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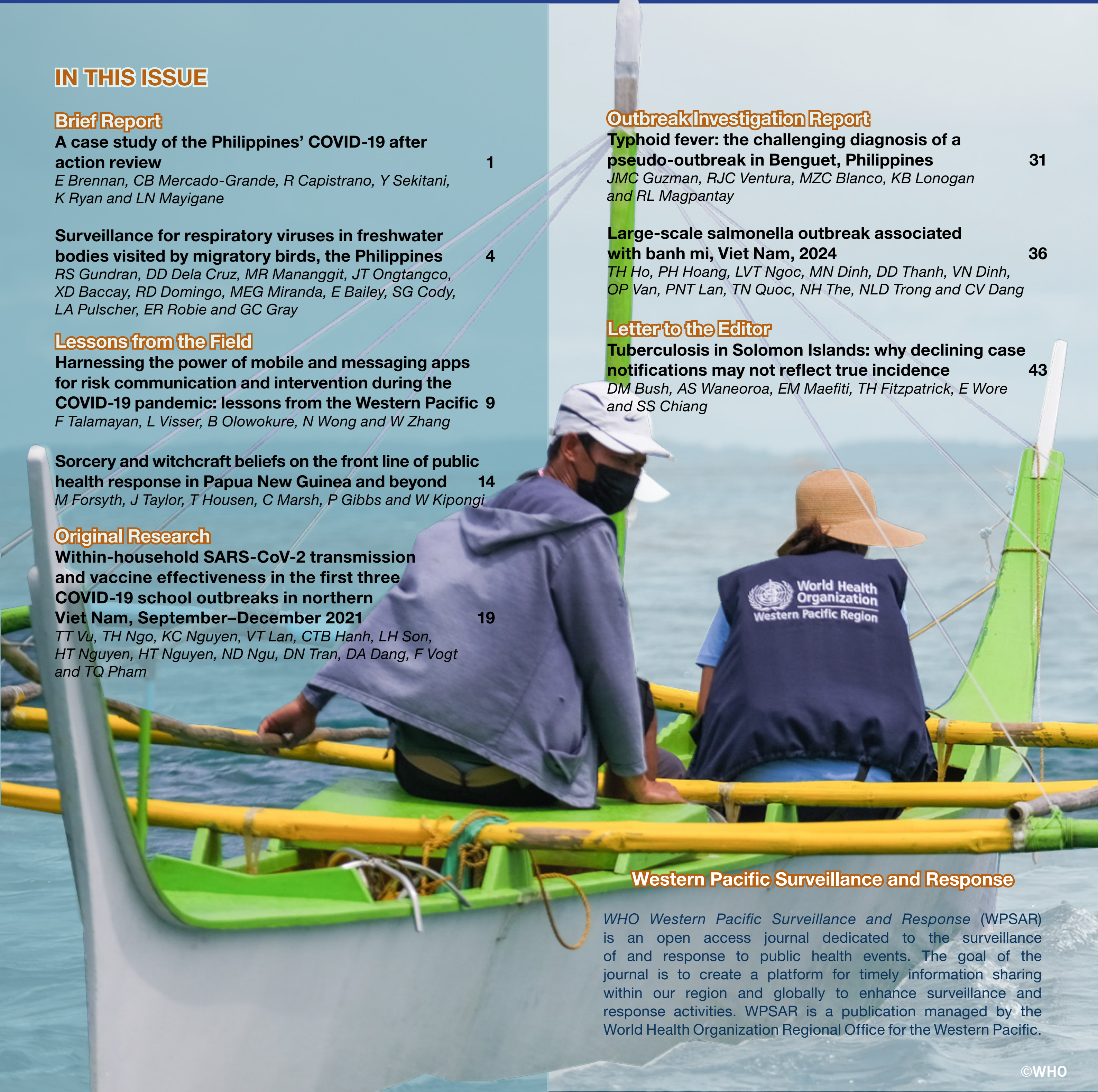

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Western Pacific Surveillance and Response

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A case study of the Philippines' COVID-19 after action review

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Health system performance depends on continual learning.[1] The need for such learning is most visible during and after protracted health emergencies. After action reviews (AARs) are one tool for health system learning. A 2019 systematic review of AARs noted that the tool "contributes to a culture of continuous personal, collective and institutional learning aimed at the gathering of lessons learned and best practices."[2] Key features of AARs include effective leadership engagement, the equal participation of team members, the inclusion of stakeholders, a positive and safe environment for feedback, and the generation of collective knowledge.[2–4] When effectively employed, AARs can lead to evidence-based improvements in health emergency preparedness, response and resilience.

On 5 May 2023, the Director-General of the World Health Organization (WHO) lifted the status of public health emergency of international concern from COVID-19 upon the recommendation of the International Health Regulations (2005) Emergency Committee. The report by the Emergency Committee recommended that "States Parties should update respiratory pathogen pandemic preparedness plans [by] incorporating learnings from national and subnational after action reviews."[5]

Following this recommendation, WHO developed the *Guidance for conducting a country COVID-19 after action review (AAR)*.[6] The Guidance was reviewed during consultations with both internal and external experts. In June 2023, the Philippines became the first country to conduct a COVID-19 AAR using WHO's new methodology. A draft of the Guidance and tools were used to design the Philippines' COVID-19 AAR. Following the AAR, a writing workshop was conducted in July 2023 to translate the AAR's findings into the Philippine Pandemic Preparedness, Response and Resilience Plan.

PROCESS

The Philippines' COVID-19 AAR was coordinated by the Secretariat of the Inter-Agency Task Force for the Management of Emerging Infectious Diseases, a body that was reactivated by the executive government on 28 January 2020 to respond to the COVID-19 outbreak. The Inter-Agency Task Force is an intersectoral collaborative body established in 2014 to prevent, prepare for and respond to outbreaks of emerging infectious diseases in the Philippines.

A 2-day in-person COVID-19 AAR (15–16 June 2023), followed by a 2-day in-person writing workshop (6–7 July 2023), were both held in Manila, Philippines. Focus groups and key informant interviews were conducted to provide further depth and breadth to insights about cross-cutting aspects. Multiple agencies were represented, including from the private sector, academia and the medical sector, as well as offices of the government. Throughout the process, working groups included representatives from diverse agencies.

The overall objectives of the process were to review and document the lessons learned about the Philippines' preparedness for and response to the COVID-19 pandemic, to identify corrective actions and policies implemented, and to inform the drafting of the Philippine Pandemic Preparedness, Response and Resilience Plan.

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COVID-19 after action review

The Philippines' COVID-19 AAR was based on the Philippines National Action Plan against COVID-19 following WHO's methodology.[6] The scope and methods proposed in the Guidance were adapted to meet the country's needs and to align with its response, based on its prevent, detect, isolate, treat, reintegrate and vaccinate (PDITR+V) strategy:[7]

- prevent – implement health promotion and ensure adherence to public health and social measures;
- detect – implement surveillance, testing and contact tracing;
- isolate and quarantine – monitor quarantine facilities at all levels;
- treat – rely on the patient referral system, hospital readiness and case management;
- reintegrate – ensure economic recovery, social healing, awareness of possible reinfection, minimum health standards; and
- vaccinate.

