealand.

METHODS

Study populations

The study was conducted using data from five regions: New South Wales (NSW) and Western Australia (WA) in Australia; and Auckland, Canterbury and Wellington in New Zealand. These represent geographically diverse locations (**Fig. 1**) that experienced different levels of COVID-19 restrictions and SARS-CoV-2 activity.

Laboratory-based surveillance

Laboratory data routinely collected as part of regional public health surveillance were prospectively collated. Data were provided by (i) Centre for Infectious Diseases and Microbiology Laboratory Services, NSW Health Pathology-Institute of Clinical Pathology and Microbiology Research (ICPMR), Westmead, NSW; (ii) PathWest Laboratory Medicine, WA; (iii) Institute of Environmental Science and Research (ESR), Wellington, and Auckland and Counties Manukau District Health Boards, Auckland; and (iv) Canterbury Health Laboratories, Christchurch. Respiratory specimens underwent nucleic acid amplification testing (NAAT) using semi-quantitative real-time reverse transcription polymerase chain reaction (PCR) or transcription-mediated amplification testing. In addition, respiratory specimens underwent rapid PCR testing at Canterbury Health Laboratories for influenza and RSV, and rapid PCR testing for influenza at ESR.

ICPMR and PathWest laboratories are major diagnostic hubs that provide state-wide testing for respiratory viruses, in both hospitalized and community populations. ESR data included laboratory-based respiratory virus testing results from specimens ordered by clinicians for hospital inpatients and outpatients during normal clinical practice from two hospital laboratories in Auckland (LabPLUS and Counties Manukau District Health Board Lab). Data from ESR also included testing results (severe acute respiratory infection, influenza-like illness [ILI]) from its National Influenza Centre for public health surveillance and from Wellington-based community cohorts. Canterbury Health Laboratories is a reference laboratory that provides services to general practice surgeries and hospitals in the Canterbury District Health Board region. The proportion of positive tests (referred to as virus activity) was calculated and smoothed using a 3-week, centred moving average.

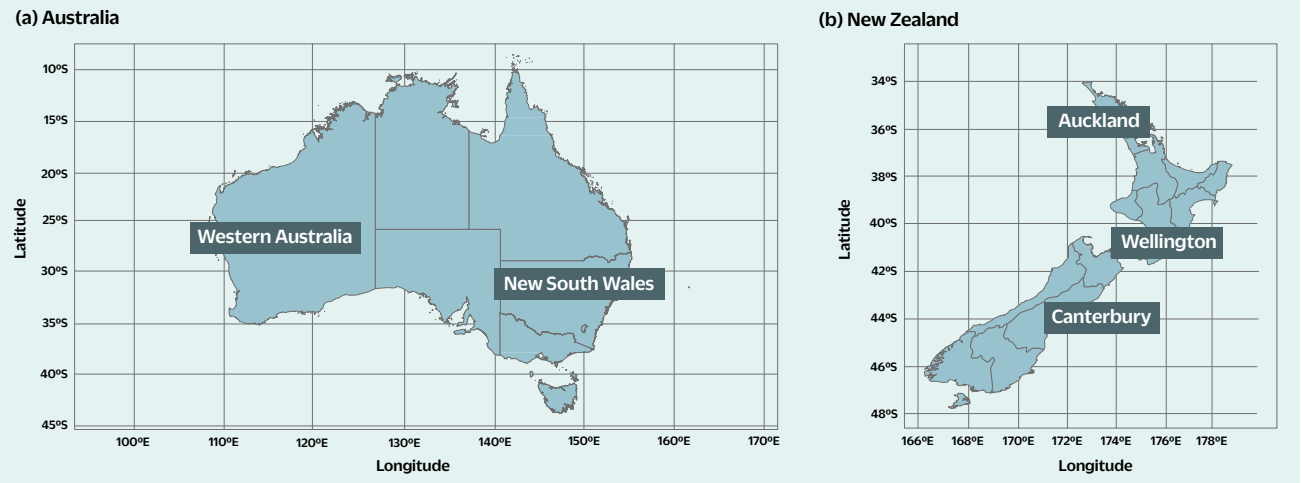
COVID-19 notification data

Australian and New Zealand COVID-19 notification data were sourced from Our World in Data (https://ourworldindata.org) on 7 March 2022.[9]

Public health and social measures

Different PHSMs were adopted by the five study regions (NSW, WA, Auckland, Canterbury and Wellington) (**Supplementary Table 1**). Moreover, the intensity of these measures changed throughout the study period.[10,11] Google mobility data sourced on 6 October 2021 were used as an indicator of compliance with PHSMs.[12] Using mapping apps, Google mobility data capture the daily movements of people with an Android device relative to a baseline period. Google provides these data in the form

Fig. 1. **Geographical representation of the five study regions in (a) Australia and (b) New Zealand**



of COVID-19 community mobility reports, expressed as a daily percentage change relative to a 5-week baseline period (3 January–6 February 2020) for six key mobility categories.[12] For each of the five regions, the daily average percentage change for three mobility categories (retail and recreation, transit stations, workplaces) was calculated. The other mobility categories (i.e. grocery and pharmacy, parks, residential) were excluded, as these activities were allowed even during periods of the most restrictive PHSMs in all regions and thus unlikely to reflect PHSM compliance. The proportion of change from baseline was smoothed using a 3-week, centred moving average, and plotted in a time series along with local PHSMs and respiratory virus activity.

Data were analysed using R version 4.0.4 (R Project for Statistical Computing).

RESULTS

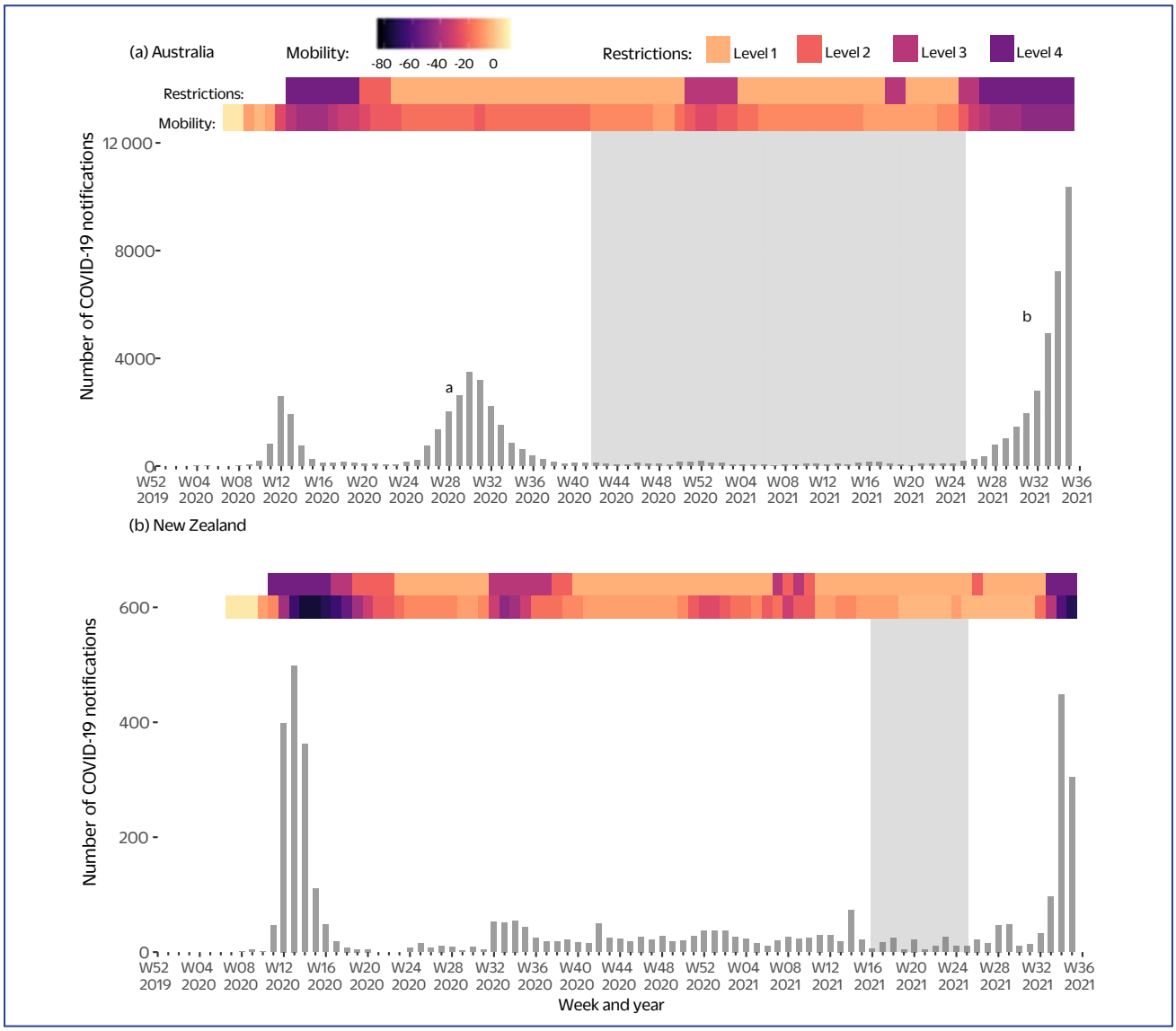
The amount of respiratory specimen testing for influenza and other respiratory viruses varied by region and year. In February 2020, both countries experienced their first wave of COVID-19 notifications (**Fig. 2**), and in response, respiratory virus testing (excluding COVID-19) in all regions increased (**Fig. 3**). By August 2021, the end of our study period, respiratory virus testing rates in all regions had not returned to their usual seasonal patterns.

In all regions, influenza was the most commonly detected respiratory virus in 2017–2019, followed by rhinoviruses and RSV. In contrast, between April 2020 and August 2021, the most commonly detected (non-COVID-19) respiratory viruses were rhinoviruses and RSV, followed by PIV-1–3 in all regions. All of these non-COVID-19 respiratory virus outbreaks occurred in the absence of any substantial SARS-CoV-2 circulation (**Fig. 2**).

Mobility data showed that mobility in all five regions dropped below baseline levels before or shortly after the introduction of COVID-19 restrictions. In NSW, restrictions were introduced on 18 March 2020 (week 11), with a reduction in mobility observed in week 11 (**Fig. 3**). In WA, restrictions were introduced on 23 March 2020 (week 12), with a reduction in mobility observed from week 10. In Auckland, Wellington and Canterbury, restrictions were introduced on 21 March 2020 (week 11), with a reduction in mobility observed in week 12 (**Fig. 3**, **Supplementary Table 1**).[11] The only region reporting mobility above baseline levels after the introduction of restrictions was Canterbury, which peaked at 2% above baseline in week 19, 2021 (**Fig. 3**).

Overall, mobility data showed an inverse relationship with restriction levels, with mobility decreasing as restrictions increased in all regions (**Fig. 3**). In all regions, outbreaks of rhinoviruses, RSV, PIV-1–3 and adenoviruses in 2020–2021 coincided with lower levels of restrictions and higher levels of population mobility (**Fig. 3**). In contrast, increases in hMPV activity were for the most part observed at a time when mobility levels were decreasing; the only exception was WA, where hMPV activity increased as mobility increased (**Fig. 3**).

Fig. 2. **New weekly COVID-19 notifications in (a) Australia and (b) New Zealand against mobility data and level of restrictions, 2020–2021 (up to week 36, 2021)**



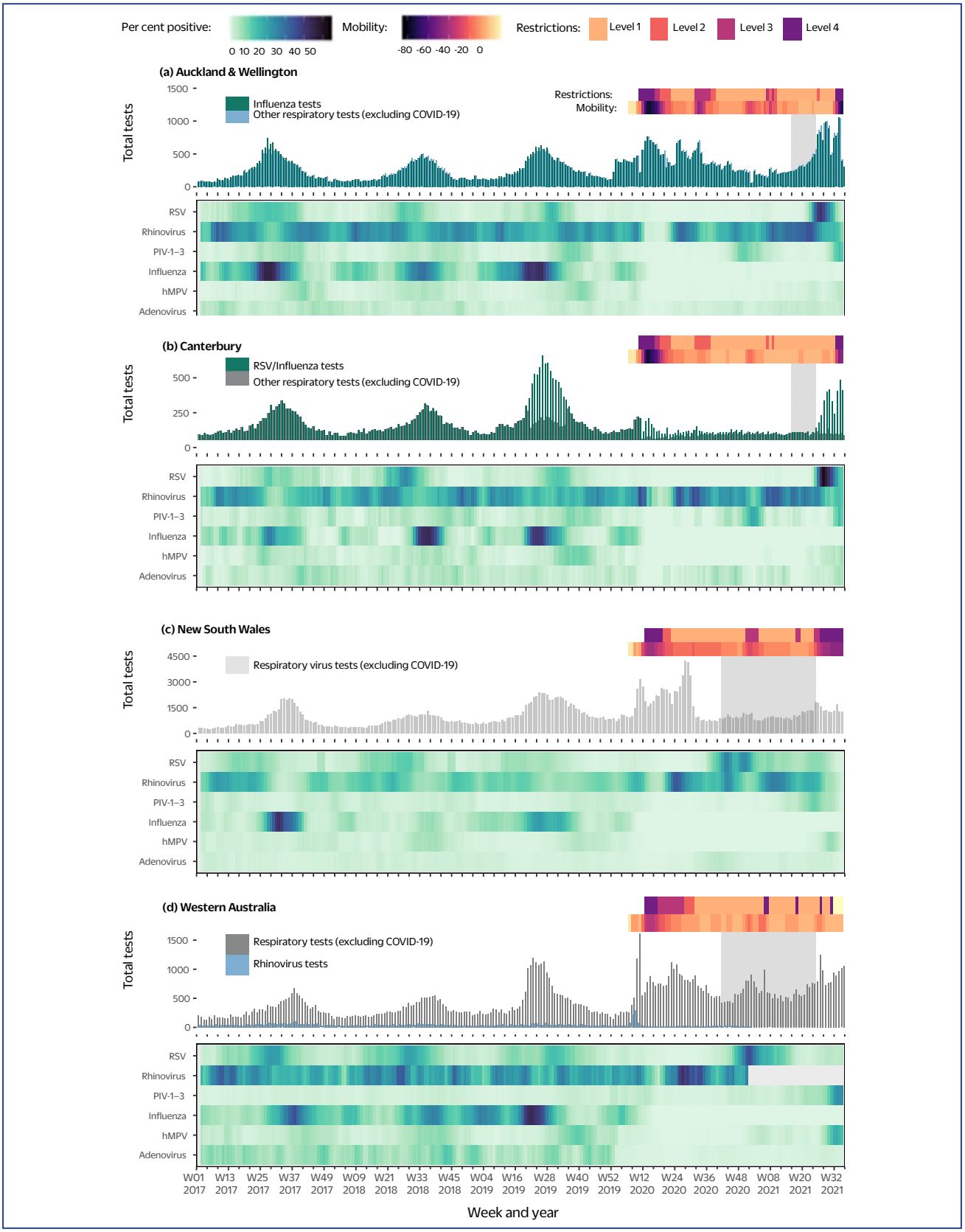
COVID-19 notifications (3-week moving average). Google mobility data are expressed as a percentage change from a 5-week baseline period. Restriction levels are summarized in Supplementary Table 1. The highest level of restrictions and corresponding Google mobility in each region are displayed (NSW in Australia; Auckland and Wellington in New Zealand). Grey shading indicates the period of quarantine-free travel between Australia (16 October 2020 to 22 June 2021) and New Zealand (19 April to 22 June 2021). In the case of Australia, the peak labelled (a) indicates a time when COVID-19 cases were driven by an outbreak in Victoria, while the peak labelled (b) indicates a time when COVID-19 cases were driven by outbreaks in NSW and Victoria.

DISCUSSION

We observed variable respiratory virus activity in five regions of Australia and New Zealand following the start of the COVID-19 pandemic in February 2020, with the notable exception of influenza, which did not circulate in either Australia or New Zealand during the pandemic period studied. After the relaxation of PHSMs in May 2020, adenovirus and rhinovirus activity increased above 2017–2019 levels in most regions (**Fig. 3**). In comparison, hMPV activity only began to rise in the autumn/winter of 2021 (i.e. May to August) after 18 months of low activity. RSV and PIV-1–3 both showed a delay in their usual seasonal pattern. Once they returned, both viruses experienced rates of activity above their 2017–2019 levels; however, in both cases, the timing of the increased activity differed between the two countries. Below we discuss some of the factors that likely contributed to these observed patterns in post-pandemic non-COVID-19 respiratory virus activity.

The nature of the relationship between infectious disease activity and mobility – specifically how, where and when people move – is well established.[13] Generally

Fig. 3. **Seasonal respiratory virus activity in selected regions of (a, b) New Zealand and (c, d) Australia against mobility data and level of restrictions, 2017–2021 (up to week 36, 2021)**



Google mobility data are expressed as a percentage change from a 5-week baseline period. Restriction levels are summarized in Supplementary Table 1. Grey shading indicates the period of quarantine-free travel between Australia (16 October 2020 to 22 June 2021) and New Zealand (19 April to 22 June 2021). Virus activity is denoted by the percentage of samples testing positive for respiratory viruses (3-week moving average) and is shown as a heat map by week.

hMPV: human metapneumovirus; PIV-1–3: parainfluenza virus types 1, 2 and 3; RSV: respiratory syncytial virus.

speaking, as mobility increases, the number of contacts or interactions between contagious and susceptible individuals also increases, resulting in an increase in virus prevalence and an outbreak of a communicable disease. The reverse is also generally true; as mobility declines, so too does respiratory virus activity. We observed reductions in population mobility coinciding with increased PHSMs in all five regions since March 2020. Overall, mobility remained below the pre-pandemic baseline in all regions, apart from a short period in Canterbury.

An early measure to contain the spread of SARS-CoV-2 was the closure of schools, with classes moving to online and home learning. Schools in New Zealand and WA reopened on 18 May 2020, while in NSW schools never officially closed but students were encouraged to learn from home from 24 March to 22 May 2020.[10,11] The initial decline and subsequent resurgence of adenoviruses and rhinoviruses in 2020 corresponded with the relaxation of some PHSMs and the reopening of schools, supporting the role of children in their circulation. Interestingly, the subsequent reintroduction of more restrictive PHSMs including school closures did not appear to reduce their activity. Possible explanations for this observation include the non-enveloped features of rhinoviruses and adenoviruses (which may make them more durable),[14] and post-COVID-19 changes in respiratory testing patterns.

Non-enveloped viruses such as adenoviruses and rhinoviruses are unique among the viruses included in this study in that they have some heat-resistant properties and can survive some disinfection processes including handwashing.[14] In addition, it has been suggested that surgical face masks are not particularly effective at reducing the emission of rhinovirus particles (aerosols and droplets).[15] Given that in both countries mandatory mask use was limited to times with stricter restrictions and only recommended at other times (**Supplementary Table 1**), it seems likely that at least some of the COVID-19 infection control measures may have been less effective against adenovirus and rhinovirus transmission and this allowed these viruses to continue to circulate despite the reintroduction of more restrictive PHSMs.

Changes in the volume of, and in the way in which the public accessed, respiratory virus testing may also have played a role in the observed patterns of adenovirus and rhinovirus activity.[16] In both countries, COVID-19 testing centres were established within and outside medical facilities, providing the community with free and rapid access to SARS-CoV-2 testing. While most of the new capacity provided by the private laboratories was restricted to SARS-CoV-2 only, a number of public health laboratories continued to screen samples for other respiratory viruses.[17,18]

Although all regions experienced a reduction in testing capacity during the early stage of the pandemic due to pressures on staff availability, testing reagents and equipment,[17,18] NSW, WA, Auckland and Wellington were able to increase their testing rates for other respiratory viruses. The introduction of rapid SARS-CoV-2 NAAT and multiplex NAAT, which target SARS-CoV-2 and other respiratory viruses simultaneously, likely played a role in enabling these regions to not only maintain but even increase their testing rates for non-SARS-CoV-2 respiratory viruses.[19] The relatively lower levels of testing in Canterbury can be attributed to the inclusion of data captured by public health surveillance programmes in the Auckland and Wellington datasets, whereas the Canterbury dataset only included the results of testing in hospitals and general practice surgeries. Additionally, after the closure of international borders in New Zealand, Canterbury implemented a stricter respiratory virus testing triaging system, which limited availability of multiplex respiratory virus testing to hospitalized patients. However, while increased testing may explain the increased detection of rhinoviruses and adenoviruses in 2020, it is unlikely to be a major contributor to the observed resurgence in adenovirus and rhinovirus activity, given the concurrent increase in activity of both viruses in Canterbury, where respiratory virus testing rates were significantly lower than in Auckland and Wellington.

We consider it unlikely that stringent PHSMs alone resulted in substantial decreases in the transmission of influenza and some other respiratory viruses that we observed during 2020 and suggest that viral displacement and interference could have played a contributory role. Viral interference between respiratory viruses, whereby two viruses interact within a host, has been well documented.[20,21] For example, a rhinovirus outbreak in 2009 is believed to have delayed the arrival of the 2009 influenza A (H1N1) pandemic in some European countries.[22,23] Evidence of similar interactions between SARS-CoV-2 and other viruses is now beginning to emerge; one recent study found prior infection with

rhinoviruses reduced the ability of SARS-CoV-2 to replicate in respiratory tract epithelium,[24] suggesting that the immune-mediated effects of rhinoviruses, a common and generally mild respiratory virus, might provide a low level of protection against both SARS-CoV-2 infection and severe COVID-19 disease. Similarly, viral displacement and interference may have contributed to the delayed rise in hMPV, a rise that we observed only towards the end of the study period at a time when RSV activity was either low (as in NSW and WA) or waning after an outbreak (as in Auckland, Canterbury and Wellington). Evidence to support this hypothesis comes from a pre-pandemic study on circulating respiratory viruses conducted in Victoria, Australia, which found that RSV protected against a subsequent hMPV infection.[21]

Domestic and international travel have previously been linked to the introduction and subsequent spread of influenza,[25,26] and our data suggest that the lifting of restrictions may have played a role in the spread of several non-COVID-19 respiratory viruses. After March 2020, international travel was severely limited in both countries, and strict border restrictions were in place throughout 2020–2021 (**Supplementary Table 1**). Apart from short-lived travel bubbles between some Australian states and New Zealand, both countries required all international arrivals to undergo government-managed 14-day quarantine. Additionally, during COVID-19 outbreaks, domestic travel was severely restricted, with travellers from locations with current COVID-19 outbreaks prevented from entering another region or required to self-isolate on arrival for 14 days and to restrict movement within these cities (**Supplementary Table 1**). However, shortly after New Zealand allowed people from Australia to enter the country without quarantining, a resurgence in RSV activity was observed, leading to speculation that Australian travellers reseeded RSV in New Zealand in April 2021.

Before the travel bubble with Australia was introduced, RSV activity was below 1% in New Zealand but above 5% in NSW and WA. This, coupled with the fact that there is no known non-human reservoir for RSV,[27] does suggest international travel was the most likely cause of the increased RSV activity observed in New Zealand in 2021. Sequencing data support the hypothesis that RSV was imported from NSW into Victoria, Australia in 2020 after the second COVID-19 wave.[28] However, the lifting of travel restrictions does not explain the rise of RSV in WA in 2020 or the second out-of-season peak that was seen at the end of 2021.[29] In contrast, RSV activity in NSW returned to its normal seasonality in 2021, with no out-of-season activity reported during the 2021–2022 summer season.[30]

In both countries, high influenza vaccination rates could have contributed to the observed low influenza activity. This is unlikely to have been a key factor, as in 2020, Australia and New Zealand reported their highest-ever rates of influenza vaccinations.[31,32] However, influenza vaccination rates were significantly lower in both countries in 2021,[31,32] possibly due to interference with COVID-19 vaccination campaigns and complacency due to low influenza activity. It is highly improbable that circulating influenza viruses were less transmissible as influenza viruses have continued to circulate in various parts of the world such as Western Africa and China since the start of the COVID-19 outbreak.[33]

Past pandemics have shown that we need to be prepared for unpredictable resurgences in respiratory viruses, including out-of-season outbreaks.[22,34] In this respect at least, the COVID-19 pandemic is not exceptional. The observed out-of-season outbreaks of RSV[28] were not entirely unexpected given that modelling studies had predicted an RSV resurgence after the relaxation of PHSMs. It is also likely that RSV seasonality will take several years to return to its pre-pandemic pattern.[35] As fewer people are exposed to (and infected with) respiratory viruses, population immunity decreases and the chance of more substantial outbreaks increases. When influenza returns, low rates of influenza vaccination and a possible mismatch between circulating viruses and vaccines (due to low influenza numbers in 2020 and 2021 and geographic differences in virus circulation) could increase population susceptibility and lead to larger outbreaks with more cases of severe disease. As COVID-19 vaccination rates rise and countries relax PHSMs, including easing of travel restrictions and reopening borders, respiratory virus activity will need to be closely monitored.[36,37]

This study has several limitations. First, laboratory surveillance is passive and subject to selection bias due to the subjectivity of health-care providers testing patients and variations in health-seeking behaviours. Moreover, rapid PCR testing at Canterbury Health Laboratories and reported by ESR only detects influenza A/B viruses and

RSV, whereas standard multiplex PCR testing used by the other surveillance programmes and laboratories is capable of detecting a wider range of clinically relevant respiratory viruses, including human rhinoviruses, hMPV, PIV and human adenoviruses. Additionally, it is difficult to determine the proportion of testing that was provided by public health laboratories as testing conducted by private pathology services was not included in this analysis. The impact of changes in testing processes and reporting mechanisms at public health laboratories overburdened with SARS-CoV-2 testing over the period of our analysis is also difficult to assess.

Finally, it is unlikely that our baseline mobility is a true reflection of pre-pandemic mobility. Google mobility data reflected the movement of people with an Android device using mapping apps relative to a 5-week baseline period (3 January–6 February 2020). Google mobility baseline data in Australia were collected during the 2019–2020 bushfire season, with active bushfires in NSW and WA occurring during the entire 5-week baseline period. Furthermore, the baseline period largely coincided with school holidays in Australia and New Zealand, a period during which mobility patterns are different.[38]

CONCLUSION

Seasonal respiratory virus circulation patterns have been disrupted during the COVID-19 pandemic. Epidemics of some viruses such as RSV have been observed out of season and with greater intensity than in the past. It is likely to take several years for respiratory viruses to return to their characteristic, pre-pandemic seasonal patterns. During this period, health-care systems should not rely on historical seasonal patterns to inform resource allocation and interventions. This study also serves to underscore the importance of surveillance systems with real-time data that can signal relevant epidemiological information back to clinicians and so prompt timely public health action and response.

Conflicts of interest

The authors have no conflicts of interest to declare.

Ethics statement

Laboratory-based respiratory virus surveillance data were collected following relevant Public Health Acts in each region under public health surveillance. As a result, ethical approval was not deemed necessary for the collection and use of these data.