During working group discussions, emphasis was placed on selected pillars from the WHO Guidance:

- country-level coordination, planning and monitoring;
- national legislation and financing;
- mass gatherings;
- infection prevention and control;
- operational support and logistics for managing supply chains and ensuring workforce resilience; and
- risk communication and community engagement, and infodemic management.

Each multisectoral working group identified the challenges, impacts and enabling or limiting factors encountered during the COVID-19 pandemic. The working groups then recommended strategic actions for both the short term (12–24 months) and long term (5 years). These were ordered by priority and prepared for use in the second phase of the process, the writing workshop.

Writing workshop

The writing workshop was designed according to the draft Asia Pacific Health Security Action Framework,[8] replacing the Asia Pacific Strategy for Emerging Diseases and Public Health Emergencies,[9] which enabled it to incorporate lessons learned from the COVID-19 pandemic. The draft Framework was later endorsed by Member States in the Western Pacific Region.[10]

The multisectoral writing groups prioritized addressing the strategic actions from the AAR discussions to develop up to 10 activities to be undertaken during the next 12–24 months. Working groups explored the feasibility (difficult or easy) and impact (high or low) of each activity, which allowed them to be prioritized. Implementation pathways were mapped for each activity. Barriers to completing each activity were discussed and mitigation measures were identified, as well as policy pathways that could help overcome barriers. To facilitate implementation, performance indicators and completion deadlines were also identified for each proposed activity.

DISCUSSION

During the AAR process, participants cited the importance of the multiagency nature of discussions, which allowed for systems thinking and overall ownership for planning and implementing strategic actions going forward. Participants also appreciated the flexibility of the discussions, which allowed for deep exploration of root causes and corrective actions.

The prioritization of activities and identification of barriers to implementation were two core elements of the writing workshop that helped reveal clear policy pathways for the short-term action plans. Participants reflected on how prioritizing enabled them to reduce an otherwise overwhelming number of potential activities to a more manageable number of time-bound and impactful ones. During the working groups, some participants noted feeling empowered by identifying barriers to implementation. They noted the value of charting a course to remove known and foreseeable bottlenecks.

Reflecting on the process, one participant noted that everybody wants to talk about their experiences and best practices, but organizing input and writing are quite a challenge. The COVID-19 AAR and writing workshop provided a pathway to address these obstacles. The process allowed for the capture and codification of knowledge and for collaborative translation into proposed policies. Insights from the COVID-19 AAR and writing workshop are being transformed into an actionable Philippine Pandemic Preparedness, Response and Resilience Plan. The lessons identified may in turn inform other planning and preparedness workstreams, such as supporting the Joint External Evaluation process, the States Parties Self-Assessment Annual Report and National Action Plans for Health Security.

The Philippines' COVID-19 AAR is a model for conducting future AARs on COVID-19 and other protracted health emergencies. The authors encourage countries to employ WHO's methodology for COVID-19 AARs and to share their experiences to ensure intercountry learning.

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Conflicts of interest

EB, RC, YS, KR and LNM are employed by WHO.

Ethics statement

Formal ethical approval was not sought as research was not undertaken.

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Surveillance for respiratory viruses in freshwater bodies visited by migratory birds, the Philippines

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Migratory birds are known to spread influenza viruses, and the Philippines is a common stopover for several species that fly long distances.[1] Influenza A viruses are a particular global health concern because of their zoonotic potential, impacting not only humans but also animals and wildlife. In 2005, thousands of migratory birds died from avian influenza at a major migratory stopover point in western China.[2] The Philippines is an important aggregation and breeding site for migratory birds that are distributed across central Asia. In September, they migrate southwards from China to Myanmar and over the Himalayas to India, returning to China around April. Through this migration, avian influenza viruses can spill over to new bird species, including domestic poultry, across countries and potentially to humans.[2]

In the Philippines, ducks are a common domestic avian species and an important source of meat and eggs for the communities that raise them. However, since outbreaks of highly pathogenic avian influenza (HPAI) occurred in the Philippines in 2017, duck production in both commercial and backyard settings has decreased, resulting in economic strain and food insecurity.[3,4] Government authorities suspected the HPAI outbreaks were linked to bird migration.[3] However, because of the temporary nature of migratory birds' residence across their flyways, trapping and sampling them is difficult, prompting researchers to seek alternative ways to detect HPAI viruses. Sampling from water bodies frequented by migratory bird populations has been proposed as an efficient and effective alternative means of detecting the viruses.[5] In the Philippines, water bodies such as riverbanks, creeks, marshlands, irrigation canals, rice fields and bird sanctuaries are known to harbour migratory bird populations and are likewise used as grazing sites for domestic ducks.

Sampling water to study the prevalence of avian influenza viruses began in the late 1970s and has been periodically used since then.[6] In one 2014 study in China, investigators were able to culture H5N1 and H9N2 avian viruses from natural water bodies for up to 45 days after migratory birds had stopped there.[6] In 2020, water sampling became even more widely used due to the COVID-19 pandemic,[7] during which the discovery of severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) in water bodies was reported, and since then wastewater-based epidemiology has been applied as an early surveillance tool.[8] In this paper, we employed water sampling as a method for assessing avian-to-avian transmission and the potential for spillover of HPAI virus

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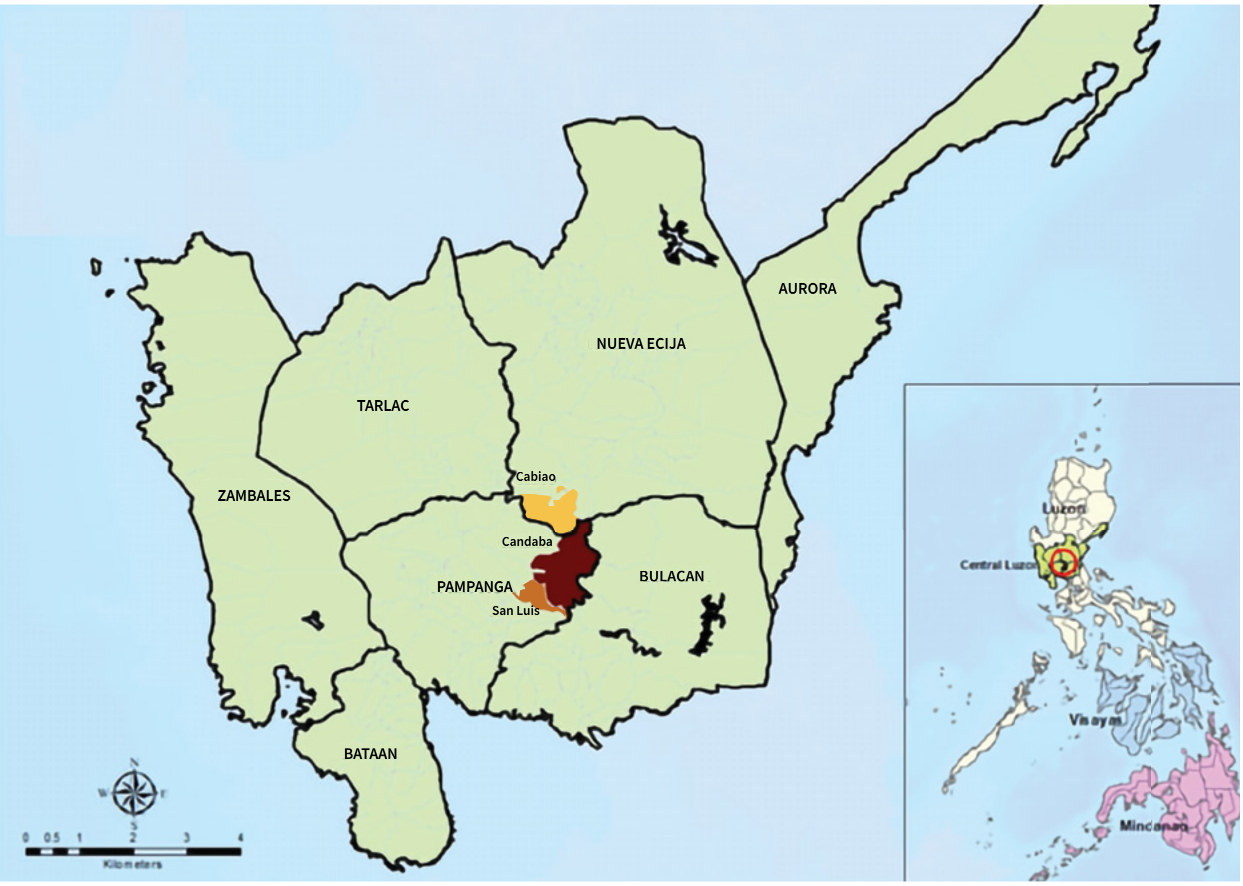
Fig. 1. **Map of Central Luzon Region, the Philippines, showing the three municipalities where water sampling was conducted (Cabiao, Nueva Ecija province; Candaba and San Luis, Pampanga province), 2019–2020**