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References

1. Willis O. Australia is flattening the curve. But should we try to squash it like New Zealand? Sydney: ABC News; 2020. Available from: https://www.abc.net.au/news/health/2020-04-15/coronavirus-elimination-australia-new-zealand/12150302, accessed 23 July 2023.
2. Huang QS, Wood T, Jelley L, Jennings T, Jefferies S, Daniells K, et al. Impact of the COVID-19 nonpharmaceutical interventions on influenza and other respiratory viral infections in New Zealand. Nat Commun. 2021;12(1):1001. doi:10.1038/s41467-021-21157-9 pmid:33579926
3. Iuliano AD, Roguski KM, Chang HH, Muscatello DJ, Palekar R, Tempia S, et al. Estimates of global seasonal influenza-associated respiratory mortality: a modelling study. Lancet. 2018;391(10127):1285–300. doi:10.1016/S0140-6736(17)33293-2 pmid:29248255
4. Jin X, Ren J, Li R, Gao Y, Zhang H, Li J, et al. Global burden of upper respiratory infections in 204 countries and territories, from 1990 to 2019. EClinicalMedicine. 2021;37:100986. doi:10.1016/j.eclinm.2021.100986 pmid:34386754
5. Wang X, Li Y, Deloria-Knoll M, Madhi SA, Cohen C, Arguelles VL, et al. Global burden of acute lower respiratory infection associated with human parainfluenza virus in children younger than 5 years for 2018: a systematic review and meta-analysis. Lancet Glob Health. 2021;9(8):e1077–87. doi:10.1016/S2214-109X(21)00218-7 pmid:34166626
6. Kinder JT, Moncman CL, Barrett C, Jin H, Kallewaard N, Dutch RE. Respiratory syncytial virus and human metapneumovirus infections in three-dimensional human airway tissues expose an interesting dichotomy in viral replication, spread, and inhibition by neutralizing antibodies. J Virol. 2020;94(20):e01068-20. doi:10.1128/JVI.01068-20 pmid:32759319
7. Martin ET, Kuypers J, Chu HY, Foote S, Hashikawa A, Fairchok MP, et al. Heterotypic infection and spread of rhinovirus A, B, and C among childcare attendees. J Infect Dis. 2018;218(6):848–55. doi:10.1093/infdis/jiy232 pmid:29684211

8. Cassir N, Hraiech S, Nougairede A, Zandotti C, Fournier PE, Papazian L. Outbreak of adenovirus type 1 severe pneumonia in a French intensive care unit, September–October 2012. Euro Surveill. 2014;19(39):20914. doi:10.2807/1560-7917.es2014.19.39.20914 pmid:25306980
9. Ritchie H, Mathieu E, Rodés-Guirao L, Appel C, Giattino C, Ortiz-Ospina E, et al. Coronavirus pandemic (COVID-19): confirmed cases. OurWorldInData.org; 2022. Available from: https://github.com/owid/covid-19-data/tree/master/public/data, accessed 7 March 2022.
10. Implementation progress towards COVID normal: as of announcements @ 1600hrs 24 December 2020. Canberra: Australian Government, Department of the Prime Minister and Cabinet; 2021. Available from: https://www.pmc.gov.au/sites/default/files/publications/covid-19-restrictions-tracker-20201224.pdf, accessed 20 October 2021.
11. History of the COVID-19 alert system: Wellington: New Zealand Government; 2021. Available from: https://covid19.govt.nz/alert-levels-and-updates/history-of-the-covid-19-alert-system/, accessed 15 October 2021.
12. COVID-19 community mobility reports. Mountain View (CA): Google LLC; 2021. Available from: https://www.google.com/covid19/mobility/, accessed 6 October 2021.
13. Findlater A, Bogoch II. Human mobility and the global spread of infectious diseases: a focus on air travel. Trends Parasitol. 2018;34(9):772–83. doi:10.1016/j.pt.2018.07.004 pmid:30049602
14. Leung NHL. Transmissibility and transmission of respiratory viruses. Nat Rev Microbiol. 2021;19(8):528–45. doi:10.1038/s41579-021-00535-6 pmid:33753932
15. Leung NHL, Chu DKW, Shiu EYC, Chan KH, McDevitt JJ, Hau BJP, et al. Respiratory virus shedding in exhaled breath and efficacy of face masks. Nat Med. 2020;26(5):676–80. doi:10.1038/s41591-020-0843-2 pmid:32371934
16. Atmore C, Stokes T. Turning on a dime–pre- and post-COVID-19 consultation patterns in an urban general practice. N Z Med J. 2020;133(1523):65–75. pmid:33032304
17. COVID-19 testing strategy for Aotearoa New Zealand. Wellington: New Zealand Government, Ministry of Health; 2021. p. 14. Available from: https://www.beehive.govt.nz/sites/default/files/2021-10/COVID-19%20Testing%20Rapid%20Review%20Report.pdf, accessed 22 August 2022.
18. Submission: inquiry into the Victorian Government's response to the COVID-19 pandemic. Submission no. 224. Queensland: Public Pathology Australia; 2020. Available from: https://parliament.vic.gov.au/images/stories/committees/paec/COVID-19_Inquiry/Submissions/224._Public_Pathology_Australia.pdf, accessed 26 July 2022.
19. Coronavirus (COVID-19) – testing framework for COVID-19 in Australia. Canberra: Australian Government Department of Health; 2021. Available from: https://www.health.gov.au/sites/default/files/documents/2021/02/coronavirus-covid-19-testing-framework-for-covid-19-in-australia.pdf, accessed 22 August 2022.
20. Nickbakhsh S, Mair C, Matthews L, Reeve R, Johnson PCD, Thorburn F, et al. Virus-virus interactions impact the population dynamics of influenza and the common cold. Proc Natl Acad Sci U S A. 2019;116(52):27142–50. doi:10.1073/pnas.1911083116 pmid:31843887
21. Price OH, Sullivan SG, Sutterby C, Druce J, Carville KS. Using routine testing data to understand circulation patterns of influenza A, respiratory syncytial virus and other respiratory viruses in Victoria, Australia. Epidemiol Infect. 2019;147:e221. doi:10.1017/S0950268819001055 pmid:31364539
22. Mak GC, Wong AH, Ho WY, Lim W. The impact of pandemic influenza A (H1N1) 2009 on the circulation of respiratory viruses 2009–2011. Influenza Other Respir Viruses. 2012;6(3):e6–10. doi:10.1111/j.1750-2659.2011.00323.x pmid:22212717
23. Casalegno JS, Ottmann M, Duchamp MB, Escuret V, Billaud G, Frobert E, et al. Rhinoviruses delayed the circulation of the pandemic influenza A (H1N1) 2009 virus in France. Clin Microbiol Infect. 2010;16(4):326–9. doi:10.1111/j.1469-0691.2010.03167.x pmid:20121829
24. Dee K, Goldfarb DM, Haney J, Amat JAR, Herder V, Stewart M, et al. Human rhinovirus infection blocks severe acute respiratory syndrome coronavirus 2 replication within the respiratory epithelium: implications for COVID-19 epidemiology. J Infect Dis. 2021;224(1):31–8. doi:10.1093/infdis/jiab147 pmid:33754149
25. Bedford T, Cobey S, Beerli P, Pascual M. Global migration dynamics underlie evolution and persistence of human influenza A (H3N2). PLoS Pathog. 2010;6(5):e1000918. doi:10.1371/journal.ppat.1000918 pmid:20523898
26. Geoghegan JL, Saavedra AF, Duchene S, Sullivan S, Barr I, Holmes EC. Continental synchronicity of human influenza virus epidemics despite climatic variation. PLoS Pathog. 2018;14(1):e1006780. doi:10.1371/journal.ppat.1006780 pmid:29324895
27. Di Mattia G, Nenna R, Mancino E, Rizzo V, Pierangeli A, Villani A, et al. During the COVID-19 pandemic where has respiratory syncytial virus gone? Pediatr Pulmonol. 2021;56(10):3106–9. doi:10.1002/ppul.25582 pmid:34273135
28. Eden JS, Sikazwe C, Xie R, Deng YM, Sullivan SG, Michie A, et al. Off-season RSV epidemics in Australia after easing of COVID-19 restrictions. Nat Commun. 2022;13(1):2884. doi:10.1038/s41467-022-30485-3 pmid:35610217
29. Paediatric respiratory pathogen report week 52, 27th December 2021 – 02nd January 2021. Perth: PathWest Laboratory Medicine WA; 2022. Available from: https://ww2.health.wa.gov.au/~/media/Corp/Documents/Health-for/Infectious-disease/Paediatric-Respiratory-Pathogen-Weekly-Report/2021/Paediatric-Respiratory-Pathogen-Report-Week-52.pdf, accessed 26 July 2022.
30. COVID-19 weekly surveillance in NSW: epidemiological week 51 ending 25 December 2021. Sydney: NSW Government, Ministry of Health; 2022. Available from: https://www.health.nsw.gov.au/Infectious/covid-19/Documents/covid-19-surveillance-report-20220107.pdf, accessed 26 July 2022.
31. Influenza dashboard: vaccination. Porirua, New Zealand: Institute of Environmental Science and Research; 2021. Available from: https://www.esr.cri.nz/our-services/consultancy/flu-surveillance-and-research, accessed 22 October 2021.
32. Van Buynder PG, Newbound A, MacIntyre CR, Kennedy AT, Clarke C, Anderson J. Australian experience of the SH21 flu vaccination program during the COVID-19 vaccine program. Hum Vaccin Immunother. 2021;17(11):1–6. doi:10.1080/21645515.2021.1967042 pmid:34542384
33. Influenza surveillance outputs. Geneva: World Health Organization Global Influenza Programme; 2022. Available from: https://www.who.int/teams/global-influenza-programme/surveillance-and-monitoring/influenza-surveillance-outputs, accessed 9 March 2022.
34. Lo JY, Tsang TH, Leung YH, Yeung EY, Wu T, Lim WW. Respiratory infections during SARS outbreak, Hong Kong, 2003. Emerg Infect Dis. 2005;11(11):1738–41. doi:10.3201/eid1111.050729 pmid:16318726

35. Baker RE, Park SW, Yang W, Vecchi GA, Metcalf CJE, Grenfell BT. The impact of COVID-19 nonpharmaceutical interventions on the future dynamics of endemic infections. Proc Natl Acad Sci U S A. 2020;117(48):30547–53. doi:10.1073/pnas.2013182117 pmid:33168723

36. Roadmap for easing COVID-19 restrictions. Sydney: NSW Government; 2021. Available from: https://www.nsw.gov.au/covid-19/easing-covid-19-restrictions, accessed 13 October 2021.

37. New Zealand PM Jacinda Ardern abandons plans for COVID-19 elimination as Auckland plans to reopen in phases. ABC News; 2021. Available from: https://www.abc.net.au/news/2021-10-04/new-zealand-extends-auckland-lockdown-but-eases-some-coronavirus/100512666, accessed 26 July 2022.

38. Ruktanonchai NW, Sadilek A, Woods D, Tatem AJ, Steele JE, Sorichetta A. Practical geospatial and sociodemographic predictors of human mobility. Sci Rep. 2021;11(1):15389. doi:10.1038/s41598-021-94683-7 pmid:34321509

Epidemiology and antimicrobial resistance profile of invasive non-typhoidal *Salmonella* from the Philippines Antimicrobial Resistance Surveillance Program, 2014–2018

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Objective: The epidemiology of invasive non-typhoidal *Salmonella* (iNTS) in the Philippines is not well elaborated. The present study describes the serotype distribution and antimicrobial susceptibility patterns of iNTS in the Philippines from 2014 to 2018.

Methods: Invasive NTS isolates were collected through the Department of Health's Antimicrobial Resistance Surveillance Program (ARSP). The identification of the isolates was confirmed using automated (Vitek®, bioMérieux, Marcy l'Étoile, France) and conventional methods. The isolates were serotyped using the slide agglutination method, and susceptibility testing was performed using Clinical and Laboratory Standards Institute guidelines. Demographic data were collected from the ARSP database.

Results: There were 138 isolates collected from human invasive specimens with 97.8% from blood samples. The most common serotypes were *Salmonella* Enteritidis (n = 84, 60.9%) and *Salmonella* Typhimurium (n = 18, 13.0%). Most of the isolates were from males (n = 88, 63.8%) and from the 0–5-year age group (n = 61, 44.2%). The proportions of iNTS isolates resistant to first-line antibiotics were as follows: ampicillin (23.2%), chloramphenicol (9.6%), ciprofloxacin (8.7%), ceftriaxone (2.2%) and trimethoprim-sulfamethoxazole (8.8%). The proportion of isolates with multi-drug resistance was 13.0% (18/138) with the most common resistance profile being resistance to ampicillin-chloramphenicol-ciprofloxacin from *Salmonella* Enteritidis isolates (n = 5).

Discussion: Resistance to first-line antibiotics limits the therapeutic choices for *Salmonella* infection. Relevant local antimicrobial resistance data on iNTS may support appropriate empiric therapy among vulnerable populations.

Salmonella enterica causes a wide range of infections among humans. Of its six subspecies, *S. enterica* subspecies enterica was solely associated with diseases among warm-blooded animals.[1] Only a small subset of serovars included in this subspecies can cause systemic infection-like typhoidal illnesses (*S*. Typhi and *S*. Paratyphi serovars).[2] However, the majority of this subspecies can commonly induce self-limiting diarrhoea, which is referred to as non-typhoidal *Salmonella* (NTS) gastroenteritis.[3] Invasive (bloodstream and extra-intestinal) NTS (iNTS) was also observed among persons living with HIV and immunocompromised children.[4] *S. enterica* serovars Typhimurium and Enteritidis were the two most common NTS associated with systemic infections that show features of typhoid fever. Globally, there were over 2.1 million cases and 416 000 deaths per year from iNTS infections, with a case fatality rate of more than 20% in children even with the suggested treatment.[5]

The epidemiology and antimicrobial resistance pattern of iNTS in Asia is not well documented, with limited reports from India, Taiwan (China) and Thailand.[6] There are no local data on serotype distribution and susceptibility profile of iNTS in the Philippines. Antimicrobial resistance data on iNTS isolates are

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of paramount importance as antibiotic treatment of infections due to these isolates is necessary.[7] NTS gastroenteritis is usually non-fatal to immunocompetent individuals; however, invasive infection due to NTS could be fatal to immunocompromised populations such as those suffering from malnutrition and people living with HIV.[8] With 21.5% of children <5 years old in the Philippines being underweight[9] and with the sustained rapid increase in new HIV infections in the country, relevant local antimicrobial resistance (AMR) data on iNTS may support appropriate empiric therapy among vulnerable populations.[10]

This study describes the epidemiology of NTS serotypes causing invasive infections and the antimicrobial resistance patterns of these isolates in the Philippines from 2014 to 2018.

METHODS

Study setting and population

The Philippines Department of Health (DOH) Antimicrobial Resistance Surveillance Program (ARSP) is a sentinel laboratory-based surveillance system of antimicrobial-resistant aerobic bacteria detected from clinical specimens. Culture and antimicrobial susceptibility data are collected from 24 tertiary hospitals located in 16 regions of the Philippines. There are eight sentinel sites in the National Capital Region and one or two sentinel sites in each of the other regions. All sentinel sites implement standard methods for culture and susceptibility testing based on the WHO manual for the laboratory identification and antimicrobial susceptibility testing of bacterial pathogens of public health importance in the developing world[11] and updated Clinical Laboratory Standards Institute (CLSI) references for antibiotic susceptibility testing and quality control.[12,13] The sentinel sites participate in an external quality assessment scheme conducted by the reference laboratory to ensure the quality of laboratory results. Staff from the Antimicrobial Resistance Surveillance Reference Laboratory (ARSRL) conduct periodic monitoring visits to sentinel sites to ensure that laboratory protocols are consistently being observed.

Data collection

Microbiological and demographic data from sentinel sites were entered into WHONET, a database designed for the management and analysis of microbiology laboratory data focusing on the analysis of antimicrobial susceptibility test results. A data extraction tool was used by ARSP to collect data from the WHONET database. Information on the age, sex, sentinel site, specimen type and initial serotyping result was collected for each isolate.

Isolates included in this study were positive for NTS. They were isolated either alone or in combination with another pathogen from blood, cerebrospinal fluid, tissue, fluid or respiratory specimens from January 2014 to December 2018. Only the first isolate from patients with multiple positive blood cultures for the same NTS serogroup and antimicrobial susceptibility profile was included in the study.

Microbiological procedures

All isolates received by the ARSRL were confirmed using both automated (Vitek®, bioMérieux, Marcy l'Étoile, France) and conventional methods at the reference laboratory. The isolates were serotyped using the Sven Gard method for slide agglutination using Denka Seiken antisera (Tokyo, Japan) and S&A Reagents serotest (Bangkok, Thailand). The antigenic formulae obtained were classified according to the White–Kauffmann–Le Minor scheme, as recommended by the WHO Collaborating Centre for Reference and Research on *Salmonella*.[2]

Antimicrobial susceptibility testing for ampicillin, ceftriaxone, chloramphenicol, ciprofloxacin and trimethoprim-sulfamethoxazole was performed using both automated (Vitek®) and conventional methods (Kirby Bauer disk diffusion and gradient diffusion method). Antimicrobial susceptibility results were interpreted using CLSI interpretive criteria (M100Ed28E). The proportion of the isolates that were resistant was generated using WHONET 5.6 software with only the first isolate per calendar year included. Quality control analyses for iNTS serotyping and antimicrobial susceptibility testing were conducted using *Escherichia coli* ATCC 25922.

RESULTS

There were 138 isolates collected from ARSP from 2014 to 2018. Among the isolates, 130 were characterized to serotypes and eight were assigned to serogroups. The most common serotypes were *Salmonella* Enteritidis (*n* = 84, 60.9%) and *Salmonella* Typhimurium (*n* = 18, 13.0%; **Table 1**).

The majority of isolates were from blood samples (*n* = 135, 97.8%), while three were from cerebrospinal fluid (2.2%). Most of the isolates were collected from Luzon (*n* = 63, 46.4%) (**Table 2**). Invasive NTS isolates were more common in males (*n* = 88, 63.8%) than females (*n* = 50, 36.2%). The 0–5-year age group (*n* = 61, 44.2%) had the highest proportion of iNTS isolates (**Fig. 1**), with most paediatric patients infected with *Salmonella* Enteritidis. The number of isolates increased annually, with the highest number collected in 2018 (**Table 1**).

The proportion of isolates resistant to antibiotics over the 5-year study period was less than 10% for each antibiotic, except for ampicillin, which was 23.2% (**Table 3**). Resistance to ciprofloxacin and ceftriaxone was present in 2015 and 2016 and persisted in 2018. The proportion of isolates resistant to chloramphenicol, ciprofloxacin, trimethoprim-sulfamethoxazole, ampicillin and ceftriaxone was highest in 2016, with a subsequent decrease of resistance in 2017 (**Fig. 2**). The observed decreases in 2017 were all statistically significant. In 2018, the proportion of isolates resistant to all antibiotics increased except for ceftriaxone; however, these increases were not significant (**Fig. 2**).

There were 18 multidrug-resistant (MDR) isolates (**Table 4**), that is, they were resistant to at least three antibiotic classes, giving an overall MDR proportion of 13.0%. The most common MDR resistance profile was resistance to ampicillin-chloramphenicol-ciprofloxacin, and these isolates were all *Salmonella* Enteritidis (*n* = 5 isolates).

Table 1. **Frequency of invasive non-typhoidal *Salmonella* isolates from the Antimicrobial Resistance Surveillance Program, the Philippines, 2014–2018 (*N* = 138)**

Salmonella serotype/ serogroup	2014	2015	2016	2017	2018	TOTAL
Enteritidis	4	14	13	26	27	84
Typhimurium	4	1	6	3	4	18
Virchow	2	–	1	1	1	5
Group C	–	–	1	–	3	4
Choleraesuis var. Kunz	1	1	1	–	–	3
Group B	1	–	–	2	–	3
Anatum	–	–	–	1	1	2
Kentucky	–	–	–	1	1	2
Stanley	–	1	–	–	1	2
Aberdeen	–	1	–	–	–	1
Ajiobo	–	–	–	–	1	1
Choleraesuis	–	1	–	–	–	1
Derby	–	–	–	–	1	1
Eastbourne	–	1	–	–	–	1
Emek	–	1	–	–	–	1
Group A	–	–	–	1	–	1
Heidelberg	–	–	1	–	–	1
Hillingdon	–	–	1	–	–	1
Javiana	1	–	–	–	–	1
Nessziona	–	–	–	–	1	1
Ohio	–	–	1	–	–	1
Rissen	1	–	–	–	–	1
Saintpaul	–	–	–	–	1	1
Tallahassee	–	–	–	1	–	1
TOTAL	**14**	**21**	**25**	**36**	**42**	**138**

DISCUSSION

The most common iNTS identified from the ARSP between 2014 and 2018 were *Salmonella* Enteritidis and *Salmonella* Typhimurium. This finding is similar to that identified in the Typhoid Fever Surveillance in Africa Program in 2010–2014,[14] the Hospital for Tropical Diseases in Viet Nam in 2008–2013,[15] from 461 iNTS isolates collected in India in 2010–2020,[16] and from genome sequencing-confirmed invasive *Salmonella* isolates collected from tertiary hospitals in the Nigeria Antimicrobial Surveillance Network.[17]

More adult males were affected by iNTS infections compared with adult females. Although such distribution may be attributed to male behavioural factors such as higher risks in food handling, preparation and consumption,[18] it could likewise be a factor of the prevailing sex ratio in the country, as there were more males than females in the Philippines from 2014 to 2018.[19] Most iNTS isolates were from patients aged 0–5

Table 2. **Invasive non-typhoidal *Salmonella* serotypes per region from the Antimicrobial Resistance Surveillance Program, the Philippines, 2014–2018**

Salmonella serotype	Region			
	Luzon[a]	Visayas[b]	Mindanao[c]	National Capital Region
Enteritidis	41	17	12	14
Typhimurium	10	2	5	1
Virchow	2	–	2	1
Group C	2	2	–	–
Choleraesuis var. Kunz	2	–	–	1
Group B	2	1	–	–
Anatum	1	1	–	–
Kentucky	–	2	–	–
Stanley	1	–	1	–
Other	2	10	–	2
TOTAL	**63**	**35**	**20**	**19**

[a] Luzon contains seven sentinel sites.
[b] Visayas contains four sentinel sites.
[c] Mindanao contains five sentinel sites.

Table 3. **Cumulative proportion of invasive non-typhoidal *Salmonella* isolates that were resistant by antibiotic, Antimicrobial Resistance Surveillance Program, the Philippines, 2014–2018**

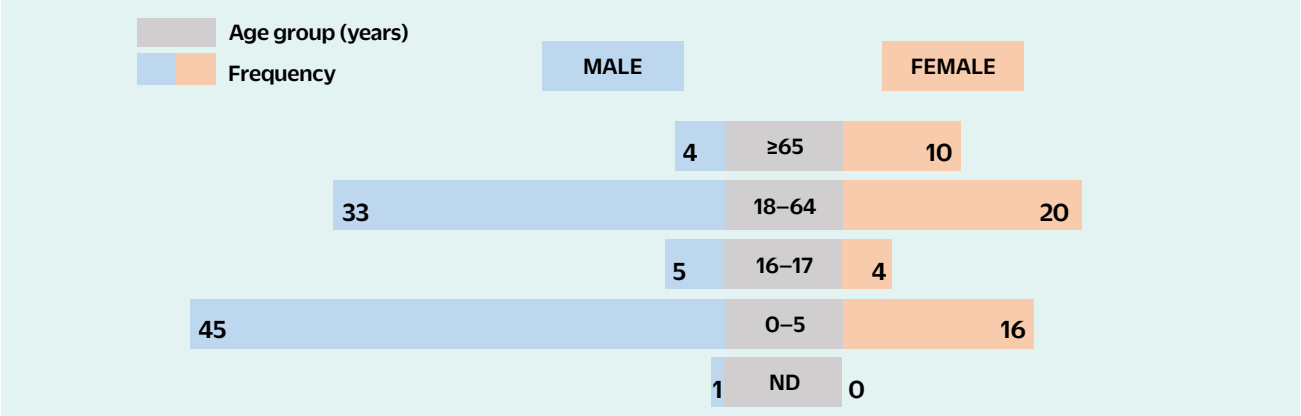
Antibiotic	% resistant	95% confidence interval
Ampicillin	23.2	16.6–31.3
Cefotaxime	1.4	0.2–5.6
Ceftriaxone	2.2	0.6–6.8
Chloramphenicol	9.6	5.4–16.2
Ciprofloxacin	8.7	4.8–15.0
Trimethoprim-sulfamethoxazole	8.8	4.8–15.2

years. Underdeveloped immune systems, malnutrition and presence of comorbidities may predispose this age group to iNTS infections.[3,20]

Invasive NTS infections were higher in Luzon, which has both rural and urban areas. Luzon is the largest and most populous island in the Philippines, which may be the reason for the higher number of reported cases from this island group in the study. Cruz Espinoza et al. concluded in their study that salmonellosis is mainly a disease of high-density population,[20] and in Luzon, there are urban in-migration generating slum areas with poor water access and poor hygiene practices[21] that may increase the risk of food and waterborne diseases among residents. Having 15 of the 24 sentinel sites of the ARSP located in Luzon likely contributed to the preponderance of iNTS infections from Luzon. Variations in the diagnostic practices of physicians and capacities of the laboratories in the different sentinel sites may have also contributed to differences in the number of iNTS in the different island groups shown in this study.

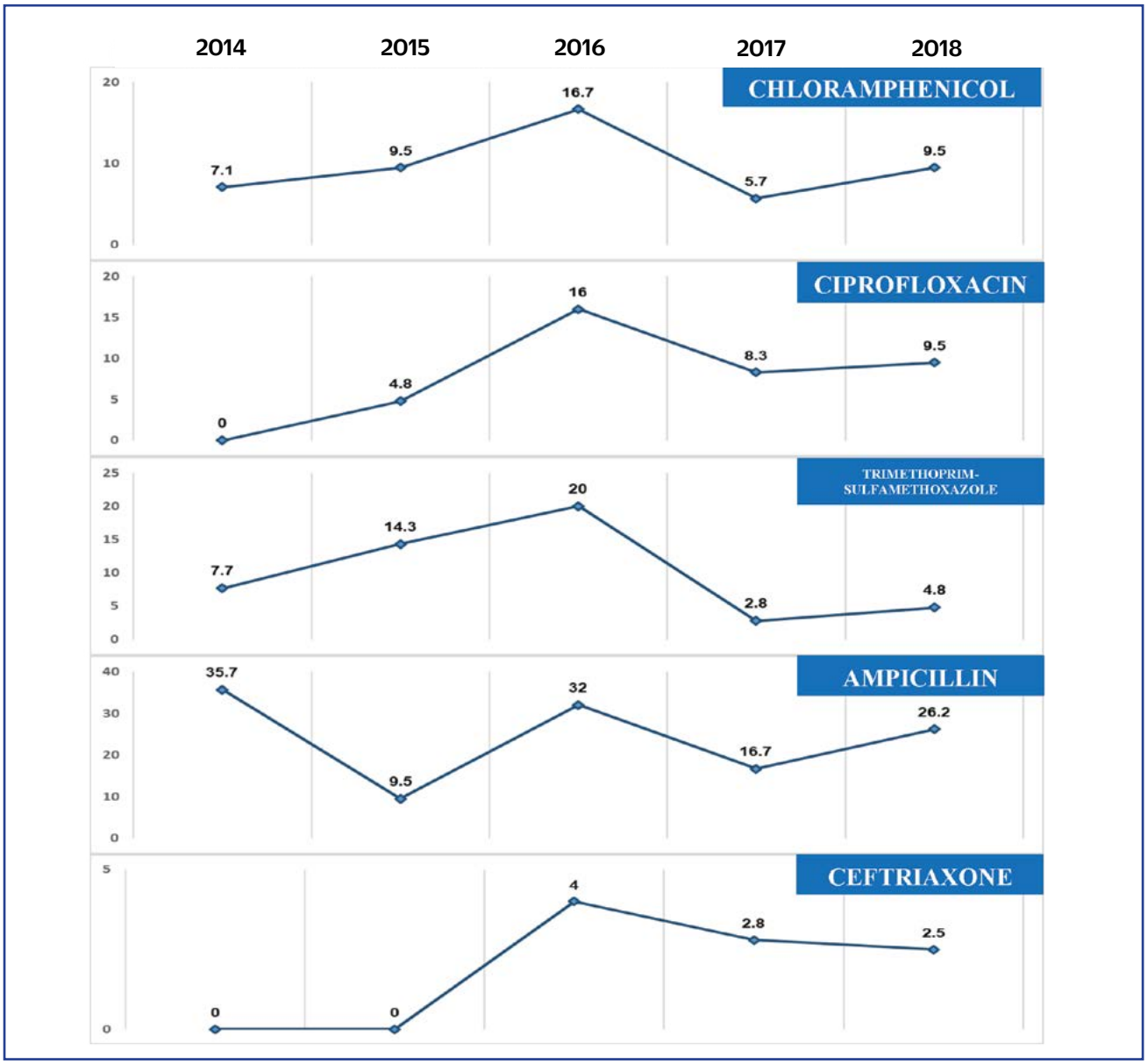
The proportion of iNTS isolates resistant to first-line antibiotics (chloramphenicol, ampicillin,

Fig. 1. **Frequency of invasive non-typhoidal *Salmonella* isolates by age group and sex, Antimicrobial Resistance Surveillance Program, the Philippines, 2014–2018**



ND: no data.

Fig. 2. **Annual antimicrobial resistance rates of invasive non-typhoidal *Salmonella* isolates, Antimicrobial Resistance Surveillance Program, the Philippines, 2014–2018**



trimethoprim-sulfamethoxazole, ceftriaxone) remained below 10%, except for ampicillin at 23%. This is relatively low compared with neighbouring Thailand, which has reported resistance to ampicillin as high as 68.2%.[6] Among iNTS isolates from children in Taiwan (China), resistance to ceftriaxone and ciprofloxacin was noted to be 5.6% and 30.6%, respectively.[22] That there was resistance to the locally recommended empiric treatment of severe NTS infections of ciprofloxacin, a fluoroquinolone, and ceftriaxone, a third-generation cephalosporin,[23,24] is a concern.

Among the iNTS isolates in this study, MDR was relatively low, with the most common resistance profile being to ampicillin, chloramphenicol and ciprofloxacin among *Salmonella* Enteritidis isolates. Low local MDR rates may allow for wider empiric treatment selection for iNTS infections. Continued emergence of resistance to these antibiotics may further limit treatment options for iNTS.

The isolates in this study were from regional hospitals that are sentinel sites for the ARSP. These

Table 4. **Multidrug-resistant[a] invasive non-typhoidal *Salmonella* isolates, Antimicrobial Resistance Surveillance Program, the Philippines, 2014–2018**

Resistance profile	Frequency
AMP-CHL-CIP	5
AMP-CIP-SXT	3
AMP-CHL-CIP-SXT	3
CHL-CIP-SXT	2
AMP-CHL-SXT	2
CRO-CHL-CIP	1
AMP-CRO-CTX-CHL-CIP	1
AMP-CRO-CTX-CIP-SXT	1
Total	**18**

[a] Resistant to three or more drug classes.

AMP: ampicillin; CHL: chloramphenicol; CIP: ciprofloxacin; CRO: ceftriaxone; CTX: cefotaxime; SXT: trimethoprim-sulfamethoxazole.

hospitals cater to patients from towns and cities within the hospital vicinity and may not be representative of all hospital patients in the Philippines. There may be resistance variations in local areas not represented in programme data. Given that the ARSP data are from routine clinical samples, and not all patients have samples taken, there may be differences in isolates selected for microbiological culture, which may also introduce bias in the resistance data presented. In addition, the small number of isolates included in this study is a limitation, as the performance of culture and susceptibility tests in the sentinel sites is dependent on the diagnostic habits of the clinicians.

Conclusion

To our knowledge, this study is the first extensive report of iNTS for the Philippines, which showed that in 2014–2018, the most common serotypes among iNTS in the Philippines were *Salmonella* Enteritidis and *Salmonella* Typhimurium. Continued surveillance of AMR among iNTS may support appropriate empiric therapy among vulnerable populations and can contribute to the reduction of the selection and spread of resistant infections. Genomic epidemiology of resistant iNTS may lead to a better understanding of transmission patterns and emergence of resistance among these bacteria and may inform varied control measures including vaccine development.

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Conflicts of interest

The authors have no conflicts of interest to declare.

Ethics statement

This study was evaluated and approved by the Institutional Review Board of the Research Institute for Tropical Medicine, Department of Health, Philippines (2020-20).

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References

1. Porwollik S, Boyd EF, Choy C, Cheng P, Florea L, Proctor E, et al. Characterization of Salmonella enterica subspecies I genovars by use of microarrays. J Bacteriol. 2004;186(17):5883–98. doi:10.1128/JB.186.17.5883-5898.2004 pmid:15317794
2. Popoff MY, Bockemühl J, Gheesling LL. Supplement 2002 (no. 46) to the Kauffmann-White scheme. Res Microbiol. 2004;155(7):568–70. doi:10.1016/j.resmic.2004.04.005 pmid:15313257
3. Crump JA, Sjölund-Karlsson M, Gordon MA, Parry CM. Epidemiology, clinical presentation, laboratory diagnosis, antimicrobial resistance, and antimicrobial management of invasive Salmonella infections. Clin Microbiol Rev. 2015;28(4):901–37. doi:10.1128/CMR.00002-15 pmid:26180063
4. Haselbeck AH, Panzner U, Im J, Baker S, Meyer CG, Marks F. Current perspectives on invasive nontyphoidal Salmonella disease. Curr Opin Infect Dis. 2017;30(5):498–503. doi:10.1097/QCO.0000000000000398 pmid:28731899
5. Ao TT, Feasey NA, Gordon MA, Keddy KH, Angulo FJ, Crump JA. Global burden of invasive nontyphoidal Salmonella disease, 2010(1). Emerg Infect Dis. 2015;21(6):941–9. doi:10.3201/eid2106.140999 pmid:25860298
6. Whistler T, Sapchookul P, McCormick DW, Sangwichian O, Jorakate P, Makprasert S, et al. Epidemiology and antimicrobial resistance of invasive non-typhoidal Salmonellosis in rural Thailand from 2006–2014. PLoS Negl Trop Dis. 2018;12(8):e0006718. doi:10.1371/journal.pntd.0006718 pmid:30080897
7. Shrestha KL, Pant ND, Bhandari R, Khatri S, Shrestha B, Lekhak B. Re-emergence of the susceptibility of the Salmonella spp. isolated from blood samples to conventional first line antibiotics. Antimicrob Resist Infect Control. 2016;5:22. doi:10.1186/s13756-016-0121-8 pmid:27231547
8. Crump JA, Heyderman RS. A perspective on invasive Salmonella disease in Africa. Clin Infect Dis. 2015;61(Suppl 4):S235–40. doi:10.1093/cid/civ709 pmid:26449937

9. Situation of children in the Philippines 2017. Manila: UNICEF Philippines; 2017. Available from: https://www.unicef.org/philippines/media/561/file/Situation%20Analysis%20of%20Children%20in%20the%20Philippines%20brief.pdf, accessed 29 December 2022.

10. A briefer on the Philippine HIV estimates, 2020. Manila: Epidemiology Bureau, Department of Health; 2020. Available from: https://doh.gov.ph/sites/default/files/publications/A%20Briefer%20on%20the%20PH%20Estimates%202020_08232021.pdf, accessed 29 December 2022.

11. Ajello G, Bopps C, Elliott J, Facklam R, Knapp JS, Popovic T, et al. Manual for the laboratory identification and antimicrobial susceptibility testing of bacterial pathogens of public health importance in the developing world: haemophilus influenzae, Neisseria meningitidis, Streptococcus pneumoniae, Neisseria gonorrhoea, Salmonella serotype Typhi, Shigella, and Vibrio cholerae. Geneva: World Health Organization; 2003. Available from: https://apps.who.int/iris/handle/10665/68554, accessed 29 December 2022.

12. M07: Methods for dilution antimicrobial susceptibility tests for bacteria that grow aerobically, 11th edition. Wayne (PA): Clinical and Laboratory Standards Institute; 2018.

13. M45: Methods for antimicrobial dilution and disk susceptibility testing of infrequently isolated or fastidious bacteria, 3rd edition. Wayne (PA): Clinical and Laboratory Standards Institute; 2016.

14. Marks F, von Kalckreuth V, Aaby P, Adu-Sarkodie Y, El Tayeb MA, Ali M, et al. Incidence of invasive salmonella disease in sub-Saharan Africa: a multicentre population-based surveillance study. Lancet Glob Health. 2017;5(3):e310–23. doi:10.1016/S2214-109X(17)30022-0 pmid:28193398

15. Phu Huong Lan N, Le Thi Phuong T, Nguyen Huu H, Thuy L, Mather AE, Park SE, et al. Invasive non-typhoidal Salmonella infections in Asia: clinical observations, disease outcome and dominant serovars from an infectious disease hospital in Vietnam. PLoS Negl Trop Dis. 2016;10(8):e0004857. doi:10.1371/journal.pntd.0004857 pmid:27513951

16. Jacob JJ, Solaimalai D, Rachel T, Pragasam AK, Sugumar S, Jeslin P, et al. A secular trend in invasive non-typhoidal Salmonella in South India, 2000–2020: identification challenges and antibiogram. Indian J Med Microbiol. 2022;40(4):536–40. doi:10.1016/j.ijmmb.2022.07.015 pmid:35987666

17. Ikhimiukor OO, Oaikhena AO, Afolayan AO, Fadeyi A, Kehinde A, Ogunleye VO, et al. Genomic characterization of invasive typhoidal and non-typhoidal Salmonella in southwestern Nigeria. PLoS Negl Trop Dis. 2022;16(8):e0010716. doi:10.1371/journal.pntd.0010716 pmid:36026470

18. Frasson I, Bettanello S, De Canale E, Richter SN, Palù G. Serotype epidemiology and multidrug resistance patterns of Salmonella enterica infecting humans in Italy. Gut Pathog. 2016;8:26. doi:10.1186/s13099-016-0110-8 pmid:27252785

19. Male to female sex ratio 2014–2018 [website]. Philippine Statistics Authority. Available from: https://psa.gov.ph/gender-stat/wmf, accessed 27 November 2019.

20. Cruz Espinoza LM, Nichols C, Adu-Sarkodie Y, Al-Emran HM, Baker S, Clemens JD, et al. Variations of invasive Salmonella infections by population size in Asante Akim North Municipal, Ghana. Clin Infect Dis. 2016;62(Suppl 1):S17–22. doi:10.1093/cid/civ787 pmid:26933015

21. Boquet Y. 7107 islands. In: Boquet Y. The Philippine archipelago. Cham (Switzerland): Springer; 2017:16.

22. Chang YJ, Chen YC, Chen NW, Hsu YJ, Chu HH, Chen CL, et al. Changing antimicrobial resistance and epidemiology of non-typhoidal Salmonella infection in Taiwanese children. Front Microbiol. 2021;12:648008. doi:10.3389/fmicb.2021.648008 pmid:33868207

23. The national antibiotic guidelines 2018. Manila: Pharmaceutial Division, Department of Health; 2018. Available from: https://pharma.doh.gov.ph/the-national-antibiotic-guidelines, accessed 4 May 2023.

24. Philippine clinical practice guidelines on the management of acute infectious diarrhea in children and adults: reference manual. Manila: Department of Health; 2019. Available from: https://doh.gov.ph/node/17952, accessed 4 May 2023.

Outbreak of foodborne disease in a boarding school, Negeri Sembilan state, Malaysia, 2021

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Objective: Foodborne disease is a significant global public health concern, with *Bacillus cereus* being a frequent cause of outbreaks. However, due to the relatively mild symptoms caused by infection with *B. cereus*, the shorter duration of illness and the challenges of testing for it in both stool and food samples, outbreaks are often underreported. This report describes the epidemiology of cases of foodborne illness, the causative agent and risk factors associated with an outbreak in a boarding school in Seremban district, Negeri Sembilan state, Malaysia, that occurred in November 2021.

Methods: Epidemiological, environmental and laboratory investigations were performed. A case was defined as any person with abdominal pain, vomiting or diarrhoea that occurred after consuming food served by the canteen at the school. The data were analysed using Microsoft Excel and the Statistical Package for the Social Sciences (SPSS).

Results: A total of 152 cases were identified among the 597 students, giving an attack rate of 25.5%. All cases were females aged 13–17 years. They presented with abdominal pain (100%), nausea (97.4%, 148), vomiting (78.3%, 119) or diarrhoea (61.8%, 94), or a combination of these. The mode of transmission of the outbreak was a continual common source. The foods associated with becoming a case were beef rendang (a dry curry) (odds ratio [OR]: 20.54, 95% CI: 4.89–86.30), rice (OR: 19.62, 95% CI: 2.62–147.01), rice cubes (OR: 18.17, 95% CI: 4.31–76.55) and vermicelli (OR: 17.02, 95% CI: 4.03–71.86). Cross-contamination and inadequate thawing and storage temperatures contributed to the outbreak.

Discussion: This outbreak of foodborne illness at a boarding school was likely caused by *B. cereus*. The findings highlight the importance of proper food preparation, temperature monitoring, hygiene practices among food handlers and compliance with food safety guidelines.

Foodborne diseases continue to be a public health concern globally, contributing to morbidity and mortality, and associated with substantial economic costs.[1] During the past decade, the national annual incidence of foodborne diseases in Malaysia has been decreasing, with the incidence reported as 50.1/100 000 population in 2019.[2] Data from *e-Wabak*, the communicable disease monitoring system run by the Ministry of Health in Malaysia, reported 46 outbreaks of foodborne disease in Seremban district, Negeri Sembilan state, between 2017 and 2021, with 18 (39.1%) involving educational institutions. Eleven (61.1%) of these outbreaks occurred at secondary schools, followed by 4 (22.2%) at primary schools and 3 (16.7%) at colleges.[3]

Food poisoning associated with *Bacillus cereus* causes diarrhoea or vomiting,[4] which is generally mild and self-limiting. Emetic syndrome develops upon ingesting the preformed toxin in contaminated foods such as rice or rice products.[4,5] Diarrhoeal syndrome, commonly associated with contaminated fish, vegetables or meat, is caused by heat-labile toxins, which have a longer incubation period.[5,6] The incubation period for the emetic syndrome is 0.5 to 6 hours, and for diarrhoeal syndrome it ranges from 8 to 16 hours.[7]

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B. cereus can withstand unfavourable conditions[8] and survives cooking processes, forming spores that can multiply and produce toxins in cooked rice.[9]

On 22 November 2021, the Seremban District Health Office was notified by a local hospital about cases of food poisoning occurring among boarding school students. The outbreak was confirmed by the rapid assessment team, consisting of doctors and environmental health assistant officers. The aim of this report is to describe the epidemiology of the outbreak, the steps taken to determine the causative pathogen and the contaminated foods and risk factors, and highlight recommendations to prevent future outbreaks.

METHODS

Outbreak location

The outbreak occurred in a secondary-level boarding school attended by 597 female students in Seremban district, Negeri Sembilan state, an urban area in Malaysia.

Epidemiological investigation

A case was defined as any person who developed abdominal pain, vomiting or diarrhoea after consuming any food or drinks at the boarding school canteen from 19 November 2021 at 06:30 to 21 November 2021 at 22:00. Active case-finding was conducted through face-to-face interviews, guided by a standardized Ministry of Health food poisoning questionnaire. Data were gathered about the sociodemographic characteristics of the cases, their symptoms, time of symptom onset and food consumption history. Records from government and private health-care facilities were reviewed to identify similar cases that may have been linked to the outbreak of foodborne illness through formal requests made to the relevant authorities.

An unmatched case–control study was conducted due to the challenges of recruiting participants during the coronavirus disease (COVID-19) pandemic and of conducting a field study. Individuals were eligible for inclusion if they had been exposed to the food prepared and served by the boarding school canteen during 19 to 21 November 2021. Participants were recruited using convenience sampling. The control group was defined as those who consumed the same food but did not experience any symptoms.

The attack rate of all students was determined, and the odds ratio (OR) was calculated for all reported food exposures. *P* values were calculated using Fisher's exact test, with statistical significance defined as $P<0.05$. The data were verified by cross-checking with health-care facility and school records. Then the data were transformed into a line list using Microsoft Excel (2021). All data were collected in hardcopy form and kept confidential in locked storage by the Seremban District Health Office. Data were analysed using the IBM Statistical Package for the Social Sciences (SPSS) version 26 (Chicago, IL, USA).

Laboratory investigation

Samples were collected for testing on 22 November 2021. Proxy food samples, hand swabs from food handlers and swabs from kitchen utensils were tested by culture and sensitivity for *B. cereus*, *Escherichia coli*, coliform bacteria, *Salmonella* species and *Staphylococcus aureus*. Rectal swabs from patients and food handlers were tested for enteric pathogens by culture and for sensitivity. Test results were obtained from the Public Health Laboratory Information System.

Environmental investigation

An environmental investigation was conducted to assess the physical environment by examining factors such as the water source, food storage areas, sanitation practices, ventilation systems and other possible sources of contamination. The food preparation process was assessed using Hazard Analysis Critical Control Point standards. Food handlers were questioned about their typhoid vaccination status and their attendance at food handling courses, as guided by the Ministry of Health's risk-based food premises inspection form, amendment 2018.

RESULTS

Epidemiological investigation

A total of 152 cases were identified among the 597 students who lived at the boarding school, giving an

attack rate of 25.5%. For the case–control study, there were 152 cases and 200 controls, for a ratio of 1:1.3. All cases were female and aged 13–17 years. They presented with abdominal pain (100%), nausea (97.4%, 148), vomiting (78.3%, 119) or diarrhoea (61.8%, 94), or a combination of these. All cases were treated as outpatients and none died.

The epidemic curve suggests an outbreak with a continual source, as indicated by the multiple peaks (**Fig. 1**), with a suggested first exposure at breakfast on 20 November 2021. The epidemic curve also suggests that there was ongoing exposure because the onset of symptoms for the first case was on 20 November 2021 at 16:00, and the onset for the last case was on 22 November 2021 at 07:30.

The food served by the canteen operator during 20 and 21 November 2021 with the highest ORs included beef rendang and rice cubes, served during breakfast on 20 November (OR: 20.54, 95% CI: 4.89–86.30 for the beef rendang; OR: 19.62, 95% CI: 2.62–147.01 for the rice cubes); white rice served during lunch (OR: 9.64, 95% CI: 4.32–76.55); white rice and chicken curry served during dinner on the same day (OR: 19.62, 95% CI: 2.62–147.01); and vermicelli and spicy soy sauce served during breakfast on 21 November (OR: 17.02, 95% CI: 4.03–71.86) (**Table 1**). Leftover food was not consumed by students or staff.

Environmental investigation

The assessment of food processing showed a temperature monitoring violation, as there was no temperature monitoring when raw food was received or during its storage in the chiller and freezer. The beef was defrosted for less than 1 hour. The beef was boiled in 40-kg quantities in a cauldron without temperature monitoring for 20 minutes, which may have contributed to uneven and insufficient heating. The rice was washed before cooking and was cooked in a large pot, with approximately 5 kg rice per pot. It was cooked fresh for each meal and was not served again.

During inspection of the premises, flies were noted in the kitchen due to non-functioning fly traps. Hand-washing stations were not equipped with soap. Otherwise, the overall cleanliness of the premises was rated at 96.6%. All 14 food handlers were asymptomatic and had received typhoid vaccinations and attended food safety training.

Laboratory investigation

The samples collected included five proxy foods (stir fry macaroni, white bread, fried chicken, soto vermicelli and chocolate cake), one sample of boiled water, 24 rectal swabs from 17 cases and seven food handlers, seven swabs from food preparers' hands, seven environmental samples and 15 water samples from drinking-water dispensers at the school. The laboratory investigation yielded *B. cereus* (<4000 colony forming units [CFU]/g) from the hand swab of one food preparer (staff member A) who worked the morning shifts on 20 and 21 November. Samples from two chopping boards also yielded *B. cereus* and *E. coli* (**Table 2**). The proxy food samples and the rice-scooping spoon yielded coliforms (**Table 2**).

Outbreak control measures

Following the outbreak, all activities at the canteen were temporarily suspended in accordance with Malaysia's Infectious Disease Control Act 1988. This allowed the kitchen operator to take necessary measures to ensure compliance with food and hygiene regulations before resuming operations. Food handlers were reminded to monitor temperatures closely, while the district health educator delivered talks to the food handlers and students as well as distributed informational pamphlets to students and teachers. To prevent future outbreaks, it is important to emphasize how to handle food safely and to educate food handlers, school administrators and students about food safety as well. A subsequent inspection was done to ensure that all necessary actions had been taken promptly.

DISCUSSION

Investigating outbreaks of foodborne illnesses enables possible sources of infection to be identified. This outbreak was most likely caused by *B. cereus* cross-contamination and poor temperature monitoring. In this outbreak, there were cases with emetic and diarrhoeal symptoms, suggesting a mixed source of *B. cereus*.[5]

The longer incubation periods observed and the continual common source pattern evidenced by the epidemiological curve, characterized by a gradual rise in

Fig. 1. **Epidemic curve of an outbreak of foodborne illness in a boarding school canteen, by date and time of symptom onset, Seremban district, Negeri Sembilan state, Malaysia, 20–22 November 2021**

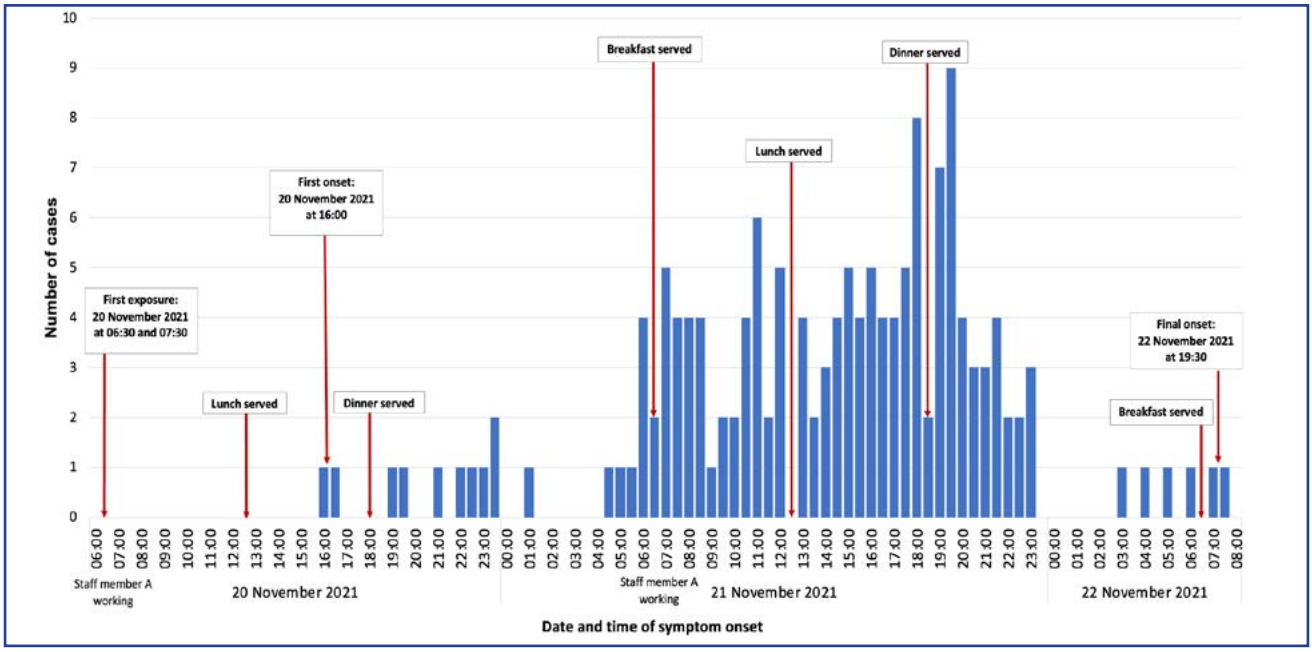

Table 1. **Case–control analysis of an outbreak of foodborne illness in a boarding school canteen, Seremban district, Negeri Sembilan state, Malaysia, 20–22 November 2021**[a]

Type of food	Cases (n = 152)			Controls (n = 200)			Odds ratio (95% CI)	P
	Exposed	Not exposed	Total	Exposed	Not exposed	Total		
20 November 2021 – Breakfast, 06:30 to 07:30								
Rice cubes[b]	**150**	**2**	**152**	**161**	**39**	**200**	**18.17 (4.31–76.55)**	**< 0.001**
Beef rendang[c]	**150**	**2**	**152**	**157**	**43**	**200**	**20.54 (4.89–86.30)**	**< 0.001**
Peanut gravy	148	4	152	140	60	200	15.86 (5.61–44.78)	< 0.05
Malted chocolate drink	147	5	152	129	71	200	16.18 (6.34–41.31)	< 0.05
20 November 2021 – Lunch, 12:30 to 13:30								
White rice	**151**	**1**	**152**	**188**	**12**	**200**	**9.64 (1.24–74.96)**	**< 0.05**
Fried spicy stuffed torpedo scad	**151**	**1**	**152**	**187**	**13**	**200**	**10.50 (1.36–81.16)**	**< 0.05**
Turmeric fried prawns	150	2	152	181	19	200	7.87 (1.80–34.35)	< 0.05
Cabbage cooked in coconut broth	150	2	152	179	21	200	8.80 (2.03–38.14)	< 0.05
20 November 2021 – Dinner, 18:00 to 19:00								
White rice	**151**	**1**	**152**	**177**	**23**	**200**	**19.62 (2.62–147.01)**	**< 0.05**
Chicken curry	**151**	**1**	**152**	**177**	**23**	**200**	**19.62 (2.62–147.01)**	**< 0.05**
Stir fry vegetables	149	2	152	170	30	200	13.15 (3.09–55.95)	< 0.05
Red apple	146	6	152	170	30	200	4.29 (1.74–10.60)	< 0.05
Plain water	150	2	152	170	30	200	13.24 (3.11–56.32)	< 0.05
21 November 2021 – Breakfast, 06:30 to 07:30								
Vermicelli	**150**	**2**	**152**	**163**	**37**	**200**	**17.02 (4.03–71.86)**	**< 0.05**
Spicy soy sauce	**150**	**2**	**152**	**163**	**37**	**200**	**17.02 (4.03–71.86)**	**< 0.05**
Malted drinks	147	5	152	150	50	200	9.8 (3.80–25.27)	< 0.05

CI: confidence interval.