strains from migrating birds to domestic poultry in the Philippines.

METHODS

Sample collection

Three areas visited by migratory birds in the Central Luzon Region of the Philippines were selected for sampling: Cabiao in Nueva Ecija province, San Luis in Pampanga province and Candaba in Pampanga province (**Fig. 1**). From October 2019 to August 2020, samples of environmental water were collected on five different occasions from six bodies of water, such as bird sanctuaries, riverbanks, creeks, marshlands, irrigation canals and rice fields, where migratory birds and ducks are typically seen during the migration season and where commercial and backyard ducks also commonly graze. In the Philippines, the southward migration of birds typically peaks between September and November, while the northward migration peaks between February and April. Google Maps was used to create a sampling grid to determine the sampling points. Samples were then randomly collected from within the identified sampling points. From each identified sampling spot for each body of water, 10 water samples of 50 millilitres (mL) each were taken at least 5 metres apart. Next, for each group of 10 samples, the samples were combined and then divided into two pools for each body of water from each municipality.

During sample collection, the following information was obtained: date and time the sample was collected, water temperature, water pH, type of vegetation in the area, and presence or absence of migratory birds. Fifty mL of viral transport medium was added to each 50-mL sample, and these 100-mL field samples were transported at ambient temperature for testing at the Regional Avian Influenza Diagnostic Laboratory in Pampanga, Philippines.

Laboratory testing

Samples were processed and molecularly screened for adenovirus, enterovirus, coronavirus, influenza A virus and influenza C virus based on previously published methods.[9] The 100-mL water samples were vortexed and a 200-μL sample from each was pooled by location and date into one sample before nucleic acid extraction. RNA and DNA were extracted from the samples using the QIAamp MinElute Virus Spin Kit (Qiagen, Germantown, MD, USA). Samples were then screened by quantitative reverse transcription–polymerase chain reaction (qRT–PCR) for the influenza A virus matrix gene using primers and probes. Samples were also examined by qRT–PCR or qPCR assays for influenza C virus, adenovirus, seasonal coronaviruses and enteroviruses.[9] Samples positive for influenza A underwent haemagglutinin subtyping at the Research Institute for Tropical Medicine in Manila, Philippines.

RESULTS

From October 2019 to August 2020, a total of 180 samples were collected (60 samples per municipality). This resulted in 36 pooled samples, 12 from each municipality.

The samples were collected in waters of different pH (range: 7.0–9.3), varying temperatures (range: 26–38 °C) and different vegetation types (**Table 1**). Various wild birds were observed in the waters including brown and white sparrows (*Passer montanus*), buff-banded rails (*Gallirallus philippensis*), mallard ducks (*Anas platyrhynchos*), storks (*Anastomus oscitans*) and wild ducks (*Anas luzonica*) (**Table 1**).

Of the pooled samples, one pool (2.78%) from a creek in Cabiao was positive for influenza A virus, and two pools (5.55%) were positive for enterovirus: one from a riverbank in Candaba and one from a rice field in San Luis (**Table 1**). The detection of influenza A virus was consistent with the H9 virus identified by haemagglutinin subtyping. The molecular assays for influenza C virus, adenovirus and seasonal coronaviruses on the pooled specimens were all negative.

DISCUSSION

The Philippines serves as a crucial stopover and wintering site for many migratory bird species.[10–15] As a common resting place for migratory birds, the country is at risk for an avian influenza spillover to domestic poultry, and potentially humans, due to the mixing of many wild bird species from across Australia, Asia and Oceania. Environmental sampling of various water bodies frequented by both domestic and wild birds yielded one pooled sample positive for influenza A virus from an area that, at the time of sampling, was inhabited by brown sparrows and storks. Two pooled samples were also positive for enterovirus. The first was collected in an area where brown sparrows were present and the second where storks were present. Notably, these same species were also seen frequenting sites where no virus was identified in the samples. Both kinds of birds are migratory and not permanent residents of the Philippines, confirming that the selected sites do serve as resting spots for such migratory birds, which may visit these waters twice annually. Influenza A virus may be transmitted from the carrier to the environment through faeces, which could then be spread to new avian species through contaminated water bodies. Similarly, enteroviruses can also be spread through environmental water sources.[16]

This pilot study was limited in that relatively few ($n = 180$) specimens were collected in a relatively narrow geographical region on five occasions during a 10-month period. Additionally, relatively few viruses were detected in these samples, and detailed characterization of the influenza A and enteroviruses that were detected was not performed. Our study was further limited in that the adenovirus assay used in this study was developed to detect human adenoviruses and may have missed non-human adenovirus strains. Hence, the sampling was not comprehensive, and important viruses may not have been detected. Regardless, our study found evidence that freshwater bodies can harbour influenza A virus. The virus can be shed by migratory birds through their faeces, and such contaminated water bodies may transmit the virus to livestock and possibly to humans. These results highlight the significant risk posed by the practice of allowing domestic ducks to forage near freshwater bodies visited by migratory birds. Ducks, once infected, can potentially

Table 1. **Summary of water samples collected from three municipalities in the Philippines, 2019–2020**