[a] Foods in bold are suspected to have been associated with the outbreak.

[b] Rice cubes are compacted rice that is boiled and subsequently cut into small cubes.

[c] Beef rendang is a dry curry that is prepared using coconut milk and spices.

Table 2. **Laboratory results from an outbreak of foodborne illness in a boarding school canteen, Seremban district, Negeri Sembilan state, Malaysia, from samples collected on 22 November 2021**

Type of specimen	Test and method	No. of samples	Test result		Organism identified
			Positive	Negative	
Samples from cases and food handlers					
Hand swabs (food handler)	Culture and sensitivity for enteric pathogens	7	1	6	*Bacillus cereus* (<4000 CFU/g) from staff member A
Rectal swabs (food handlers and cases)		24	0	24	–
Samples from food and water					
Stir fry macaroni	*B. cereus* (ISO 7932:2004 [E])[a] *Escherichia coli* (AOAC 991.14) Coliform (AOAC 991.14) *Salmonella species* (ISO 6579-1:2017 [E]) *Staphylococcus aureus* (AOAC 2003.07-2006)	1	1	0	Coliform (1300 CFU/g)
White bread		1	1	0	Coliform (30 000 CFU/g)
Fried chicken		1	0	1	–
Soto vermicelli[b]		1	0	1	–
Chocolate cake		1	0	1	–
Water (from drinking-water dispenser)	Coagulase-positive *Staphylococci* (ISO 6888-1:1999/ Amd.1.2003 [E])	1	0	1	–
Drinking-water dispenser		1	0	1	–
Filtered water dispenser		1	0	1	–
Samples from kitchen utensils					
Cutting board (sample 1)	*B. cereus* (ISO 7932:2004 [E]) *E. coli* (AOAC 991.14) Coliform (AOAC 991.14) *S. aureus* (AOAC 2003.07-2006)				*B. cereus* (<4000 CFU/g) *E. coli* (700 CFU/g) Coliform (350 000 CFU/g)
Cutting board (sample 2)		1	1	0	*B. cereus* (<4000 CFU/g) *E. coli* (100 CFU/g) Coliform (34 000 CFU/g)
Rice spoon		1	1	0	Coliform (6500 CFU/g)
Ladle		1	0	1	–
Tip of water bottle		1	0	1	–
Pan surface		1	0	1	–

AOAC: Association of Official Analytical Collaboration International; CFU: colony forming units; ISO: International Organization for Standardization; –: indicates no findings.

[a] The letter E after an ISO standard indicates that it was published in English.

[b] Soto vermicelli is a plain soup eaten with vermicelli noodles.

the number of cases and numerous peaks over time, can be explained by multiple contamination incidents occurring over 2 days. The food could have been continually contaminated by staff member A, kitchen equipment or contaminated food. The self-service buffet style of food service during which students have their meals in groups in the dining hall may also have contributed to this type of epidemiological curve and could have facilitated possible contamination by students.

The ORs associated with the food should be interpreted with caution due to the wide confidence intervals, which make it difficult to determine which foods were most strongly associated with illness. However, not monitoring the temperature of the raw meat could also allow B. cereus to survive the cooking process and continue multiplying,[10] which could explain the high OR for beef rendang. Multiple factors commonly contribute to outbreaks of foodborne illness, especially those related to improper storage (i.e. refrigeration) and failure to maintain proper temperatures.[11] Other sauce-based dishes, such as chicken curry and spicy soy sauce, also had a high OR since they were served with rice. Rice was often served for breakfast, lunch and dinner on the dates around the outbreak occurrence, so it is possible that rice was also responsible for this outbreak.

Despite swabbing workers' hands and kitchen equipment, only low numbers of CFUs were found; however, the positivity still indicates contamination since low numbers of *B. cereus* have caused outbreaks.[12] To improve the efficacy of hand-washing and reduce the

number of *B. cereus* spores, soap should be used and hands should be washed for at least 20 seconds.[13,14] Drying hands with disposable towels instead of cloth towels can also reduce the risk of cross-contamination.[15] The presence of *E. coli* and coliforms suggests poor hygiene practices.

The study has limitations that make it difficult to definitively confirm that *B. cereus* caused the outbreak. None of the food items from the days on which contamination likely occurred were available for testing; instead, proxy food samples were used. When tested, these proxy samples were negative for *B. cereus* toxins. In terms of the statistical analyses, multivariable analysis was not performed, and the assessment of potentially contaminated food was conducted solely using univariable analysis. Ideally, a cohort study should have been conducted, but a case–control design was adopted due to the limited number of staff and stringent standard operating procedures implemented during the COVID-19 pandemic. Recall bias may exist due to the retrospective nature of participants providing a history of their food intake, and potential confounders were not adjusted for statistically. Due to the limitations identified in this study, the definitive causative agent of the foodborne outbreak is not confirmed.

In conclusion, this outbreak investigation highlights the need for proper food handling, temperature monitoring and hygiene practices. *B. cereus* most likely caused the outbreak through cross-contamination, while the presence of *E. coli* indicated poor hygiene standards. It is necessary to ensure there are strict enforcement of and more effective control measures, continual training and frequent spot inspections to identify and address any violations in food handling and hygiene practices.

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Conflicts of interest

The authors have no conflicts of interest to declare.

Ethics statement

Ethical approval was obtained from the Medical Research and Ethics Committee, Ministry of Health, Malaysia (no. NMRR-22-00798-WMX).

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References

1. Jaffee S, Henson S, Unnevehr L, Grace D, Cassou E. The safe food imperative: accelerating progress in low- and middle-income countries. Washington (DC): World Bank; 2018. Available from: http://hdl.handle.net/10986/30568, accessed 3 February 2023.
2. Compendium of environment statistics, Malaysia 2020. Putrajaya: Department of Statistics, Malaysia; 2020: page 223. Available from: https://newss.statistics.gov.my/newss-portalx/ep/epProductFreeDownloadSearch.seam, accessed 1 February 2023.
3. Vector-borne disease and outbreak reporting system. Putrajaya: Ministry of Health, Malaysia; 2022. Available from: http://vekpro.moh.gov.my/vekpro/index.htm, accessed 10 December 2022.
4. Ehling-Schulz M, Guinebretiere M-H, Monthán A, Berge O, Fricker M, Svensson B. Toxin gene profiling of enterotoxic and emetic *Bacillus cereus*. FEMS Microbiol Lett. 2006;260(2):232–40. doi:10.1111/j.1574-6968.2006.00320.x pmid:16842349
5. Gram-positive bacteria. In: Lampel K, Al-Khaldi S, Cahill S, editors. Bad bug book: handbook of foodborne pathogenic microorganisms and natural toxins. 2nd ed. Silver Spring (MD): Center for Food Safety and Applied Nutrition, U.S. Food and Drug Administration; 2012. Available from: https://www.fda.gov/media/83271/download, accessed 27 February 2023.
6. Jeßberger N, Rademacher C, Krey VM, Dietrich R, Mohr A-K, Böhm M-E, et al. Simulating intestinal growth conditions enhances toxin production of enteropathogenic *Bacillus cereus*. Front Microbiol. 2017;8:627. doi:10.3389/fmicb.2017.00627 pmid:28446903
7. Rouzeau-Szynalski K, Stollewerk K, Messelhäusser U, Ehling-Schulz M. Why be serious about emetic *Bacillus cereus*: cereulide production and industrial challenges. Food Microbiol. 2020;85:103279. doi:10.1016/j.fm.2019.103279 pmid:31500702
8. Yu S, Yu P, Wang J, Li C, Guo H, Liu C, et al. A study on prevalence and characterization of *Bacillus cereus* in ready-to-eat foods in China. Front Microbiol. 2020;10:3043. doi:10.3389/fmicb.2019.03043 pmid:32010099
9. Osimani A, Aquilanti L, Clementi F. *Bacillus cereus* foodborne outbreaks in mass catering. Int J Hospit Manag. 2018;72:145–53. doi:10.1016/j.ijhm.2018.01.013
10. Tewari A, Singh SP, Singh R. Incidence and enterotoxigenic profile of *Bacillus cereus* in meat and meat products of Uttarakhand, India. J Food Sci Technol. 2015;52(3):1796–801. doi:10.1007/s13197-013-1162-0 pmid:25745259
11. Panisello PJ, Rooney R, Quantick PC, Stanwell-Smith R. Application of foodborne disease outbreak data in the development and maintenance of HACCP systems. Int J Food Microbiol. 2000;59(3):221–34. doi:10.1016/S0168-1605(00)00376-7 pmid:11020042

12. Carroll LM, Wiedmann M, Mukherjee M, Nicholas DC, Mingle LA, Dumas NB, et al. Characterization of emetic and diarrheal *Bacillus cereus* strains from a 2016 foodborne outbreak using whole-genome sequencing: addressing the microbiological, epidemiological, and bioinformatic challenges. Front Microbiol. 2019;10:144. doi:10.3389/fmicb.2019.00144 pmid:30809204

13. Dorotíková K, Kameník J, Bogdanovičová K, Křepelová S, Strejček J, Haruštiaková D. Microbial contamination and occurrence of *Bacillus cereus* sensu lato, *Staphylococcus aureus*, and *Escherichia coli* on food handlers' hands in mass catering: comparison of the glove juice and swab methods. Food Control. 2022;133:108567. doi:10.1016/j.foodcont.2021.108567

14. Sasahara T, Hayashi S, Hosoda K, Morisawa Y, Hirai Y. Comparison of hand hygiene procedures for removing *Bacillus cereus* spores. Biocontrol Sci. 2014;19(3):129–34. doi:10.4265/bio.19.129 pmid:25252644

15. Yap M, Chau ML, Hartantyo SHP, Oh JQ, Aung KT, Gutiérrez RA, et al. Microbial quality and safety of sushi prepared with gloved or bare hands: food handlers' impact on retail food hygiene and safety. J Food Prot. 2019;82(4):615–22. doi:10.4315/0362-028X.JFP-18-349 pmid:30907665

Descriptive analysis of a SARS-CoV-2 outbreak among health-care workers in a regional hospital in the Philippines

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Objective: On 25 July 2022, trainees from the Field Epidemiology Training Programme in Northern Luzon, Philippines were sent to conduct an epidemiological investigation of six confirmed cases of severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) among staff of a regional hospital in Mountain Province. The investigation had three objectives: to profile the cases, identify the source and mode of transmission, and recommend prevention and control measures.

Methods: Descriptive epidemiology was used to investigate the outbreak, with the standard case definition issued by the Philippine Department of Health.

Results: A total of 167 hospital personnel and interns tested positive for SARS-CoV-2 infection between 6 July and 31 August 2022, with a peak in the number of cases on 20 July. Among the cases, 57 (34%) had a history of travel, with 41 (25%) having travelled to Boracay island to attend team-building activities. Most cases were asymptomatic, and the most affected group was those aged 30–34 years. The highest number of cases occurred among nurses. It was discovered that the team-building activities on Boracay did not strictly adhere to safety protocols.

Discussion: This outbreak suggests that transmission of SARS-CoV-2 among health-care workers can occur through contact with other staff members outside of the hospital setting and highlights the importance of strict adherence to safety protocols to prevent the spread of SARS-CoV-2.

On 12 July 2022, the Provincial Epidemiology and Surveillance Unit in Mountain Province, Philippines, reported six confirmed cases of infection with severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) among employees at a regional hospital in the province. Five of the six cases (83%) had travelled to Boracay island. This outbreak was reported through the national Event-Based Surveillance and Response System. In response, on 25 July, trainees from the Field Epidemiology Training Programme (FETP) in Northern Luzon were sent to conduct an epidemiological investigation.

The regional hospital is a Department of Health (DOH) hospital located in Bauko, Mountain Province. The hospital has 100 beds and 681 employees, including casual labourers and contractual employees. It is the referral hospital for Mountain Province and neighbouring provinces. During the SARS-CoV-2 pandemic, the hospital accommodated asymptomatic to severe cases and served as a step-down facility from the infectious disease pavilion. The hospital also has a SARS-CoV-2 molecular laboratory, capable of running 192 tests at a time and providing routine testing for employees. Routine testing for SARS-CoV-2 is done every 15 days.

When the outbreak was reported in July 2022, Mountain Province was in Alert Level 1 due to a decrease in SARS-CoV-2 cases and successful roll-out of vaccinations; at Alert Level 1, travel within and outside of the province is permitted as well as 100% operational capacity in all establishments, provided the minimum public health standards are observed.

To promote better well-being and mental health among its employees after the SARS-CoV-2 pandemic,

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the hospital's management planned team-building activities outside of the province. The activities were held on Boracay island, in Malay, Aklan, during 3–21 July 2022, and planned for Bolinao, Pangasinan, during succeeding weeks; each group attended activities for 4 days. The Boracay group was divided into three teams and the Bolinao group into two teams. The Boracay group was the first to travel.

Boracay is a small island in the Western Visayas Region known for its resorts and beaches. It was at Alert Level 1 at the time of the outbreak, and an increase in the number of foreigners visiting Boracay in July was reported from the Malay Tourism Office. On 14 July, Aklan reported 43 active cases of SARS-CoV-2 infection, including five from the municipality of Malay which includes Boracay.

METHODS

The FETP trainees conducted a descriptive epidemiological analysis to investigate confirmed cases of SARS-CoV-2 infection among staff of the regional hospital in Mountain Province, Philippines. The definition of a confirmed SARS-CoV-2 case used in this study was based on the DOH memorandum order dated 7 March 2022 and included:

- any individual, irrespective of the presence or absence of clinical signs and symptoms, who had SARS-CoV-2 infection confirmed by a test conducted at the national reference laboratory, a subnational reference laboratory or a DOH-licensed SARS-CoV-2 testing laboratory, or a combination of these; OR
- any suspected or probable case of SARS-CoV-2 infection who tested positive using an antigen test in areas with outbreaks or in remote settings where reverse transcription–polymerase chain reaction (RT–PCR) is not immediately available, provided that the antigen test satisfies the recommended minimum regulatory, technical and operational specifications set by the Health Technology Assessment Council.

The line list of positive cases and case investigation forms for hospital staff were obtained from the provincial database of SARS-CoV-2 cases. From this, a separate line list of confirmed SARS-CoV-2 cases among hospital staff was created.

To gather additional information, a guided questionnaire was used to conduct interviews with key informants, including the head of the human resources department, team leaders and coordinators of teams two and three from the team-building activities (the leader of team one was unavailable), and the Health Education and Promotions Officer who joined the team-building activities on Boracay. The purpose of these interviews was to identify the activities undertaken and practices observed during the team-building that may have contributed to the spread of SARS-CoV-2 among hospital staff.

RESULTS

From 6 July to 31 August 2022, 167 personnel and interns working at the regional hospital tested positive for SARS-CoV-2. Cases were continually detected during this period, with a peak in the number of cases on 20 July (**Fig. 1**). Of the cases, 57 (34%) had a history of travel, and 41 (25%) had travelled to Boracay to attend the team-building activities. Among these cases, 19 (46%) were from the second group of attendees (13–16 July). Most cases (n = 96, 57%) were asymptomatic, and most of those who had travelled to Boracay were asymptomatic (27/41, 66%). Altogether, 96% (69/71) of cases with symptoms had mild illness. All cases recovered.

The first reported case worked in the surgery department of the hospital and was detected through routine employee testing on 6 July. The hospital reported that the case had travelled to a nearby municipality to attend a social gathering 4 days before testing. No confirmed case had been reported among hospital staff for 2 months before this case. The second case occurred in a nurse working in the outpatient department; this case was also detected during scheduled routine testing and was swabbed 3 days after returning from Boracay (**Fig. 1**).

The age range of cases was 21–64 years (median: 32 years), with the most affected age group being those aged 30–34 years (**Fig. 2**). The majority of cases occurred among females (130, 78%). Nurses accounted for the highest number of cases (60, 36%), followed by physicians (23, 14%), administrative assistants (11, 7%) and nursing attendants (8, 5%), with administrative aides,

Fig. 1. **Confirmed cases of severe acute respiratory syndrome coronavirus 2 in a regional hospital, by date of specimen collection (*N* = 167), Philippines, 1 July–31 August 2022**

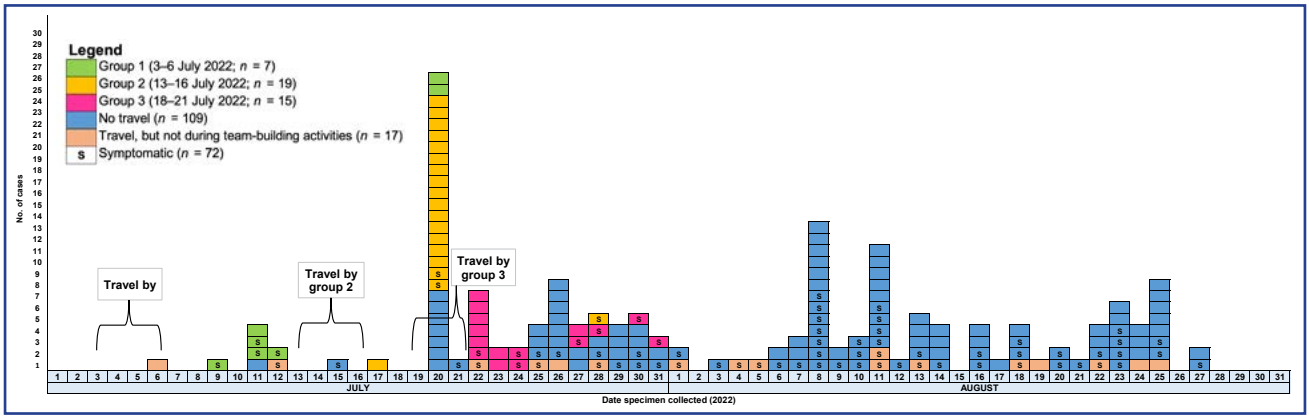
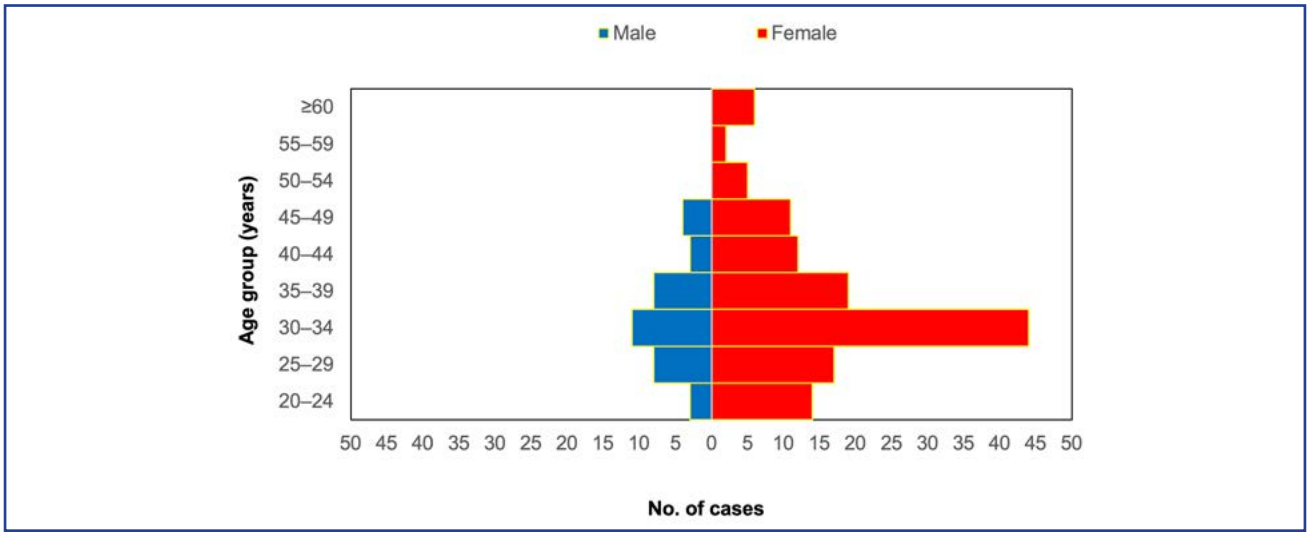


Fig. 2. **Confirmed cases of severe acute respiratory syndrome coronavirus 2 in a regional hospital, by age group and sex (*N* = 167), Philippines, 1 July–31 August 2022**



medical technologists, medical technologist interns and radiology technologists accounting for 7 cases each (4% each). The remaining cases occurred among a range of other hospital staff. Health workers were affected across all levels and wards in the hospital, and both front-line and non-front-line health workers were equally affected. Some of the cases worked in multiple areas of the hospital. All cases were fully vaccinated and had received at least one booster dose.

Key informant interviews

Staff were not required to be tested before travel; instead, attendees only had to report that they were asymptomatic. Safety briefings were conducted before and after each activity on Boracay, and team leaders were assigned as monitors. All activities were held at the beach, and meals were served buffet style to groups in an area with good ventilation and with two to three individuals per table. Two to three participants were accommodated in each room, in which there were single beds; some two-bed rooms had an additional mattress so three people could be accommodated. The bedrooms were air-conditioned. During free time, participants visited souvenir shops and fast food centres, and some went drinking at night. It was reported that the attendees did not observe physical distancing and did not wear masks while out drinking and during water sports.

Control measures

Several control measures were implemented by the regional hospital after the first six cases were reported. Swabbing of all employees every 15 days continued, with mandatory testing for the last team upon their return from travel. Cases were advised to isolate in their homes and were allowed to return to duty after completing 5 days' isolation from the date of onset of symptoms or testing, as certified by their safety officer. Members of the second team, who were not scheduled for routine testing on returning from travel, were asked to undergo testing. Hospital management postponed the later travel to Bolinao. Management also strengthened their contingency plans for outbreaks at the hospital, which included promoting stricter observance of minimum public health standards in the facility at all times.

DISCUSSION

This outbreak highlights the impact of travel and team-building activities on the transmission of SARS-CoV-2 among health-care workers. The peak of cases among hospital staff occurred on 20 July 2022, which coincided with the team-building activities on Boracay. Similar findings have been reported in a study conducted in Petaling District, Malaysia, where the authors found that social gatherings were a significant contributor to the spread of SARS-CoV-2 among health-care workers.[1] This outbreak also suggests that transmission of SARS-CoV-2 among health-care workers can occur not only through direct exposure to patients in a ward but also through contact with other staff members outside of the hospital. This is consistent with previous studies, such as that of the SARS-CoV-2 outbreak in Tasmanian health-care settings, which demonstrated that transmission among health-care workers can occur outside of patient care areas.[2]

Health-care workers are vulnerable to SARS-CoV-2 transmission not only directly from patients but also from other staff after patient care. Ongoing transmission in the hospital may have also contributed to this outbreak as evidenced by the detection of cases with no travel history. Hospital staff working in close proximity while infectious may have unknowingly contributed to the spread of SARS-CoV-2 in the hospital.[3] Our investigation revealed that some cases worked in multiple areas of the hospital, which made transmission between and among staff possible.[1] This highlights the importance of observing physical distancing and other public health measures, especially in health-care settings where staff may work in multiple areas and come into contact with a larger number of colleagues and patients. Unrecognized asymptomatic and presymptomatic infections might also contribute to transmission in these settings.[4,5]

The majority of health-care workers who travelled were asymptomatic upon detection, and this may be attributed to their vaccination history. All cases were vaccinated, and vaccinated individuals are most likely to be asymptomatic.[6] Vaccination has a substantial impact on reducing the incidence of coronavirus disease, hospitalizations and deaths, especially among vulnerable individuals with comorbidities and risk factors associated with severe disease.[7] Fully vaccinated individuals also have fewer days during which they are symptomatic and have less severe illness.[8] Most of the symptomatic cases had only mild signs and symptoms.

This study underscores the need for regular testing of health-care workers, especially before and after travel or team-building activities. In this investigation, the hospital had its own molecular laboratory so it is capable of testing staff regularly. Regular testing will help identify possible sources of infection and prevent further transmission. It is also important for health-care workers who test positive to be vigilant in identifying and reporting close contacts, as this will facilitate contact tracing and prevent further spread of the virus.

This study is only descriptive and thus is limited in its ability to determine risk factors. This limitation and the absence of testing before travel make it difficult to determine whether transmission existed in the hospital before the detection of the first case. Additionally, close contacts were not disclosed, so the study was not able to trace secondary and tertiary transmission. Despite these limitations, the study was able to provide further evidence of the risk of transmission between health-care workers outside of health-care facilities.

Therefore, it is likely that the travel to and attendance at the team-building activities contributed to this outbreak of SARS-CoV-2 among the staff and interns at this regional hospital. Not observing minimum public health standards during the activities – such as physical distancing and avoiding direct contact during meals and drinking sessions – likely contributed to transmission.

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Conflicts of interest

The authors have no conflicts of interest to declare.

Ethics statement

Ethical clearance was not required because this report used routinely available data and no personal identifying information was collected.