Municipality, province, type of water body	pH	Temperature (°C)	Vegetation type present[d]	Migratory birds present[e]	Collection date	Collection time
Cabiao, Nueva Ecija						
Riverbank	8.7	29	Camachile, tall grass, water hyacinth, water lilies	Brown sparrow	8 November 2019	14:16
Creek[a]	7.7	26	Water hyacinth, water lilies	Brown sparrow, stork	29 October 2019	15:06
Marshland	8.2	37	Camachile, para grass, vines, water spinach, wild tamarind	Stork	8 November 2019	13:28
Irrigation canal	8.4	38	Para grass	Brown sparrow, stork	8 November 2019	12:58
Rice field	–[c]	–[c]	Para grass	Stork	28 August 2020	10:36
Bird sanctuary	8.4	32	Wild spinach	Brown sparrow, buff-banded rail, stork	8 November 2019	10:45
Candaba, Pampanga						
Riverbank[b]	8.5	31	Bamboo, banana, para grass, tall grass	Brown sparrow	7 November 2019	13:01
Creek	7.0	33	Tall grass, water spinach	Brown and white sparrows, stork	31 October 2019	14:05
Marshland	7.7	32	Water hyacinth, water lilies, water spinach	Stork	31 October 2019	13:35
Irrigation canal	7.8	30	Wild tamarind	Stork	31 October 2019	13:01
Rice field	8.6	32	Para grass, water spinach	Brown sparrow, stork	8 November 2019	13:25
Bird sanctuary	7.3	31	Lotus, eucalyptus tree, water hyacinth, water lilies, wild spinach, wild tamarind	Brown sparrow, stork, wild duck	31 October 2019	13:43
San Luis, Pampanga						
Riverbank	8.3	27	Tall grass, water hyacinth, water lilies	Brown sparrow	7 November 2019	12:02
Creek	8.5	27	Carabao grass, tall grass, water hyacinth water lilies	Brown sparrow, mallard duck, stock	7 November 2019	12:15
Marshland	9.3	31	Acacia, water hyacinth, water lilies	Stork	7 November 2019	11:15
Irrigation canal	8.0	26	Tall grass	Brown sparrow	7 November 2019	10:40
Rice field[b]	8.1	27	Rice grass	Stork	31 October 2019	11:30
Bird sanctuary	8.2	27	Water spinach, water hyacinth, water lilies	Brown sparrow, stork, other birds	28 November 2019	10:45

[a] Positive for influenza A.

[b] Positive for enterovirus.

[c] Measurements not recorded.

[d] Acacia: *Acacia mangium*; bamboo: *Bambusa vulgaris*; banana: *Musa* spp.; camachile: *Pithecellobium dulce*; carabao grass: *Paspalum conjugatum*; eucalyptus tree: *Eucalyptus deglupta*; water hyacinth: *Eichhornia crassipes*; water lilies: *Nymphaea* spp.; lotus: *Nelumbo nucifera*; para grass: *Brachiaria mutica*; tall grass: *Saccharum spontaneum*; vines: *Ipomoea batatas*; water spinach: *Ipomoea aquatica*; wild spinach: *Amaranthus viridis*; wild tamarind: *Leucaena leucocephala*.

[e] Brown or white sparrow: *Passer montanus*; buff-banded rail: *Gallirallus philippensis*; mallard duck: *Anas platyrhynchos*; stork: *Anastomus oscitans*; wild duck: *Anas luzonica*.

spread the virus to other birds and sometimes to humans. This study may serve as an example of an alternative strategy for surveillance of avian influenza viruses among migratory birds. Our hope is that water surveillance might help to mitigate HPAI infections among poultry, such as the epizootics that occurred in the Philippines during 2017 and January 2022.[17]

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Conflicts of interest

The authors have no conflicts of interest to declare.

Ethics statement

As this study involved only water sampling, no ethical review was required.

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Harnessing the power of mobile and messaging apps for risk communication and intervention during the COVID-19 pandemic: lessons from the Western Pacific

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Problem: The spread of mis- and disinformation on mobile and messaging apps during the COVID-19 pandemic not only fuelled anxieties and mistrust in health authorities but also undermined the effectiveness of the overall public health response.

Context: Mobile and messaging apps help users stay informed and connected to their families, friends, colleagues and communities. However, during the COVID-19 pandemic, these apps were also one of the primary channels where mis- and disinformation were circulated.

Action: Recognizing the importance of including mobile and messaging apps in risk communication and emergency response strategies, the World Health Organization (WHO) and some countries in the WHO Western Pacific Region independently piloted initiatives to reach messaging app users, meet their evolving information needs, and streamline health ministry communication.

Outcome: The enhanced use of mobile and messaging apps enabled consistent and timely communication and improved coordination during the COVID-19 pandemic. Leveraging their features also helped identify and potentially fill crucial information gaps, mitigating the harms of mis- and disinformation and fostering stronger trust in health authorities.

Discussion: The findings from the work carried out by WHO and countries in the Western Pacific Region identified some promising innovative communication interventions using mobile and messaging apps. While these interventions should be further explored and evaluated, they have demonstrated that interventions need to be proactive, flexible, and able to adapt to changes in mis- and disinformation content being shared through messaging apps.

PROBLEM

The COVID-19 pandemic saw the spread of health-related mis- and disinformation on popular social networking messaging apps, such as WhatsApp, Facebook Messenger, Telegram and Viber, among others.[1] While these apps enable connections and the exchange of important health information, the relationships fostered between users of these platforms have also increased their susceptibility to consuming and sharing mis- and disinformation.[2] In closed social networks, characterized by intimacy and trust among contacts who generally know one another, there is a greater possibility of content being believed and shared without adequate fact-checking.[3]

In an era of expanding digital connectivity, the rapid spread of information can be both beneficial and detrimental to public health: it is useful for swiftly responding to people's concerns and filling information voids, yet it can also amplify harmful messages. The widespread circulation of mis- and disinformation exacerbates disease- or pandemic-related challenges by fuelling fears, encouraging negative health behaviours, eroding trust in health authorities and undermining the effectiveness of public health and social measures.[4]

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This work is an effort to understand communication using private messaging apps during the COVID-19 pandemic as this may help to improve public health messaging, including addressing mis- and disinformation, in future public health emergencies.

CONTEXT

Messaging apps such as Facebook Messenger, WeChat, WhatsApp and Telegram account for approximately 5 billion users globally.[5] They have extensive reach, and according to a report by the digital analysis firm Kepios, in 2023, Facebook Messenger had the majority share of the population aged 13 and above in several countries in the Western Pacific, including Mongolia (79.8%), Viet Nam (66.3%), Tonga (66.2%), New Zealand (60.6%), the Philippines (60.5%) and Fiji (59.6%).[6] The same report highlighted that 71.1% of active global Facebook/Meta users aged 16–64 years use the platform for messaging family and friends. This figure reflects users' gravitation towards free apps that support private, personal communication. The design of most messaging apps is influenced by these specific user preferences, offering a range of features from secure messaging to group chats and multimedia sharing.