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References

1. Supramanian RK, Sivaratnam L, Rahim AA, Abidin NDIZ, Richai O, Zakiman Z, et al. Descriptive epidemiology of the first wave of COVID-19 in Petaling District, Malaysia: Focus on asymptomatic transmission. Western Pac Surveill Response J. 2021;12(2):82–8. doi:10.5365/wpsar.2020.11.4.001 pmid:34540316
2. Johnston FH, Anderson T, Harlock M, Castree N, Parry L, Marfori T, et al. Lessons learnt from the first large outbreak of COVID-19 in health-care settings in Tasmania, Australia. Western Pac Surveill Response J. 2021;12(4):1–7. doi:10.5365/wpsar.2021.12.4.884 pmid:35251738
3. Sakamoto N, Ota M, Takeda T, Kosaka A, Washino T, Iwabuchi S, et al. Nosocomial outbreak of coronavirus disease in two general wards during the initial wave of the pandemic in 2020, Tokyo, Japan. Western Pac Surveill Response J. 2022;13(1):1–5. doi:10.5365/wpsar.2022.13.1.906 pmid:35494413
4. Kimball A, Hatfield KM, Arons M, James A, Taylor J, Spicer K, et al. Asymptomatic and presymptomatic SARS-CoV-2 infections in residents of a long-term care skilled nursing facility – King County, Washington, March 2020. MMWR Morb Mortal Wkly Rep. 2020;69(13):377–81. doi:10.15585/mmwr.mm6913e1 pmid:32240128
5. Tong ZD, Tang A, Li KF, Li P, Wang HL, Yi JP, et al. Potential presymptomatic transmission of SARS-CoV-2, Zhejiang Province, China, 2020. Emerg Infect Dis. 2020;26(5):1052–4. doi:10.3201/eid2605.200198 pmid:32091386
6. Pritchard E, Matthews PC, Stoesser N, Eyre DW, Gethings O, Vihta K-D, et al. Impact of vaccination on new SARS-CoV-2 infections in the United Kingdom. Nat Med. 2021;27(8):1370–8. doi:10.1038/s41591-021-01410-w pmid:34108716
7. Moghadas SM, Vilches TN, Zhang K, Wells CR, Shoukat A, Singer BH, et al. The impact of vaccination on coronavirus disease 2019 (COVID-19) outbreaks in the United States. Clin Infect Dis. 2021;73(12):2257–64. doi:10.1093/cid/ciab079 pmid:33515252
8. Tan SY, Teo SP, Abdullah MS, Chong PL, Asli R, Mani BI, et al. COVID-19 symptom duration: associations with age, severity and vaccination status in Brunei Darussalam, 2021. Western Pac Surveill Response J. 2022;13(4):1–9. doi:10.5365/wpsar.2022.13.4.941 pmid:36817502

Communicating health and science to the public: a role for scientists and academic researchers

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The coronavirus disease (COVID-19) pandemic identified valuable lessons for Australia's public health response including the need for timely, clear and open communication to the public.[1] With the launch of the World Health Organization Western Pacific Region Communication for Health (C4H) initiative,[2] insights from social, behavioural and communication sciences contribute to improved health outcomes. Close collaboration between journalists and scientists is important, particularly during a pandemic, for developing trust in science.[3] This perspective piece highlights the importance of engaging trusted scientists and academic researchers during public health emergencies while ensuring they receive communication training to confidently interact with journalists and the public.

During the COVID-19 pandemic, science evolved rapidly and government decisions were constantly updated. However, they were often challenged by the public, for example, the effectiveness and side-effects of COVID-19 vaccines and the transmission route of SARS-CoV-2. The volume of information generated during the COVID-19 pandemic was addressed during the 73rd World Health Assembly, where Member States were urged to unite to manage the "infodemic", and to combat and prevent the spread of mis- and disinformation while respecting freedom of expression.[4] Social media became an invaluable source of material for journalists, with clinicians, scientists and academic researchers posting facts and their observations using these channels. It was well-documented that automated online accounts or software robots known as "bots" disproportionately contributed to controversial conversations online and influenced opinion trends,[5] and this was amplified during the pandemic with up to 66% of bots actively posting about COVID-19.[6] In addition, beliefs in misinformation were significantly associated with lower levels of digital health literacy, the perceived threat of COVID-19, confidence in government and trust in scientific institutions.[7]

The research community generated a large number of research studies on COVID-19, with publishers supporting open access and sharing resources to rapidly disseminate scientific information.[8] Commissioning research with trusted local researchers and the rapid creation of evidence from emergency response projects were successfully utilized to inform the public health response.[9] However, conducting research is not solely about contributing to the evidence base; equally important is communicating research findings to the target audience to achieve an effective public health response.

The COVID-19 pandemic introduced unique and fast-growing challenges for health communicators. Ratzan et al.[10] suggested three areas of capacity building: the need for proactive communicators to combat false information and establish trusted leadership; the importance of planning for unpredictability whilst acknowledging the uncertainty as scientific evidence evolves; and to remain people-centred with interventions for health and media literacy. The health literacy,

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language and cultural needs of a community should also be considered when developing public health messaging about COVID-19.[11]

Despite the infodemic, lack of trust in governments, rapidly evolving science and challenges in health communication, journalists still needed to meet daily reporting deadlines. As journalists play a critical role in influencing public opinion, they have a responsibility not to publish inaccurate or misleading headlines that cause fear and diminish countermeasures against the outbreak.[12] Addressing these issues resulted in the media shifting towards the use of scientists[13] and academic researchers as spokespersons, with virologists, infectious disease specialists and epidemiologists most commonly engaging with them. These scientists and academic researchers were able to provide interpretations of new research for the public and became crucial to the public's understanding of COVID-19.

At a tumultuous time during a global pandemic when a "war of words"[14] can misguide the public, there is a need to turn to credible sources of information from experts. As an example, Australia turned to several epidemiologists and infectious disease specialists for balanced, honest, authentic and evidence-based advice, scaling up the engagement of scientists and academic researchers with the media became increasingly evident. It is critical for scientists and academic researchers to further develop their science communication skills and to be confident when collaborating with journalists as the media continually seeks experts for commentary. Building strong relationships with journalists may help combat misinformation and misconceptions of science and research and might reinforce important messages from government-funded public health campaigns. Considering the insights gained from the COVID-19 pandemic, it is time to prioritize and invest in science communication training and build capacity for scientists and academic researchers to engage with the media. Equipping infectious disease experts, virologists, epidemiologists and many other academic researchers with effective public engagement and science communication skills may enable them to become influential champions in rebuilding trust in science during future disease outbreaks.

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References

1. Basseal JM, Bennett CM, Collignon P, Currie BJ, Durrheim DN, Leask J, et al. Key lessons from the COVID-19 public health response in Australia. Lancet Reg Health West Pac. 2023;30:100616. doi:10.1016/j.lanwpc.2022.100616 pmid:36248767
2. Communication for health in the WHO Western Pacific Region. Manila: WHO Regional Office for the Western Pacific; 2021. Available from: https://apps.who.int/iris/handle/10665/346654, accessed 25 June 2023.
3. Beilstein CM, Lehmann LE, Braun M, Urman RD, Luedi MM, Stüber F. Leadership in a time of crisis: lessons learned from a pandemic. Best Pract Res Clin Anaesthesiol. 2021;35(3):405–14. doi:10.1016/j.bpa.2020.11.011 pmid:34511228
4. Managing the COVID-19 infodemic: promoting healthy behaviours and mitigating the harm from misinformation and disinformation. Geneva: World Health Organization; 2020. Available from: https://www.who.int/news/item/23-09-2020-managing-the-covid-19-infodemic-promoting-healthy-behaviours-and-mitigating-the-harm-from-misinformation-and-disinformation, accessed 25 June 2023.
5. Yuan X, Schuchard RJ, Crooks AT. Examining emergent communities and social bots within the polarized online vaccination debate in Twitter. Soc Media Soc. 2019;5(3). doi:10.1177/2056305119865465
6. Himelein-Wachowiak M, Giorgi S, Devoto A, Rahman M, Ungar L, Schwartz HA, et al. Bots and misinformation spread on social media: implications for COVID-19. J Med Internet Res. 2021;23(5):e26933. doi:10.2196/26933 pmid:33882014

7. Pickles K, Cvejic E, Nickel B, Copp T, Bonner C, Leask J, et al. COVID-19 misinformation trends in Australia: prospective longitudinal national survey. J Med Internet Res. 2021;23(1):e23805. doi:10.2196/23805 pmid:33302250

8. de las Heras-Pedrosa C, Jambrino-Maldonado C, Rando-Cueto D, Iglesias-Sánchez PP. COVID-19 study on scientific articles in health communication: a science mapping analysis in Web of Science. Int J Environ Res Public Health. 2022;19(3):1705. doi:10.3390/ijerph19031705 pmid:35162726

9. Campbell D, Edwards B, Milat A, Thackway S, Whittaker E, Goudswaard L, et al. NSW Health COVID-19 Emergency Response Priority Research program: a case study of rapid translation of research into health decision making. Public Health Res Pract. 2021;31(4):3142124. doi:10.17061/phrp3142124 pmid:34753169

10. Ratzan SC, Sommariva S, Rauh L. Enhancing global health communication during a crisis: lessons from the COVID-19 pandemic. Public Health Res Pract. 2020;30(2):e3022010. doi:10.17061/phrp3022010 pmid:32601655

11. McCaffery KJ, Dodd RH, Cvejic E, Ayrek J, Batcup C, Isautier JMJ, et al. Health literacy and disparities in COVID-19–related knowledge, attitudes, beliefs and behaviours in Australia. Public Health Res Pract. 2020;30(4):e30342012. doi:10.17061/phrp30342012 pmid:33294907

12. Shimizu K. 2019-nCoV, fake news, and racism. Lancet. 2020;395(10225):685–6. doi:10.1016/S0140-6736(20)30357-3 pmid:32059801

13. Mazer BL. Lessons in public (mis)communication about the laboratory from the COVID-19 pandemic. J Clin Microbiol. 2021;59(4):e02917-20. doi:10.1128/JCM.02917-20 pmid:33478980

14. McLaws ML. WHO global and local epidemiology and a perspective of communication during the pandemic. Presented at: The Australasian Medical Writers Association Annual Conference (online); 19 November 2020.

Financing for tuberculosis prevention, diagnosis and treatment services in the Western Pacific Region in 2005–2020

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Objective: This paper provides an overview of financing for tuberculosis (TB) prevention, diagnostic and treatment services in the World Health Organization (WHO) Western Pacific Region during 2005–2020.

Methods: This analysis uses the WHO global TB finance database to describe TB funding during 2005–2020 in 18 low- and middle-income countries (LMICs) in the Western Pacific Region, with additional country-level data and analysis for seven priority countries: Cambodia, China, the Lao People's Democratic Republic, Mongolia, Papua New Guinea, the Philippines and Viet Nam.

Results: Funding for the provision of TB prevention, diagnostic and treatment services in the 18 LMICs tripled from US$ 358 million in 2005 to US$ 1061 million in 2020, driven largely by increases in domestic funding, which rose from US$ 325 million to US$ 939 million over the same period. In the seven priority countries, TB investments also tripled, from US$ 340 million in 2005 to US$ 1020 million in 2020. China alone accounted for much of this growth, increasing its financing for TB programmes and services five-fold, from US$ 160 million to US$ 784 million. The latest country forecasts estimate that US$ 3.8 billion will be required to fight TB in the seven priority countries by 2025, which means that unless additional funding is mobilized, the funding gap will increase from US$ 326 million in 2020 to US$ 830 million by 2025.

Discussion: Increases in domestic funding over the past 15 years reflect a firm political commitment to ending TB. However, current funding levels do not meet the required needs to finance the national TB strategic plans in the priority countries. An urgent step-up of public financing efforts is required to reduce the burden of TB in the Western Pacific Region.

Tuberculosis (TB) remains a major public health concern, responsible for 10.6 million people falling ill and 1.6 million (including 187 000 people with HIV) dying globally in 2021.[1] Worldwide, TB is the 13th leading cause of death and in 2021 was the second leading infectious killer after coronavirus disease (COVID-19). Currently, TB kills more people than HIV-related disease and is a major contributor to antimicrobial resistance-related deaths.[1] Despite a steady decline in the TB disease burden over the past two decades, progress towards the target of reducing TB deaths by 90% from 2015 levels by 2030 – a target set by the World Health Organization (WHO) End TB Strategy and the United Nations (UN) Sustainable Development Goals (SDGs) – has been slow. Furthermore, the COVID-19 pandemic has reversed years of progress in providing TB services and reducing the TB disease burden.

Since 2002, WHO has been monitoring the funding of TB prevention, diagnostic and treatment services, based on data supplied by national TB programmes (NTPs), as part of its annual rounds of global TB data collection. Findings have been published in global TB reports and in the scientific literature. The latest annual rounds of data collection reflect the evolution in global TB strategies and capture investments in the implementation of new drug regimens, provider-initiated screening, novel diagnostics and the introduction of digital tools for surveillance and case management. These most recent data on global TB spending have revealed changes in the current TB financing landscape,

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shaped largely by shifts in government and external donor agency priorities at the global and regional levels.

Adequate and sustainable financing is essential for achieving universal health coverage, including access to quality TB services. Given the ambitious targets to end TB by 2030, levels of domestic and international funding for TB response based on historical allocations are now no longer adequate to meet the investments required by current global and country response plans.[2] Recognizing this shortfall and the need to accelerate the investment response, in 2018 world leaders attending the first United Nations High-Level Meeting (UNHLM) on TB committed to mobilizing US$ 13 billion a year to finance TB prevention, diagnosis and treatment by 2022 and US$ 2 billion a year to support TB research.[3] It is anticipated that world leaders will renew their commitment to accelerate the investment response to end TB at the second UNHLM on TB, scheduled to take place in 2023. According to WHO estimates, in 2020, with the COVID-19 pandemic altering access and delivery models for TB services, funding availed for TB prevention, diagnosis and treatment in 136 low- and middle-income countries (LMICs) totalled US$ 5.3 billion, less than half (41%) of the annual investments required to fund the global TB response to meet End TB targets. At US$ 901 million in 2019, funding for TB research also fell short of annual global investment targets (45%).[1]

The WHO Western Pacific Region is home to a quarter of the world's population (1.9 billion people) across 37 countries and areas, including 18 LMICs. In 2020, the Western Pacific Region accounted for 18% of the estimated global TB incidence, 19% of globally reported TB cases and 6% of estimated global TB deaths.[1,4] This demographically diverse region comprises both large countries with populations exceeding 1 billion people and small Pacific island countries and areas with just a few thousand residents. The Region is also diverse in terms of the TB burden, with some countries in the pre-elimination stage (defined as <10 TB cases per 1 million people) while others have high or intermediate TB burdens.[5] China, Mongolia, Papua New Guinea, the Philippines and Viet Nam are on the current list of 30 high-TB burden countries (2021–2025), and Cambodia is on the global TB watchlist.[1] Kiribati, the Lao People's Democratic Republic, Malaysia and the Marshall Islands are also among the 10 countries classified as regional priority countries for TB in the Western Pacific Region.[2]

In line with the global End TB Strategy, the *Western Pacific Regional Framework to End TB: 2021–2030* reaffirmed the importance of adequate financing for TB, effective financial management, and transition from external to domestic funding through strong political commitment and accountability.[2] In order to provide background to the regional TB framework and to inform its investment forecasts, this paper describes historic trends in financing for TB prevention, diagnostic and treatment services in the Western Pacific Region for the period 2005–2020, focusing on 18 LMICs that together accounted for 96% of the Region's notified cases in 2020. In addition, it presents estimated TB funding requirements for 2021–2025 for seven TB priority countries, based on information reported in their national strategic plans (NSPs). The seven priority countries are Cambodia, China, the Lao People's Democratic Republic, Mongolia, Papua New Guinea, the Philippines and Viet Nam.

METHODS

This descriptive analysis used data from the WHO global TB finance database, as of October 2021. This database contains data on yearly budgets, expenditure and use of TB health services,[4] information that countries and areas are required to report annually via WHO's global TB data collection system.[6] It also includes data on spending on inpatient and outpatient care, as estimated by WHO.[1]

This analysis distinguishes two major sources of TB financing: domestic and international donor funding. Total domestic funding for tuberculosis captures (1) "domestic" funding, which is funding for selected national TB programmes as reported by countries to WHO, as well as (2) "estimated domestic funds" for inpatient and outpatient care, which is estimated by WHO. International funding includes donor-funded TB investments as reported by national TB programmes to WHO. The methods used to estimate TB funding and costs are described in greater detail elsewhere.[7]

For the group of 18 LMICs in the Western Pacific Region, data from the WHO TB finance database were used to review trends in TB funding, disaggregated by funding source and by category of expenditure over the period 2005–2020.[7] For the seven priority countries, country-level funding data for 2005–2020 were examined, overall and by funding source, and by category

of expenditure for 2020. For the seven priority countries, the analysis also included comparisons of the amount of domestic funding (as a proportion of total TB funding) between 2015 and 2020 and implementation rates (the proportion of spent funds to received funds) during 2015–2020. Country-reported TB budget requirements, forecasted funding gaps (i.e. the difference between the budget required and the expected funding for subsequent years at the time of reporting) and actual funding gaps (i.e. the difference between the budget required and the actual received funding) were also calculated for each year during 2005–2020. Projected funding gaps for 2021–2025 were calculated from required annual budgets provided in NSPs; for the three countries where this information was not available, the budget required was projected using the average annual change in required funding for previous years (for China, this was for 2015–2020, for Mongolia, 2019–2023 and for the Philippines, 2024–2025). Anticipated availability of domestic and international funds to meet the NSP needs for 2021–2025 were estimated using the average annual change in received funding for 2021–2025 and assuming recent patterns would continue. Finally, we estimated the impact of the COVID-19 pandemic on TB financing in 2020 using country-reported information on re-allocation of TB budgets to the COVID-19 response. This information was collected through an online WHO survey added to 2020's annual TB data collection round, complemented by – in the case of the Philippines – data from the Philippine Department of Health.

Data analyses and visualizations were performed using the statistical software package R 3.6.2 (Comprehensive R Archive Network: https://cran.r-project.org/).

RESULTS

TB financing patterns in 18 LMICs

Total funding for TB prevention, diagnostic and treatment services in the group of 18 LMICs in the Western Pacific Region more than tripled in 15 years, from US$ 358 million in 2005 to US$ 1061 million in 2020 (**Fig. 1A**). Since 2015, when the End TB Strategy was launched, total TB funding increased by 1.4 times, largely driven by a rise in domestic funding, which increased from US$ 325 to US$ 939 million between 2005 and 2020. International funding for TB response in the Western Pacific Region increased from US$ 33 million in 2005 to a peak of US$ 185 million in 2013 before falling back to US$ 122 million in 2020. Throughout this 15-year period, the Global Fund to Fight AIDS, Tuberculosis and Malaria has provided a substantial proportion of the international funds; in 2020, 81% of the donor funding came from the Global Fund.

Domestic funding as a percentage of total funding received for TB declined during the 2000s, dropping to its lowest levels between 2011 and 2013, but since then has increased to similar levels to those seen in the mid-2000s (**Fig. 1B**). By 2020, domestic sources accounted for 88.5% of the total TB funding among the 18 LMICs (US$ 939 of the US$ 1061 million).

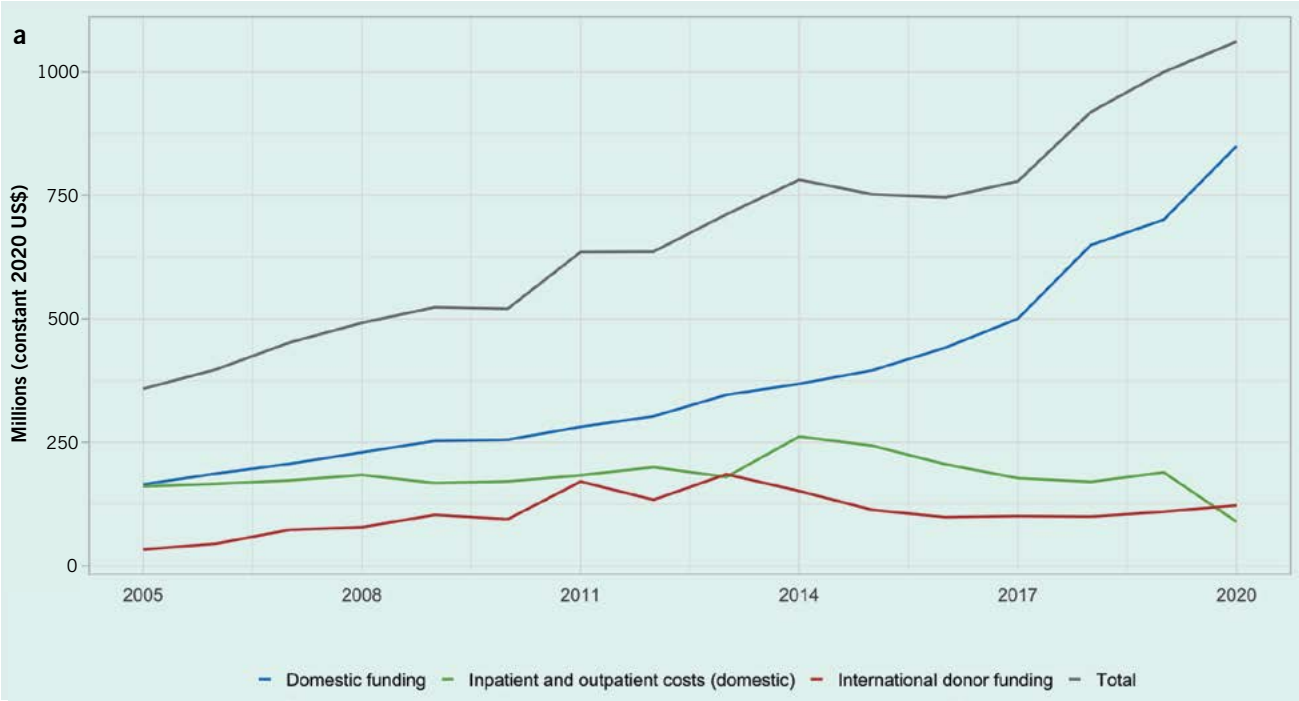
Averaged across the 18 LMICs and the period 2005–2020, drug-susceptible TB (DS-TB) programme management costs accounted for the largest proportion (37%) of total TB expenditures, followed by staff costs (25%), DS-TB drugs (11%) and drug-resistant TB (DR-TB) drugs (9%). Spending by category of expenditure for each year between 2005 and 2020 is shown in **Fig. 2**.

TB financing patterns in seven regional priority countries

Funding for TB prevention, diagnostic and treatment services in the seven priority countries increased from US$ 340 million in 2005 to US$ 658 million in 2015 and US$ 1020 million in 2020. In 2020, China alone accounted for 77% of the total amount of available funding for TB in the 18 LMICs in the Western Pacific Region (US$ 1.06 billion), with a quintupling of its (mostly domestic) funding for TB between 2005 and 2020 (**Fig. 3**). Funding the TB response in the other six countries increased from US$ 180 million in 2005 to US$ 315 million in 2015, before falling back to US$ 236 million in 2020. Large increases in the total funding available for TB were observed in the late 2000s in the Lao People's Democratic Republic and in the Philippines, and in the 2010s in Viet Nam. Cambodia mobilized substantial international funding in the late 2000s and early 2010s, while Mongolia increased both its domestic and international allocations for TB response between 2008 and 2012 (**Fig. 3**).

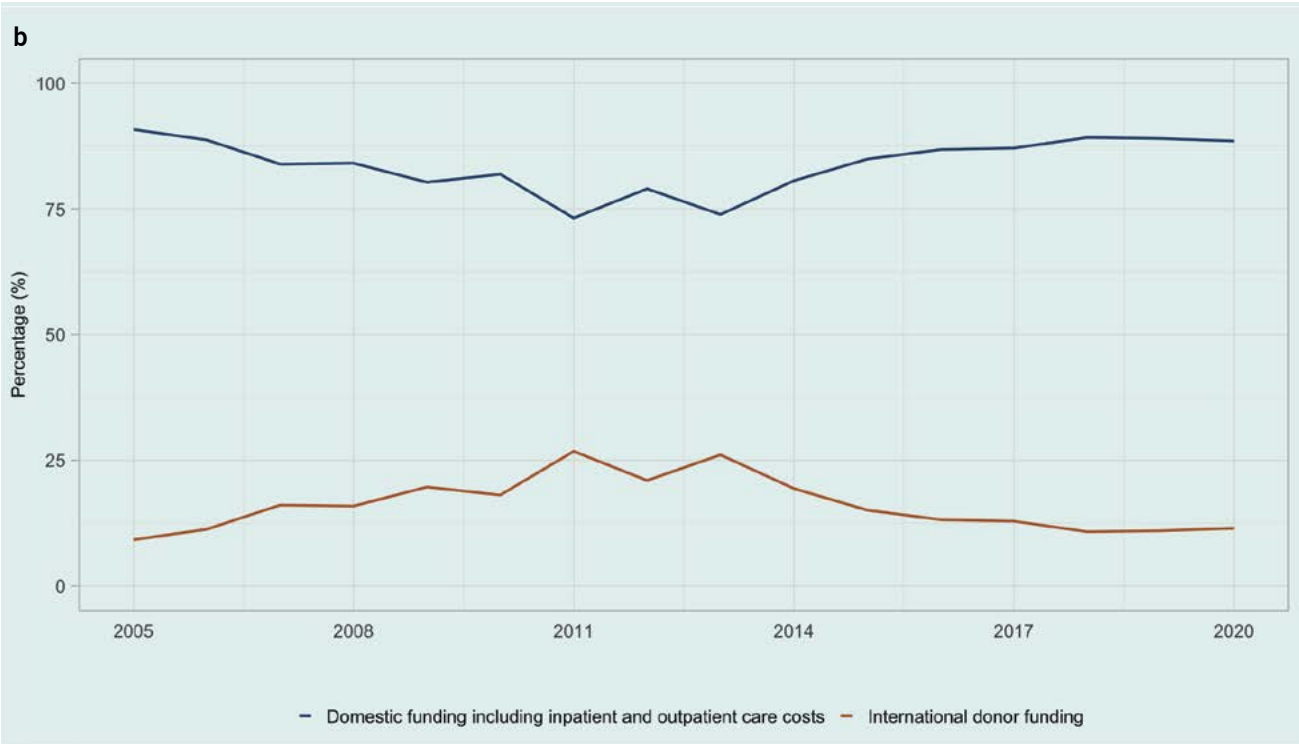
In 2020, received funding as a percentage of the total budget required averaged 70% in the seven priority

Fig. 1. **Funding for TB prevention, diagnostic and treatment services in 18 low- and middle-income countries in the Western Pacific Region, 2005–2020: (a) Total funding (US$ millions); (b) Domestic and international donor funding as a percentage of total funding (%)**



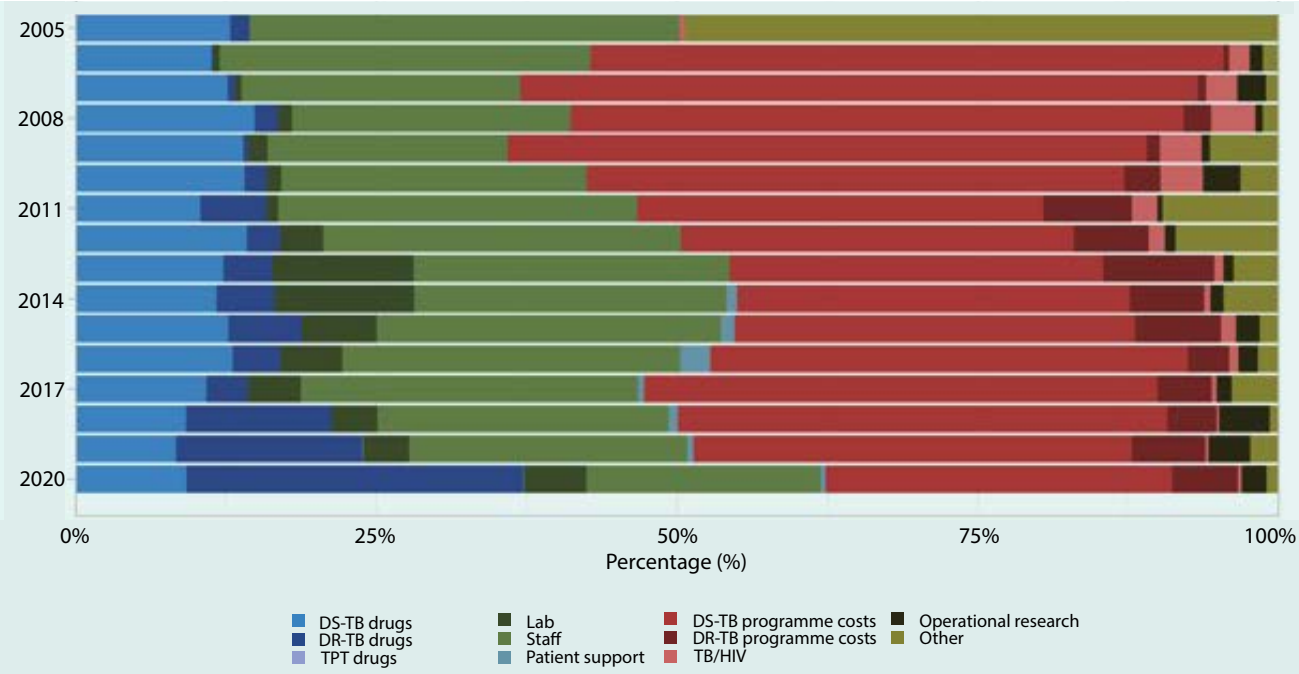
Domestic funding only includes public funding reported by national TB programmes to WHO; inpatient and outpatient care costs that were estimated independently by WHO are shown as a separate category.