Despite the popularity and practical benefits of messaging apps, WHO recognized and highlighted their role as disseminators of rumours and mis- and disinformation, especially during the COVID-19 pandemic.[7] In Singapore, it has been reported that Telegram has become a source for the circulation of misinformation through chat groups that have attracted a large following.[8] Members of these groups questioned the safety and effectiveness of mRNA COVID-19 vaccines and prompted others to explore the use of ivermectin for curing COVID-19.[9] Viber chat groups have played a significant role in the spread of COVID-19 misinformation in the Philippines, causing panic among citizens and leading to potential superspreader events.[10] In Australia, a study revealed that individuals who endorsed COVID-19 misinformation on social media exhibited lower levels of confidence in government, trust in scientific institutions, perceived COVID-19 threat and digital health literacy.[11]

ACTION

With increasing numbers of people turning to social media for news and information, achieving maximum reach, engagement and impact necessitated the adoption of innovative communication strategies and interventions. WHO and countries in the WHO Western Pacific Region independently explored various approaches to fill information voids and reduce the spread of mis- and disinformation, ranging from creating shareable content to engaging key influencers. They also piloted initiatives to use platform features in their emergency response and connect with mobile and messaging app users through broadcast channels and interactive chatbots (that is, computer programmes that simulate conversation with human users to provide them with the information or assistance they need).[12]

For instance, Singapore's Ministry of Communications and Information launched broadcast channels on Telegram and X (previously Twitter) to complement their existing Facebook, Instagram and WhatsApp channels and offer more options for the public to obtain information on COVID-19.[13] In early 2020, the Government of Australia launched a COVID-19 WhatsApp bot (decommissioned in 2022).[14] The Philippine Department of Health also created a chatbot service called Knowledge Informs Responsible Action (KIRA), which is accessible through popular messaging apps such as Facebook Messenger and Viber.[15] At the height of the COVID-19 pandemic, these apps had the capacity to spread messages with great velocity due to the millions of members.

The pandemic prompted the development of new chatbot features and functions to understand and meet people's evolving needs. For example, KIRA enabled the Philippine Department of Health to capture public sentiment towards COVID-19 vaccination, track citizens' satisfaction with their vaccination programme and receive reports on online mis- and disinformation. This approach enabled health authorities to disseminate relevant health information and implement evidence-based COVID-19 responses. Meanwhile, the COVID-19 WhatsApp bot in Australia had a registration feature specifically for self-isolation.[14] Another example is Viet Nam's local messaging app Zalo, which offered users affected by COVID-19 the option to seek or provide emergency support and receive remote medical advice in Ho Chi Minh City, Đồng Nai, Bình Dương and Long An.[16] Overall, these initiatives showcase the adaptability of messaging apps in addressing varied public health needs.

In addition to collecting data and disseminating health information, messaging apps were also used to streamline ministry communication and decision-making. For example, in Cambodia, the Ministry of Health informed the authors that Telegram was adopted as a tool to improve coordination among various government agencies.

At the regional level, WHO conducted preliminary research in 2021 to determine ways that ministries and institutions could mitigate the potential harms of the unchecked spread of COVID-19 and vaccine-related mis- and disinformation. Insights from the research were used to design and implement capacity-building initiatives that could reinforce the use of mobile and messaging apps for combating mis- and disinformation.

OUTCOME

The spread of mis- and disinformation online pointed to the need for better integration of digital platforms, especially mobile and messaging apps, into the planning and operationalization of public health strategies. Several lessons were identified from the COVID-19 experience, including the effectiveness of mobile and messaging apps in streamlining the COVID-19 response, delivering accurate health information, mitigating the harmful effects of mis- and disinformation and coordinating inter-agency communications.

Messaging apps also played a role in improving people's well-being and building greater trust in health authorities. A study of the psychological well-being of 1145 adults in Singapore revealed that exposure to government WhatsApp messages helped to reduce depressive symptoms associated with receiving COVID-19 updates, while increased trust in official WhatsApp messages helped to decrease people's anxiety during the pandemic.[17] Singapore's successful use of messaging apps to disseminate information during the pandemic highlighted the effectiveness of a multiplatform, multilanguage and multiformat approach in providing reliable and timely updates to the public. The strategy not only provided the public with accurate and up-to-date information but also fostered trust between the government and the population.[18]

Embracing the features of mobile and messaging apps helped enhance response capabilities and interaction with health authorities' target audience. In January 2022, Viet Nam's Ministry of Information and Communication reported that over 100 000 people received aid through Zalo's Connect feature.[19] KIRA's July 2022 statistical analysis revealed that their content had been used by 1 million users from over 1400 local governments in the Philippines, resulting in almost 35 million interactions.[20] Through KIRA, messaging app users were able to input their questions and receive responses, functioning as hotlines akin to online customer service provided by private companies.

The Cambodian Ministry of Health informed the authors that Telegram promoted swift inter-agency coordination during the COVID-19 pandemic. The app was used to share critical information and guidance and flag emerging mis- and disinformation. This strategy enabled the development of consistent messaging and quick action against mis- and disinformation. However, despite the app's advantages, one challenge that emerged was maintaining comprehensive records of these communications. The absence of proper archiving in messaging apps makes it difficult to retrieve official communication or verify previously discussed information. These apps often support various media types such as text, images, audio and video. Thus, it is problematic to track and organize diverse data formats into coherent records.

Despite the challenges revealed by WHO and countries in the Western Pacific Region, experience and lessons learnt demonstrated the importance of disseminating clear, timely and consistent health messages to effectively address questions about COVID-19 and vaccines.

DISCUSSION

Various actions taken by WHO and countries in the Western Pacific Region during the COVID-19 pandemic offer valuable insights into both the potential and challenges of leveraging mobile and messaging apps for risk communication and health emergency response. Singapore's multiplatform strategy, Australia's WhatsApp bot and Viet Nam's Zalo app demonstrated innovative uses of technology to meet specific local needs, showcasing adaptability and responsiveness. Integrating the KIRA chatbot into popular messaging apps in the Philippines enhanced the Department of Health's ability to listen and respond to people's questions and evolving needs.[15] The use of messaging apps for inter-agency coordination, as observed in Cambodia, also highlighted their versatility beyond their conventional functions.

This trend could also be observed globally. International organizations such as WHO and the United Nations Children's Fund (UNICEF) spearheaded online initiatives to improve global understanding of COVID-19. WHO rolled out the WHO Health Alert Chatbot on WhatsApp and Facebook in early 2020, offering information on the latest COVID-19 figures and cases, guidelines for self-protection, frequently asked questions, travel advisories, news and press releases in different formats.[21] UNICEF launched the U-Report COVID-19 Information Chatbot in the same year to enhance risk communication and community engagement around COVID-19.[22] Information in both chatbots is available in multiple languages. This holds immense significance as it ensures inclusivity and accessibility for messaging app users, transcends language barriers and empowers individuals to access accurate COVID-19 information in the language with which they are most comfortable.

Despite the benefits of integrating mobile and messaging apps into various risk communication strategies, there are significant challenges, particularly in maintaining people's trust and protecting their privacy during data collection processes. Mobile and messaging apps are, in most cases, encrypted to protect the data and content of their users. For health authorities, this means data are unavailable to identify people's information needs. There is also concern over authorities' potential privacy breaches.[23] Consent is not regularly obtained for messaging apps, and confidentiality, privacy, data security and record-keeping remain areas of concern.[24]

In summary, by leveraging messaging app features such as broadcast messages and chatbots, various countries were able to provide messaging app users access to accurate health information and an avenue to inform ministries of their needs. The rapid circulation of accurate and well coordinated health messages on messaging apps helped achieve two things: pre-empt information voids that could be filled with mis- and disinformation; and foster trust in health authorities. Examples from the Western Pacific Region demonstrate the value of exploring how these pilots could be applied to a wider range of health communication strategies, extending beyond emergency response. Given that our results are based on a small subset of the overall conversations on mobile and messaging apps, these interventions should be further evaluated to determine which approaches, or combination of approaches, may be most effective.

Conflicts of interest

The authors have no conflicts of interest to disclose.

Ethics statement

Formal ethics approval was deemed unnecessary as research was not undertaken.

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Sorcery and witchcraft beliefs on the front line of public health response in Papua New Guinea and beyond

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Problem: Many communities refer to sorcery or witchcraft to explain misfortunes such as sickness, death and disability. The effects of these beliefs on public health service delivery have long been overlooked. Beliefs in sorcery and witchcraft are significant challenges for health-care workers to understand to deliver better health outcomes and avoid inadvertently triggering accusations of witchcraft that may lead to violence.

Context: This paper examines the impacts of accusations of sorcery and related violence on the provision of health care in Papua New Guinea.

Action: The discussion focuses on a workshop held in Papua New Guinea in September 2022 with health extension officers on the topic of health-care delivery and sorcery accusations.

Lessons learned: The workshop confirmed the challenges that beliefs in sorcery and witchcraft present for health extension officers and suggested several strategies that could be used to navigate them. It identified several possible future measures that those on the front line of community health-care delivery considered most important in responding to the issue. These included educating health-care workers on how to effectively address sorcery beliefs when delivering health care and developing communication techniques on the causes of death and sickness that avoid triggering sorcery accusations.

Discussion: This paper reviews the findings of the workshop in the broader context of the effects of beliefs in witchcraft on public health delivery globally. Because of the close connections between sorcery beliefs and health, equipping health-care workers and field epidemiologists with strategies to address these beliefs effectively is critical to delivering better health care, facilitating timely response to public health events, and helping to prevent violence related to sorcery accusations. This need exists in all countries where sorcery beliefs related to health, illness, disability and death are prevalent.

PROBLEM

Across the globe today, many communities refer to sorcery or witchcraft to explain misfortune of all kinds, including sickness, death and disability.[1] This is certainly the case in Papua New Guinea, a highly diverse country of approximately 9 million people, where belief in sorcery is widespread across all sectors of society, including among those in leadership positions, the justice sector and health care.[2] We discuss the implications of these beliefs for public health professionals. While beliefs in sorcery and witchcraft also play a role in traditional healing practices, our focus is on the harmful results of these beliefs and is not intended to advocate against traditional healers per se, as it is recognized that they can and do play an important role in primary health care. The question of the extent to which traditional healers, diviners and religious leaders can play a positive role in helping to prevent the harms generated by witchcraft beliefs is an important one requiring further research. While this paper focuses on Papua New Guinea, sorcery beliefs are widespread in many places worldwide.[3] Even in high-income countries, there has been increased recognition of the harms generated by witchcraft beliefs. For example, in 2012, the United Kingdom of Great Britain and Northern Ireland published a national action plan to tackle child abuse linked to faith or

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belief, which includes concepts of witchcraft and spirit possession.[4] However, at present, sorcery beliefs in the provision of health services receive hardly any attention or resources.

CONTEXT

Sorcery beliefs and violence in Papua New Guinea

In Papua New Guinea, the term "sorcery" is used to represent the belief that one human being is capable of harming another by magical or supernatural means, as well as the practices associated with that belief.[2] While not new, these beliefs have gained greater attention recently due to the harm that can follow accusations of sorcery and concerns that violence is spreading across the country.[5] The scope of harm caused by sorcery accusation-related violence (SARV) is unknown. Even when cases are reported, the fragmented nature of data collation in Papua New Guinea makes it difficult to obtain a reliable account of overall case numbers. A recent 4-year study on SARV that took place in four provinces of Papua New Guinea recorded 1039 cases affecting 1554 people.[6] Victims of SARV include men, women, young and elderly people across the socioeconomic spectrum. However, in some places, women are targeted and often are most severely impacted.[1,6]

The traumatic impacts of SARV are wide-ranging for accused individuals, their families and the affected community. The impacts on children are extremely severe, including: witnessing parents, close relatives or community members being tortured and killed; stigmatization in school and the community; and exclusion from school resulting in poor educational outcomes.[5] Such experiences can lead to feeling ashamed and isolated and living in fear. Also, children are often accused due to the belief that sorcery is passed down through bloodlines. Many children develop the belief that sorcery is real and accept torture (of accused persons) as the norm.[7]

Harm from SARV is compounded by the fact that it is not properly addressed by the legal system.[8] Despite adequate criminal legislation, cases often go unreported as witnesses or victims fear community retaliation, while others may not believe the police will take their complaints seriously. This lack of accountability and justice can contribute to a culture of impunity, where individuals feel empowered to continue perpetrating acts of violence. This promotes a cycle of fear and mistrust, potentially further spreading the risk of accusation and violence.[9]

Sorcery beliefs and health in Papua New Guinea

Sorcery beliefs and accusations in Papua New Guinea tightly intertwine with health, as people often blame sickness and death on sorcery.[10] This has two main implications for public health professionals. First, it can significantly impact the ability of health-care workers and field epidemiologists to provide appropriate interventions. Sorcery beliefs may delay or deter people from seeking medical assistance or make them less likely to follow medical advice.[11] For example, if a community believes a child's death was caused by sorcery, people may be reluctant to allow a field epidemiologist to investigate its real cause, and instead call a "diviner" to ascertain if sorcery caused it.[12] This can make it difficult to identify the source of an infection or disease and delay the steps needed to prevent its further spread.

Second, sorcery beliefs can lead to violence following an incidence of sickness or death, where people blame the death or sickness on a particular individual. Individuals accused of sorcery may be attacked, killed or tortured. Accusations can spiral out of control, sometimes involving multiple deaths, property destruction and the dislocation of entire communities.[13] Also, health-care workers can inadvertently trigger accusations in their communications about the cause of death. One way this occurs in Papua New Guinea is through the common practice of telling people that illnesses are *sik bilong ples* (the sickness of the area), which is interpreted as culture-related and caused by sorcery. Health-care professionals may make such diagnoses due to a lack of biomedical explanations and appropriate tests, or to protect patient confidentiality if the patient died of an illness involving stigma, such as HIV and AIDS.

ACTION

Health-care workers and navigating sorcery beliefs in Papua New Guinea

The difficulties and challenges of sorcery beliefs facing health-care workers were the focus of the first-ever training workshop on this topic for field epidemiologists in Papua New Guinea, held in 2022. The workshop was part of the Field Epidemiology Training Program of Papua New Guinea (FETPNG). Programme fellows are health extension officers drawn from across Papua New Guinea. The workshop participants included 17 advanced field epidemiology fellows and three senior coordination staff who attended a voluntary 90-minute session facilitated by an expert in SARV in Papua New Guinea from the National Research Institute. The objectives of the workshop were to raise awareness among the fellows of the problem of SARV in Papua New Guinea and its link to health, introduce some helpful strategies to mitigate SARV risk in health care, and encourage discussion among the participants on the effective strategies they have developed, thus generating peer-to-peer learning.

The workshop was organized in response to consistent feedback from the fellows on their experiences with tension and occasional conflict in the community associated with sorcery beliefs. The fellows observed that these tensions often delayed or created barriers to outbreak response and public health intervention efforts. The workshop involved a presentation and a free discussion between the fellows focusing on their experiences of the impact of sorcery beliefs on their work, the challenges it presents, and their strategies for effectively addressing them. With their permission, the discussion was recorded, and relevant parts were transcribed.