Source: Global tuberculosis databases.[4]



Source: Global tuberculosis databases.[4]

Fig. 2. **Average spending by category of expenditure[a] (as reported in national TB strategic plans) by 18 low- and middle-income countries in the Western Pacific Region, 2005–2020 (% of total)**

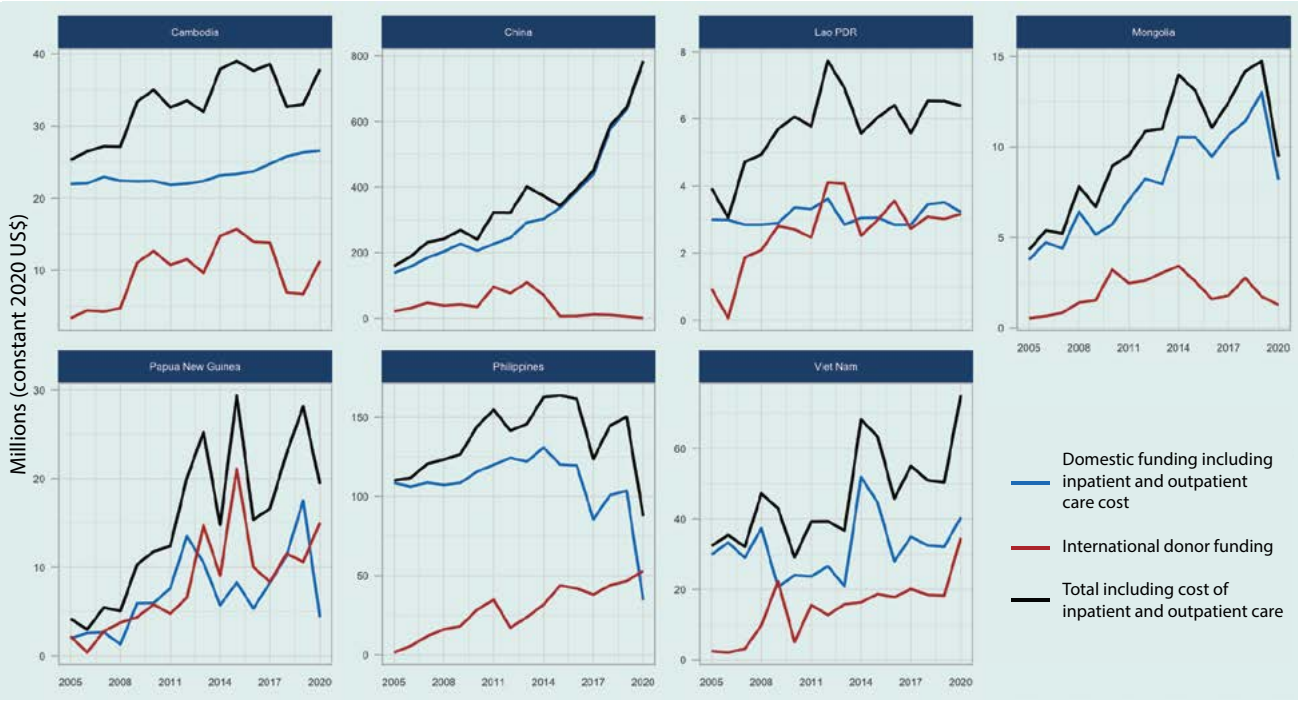


DR-TB: drug-resistant tuberculosis; DS-TB: drug-susceptible tuberculosis; TPT: tuberculosis preventive treatment.

[a] TB spending as reported by countries to WHO through annual rounds of TB data collection. Except for China, these exclude costs of delivering care for TB at facilities.

Source: Global tuberculosis databases.[4]

Fig. 3. **Funding for TB prevention, diagnostic and treatment services in seven priority countries in the Western Pacific Region, total amount and by funding source, 2005–2020 (US$ millions)**



Source: Global tuberculosis databases.[4]

countries (US$ 952 million of US$ 1.36 billion), with large differences across countries ranging from 37% to 158% (**Table 1**). Expenditure as a proportion of received funding averaged 99% (US$ 940 million of US$ 952 million), and in no country was lower than 84%.

In 2020, domestic funding for TB across the seven priority countries totalled US$ 902 million or 88% of the total investment in TB responses (US$ 1.02 billion), with China fully funding domestically (**Fig. 3**), while the other six countries funded on average 54% of the total cost of their programmes (**Table 2**). Cambodia's domestic funding for TB increased from US$ 21.0 million in 2004 to US$ 26.6 million in 2020 but was offset by a decline in international financing so that overall total TB funding decreased between 2017 and 2019. In contrast, in Viet Nam, domestic funding fluctuated over the period, rising from US$ 21 million in 2009 to US$ 51 million in 2014 but dropping back to US$ 40 million in 2020. This fluctuation was driven by changes in country-reported domestic funding – which fell from US$ 10.0 million in 2006 to US$ 1.1 million in 2019 before recovering to US$ 7.9 million in 2020 – as well as by increases in the estimated cost of delivering inpatient and outpatient care (from US$ 18 million in 2004 to US$ 32 million in 2020). Over the period covered by this report, the contribution of domestic to total funding in the Lao People's Democratic Republic has remained relatively low, at around 50%.

Domestic funding contributions in 2020 compared with those in 2015 show that the share of domestic funding available to meet total resources required by country NSPs decreased in Papua New Guinea (from 28% to 22%), the Philippines (from 73% to 40%) and Viet Nam (from 70% to 54%) but increased in China (from 98% to 100%), Cambodia (from 60% to 70%) and Mongolia (from 80% to 86%) and remained unchanged in the Lao People's Democratic Republic (50%) (**Fig. 4**).

Annual average implementation rates of domestic and international funding allocated for the TB response in the seven priority countries over the 2015–2020 period ranged from 81% in the Lao People's Democratic Republic to 100% in China (**Fig. 5**).

In 2020, inpatient and outpatient care costs in the six priority countries excluding China were estimated to be US$ 68 million (**Table 2**). The remaining US$ 952 million of the total amount of received funding for TB in the seven priority countries in 2020 (US$ 1020 million) derives from reported TB programme spending. In most countries, programme costs for DS-TB or DR-TB specific activities accounted for the largest share of TB programme expenditures (**Fig. 6**), together averaging 31% across the seven countries, with the highest percentage reported at 45% in China, followed by Cambodia (42%), Papua New Guinea (38%) and the Lao People's Democratic Republic (35%). First-line and second-line treatment drugs combined represented 33% of the total reported programme expenditure in Viet Nam, 26% in the Philippines and 24% in China (**Fig. 6**). The proportion of spending for collaborative TB/HIV activities ranged from 13% in Papua New Guinea to 4% in Viet Nam. The proportion of total TB spending for patient support ranged from 0% to 6%, for operational research from 0% to 3% and for TB preventive treatment (TPT) from 0% to 1%.

Reported and estimated funding gaps in the regional priority countries

TB funding gaps, reported by NTPs (and calculated as NSP budget requirements as a percentage of the expected amount of funding available from domestic or donor sources), have varied substantially not only within individual countries during 2005–2020 but also between the seven priority countries, as shown by the solid line in **Fig. 7**. Large funding gaps were consistently reported by Cambodia (ranging from 42% to 49%), the Philippines (from 37% to 70%) and Viet Nam (from 66% to 72%); in contrast, the Lao People's Democratic Republic and Mongolia reported only small or no funding gaps during most of the period 2005–2020. Fluctuating funding gaps were observed in China (from 0% to 34%) and most noticeably in Papua New Guinea (from 0% to 73%). The actual funding received exceeded the original forecast budget requirements in some years in some countries, including in China (in 2005, 2013 and 2017), the Lao People's Democratic Republic (in 2007, 2016, 2017 and 2020), Mongolia (2005, 2007–2009, 2013 and 2020) and Papua New Guinea (2013), pointing to successful funding mobilization periods in the midst of persistent potential funding gaps.

TB funding requirements for the seven priority countries are projected to be around US$ 2.8 billion by

Table 1. **Budgets, expenditure and received funding for TB prevention, diagnostic and treatment services reported by seven countries in the Western Pacific Region, total and proportion available and implementation rates, 2020 (current US$ millions)**

Country	Funding			Total received funding as a proportion of total budget required (B)/(A) x 100	Total expenditure as a proportion of received funding (C)/(B) x 100
	Total budget required (A)	Total received funding (B)	Total expenditure (C)		
Cambodia	33	17	14	51%	86%
China	994	785	785	79%	100%
Lao PDR	2	4	3	158%	84%
Mongolia	6	5	5	95%	100%
Papua New Guinea	34	17	17	50%	100%
Philippines	217	81	80	37%	100%
Viet Nam	71	43	36	60%	85%
Total	1357	952	940	70%	99%

Lao PDR: Lao People's Democratic Republic.

Source: Global tuberculosis databases.[4]

Table 2. **Funding for TB prevention, diagnostic and treatment services, available funding from domestic and international donor sources in seven priority countries in the Western Pacific Region, 2020 (current US$ millions)**

Country	Funding			Source of funding (% of total)			
					International donor funding		
	Total received funding (A)	Estimated inpatient and outpatient care costs (B)	Estimated total resources required for TB care (A+B)	Domestic funding	Global Fund	USAID	Other[a]
China	785	–	785	100%	0%	0%	0%
Cambodia	17	21	38	70%	22%	3%	5%
Lao PDR	4	2	6	50%	50%	0%	0%
Mongolia	5	4	9	87%	11%	0%	2%
Papua New Guinea	17	2	19	22%	58%	0%	20%
Philippines	81	7	88	39%	46%	15%	0%
Viet Nam	43	32	75	54%	45%	1%	0%
Total	952	68	1020	88%	10%	1%	1%

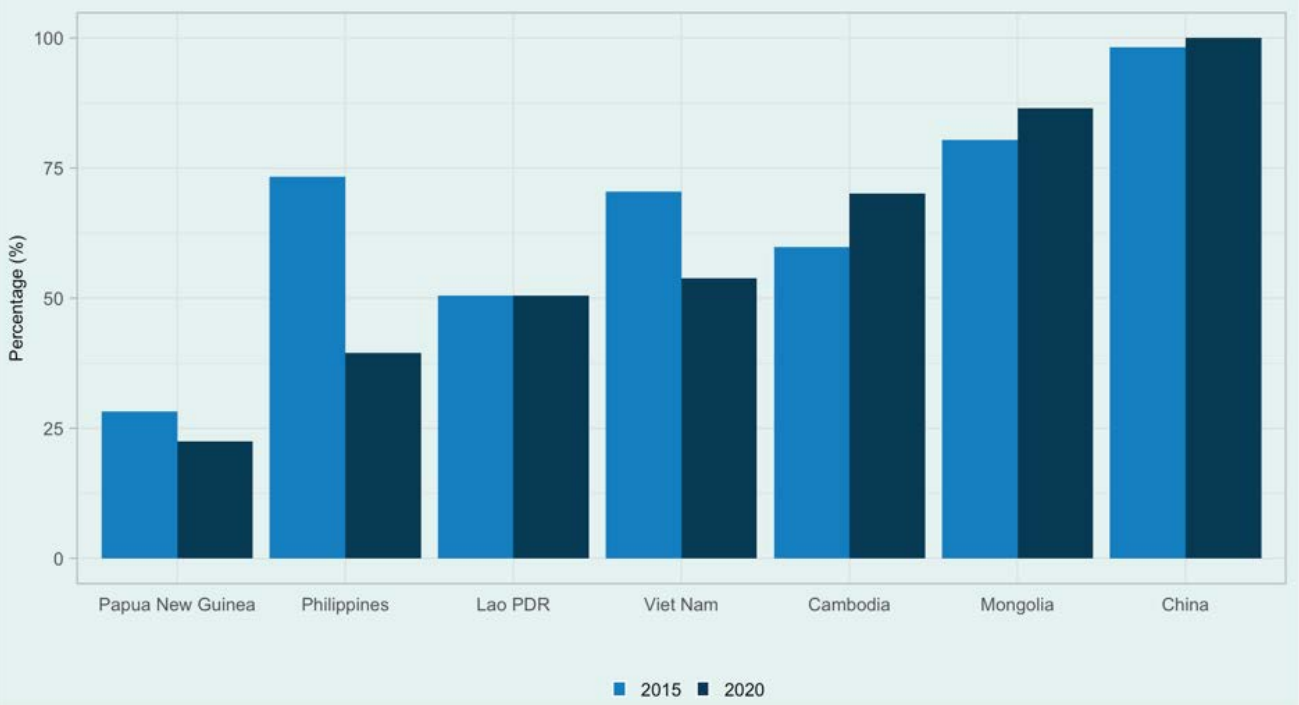
Lao PDR: Lao People's Democratic Republic; USAID: United States Agency for International Development.

[a] Includes grants.

Source: Global tuberculosis databases.[4]

2025. With available funding assumed to double, from US$ 1.02 billion in 2020 to US$ 2 billion in 2025, this translates into an anticipated funding gap of US$ 830 million in 2025. Given that the funding gap in 2020 was estimated to be US$ 326 million, this represents a considerable widening of the funding gap over the period 2020–2025, from 24% to 30%. The average projections mask considerable variation between countries; between 2020 and 2025, funding gaps are projected to increase from 49% to 51% in Cambodia, from 11% to 16% in China, from 0% to 52% in the Lao People's Democratic Republic, from 5% to 64% in Papua New Guinea and from 66% to 74% in Viet Nam (**Fig. 8**).

Fig. 4. **Contribution of domestic financing for TB prevention, diagnostic and treatment services in seven priority countries in the Western Pacific Region, 2015[a] and 2020 (as % of total received funding)**



Lao PDR: Lao People's Democratic Republic.

[a] 2015 data for Papua New Guinea were estimated by the WHO Global TB Programme as they were not reported in 2015, 2018 and 2019.

Source: Global tuberculosis databases.[4]

Domestic funding for TB during the COVID-19 pandemic

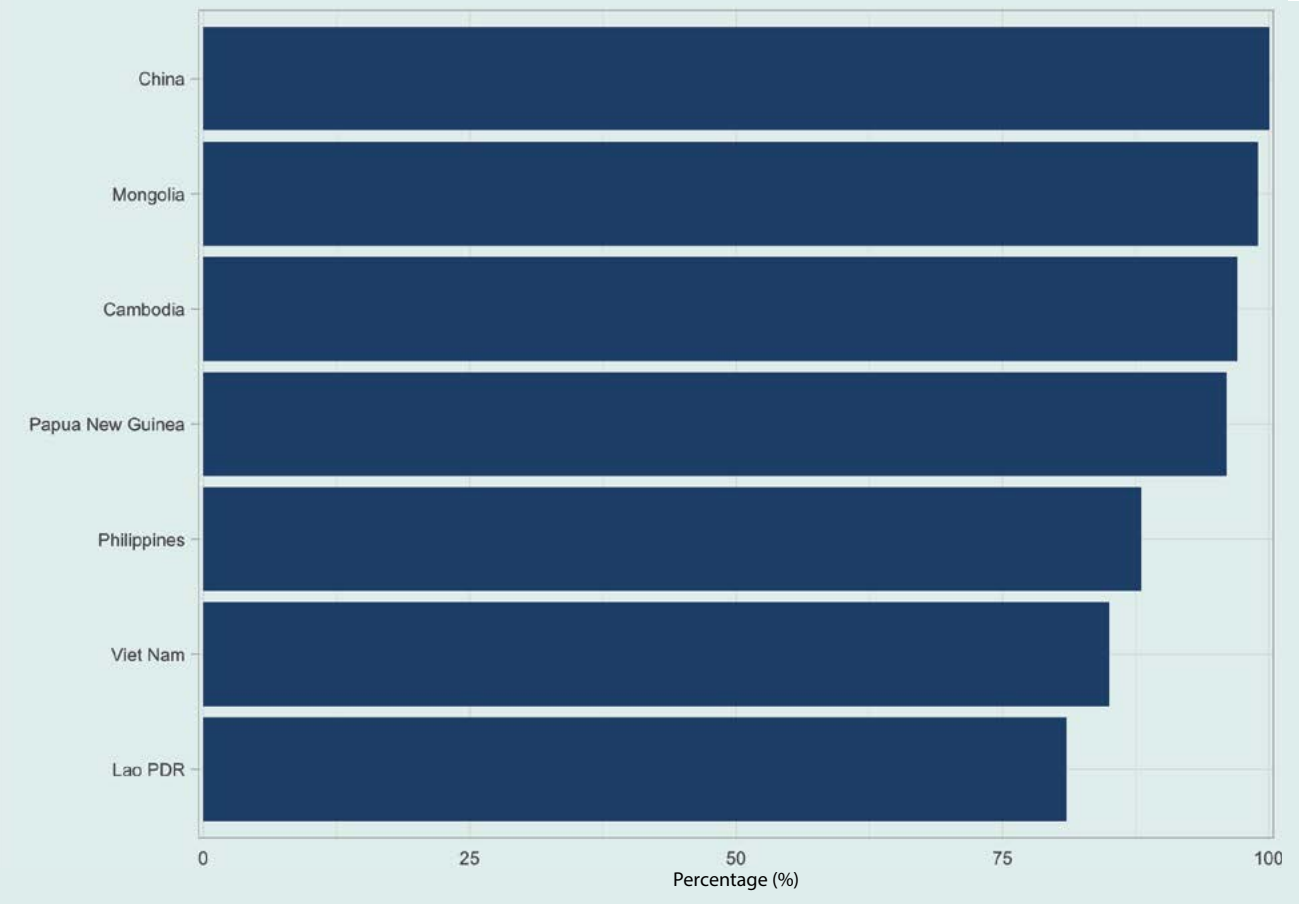
Five countries in the Western Pacific Region, including four priority countries, reported that part of their NTP budget was re-allocated to the COVID-19 response in early 2020. In the Philippines, the national budget allocated for NTP declined by 45%, from US$ 19 million in 2020 to US$ 10 million in 2021.

DISCUSSION

Total spending on TB prevention, diagnostic and treatment services in the seven priority countries in the Western Pacific Region increased by nearly 60%, from US$ 658 million in 2015 to US$ 1020 million in 2020. This was mostly driven by increases in the amount of available domestic funding, which rose from US$ 547 million in 2015 to US$ 902 million in 2020. Much of this recent surge in domestic funding has occurred in China, which alone accounted for almost three quarters (74%) of the total amount of available domestic funding in 2020 (US$ 902 million). Among the other six priority countries, including the Lao People's Democratic Republic, Papua New Guinea, the Philippines and Viet Nam, the level of domestic funding (as a proportion of total funding) has remained largely unchanged, and these countries remain reliant on donor funding. For these seven priority countries, it is anticipated that the funding gap will reach 30% by 2025, up from 24% in 2020. This projected further widening of the funding gap stems from the assumption that domestic and international funding availability remains unchanged while resource requirements to meet country TB targets will increase. Although data are limited at present, evidence suggests that the COVID-19 pandemic has impacted the allocation of funding for TB prevention, diagnostic and treatment services in 2020 across the Region.

Despite the progress made by countries to mobilize funding for TB prevention, diagnosis and treatment, at US$ 1061 million, available funding in 2020 was just 44% of the annual target set for LMICs in the Western Pacific Region,[8] indicating an urgent need for more investment. While the observed increase in domestic funding in the 18 LMICs and the seven priority countries overall

Fig. 5. **Implementation rates[a] of domestic and international funding allocated for TB prevention, diagnostic and treatment services in seven priority countries in the Western Pacific Region, 2015–2020**



Lao PDR: Lao People's Democratic Republic.

[a] Defined as spent funds as a percentage of total received funds.

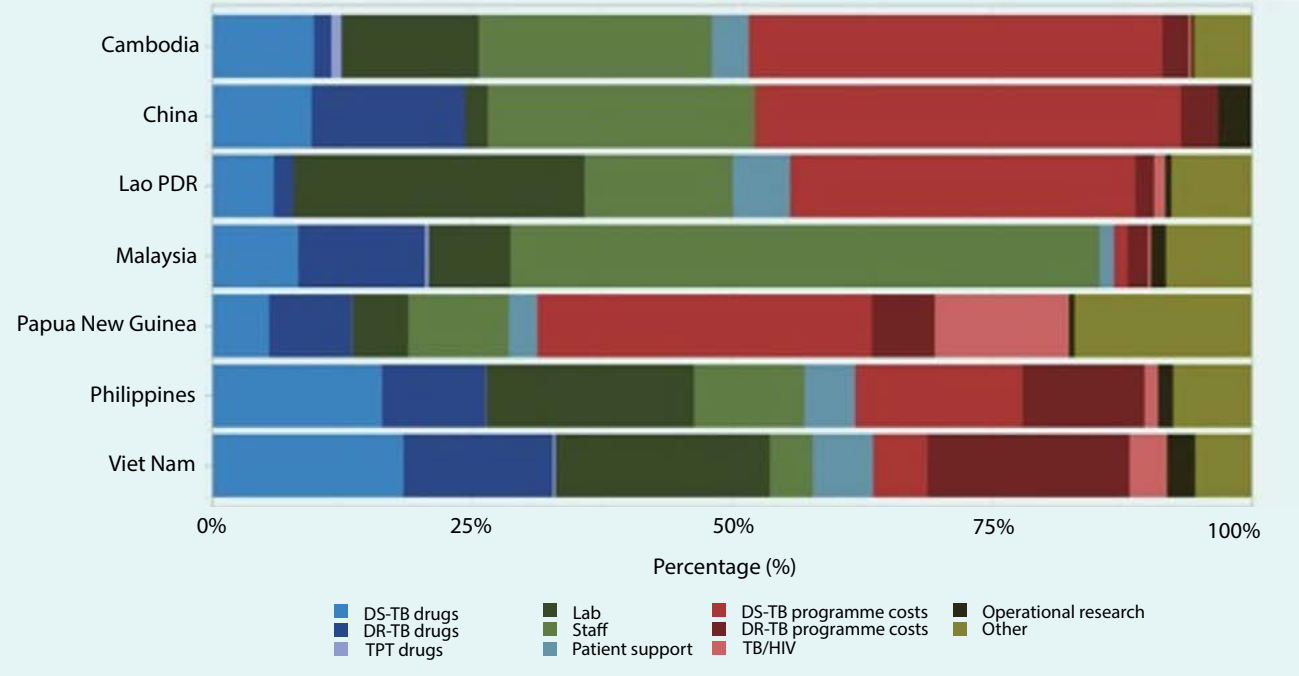
Source: Global tuberculosis databases.[4]

reflects a firm political commitment to ending TB in the Region, further domestic funding increases are critical, especially in countries that rely on external funding such as in Cambodia, the Lao People's Democratic Republic, Papua New Guinea, the Philippines and Viet Nam. This is particularly important given that steady economic growth across all LMICs in the Region has meant that sources of external funding are generally declining, placing a greater onus on domestic funding to maintain essential public health functions for TB prevention, diagnosis and treatment.[9] Moreover, external funding is often tied to specific TB intervention areas and cannot be used to fund core programme staff or TB care delivery at the facility level. Implementation of all received funding has been challenging in a few countries that are still reliant on donor funding (e.g. the Lao People's Democratic Republic, the Philippines and Viet Nam).

Analysis of TB investments by intervention area showed that TB programme priorities have changed over time. A rise in the number of DR-TB cases enrolled in care (these increased by 70% in the Region from 2015 to 2020)[4] are likely to be behind recent allocation increases for second-line drugs regionally and, in particular, in countries with high multidrug-resistant TB (MDR-TB) burdens (China, Mongolia, Papua New Guinea, the Philippines and Viet Nam). Given that increases in funding for second-line drugs is often at the expense of other programme components, global efforts to reduce prices of DR-TB drugs and expand the use of shorter MDR-TB regimens remain essential.

Allocation of TB funding to TPT, patient support and operational research remains low, collectively accounting for less than 6% of total NSP spending in

Fig. 6. **Spending on TB prevention, diagnostic and treatment services[a] by expenditure category in seven priority countries in the Western Pacific Region, 2020**



DR-TB: drug-resistant tuberculosis; DS-TB: drug-susceptible tuberculosis; Lao PDR: Lao People's Democratic Republic; TPT: tuberculosis preventive treatment.

[a] Excludes inpatient and outpatient care costs in all countries but China.

Source: Global tuberculosis databases.[4]

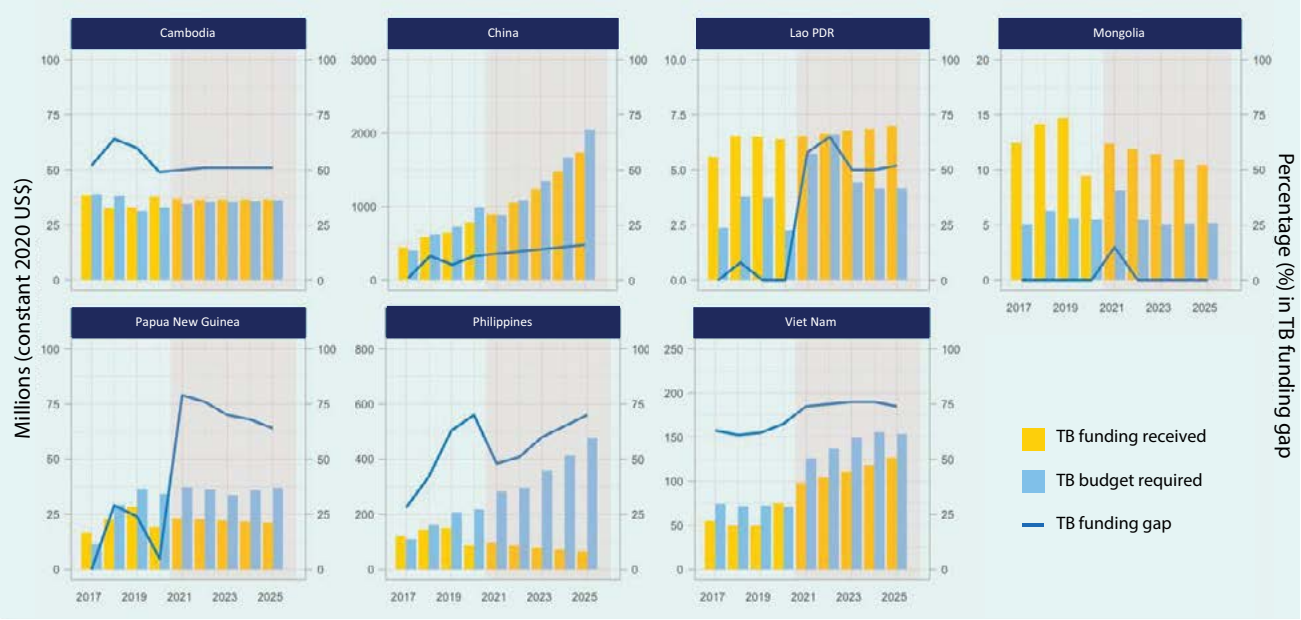
Fig. 7. **TB funding received, budgets required for national strategic plans and NTP-reported funding gaps[a] in seven priority countries in the Western Pacific Region, 2005–2020**

Lao PDR: Lao People's Democratic Republic; NTP: National TB Programme.

[a] TB funding gap reported by NTP is the difference between the budget required and the expected funding at the time of reporting. The actual received funding (i.e. TB spending) might be higher than expected. This was the case for China where the received funding exceeded the budget required in 2005, 2013 and 2017.

Source: Global tuberculosis databases.[4]

Fig. 8. **TB funding received, budgets required for national strategic plans and NTP-reported funding gaps[a] in seven priority countries in the Western Pacific Region, 2017–2025**



Lao PDR: Lao People's Democratic Republic.

Numbers in the red-shaded areas are projections

Source: Global tuberculosis databases.[4]

most countries. Despite commitments made by world leaders at the 2018 UNHLM to treat 30 million people with TB infection during 2018–2022, by the end of 2020, only 8.7 million people had received TPT.[1] Increased funding for this intervention is thus essential if TPT targets are to be met. Patient support interventions aimed at reducing barriers to accessing TB services such as in-kind, vouchers, cash allowances and nutrition support are also widely seen as increasingly important, especially in countries where high proportions of TB-affected families face catastrophic costs. Over one third (34%) of TB-affected families in Papua New Guinea are unable to afford the cost of TB treatment; this proportion rises to 92% in Solomon Islands.[1] Efforts are also needed to increase social protection measures for TB-affected families, interventions which often fall outside health or TB budgets. While TB research outputs in the Region as a whole increased by 8.8% annually between 2000 and 2018, there are still major knowledge gaps in some countries such as the Lao People's Democratic Republic and Mongolia.[10] Operational research can generate context-specific evidence to inform decision-making and improvements to national programmes, and thus requires adequate funding.

Projected increases in TB investment in the seven priority countries (from US$ 1.02 billion in 2020 to US$ 2 billion in 2025) are likely to be insufficient to mitigate existing funding gaps. Instead, gaps are projected to increase further, from US$ 326 million in 2020 to US$ 830 million in 2025. While the competing priorities of the COVID-19 response may impact these funding gaps in the short term, health system-wide improvements made during the pandemic may, in the longer term, enhance TB prevention, diagnosis and treatment by facilitating accelerated uptake of digital tools and collaboration between disease programmes and sectors,[11] increasing efficiencies, and expanding use of personalized and remote patient support.[12] The pandemic has also highlighted the importance of sufficiently funded and resilient health systems,[13] not just for COVID-19 response but for all infectious disease control and prevention services.

This descriptive analysis has several limitations. Firstly, WHO TB financing data for LMICs from 2003 to 2020 were not complete, especially in the early 2000s when global reporting of TB financing data was relatively new. Therefore, the observed patterns may not have accurately captured the real situation for the

early reporting years. Secondly, unlike recent financial modelling studies,[14] WHO estimates of government and international funding for TB only included public spending (i.e. private spending was not included); moreover, no additional imputations (beyond what is already included in WHO TB finance data) were made for missing data (by intervention) or for out-of-pocket and private spending. Funding of TB services by local governments outside of the national TB budget and by other health programmes through integrated approaches was also not included. Thirdly, differences in the categorization of budgets and funding streams between countries are likely to lead to under- and overestimation of funding proportions by category. For example, drugs for TPT may be reported as DS-TB drugs in some countries. Fourthly, the assumptions used to project available funding and to impute missing forecasts by country-year were made by the authors without consultation with individual countries. Possible future changes in the costs of drugs and diagnostics were also not considered, and therefore the calculated funding gap may also be an under- or overestimate.

Despite these limitations, this report provides an overview of domestic and international spending on TB prevention, diagnostic and treatment services in the Western Pacific Region between 2005 and 2020. It also provides a more detailed, short-term (2015–2020) assessment of TB funding and expenditure in seven priority countries that collectively account for 85% of the Region's notified cases. Periodic analysis and reporting of TB funding, budget and expenditure data remain essential not only to monitor TB financing, identify major funding gaps and inform corrective actions, but also to advocate for government commitment to the goal of ending TB.[15] This analysis clearly shows that if the Western Pacific Region is to achieve its End TB Strategy targets, additional funding needs to be mobilized. The economic case for doing so is strong. Economic modelling from four high-TB burden countries in the Region has demonstrated that TB care and prevention is an extremely profitable investment that provides a multi-fold return on investment.[16] An evaluation of the economic impact of TB mortality in 120 LMICs, including the 18 LMICs in the Western Pacific Region, estimated that the cost of not investing enough in TB care to meet the 2030 targets would result in 31.8 million (95% confidence interval [CI], 25.2–39.5 million) deaths, which corresponds to an economic loss of US$ 17.5 trillion (95% CI, 14.9–20.4 trillion) during 2020–2050 globally.[17] The *Western Pacific Regional Framework to End TB: 2021–2030*, endorsed by Member States in October 2021, reiterated the importance of securing sustainable and adequate financing for TB programmes through a whole-of-government and multisectoral approach.[2] Securing high-level political commitment, ensuring coordination across sectors, and shaping a national response to TB as part of the drive towards the goal of universal health coverage will be key to advancing policy dialogue to achieve sustainable and adequate financing for TB.

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Conflicts of interest

The authors have no conflicts of interest to declare.

Ethics statement

As this report used routinely available data and no personal identifying information was collected, ethical clearance was not required.

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References

1. Global tuberculosis report 2022. Geneva: World Health Organization; 2022. Available from: https://apps.who.int/iris/handle/10665/363752, accessed 23 June 2022.
2. Western Pacific regional framework to end TB: 2021–2030. Manila: WHO Regional Office for the Western Pacific; 2021. Available from: https://apps.who.int/iris/handle/10665/352278, accessed 23 June 2022.
3. Political declaration of the UN general assembly high-level meeting. New York: United Nations; 2018. Available from: https://cdn.who.int/media/docs/default-source/documents/tuberculosis/political-declaration-un-general-assembly-tb-tuberculosis77cd7a27-7e8d-4fbb-9729-a5dbd505798f.pdf?sfvrsn=4f4090dc_1&download=true, accessed 23 June 2022.
4. Global tuberculosis databases. Geneva: World Health Organization; 2021. Available from: https://www.who.int/teams/global-tuberculosis-programme/data, accessed 23 June 2022.

5. Towards tuberculosis elimination: an action framework for low-incidence countries. Geneva: World Health Organization; 2014. Available from: https://apps.who.int/iris/handle/10665/132231, accessed 23 June 2022.

6. The WHO global TB data collection system. Geneva: World Health Organization; 2022. Available from: https://extranet.who.int/tme/, accessed 23 June 2022.

7. Box 6.1: Methods used to compile, review, validate and analyse financial data reported to WHO. In: Global tuberculosis report 2019. Geneva: World Health Organization; 2019. Available from: https://apps.who.int/iris/handle/10665/329368, accessed 23 June 2022.

8. Stop TB Partnership. The paradigm shift: global plan to end TB 2018–2022. Geneva: World Health Organization; 2019. Available from: https://stoptb.org/assets/documents/global/plan/GPR_2018-2022_Digital.pdf, accessed 23 June 2022.

9. Regional framework for action on transitioning to integrated financing of priority public health services in the Western Pacific. Manila: WHO Regional Office for the Western Pacific; 2018. Available from: https://apps.who.int/iris/handle/10665/274718, accessed 23 June 2022.

10. Morishita F, Yamanaka T, Islam T. Intensified research on tuberculosis in the Western Pacific Region: a bibliometric analysis, 2000–2019. Western Pac Surveill Response J. 2020;11(4):24–31. doi:10.5365/wpsar.2020.11.3.003 pmid:34046238

11. Programmatic innovations to address challenges in tuberculosis prevention and care during the COVID-19 pandemic. Geneva: World Health Organization; 2021. Available from: https://apps.who.int/iris/handle/10665/341307, accessed 23 June 2022.

12. End TB app suite. Manila: Department of Health, Philippines; 2022. Available from: https://ntp.doh.gov.ph/resources/downloads/endtb-appsuite/, accessed 23 June 2022.

13. Micah AE, Cogswell IE, Cunningham B, Ezoe S, Harle AC, Maddison ER, et al. Tracking development assistance for health and for COVID-19: a review of development assistance, government, out-of-pocket, and other private spending on health for 204 countries and territories, 1990–2050. Lancet. 2021;398(10308):1317–43. doi:10.1016/S0140-6736(21)01258-7 pmid:34562388

14. Su Y, Garcia Baena I, Harle AC, Crosby SW, Micah AE, Siroka A, et al. Tracking total spending on tuberculosis by source and function in 135 low-income and middle-income countries, 2000–17: a financial modelling study. Lancet Infect Dis. 2020;20(8):929–42. doi:10.1016/S1473-3099(20)30124-9 pmid:32334658

15. Multisectoral accountability framework to accelerate progress to end tuberculosis by 2030. Geneva: World Health Organization; 2019. Available from: https://apps.who.int/iris/handle/10665/331934, accessed 23 June 2022.

16. Estill J, Islam T, Houben RMGJ, Rudman J, Ragonnet R, McBryde ES, et al. Tuberculosis in the Western Pacific Region: estimating the burden of disease and return on investment 2020–2030 in four countries. Lancet Reg Health West Pac. 2021;11:100147. doi:10.1016/j.lanwpc.2021.100147 pmid:34327358

17. Silva S, Arinaminpathy N, Atun R, Goosby E, Reid M. Economic impact of tuberculosis mortality in 120 countries and the cost of not achieving the Sustainable Development Goals tuberculosis targets: a full-income analysis. Lancet Glob Health. 2021;9(10):e1372–9. doi:10.1016/S2214-109X(21)00299-0 pmid:34487685

Multi-source surveillance conducted by the Tokyo Metropolitan Government during the Tokyo 2020 Olympic and Paralympic Games

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The Tokyo 2020 Olympic and Paralympic Games (the Games) were held from 23 July to 5 September 2021 in Tokyo, Japan, after a 1-year delay due to the coronavirus disease (COVID-19) pandemic. The Tokyo Metropolitan Government was responsible for monitoring and responding to infectious disease outbreaks other than COVID-19 during the Games. A multi-source surveillance system was used from 1 July to 12 September 2021 for the early detection and rapid response to infectious diseases. This included routine notifiable disease surveillance, sentinel surveillance, syndromic surveillance, cluster surveillance, ambulance transfer surveillance and the Tokyo Infectious Alert system. Daily reports were disseminated summarizing the data collected from the multi-source surveillance system. No case of infectious disease under the Tokyo Metropolitan Government system required a response during the Games. The multi-source surveillance was useful for providing intelligence during the Games and, if required, could contribute to the early detection and rapid response to outbreaks during other mass gatherings. The system could be improved to overcome the challenges implied by the findings of this multi-source surveillance.

Outbreaks of infectious disease, widespread food poisoning incidents and bioterrorism attacks are more probable during mass-gathering events such as the Olympic and Paralympic Games.[1] The rapid detection of infectious diseases, potential outbreaks and other public health events at mass gatherings is crucial. Surveillance during mass gatherings is typically conducted by public health agencies that adopt additional surveillance mechanisms to augment their routine public health surveillance during the event.

The Tokyo 2020 Olympic and Paralympic Games (the Games) were held from 23 July to 5 September 2021, the 1-year delay being due to the novel coronavirus disease (COVID-19) pandemic. The Games were held during the fifth wave of COVID-19 in Japan with the arrival of the Delta variant strain while the public health response to COVID-19 was ongoing. Consequently, only players and staff members were in attendance. The Tokyo Organising Committee of the Olympic and Paralympic Games was responsible for monitoring and responding to COVID-19 during the Games, and the Tokyo Metropolitan Government (TMG) was responsible for monitoring and responding to all infectious diseases other than COVID-19.

TMG has conducted similar surveillance for mass gatherings including during the 2013 Sports Festival in Tokyo[2] and the 2019 Rugby World Cup in Japan.[3] Lessons learned from these earlier mass-gathering events were used to develop the mechanisms for the Games. This report summarizes the multi-source surveillance conducted by TMG for infectious diseases other than COVID-19 during the Games.

METHODS

Surveillance systems

Multi-source surveillance for infectious diseases other than COVID-19 for the Games was conducted by TMG from 1 July to 12 September 2021, including national holidays and weekends. Data were sourced from the following surveillance systems.

[a] Infectious Disease Control Division, Bureau of Social Welfare and Public Health, Tokyo Metropolitan Government, Tokyo, Japan.
[b] Epidemiological Information Section, Tokyo Metropolitan Institute of Public Health, Tokyo, Japan.
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Official notifiable disease surveillance

In compliance with the Act on the Prevention of Infectious Diseases and Medical Care for Patients with Infectious Diseases (the Infectious Diseases Control Law), notifiable disease surveillance requires diagnosing physicians to notify authorities of 87 diseases across five severity categories. For the Games, official notifiable disease surveillance included all diseases in categories I–IV with the exclusion of tuberculosis and three diseases in Category V (invasive meningococcal infection, measles, rubella) (**Table 1**). Notifications from the diagnosing physicians are usually published by TMG once a week; however, during the Games, they were reported in the daily Games report.

Official sentinel surveillance

In compliance with the Infectious Diseases Control Law, the sentinel surveillance system receives weekly reports from different types of sentinel sites. These reports comprise daily data collected Monday to Sunday by each site on 1–12 diseases, submitted on a weekly basis to their local public health centre (**Table 2**). During the Games, sentinel data continued to be reported weekly and were included only in the daily Games reports issued on Thursdays.

Official syndromic surveillance

In accordance with the Infectious Diseases Control Law, syndromic surveillance of cases of unknown pathogens is used to detect outbreaks. The case definitions include: a patient with fever, respiratory symptoms, rash, gastrointestinal symptoms, neurological symptoms, or other symptoms suggestive of some infectious disease; a patient needing intensive care; and a physician unable to diagnose the disease immediately based on generally accepted medical knowledge. During the Games, 36 hospitals from this system, plus two new temporary hospitals, were designated as reporting sites for syndromic surveillance.

Cluster surveillance

Cluster surveillance is conducted at residential aged-care facilities and nursery schools based on the requirements of the central government. From January 2019, TMG extended its cluster surveillance and also mandated schools, medical institutions and any other facility to notify their local public health centre when more than 10 people report or are diagnosed with the same symptom or when more than half of the users and staff of a facility share the same symptom or diagnosis during the previous 7 days. Initially, for the Games, public health centres were asked to report their cluster surveillance weekly as usual; however, this was revised to daily reporting from 11 July 2021 onwards.

Ambulance transfer surveillance

The ambulance transfer surveillance system is unique to TMG. It collects and analyses information at the time of emergency transport using data provided by the Tokyo Fire Department's Emergency Information Analysis and Management System.[4] It operated as usual during the Games.

The Tokyo Infectious Alert system

The Tokyo Infectious Alert system, another unique system operated by TMG, has been used for avian influenza (H5N1 and H7N9), Middle East respiratory syndrome (MERS) and severe acute respiratory syndrome (SARS). Doctors notify suspected cases of severe respiratory syndrome to public health centres, which collect and transfer the specimens for testing. The test results of suspected cases are delivered 24 hours a day to public health centres and medical facilities through the infectious disease control unit of TMG. This system operated as usual during the Games.

Prescription and absenteeism surveillance systems

The prescription surveillance system is a nationwide syndromic surveillance system established in 2009 that reports on the estimated number of influenza and chickenpox cases and the number of patients prescribed certain types of drugs, based on pharmacy prescriptions.[5,6] In 2021, approximately 12 000 pharmacies participated, collectively accounting for approximately 20% of all pharmacies nationwide. The estimated numbers of patients are published online each morning.

Information related to school or nursery school absenteeism is integrated and systematized into the Nursery School Absenteeism Surveillance System ((N)SASSy).[7–9] In 2021, approximately half (22 000)

Table 1. **Infectious diseases in the notifiable diseases surveillance system by severity category included in surveillance for the Tokyo 2020 Olympic and Paralympic Games, 1 July–12 September 2021**

Category	Diseases
I	Crimean-Congo haemorrhagic fever, Ebola haemorrhagic fever, Lassa fever, Marburg disease, plague, smallpox, South American haemorrhagic fever
II	Acute poliomyelitis, avian influenza (H5N1), avian influenza (H7N9), diphtheria, Middle East respiratory syndrome (only if the pathogen is MERS coronavirus), severe acute respiratory syndrome (only if the pathogen is SARS coronavirus)
III	Cholera, Enterohaemorrhagic *Escherichia coli* infection, paratyphoid fever, shigellosis, typhoid fever
IV	Anthrax, avian influenza (excluding H5N1 or H7N9), B virus disease, botulism, brucellosis, Chikungunya fever, coccidioidomycosis, dengue fever, Eastern equine encephalitis, echinococcosis, epidemic typhus, glanders, haemorrhagic fever with renal syndrome, Hantavirus pulmonary syndrome, Hendra virus infection, hepatitis A, hepatitis E, Japanese encephalitis, Japanese spotted fever, Kyasanur Forest disease, legionellosis, leptospirosis, Lyme disease, lyssavirus infection, malaria, melioidosis, monkeypox, Nipah virus infection, Omsk haemorrhagic fever, psittacosis, Q fever, rabies, relapsing fever, Rift Valley fever, Rocky Mountain spotted fever, severe fever with thrombocytopenia syndrome (only if the pathogen is SFTS virus of the genus *Phlebovirus*), tick-borne encephalitis, Tsutsugamushi disease, tularaemia, Venezuelan equine encephalitis, West Nile fever, Western equine encephalitis, yellow fever, Zika virus infection
V	Invasive meningococcal infection, measles, rubella

Table 2. **Types of sentinel sites and the diseases included in their sentinel surveillance for the Tokyo 2020 Olympic and Paralympic Games, 1 July–12 September 2021**

Classification of sentinel sites (subject)	No. of sites	Diseases
Paediatric sentinel sites (paediatric medical facilities)	264	Erythema infectiosum, exanthema subitum, group A streptococcal pharyngitis, hand, foot and mouth disease, herpangina, infectious gastroenteritis, Kawasaki disease,[a] mumps, pharyngoconjunctival fever, respiratory syncytial virus infection, undiagnosed exanthems,[a] varicella
Influenza sentinel sites (internal and paediatric medical facilities)	419	Influenza (excluding avian influenza and pandemic influenza [novel influenza or re-emerging influenza])
Ophthalmology sentinel sites (ophthalmologic facilities)	39	Acute haemorrhagic conjunctivitis, epidemic keratoconjunctivitis
General hospital sentinel sites (medical facilities, each with at least 300 beds)	25	Aseptic meningitis, bacterial meningitis (excluding cases for which the cause is identified as *Haemophilus influenzae*, *Neisseria meningitides* or *Streptococcus pneumoniae*), chlamydial pneumonia (excluding psittacosis), infectious gastroenteritis (only if the pathogen is rotavirus), influenza (excluding avian influenza and pandemic influenza [novel influenza or re-emerging influenza]), mycoplasma pneumonia

[a] Kawasaki disease and undiagnosed exanthems are diseases designated by the Tokyo Metropolitan Government; they are not based on the Act on the Prevention of Infectious Diseases and Medical Care for Patients with Infectious Diseases.

of all schools, including kindergartens, as well as approximately one fourth (7100) of nursery schools in Japan, reported to the system, thus monitoring the daily health of approximately 6 million children 18 years old or younger nationwide.

During the Games, TMG monitored prescription surveillance and (N)SASSy more closely than usual.

Procedures

Jurisdictional public health centres verified outbreak information obtained from official notifiable surveillance, official sentinel surveillance and cluster surveillance (**Fig. 1**). Data from the official syndromic surveillance and Tokyo Infectious Alert system were reported to TMG by public health centres, as were ambulance transfer surveillance

data from the Tokyo Fire Department's system. The public health centres were involved in the verification of these surveillance systems.

Risk assessment was performed by TMG with the National Institute of Infectious Diseases, Japan (NIID) following WHO guidelines for risk assessment.[10] In particular, the importance for public health was assessed in terms of severity and/or infectivity while the possibility of outbreak expansion was assessed based on the location, environment, timing and extent of occurrence.

Data from all surveillance systems were collated by TMG, with 15:00 as the daily cut-off time for reporting (**Fig. 1**). The data were summarized into daily reports which were assessed and confirmed at daily web conferences with NIID. The final report was delivered to all relevant stakeholders, including the public health centre in Tokyo, the Tokyo Medical Association, the Ministry of Health, Labour and Welfare, and the Tokyo Organising Committee of the Olympic and Paralympic Games, with 17:00 as the daily cut-off time. The daily report was not provided to the general public.

Response plan

Outbreak investigations within the athletes' village were the responsibility of the Tokyo Base of Health Support, which was responsible for providing public health services to the athletes' village during the Games. It could request support from the Tokyo Epidemic Investigation Team and the Field Epidemiology Training Program at NIID, if required (**Fig. 2**). Evaluations of unusual events and the determination of appropriate responses were conducted at the daily web conferences between TMG and NIID.

RESULTS

Preparation

Preparations for surveillance of the Games commenced in April 2021. Weekly meetings were held between the relevant TMG units and organizations including the Tokyo Organising Committee of the Olympic and Paralympic Games and the Ministry of Health, Labour and Welfare from 25 May 2021. Two practice sessions for producing daily reports were held from 19 to 20 May and from 18 to 24 June 2021. The multi-source surveillance system was set up in 3 months, including system user guides.

Surveillance system operations

The surveillance report was published daily during the Games as planned. Mechanical issues led to three instances of delayed reporting from the ambulance transfer surveillance system. There was at least a day's delay in reporting from the official notifiable disease surveillance system because the public health centre was occupied with the COVID-19 outbreak response. From 23 July, these delayed cases were reflected in the daily report as soon as they were registered. Additionally, some delays in reporting occurred on weekends. This was due to processing delays at the office that receives reports on behalf of the public health centre during nights, weekends and holidays when the centre is closed. However, the delays did not affect the daily reporting procedures. Operation of the multi-source surveillance system required 12 TMG staff members.

Results of surveillance

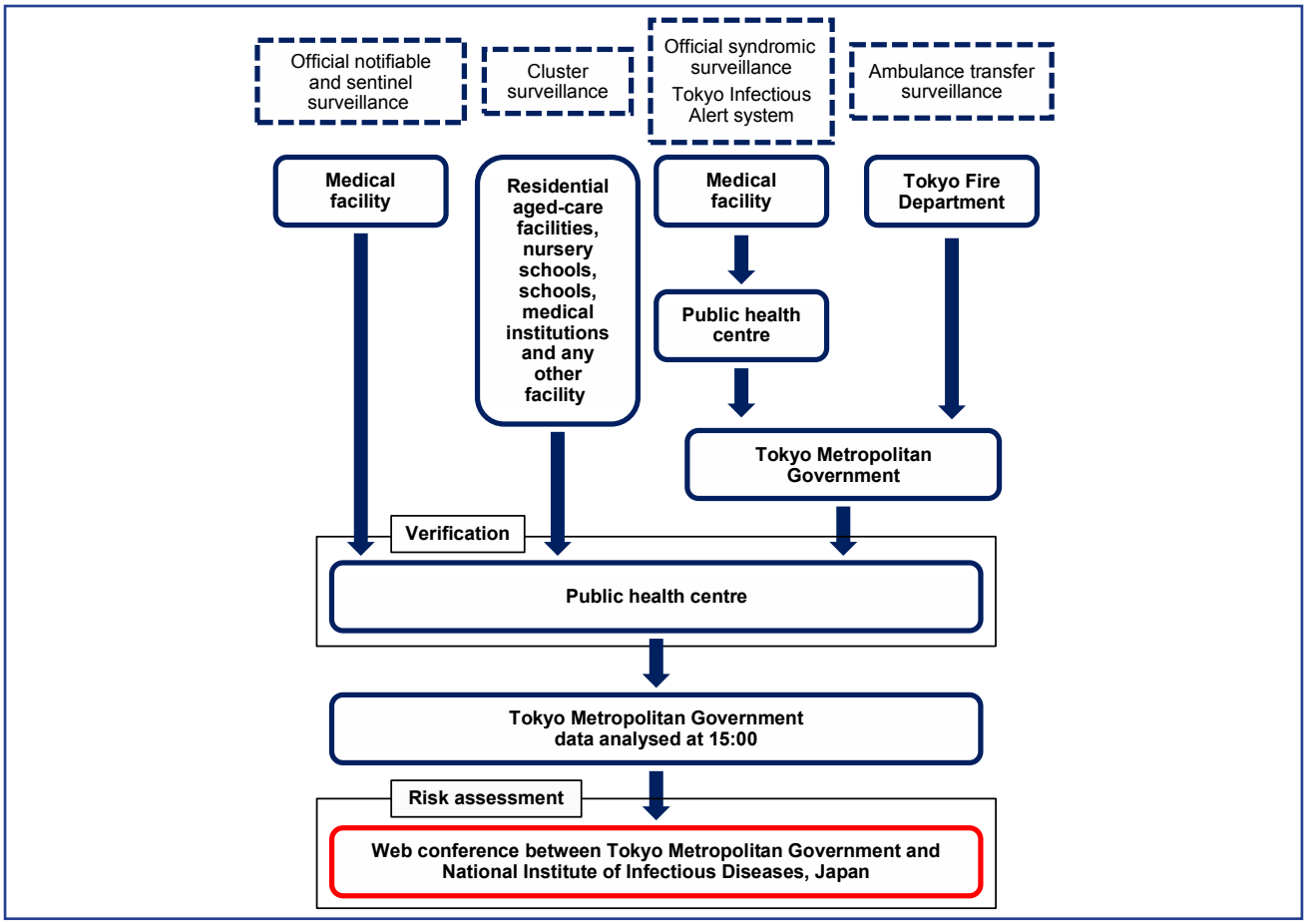
Official notifiable diseases surveillance

There were 192 cases reported from medical facilities in Tokyo through the notifiable diseases surveillance system. This included 122 enterohaemorrhagic *Escherichia coli* infection cases and 44 legionellosis cases (**Fig. 3**). There were six malaria cases, including two cases related to the Games where the patients were infected abroad before arriving in Japan. Four suspected measles cases and three suspected rubella cases were reported, which subsequently tested negative. The other reports included 10 cases of hepatitis E, two of Japanese spotted fever and one of hepatitis A. The data reported through the notifiable diseases surveillance system did not indicate any unusual occurrence that could be related to the Games.