LESSONS LEARNED

During the workshop, five fellows confirmed the negative impacts of sorcery beliefs on their ability to work effectively. One made the following observations:

> I grew up in the traditional way. There were always stories about sorcery… My dad said this isn't true, so I started not to believe it. The mindset changed over time though in the village. The common things – tuberculosis, cancers – were being blamed on sorcery… but things changed over time. I finished school and went away. When I came back – sorcery was widespread again. I would advocate that there was no such thing. One patient came in vomiting blood – a health worker was talking sorcery… these are the people we rely on to change the way people are thinking. How do we impart knowledge to the community?

Another said:

> There was one facility in a very remote place that was closed for 2 months. A health worker was diagnosed with something at the hospital and died, and the health centre closed down. The brothers-in-law killed four people who were suspected to be sorcerers. The facility was closed. What we did was discuss with the community how best to reopen the health centre. We had to compensate those who died. We settled this, and then the facility opened. We see the issues as health workers – we hear people coming in saying sorcery. What do we do? Maybe we can prevent the violence at the facility level.

Fellows explained that where sorcery was believed to have caused sickness or death in a family, or the wider community, it was hard for them to enter communities, convey risk factors and implement prevention and control measures.

During the session, the fellows provided recommendations for support needed to better address sorcery beliefs and related violence in Papua New Guinea's health-care sector. These included:

- educating health-care workers about how to navigate sorcery beliefs related to death, sickness and other health matters; for example, one fellow noted, "What would help is education at the health centre level – officers need to be trained; they should have an action plan – a *step by step* guide [when faced with sorcery accusations]";

- encouraging use of confirmatory tests to help dispel myths and confirm a medical cause/viewpoint; another fellow said, "Confirmatory tests could help dispel myths. One defaulter in the TB program – he died. Uncle came and said that I had caused this. But because I can prove why he died – that stopped the process";

- encouraging timely reporting of test results and death certificates; promptness dispels accusations and violence; for instance, a third fellow said, “One factor is that death certificate is delayed – so it’s not there in time to avert violence”; and

- developing effective ways to communicate a diagnosis of sickness or communicate the causes of death to a family member in ways that avoid triggering sorcery accusations; for example, another fellow said, “Health comes into this – a sign of disease triggers an accusation. We can spend more time educating the community like what causes fever”.

DISCUSSION

The close connections between sorcery beliefs and health mean that equipping health-care workers and field epidemiologists with strategies to address these beliefs effectively is critical to delivering better health care, facilitating timely responses to public health events and helping to prevent violence related to sorcery accusations. The effects of beliefs in sorcery and witchcraft on health-service delivery should be examined in all countries where it is common for health, illness, disability and death to be explained by reference to such beliefs. There is a great need for properly funded pilots to trial interventions such as those recommended in the workshop in Papua New Guinea to assess those that are most effective, and to share such findings both nationally and internationally. This is an intended direction of research for the authors, and further publications are planned.

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Conflicts of interest

The authors have no conflicts of interest to declare.

Ethics statement

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Within-household SARS-CoV-2 transmission and vaccine effectiveness in the first three COVID-19 school outbreaks in northern Viet Nam, September–December 2021

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Objective: The risk of transmission of severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) from schoolchildren to their household and the protective effects of vaccination in these settings remain poorly understood. We assessed the transmission dynamics of schoolchildren with SARS-CoV-2 within their households and the protective effects of coronavirus disease (COVID-19) vaccination among household members in Viet Nam.

Methods: We estimated the attack rate, vaccine effectiveness and adjusted risk ratio (aRR) of factors associated with SARS-CoV-2 transmission to household contacts of children confirmed to have COVID-19 who attended three schools in Ha Nam, Phu Tho and Thanh Hoa provinces between September and December 2021 using multivariable regression with household-level random effects.

Results: This retrospective cohort study included 157 children infected with SARS-CoV-2 and their 540 household contacts. The attack rate among household contacts was 24.6% (133/540). Overall, vaccine effectiveness among household contacts was 39% (95% confidence interval [CI]: -1 to -63), higher among males than females and higher in adults aged >40 years. COVID-19 transmission was greater among female household contacts compared with males (aRR: 1.35, 95% CI: 0.94 to 1.95), although not statistically significant, and highest among those aged 19–39 years (aRR: 2.51, 95% CI: 1.50 to 4.21). Fully vaccinated household contacts had significantly lower infection risk (aRR: 0.46, 95% CI: 0.26 to 0.84).

Discussion: We found substantial onward transmission of SARS-CoV-2 from schoolchildren to household members, and older people were more likely to be protected by vaccination. We recommend that schoolchildren and all household members living with schoolchildren receive at least two doses of a COVID-19 vaccine. Recognizing the role of schoolchildren in the onward transmission of COVID-19 is an important lesson learned by Viet Nam that can help not only in managing other outbreaks but also in protecting schoolchildren by predicting the progress of the outbreak and preparing for a timely response.

On 23 January 2020, Viet Nam announced its initial cases of coronavirus disease (COVID-19). These were quickly followed by sporadic clusters of imported and secondary cases, which subsequently transformed into clusters in the community in late March and April 2020. Public health measures were implemented across the country, including widespread social isolation, the requirement for all visitors and repatriated people to be tested for severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) and

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placed in quarantine, the implementation of intensive contact tracing and school closures, and restrictions on intercity transportation. After the final community cases were identified in late April 2021, these public health and social measures were gradually stopped in May 2021. From May until July 2021, only imported cases were detected through quarantine and immigration checkpoints, and no special public health and social measures, such as national lockdown or school closures, were carried out.[1]

In 2021, Viet Nam used emergency regulations to approve nine COVID-19 vaccines: ChAdOx1-S [recombinant] vaccine (AstraZeneca), Abdala (CIGB-66, Center for Genetic Engineering and Biotechnology), Spikevax (Moderna), Sputnik V (Gamaleya Research Institute), CoronaVac vero cell vaccine (Sinovac Life Sciences), Comirnaty (Pfizer–BioNTech), Hayat-Vax (Sinopharm), Janssen (Johnson & Johnson) and Covaxin (Bharat Biotech). Most of the vaccine doses were supplied by AstraZeneca, Gamaleya Research Institute, Sinovac Life Sciences, Pfizer–BioNTech and Moderna. Viet Nam began COVID-19 vaccinations for adults in April 2021.

From September to November 2021, several regions reopened their schools, after which several school outbreaks were caused by the SARS-CoV-2 Delta strain. Ha Nam, Phu Tho and Thanh Hoa provinces, which had reported no COVID-19 cases previously, all reported school outbreaks. Because the vaccination programme targeted only adults, all children younger than 18 years were unvaccinated. The Ministry of Health began vaccinating children aged 12–17 years against COVID-19 on 14 October 2021. Children aged 12–17 years were vaccinated in Ha Nam on 16 November 2021, in Phu Tho on 14 November 2021 and in Thanh Hoa on 30 November 2021.