Official sentinel surveillance

Respiratory syncytial virus (RSV) infection was the most frequently reported condition through the sentinel surveillance system during the Games, followed by infectious gastroenteritis (**Fig. 4**). A record high of 8.93 cases of RSV infection was reported per sentinel

Fig. 1. **Flowchart of surveillance for the Tokyo 2020 Olympic and Paralympic Games by the Tokyo Metropolitan Government, 1 July–12 September 2021**



site in week 28 (12–18 July 2021). The number of reported cases per sentinel site per week of infectious gastroenteritis was 1.44–3.69 during the Games (**Fig. 4**).

Official syndromic surveillance

No report was made through the official syndromic surveillance system during the Games.

Cluster surveillance

There were 276 clusters of RSV infection and 29 clusters of infectious gastroenteritis reported through cluster surveillance during the Games. Most cases of these two infectious diseases were reported from nursery schools. There were also two clusters of adenovirus infection and two clusters of herpangina reported. Single clusters of *Clostridioides difficile* infection, haemolytic streptococcus infection, hand, foot and mouth disease, scabies and varicella were also reported. Each of the six clusters contained multiple infectious diseases. Seventy-seven clusters were undiagnosed from nursery schools and kindergartens. However, given the ongoing RSV epidemic and the reported symptoms of mainly fever, cough and nasal mucus, the public health centres attributed the cases to RSV infections.

Fig. 5 shows the daily number of clusters reported from 11 July to 12 September 2021. Due to daily reports in cluster surveillance being issued from 11 July, there were no daily data for 1–10 July. Nevertheless, clusters reported during 1–10 July included 67 clusters of RSV infection, 11 clusters of infectious gastroenteritis, four other clusters and 17 undiagnosed clusters.

Ambulance transfer surveillance

Five aberrant cases that required follow up were detected through the ambulance transfer surveillance and reported during daily reports on 6, 16, 20 July and 22 August 2021

Fig. 2. **Response plan for potential investigations during the Tokyo 2020 Olympic and Paralympic Games, 1 July–12 September 2021**

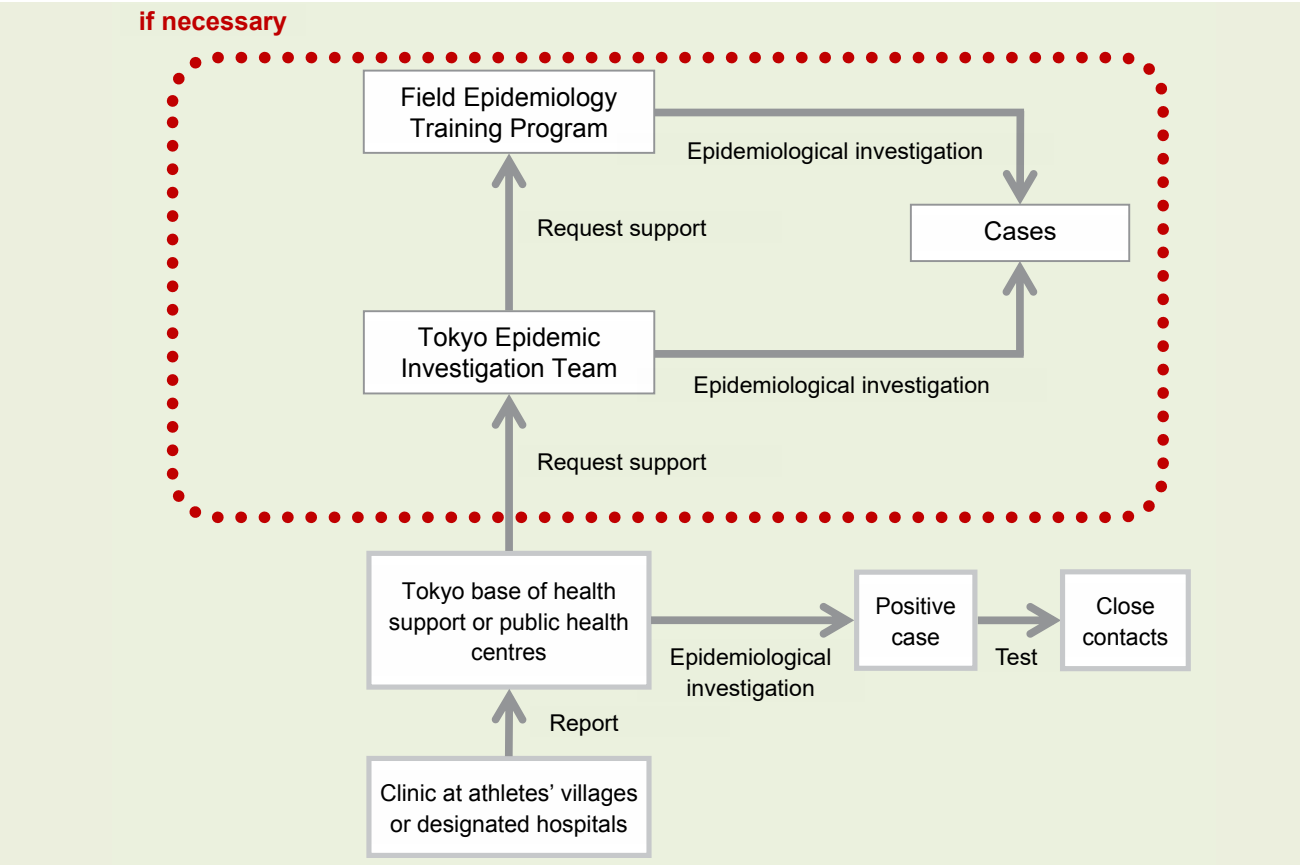


Fig. 3. **Daily reported cases from the notifiable diseases surveillance system during the Tokyo 2020 Olympic and Paralympic Games, 1 July–12 September 2021**

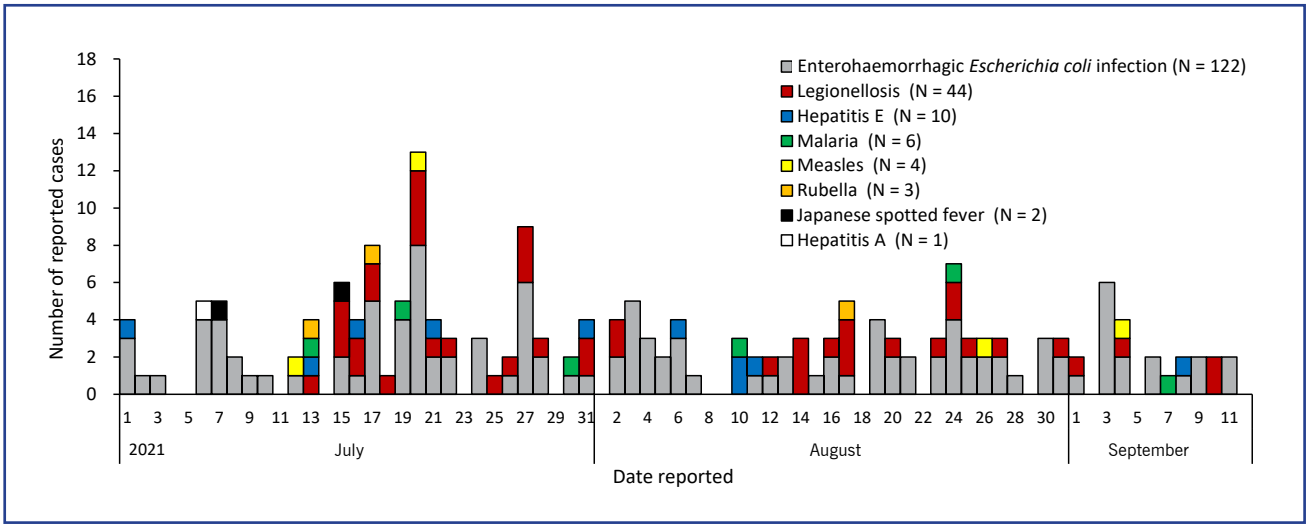


Fig. 4. **Number of cases per sentinel site per week for respiratory syncytial virus infection and infectious gastroenteritis from the sentinel surveillance system in Tokyo, 4–10 January to 20–26 September 2021**

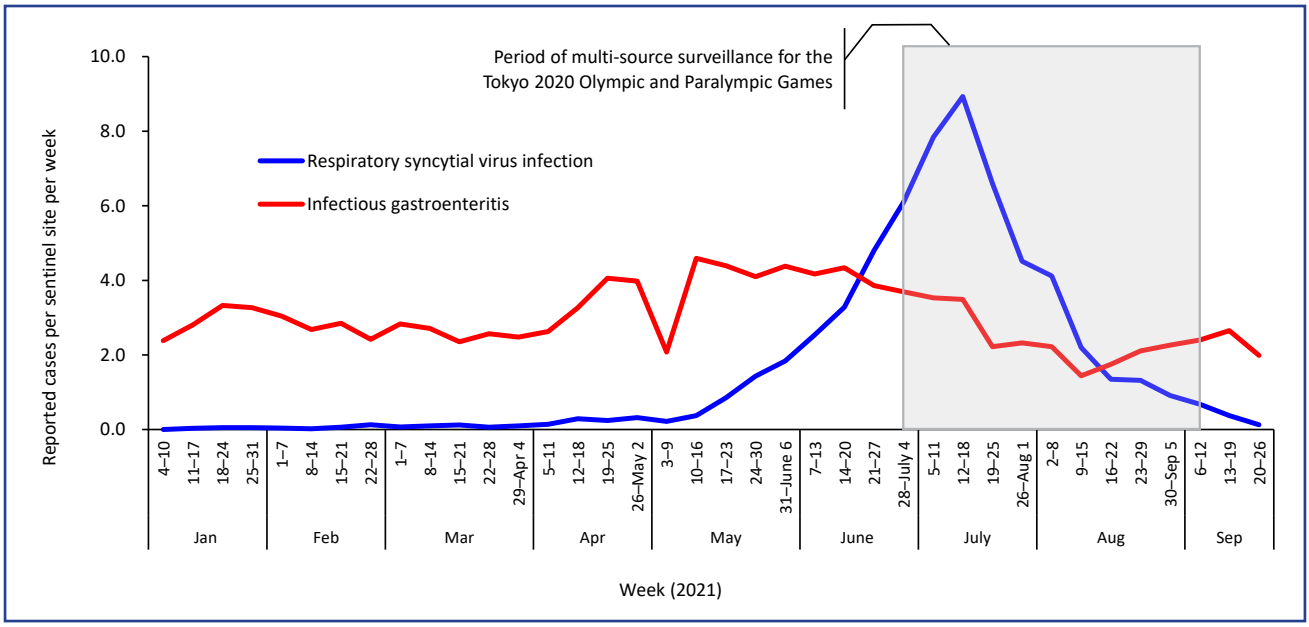
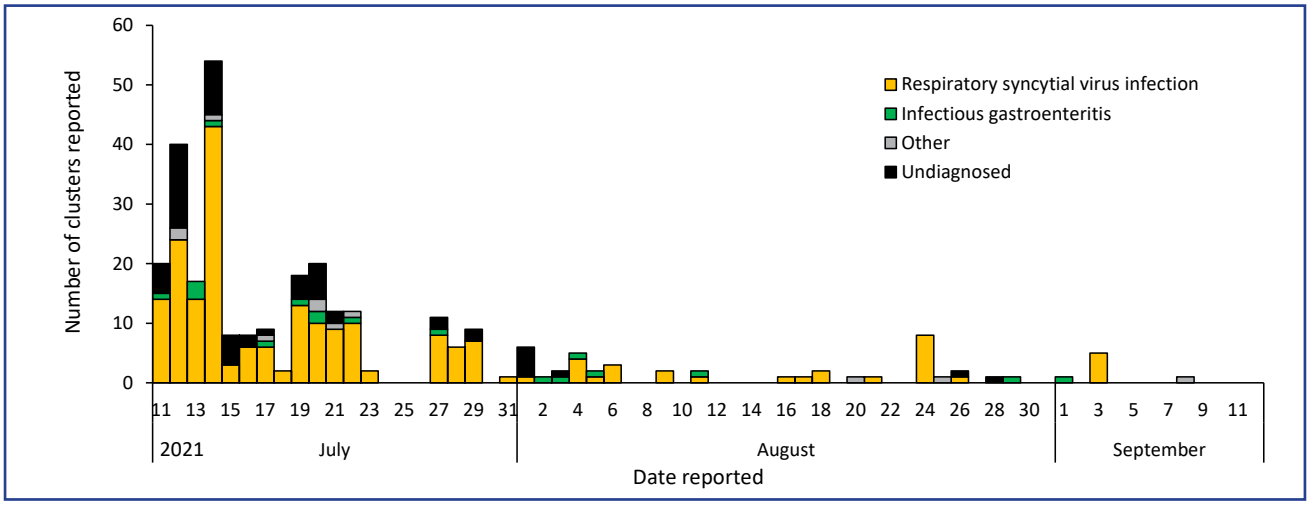


Fig. 5. **Number of clusters reported from the cluster surveillance system during the Tokyo 2020 Olympic and Paralympic Games, 11 July–12 September 2021**



(**Table 3**). Three cases were presumably attributable to infectious gastroenteritis among members of the same family while the other two were COVID-19 patients who were transferred from COVID-19 residential treatment facilities to hospital. No outbreak was observed.

Tokyo Infectious Alert system

No reports were made through the Tokyo Infectious Alert system during the Games.

Prescription surveillance

No aberration was reported through prescription surveillance during the Games.

Table 3. **Aberrations detected in ambulance transfer surveillance during the Tokyo 2020 Olympic and Paralympic Games, by detection and reporting date, 6, 16, 20 July and 22 August 2021**

Detection and reporting date	Situation	Investigation required at medical institution	Reason for not requiring investigation	Follow-up
6 July 2021	On 5 July at 14:00, three people in a city ward were rushed to the emergency room with fever, diarrhoea and vomiting	Not required, but monitoring was continued	All cases had mild symptoms and were presumed to be from one family	No further aberration
16 July 2021	On 15 July at 01:00, five people in a city were rushed to the emergency room with diarrhoea and vomiting	Not required, but monitoring was continued	All cases had mild symptoms and were presumed to be from one family	No further aberration
20 July 2021	On 19 July at 09:00, three people in a city were rushed to the hospital for fever and vomiting	Not required, but monitoring was continued	All cases were presumed to be from one family	No further aberration
22 August 2021	On 21 August at 10:00–11:00, three fever cases with COVID-19 were transported to medical facilities	Not required	The patients were being transported from a COVID-19 residential treatment facility to hospital	Not required
22 August 2021	On 21 August at 11:00–20:00, five fever cases with COVID-19 were transported to medical facilities	Not required	The patients were being transported from a COVID-19 residential treatment facility to hospital	Not required

Nursery School Absenteeism Surveillance System

No aberration requiring investigation was reported through (N)SASSy during the Games.

Response

No investigations or public health responses were required during the Games.

DISCUSSION

The multi-source surveillance conducted for the Games in Tokyo in 2021 confirmed that no cases of infectious disease were reported that required a specific public health response. Although there were diseases reported through the official notification and sentinel systems in Tokyo, none were assessed as being associated with the Games. Despite the Games being postponed to 2021 because of the COVID-19 pandemic, TMG was able to prepare the multi-source surveillance system in just 3 months and successfully operate it during the Games, incorporating lessons learned from the 2013 Sports Festival in Tokyo and the 2019 Rugby World Cup.

The countermeasures implemented to prevent transmission during the COVID-19 pandemic contributed to the low activity of other infectious diseases[11,12] and might explain why no outbreak was detected during the Games. In addition, the risks posed by mass gatherings at the Games were reduced due to the fact that only players and staff members were in attendance.

No reports were received through the official syndromic surveillance system or the Tokyo Infectious Alert system during the Games. As null reporting was not required in the official syndromic surveillance system, it is not known whether the lack of reports was due to a true lack of illness or to issues with the system itself, such as unclear case definition or insufficient awareness within medical institutions to report. Further investigation into the reasons for non-reporting and the modifications to rectify them is necessary before the official syndromic surveillance system is used for a similar event.

The prescription surveillance or (N)SASSy coverage in Tokyo was not as complete for the Games as it had been historically. This surveillance system is part of routine automatic surveillance that is conducted irrespective of high-profile and mass-gathering events. Historical data can, therefore, be used for comparison during mass-gathering events to detect aberrations.

The lack of aberrations from (N)SASSy was probably because the Games were held during the school summer holidays, when the risk of outbreaks was low. Although these systems did not report any aberrations during the Games, they are still expected to be helpful for future mass-gathering surveillance because they can provide valuable information collected with no effort or cost.

The cluster surveillance system comprised medical institutions and residential aged-care facilities that were not covered by other surveillance systems. Although the cluster surveillance worked well, the reported data were not linked to illness at the Games. This was because hospitalized patients and residents at care facilities were unlikely to come into contact with participants of the Games. Therefore, the monitoring of clusters in these populations might not be useful for future surveillance during the Games. The cluster surveillance system was incorporated into the multi-source surveillance system for the Games due to the possibility that medical staff and professional caregivers may have worked as volunteers for the Games and could have transmitted infectious diseases, which was not the case. This occurred during the PyeongChang 2018 Winter Olympic Games, where 172 cases of norovirus were observed in volunteers who stayed at hostels, with four cases of diarrhoea in the Olympic villages.[13]

The daily reports of the surveillance data and risk assessments from the Games were not shared publicly by TMG. This contrasts with the enhanced syndromic surveillance for the National Sports Festival in Wakayama[14] and the Worldwide Uchinanchu (persons of Okinawan origin) Festival,[15] where all information and related risk assessments were posted online promptly. The Infectious Diseases Control Law requires that national and local governments analyse and disseminate information relating to infectious diseases to prevent transmission and outbreaks. However, TMG did not rapidly share the surveillance information with the general public during the Games as it did not have sufficient time for coordination with relevant organizations. This shortcoming should be improved to further multi-source surveillance for mass gatherings such as the Games.

Communication between TMG and NIID was useful to multi-source surveillance for the Games. The daily web conferences held with NIID facilitated information sharing, which contributed to risk assessment. The establishment of a system of collaboration with NIID during the planning and preparation stages for future mass-gathering or politically high-profile events in Tokyo is recommended. Both cooperation and communication among stakeholders including sections within TMG, event operators, the national government and other local governments involved in future events are also needed.

The multi-source surveillance system used for the Games is likely to be utilized by TMG for future mass gatherings in Tokyo. As multi-source surveillance increases the number of information sources being assessed, it may enable earlier detection and quicker response times than the routine surveillance conducted by TMG. It combines syndromic, cluster and laboratory information in a multi-layered way to provide a comprehensive assessment of infectious diseases occurring during mass-gathering events. However, the content, surveillance systems used, reporting schedules and responses to the outbreak detected in the multi-source surveillance must be tailored to each event.

There are some limitations to this analysis. It was limited to systems operated by TMG and did not include surveillance conducted by other local government jurisdictions where some of the events were held. Thus, any infectious diseases from these jurisdictions related to the Games would have been missed by the TMG system. Additionally, because of the short preparation time, we did not collaborate with related departments such as food and environmental divisions of TMG, the Tokyo Metropolitan Police Department and quarantine stations. If these agencies had detected public health events such as an outbreak of food poisoning or bioterrorism, then our multi-source surveillance may not have detected it. Food poisoning information and mosquito surveillance are expected to be increasingly important infection control measures during multi-source surveillance of other events held in the summer months. These are the challenges for future efforts in multi-source surveillance by TMG.

In conclusion, the multi-source surveillance undertaken during the Games by TMG resulted in no confirmed case of infectious disease requiring a response. This is likely due to there being no audience presence during the Games, and to the public health and social measures implemented for the COVID-19 pandemic. Our experience from earlier mass-gathering

events contributed to our being able to establish multi-source surveillance for the Games rapidly. Further lessons learned during the Games that can be applied to future mass-gathering events are to ensure the quality of the surveillance systems, include mechanisms for informing the general public in a timely manner, improve the sharing of surveillance data conducted by other local governments, and secure the necessary collaboration with related departments within TMG.

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Conflicts of interest

The authors have no conflicts of interest to declare.

Ethics approval

Official surveillance for notifiable diseases, official sentinel surveillance and official syndromic surveillance were conducted according to Articles 12 and 14 of the Infectious Diseases Control Law. Cluster surveillance, ambulance transfer surveillance and the Tokyo Infectious Alert system were conducted by TMG based on Article 15 of the Infectious Diseases Control Law. Prescription surveillance and (N)SASSy data were published in general every day to show the situation of the previous day. Therefore, there was no need for ethical approval.

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References

1. Public health for mass gatherings: key considerations. Geneva: World Health Organization; 2015. Available from: https://www.who.int/publications/i/item/public-health-for-mass-gatherings-key-considerations, accessed 22 November 2022.
2. Shimatani N, Sugishita Y, Sugawara T, Nakamura Y, Ohkusa Y, Yamagishi T, et al. Enhanced surveillance for sports festival in Tokyo 2013: preparation for Tokyo 2020 Olympic and Paralympic Games. Jpn J Infect Dis. 2015;68(4):288–95. doi:10.7883/yoken.JJID.2014.233 pmid:25672404
3. Sugishita Y, Abe N, Somura Y. Enhanced syndromic surveillance by the Tokyo Metropolitan Government for the 2019 Rugby World Cup lessons learned for the Tokyo Olympic and Paralympic Games. Jxiv. 2022. doi:10.51094/jxiv.109
4. Sugishita Y, Sugawara T, Ohkusa Y, Ishikawa T, Yoshida M, Endo H. Syndromic surveillance using ambulance transfer data in Tokyo, Japan. J Infect Chemother. 2020;26(1):8–12. doi:10.1016/j.jiac.2019.09.011 pmid:31611069
5. Ohkusa Y, Sugawara T, Kawanohara H, Kamei M. Evaluation of the global action plan on antimicrobial resistance in Japan during its first eighteen months. Drug Discov Ther. 2018;12(3):182–4. doi:10.5582/ddt.2018.01011 pmid:29999000
6. Sugawara T, Ohkusa Y, Kawanohara H, Kamei M. Prescription surveillance for early detection system of emerging and reemerging infectious disease outbreaks. Biosci Trends. 2018;12(5):523–5. doi:10.5582/bst.2018.01201 pmid:30473564
7. Tanabe Y, Kurita J, Nagasu N, Sugawara T, Ohkusa Y. Infection control in nursery schools and schools using a School Absenteeism Surveillance System. Tohoku J Exp Med. 2019;247(3):173–8. doi:10.1620/tjem.247.173 pmid:30867342
8. Kurita J, Sugawara T, Matsumoto K, Ohkusa Y. Cost-effectiveness analysis of (Nursery) School Absenteeism Surveillance System. Pediatr Int. 2019;61(12):1257–60. doi:10.1111/ped.14023 pmid:31630471
9. Sugishita Y, Sugawara T, Ohkusa Y. Association of influenza outbreak in each nursery school and community in a ward in Tokyo, Japan. J Infect Chemother. 2019;25(9):695–701. doi:10.1016/j.jiac.2019.03.010 pmid:30962116
10. Rapid risk assessment of acute public health events. Geneva: World Health Organization; 2012. Available from: https://apps.who.int/iris/handle/10665/70810, accessed 22 November 2022.
11. Hibiya K, Iwata H, Kinjo T, Shinzato A, Tateyama M, Ueda S, et al. Incidence of common infectious diseases in Japan during the COVID-19 pandemic. PLoS One. 2022;17(1):e0261332. doi:10.1371/journal.pone.0261332 pmid:35020724
12. Sawakami T, Karako K, Song P, Sugiura W, Kokudo N. Infectious disease activity during the COVID-19 epidemic in Japan: lessons learned from prevention and control measures. Biosci Trends. 2021;15(4):257–61. doi:10.5582/bst.2021.01269 pmid:34261848
13. Kim DS, Young-Lee H, Bae KS, Baek GH, Lee SY, Shim H, et al. PyeongChang 2018 Winter Olympic Games and athletes' usage of 'polyclinic' medical services. BMJ Open Sport Exerc Med. 2019;5(1):e000548. doi:10.1136/bmjsem-2019-000548 pmid:31548900
14. Kambe C, Fujii H, Niu T, Matsuura H, Nagai N, Nakamura Y, et al. Enhanced surveillance for national (handicapped) sports games in Wakayama, Japan 2015. J Biosci. 2018;6(7):35–47. doi:10.4236/jbm.2018.67004
15. Yamakawa M, Yamauchi M, Nidaira M, Azuma T, Nakasone T, Ando F, et al. Enhanced public health surveillance for the Sixth Worldwide Uchinanchu Festival conducted by the Okinawa Prefectural Government, Japan. J Biosci. 2017;5(9):106–15. doi:10.4236/jbm.2017.59010
16. Health Science Research Group on "Health Security for Mass Gatherings/High Profile Events". Report on international symposium: mass gathering and public health preparedness during COVID-19 pandemic. Tokyo: Ministry of Health, Labour and Welfare, Japan; 2022. Available from: http://massgathering.jp/archives/542, accessed 4 May 2023.

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