The role of children in school outbreaks and within-household transmission of COVID-19 is not well understood. One study from England reported that children are less likely to transmit the illness than adults,[2] with another study from Ireland reporting no secondary transmission within a school setting.[3] An unpublished study from the United Kingdom of Great Britain and Northern Ireland found that children aged 11–18 years had the highest rate of COVID-19,[4] and those aged 5–11 years had a prevalence comparable to working-age people (Riley S, Ainslie KEC, Eales O, Walters CE, Wang H, Atchison C, et al. High prevalence of SARS-CoV-2 swab positivity and increasing R number in England during October 2020: REACT-1 round 6 interim report. medRxiv [Preprint]. 2020). In 2023, a study from the United States of America that included 110 children indicated that they could carry and spread the virus at rates similar to adults.[5] Moreover, a 2022 systematic review found lower prevalence in children compared with adults, but these rates increased with the arrival of new variants such as Omicron.[6]

Unvaccinated children infected by SARS-CoV-2 are frequently asymptomatic or have minimal symptoms; therefore, their role in disease transmission within households must be considered. Several studies have shown that transmission rates of SARS-CoV-2 within a household were higher than transmission in schools.[7-10] However, the role of vaccination status among household members has not yet been documented. Addressing these gaps will allow for a more evidence-based approach to school closures and vaccine prioritization strategies.

In this study, we aimed to assess within-household attack rates and the effect of vaccination among household members living with unvaccinated children with confirmed SARS-CoV-2 infection during three school outbreaks in Ha Nam, Phu Tho and Thanh Hoa provinces, Viet Nam, between September and December 2021.

METHODS

Study design and sampling

We used secondary data collected during three school outbreak investigations in Ha Nam, Phu Tho and Thanh Hoa. Data were available for 157 students and 540 household contacts from the three outbreaks: 23 students and 87 household contacts in Ha Nam; 91 students and 347 household contacts in Phu Tho; and 43 students and 106 household contacts in Thanh Hoa.

Case definition

A confirmed case was defined as a child who tested positive for SARS-CoV-2 by real-time reverse transcription–polymerase chain reaction (RT–PCR) and who attended one of the three implicated schools. A household contact was defined as anyone who lived in the same household as a confirmed case at the time of recruitment. When a schoolchild exhibited symptoms or was a contact of another confirmed case, the child and all household members underwent RT–PCR testing. Household members were tested regardless of symptoms. Household members who tested negative at the time the confirmed case was diagnosed and also tested negative after a 14-day period of self-quarantine were considered not to be cases.

Study variables

Outcome variable

The outcome variable was the COVID-19 test result of household members. Vaccine effectiveness was calculated using the formula: VE = (1 - RR) × 100, where RR indicates the attack rate of fully vaccinated people divided by the attack rate of those who were unvaccinated or received only one dose.

Independent variables

The demographic information for confirmed cases included age, sex (male/female) and whether they had any symptoms at the time of testing (yes/no). Symptoms were classified as yes or no for fever, cough, sneezing, fatigue, headache or abdominal pain, loss of taste or smell and trouble breathing. Age was then categorized as preschool, primary school, secondary school and high school.

We obtained demographic information for household members from data collected during the outbreak investigation, including age, sex (male/female), vaccination status (fully vaccinated, defined as having received at least two vaccination doses, or not vaccinated) and relationship to the student who was a confirmed case (parent, sibling, grandparent or uncle). The ages of household members were divided into three groups: 0–18, 19–39 and ≥40 years. The vaccines received were classified into five types: none, only AstraZeneca, only Moderna or Pfizer–BioNTech (mRNA vaccine), only CoronaVac vero cell vaccine, or a mix of two types of vaccine. Cycle threshold (Ct) values for positive schoolchildren and positive household contacts were categorized as <20, 20 to <25, 25 to <30 and ≥30.

Data management

Schoolchildren whose records lacked information about household contacts were excluded from the analysis, as were students residing in the same household as a confirmed case, contacts who were not household members, and household members whose COVID-19 test results were missing (**Supplementary Fig. 1**). Information collected from the secondary data source was confirmed with the provincial Center for Disease Control and the school, as needed.

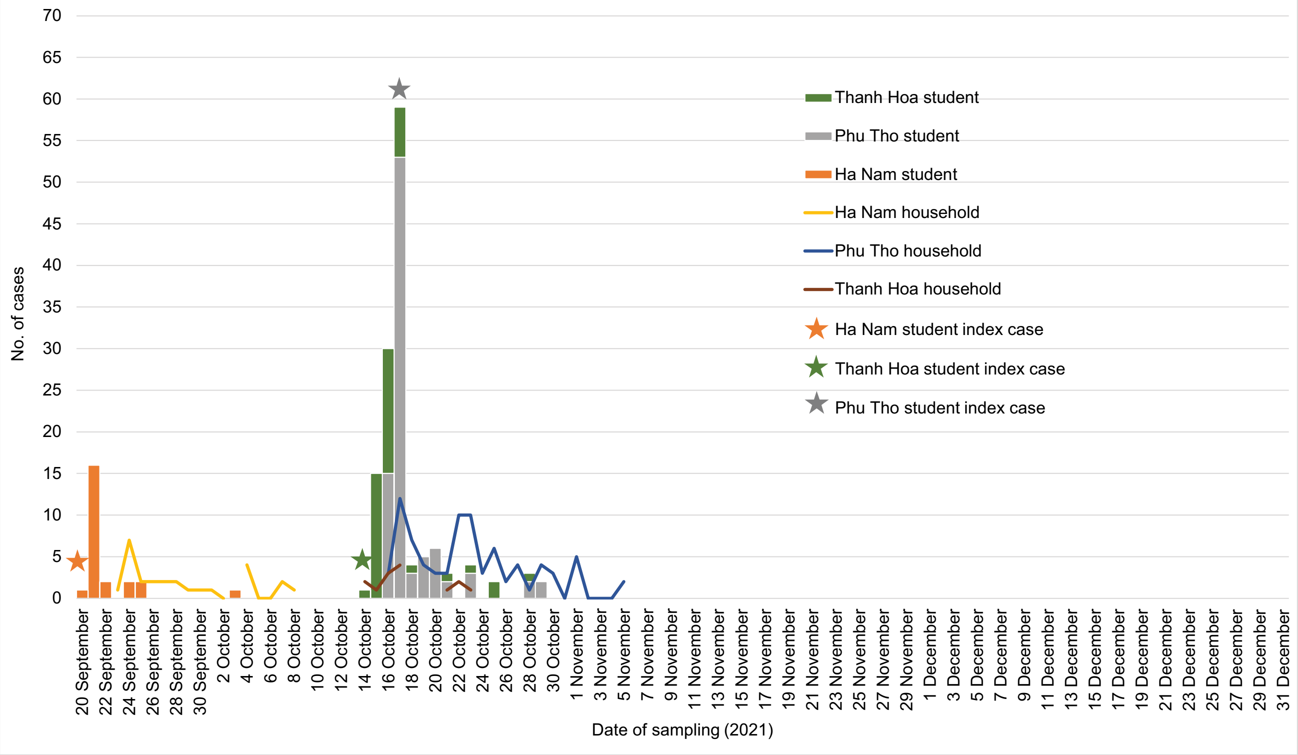
Statistical analysis

Frequencies and percentages were used for descriptive analyses to characterize confirmed cases and their household contacts. The attack rate for household contacts, which equalled the secondary attack rate for confirmed cases among schoolchildren, was calculated by dividing the number of household members with a positive COVID-19 result by the total number of people in the household. This attack rate was then divided into four groups: 0, 0 to 0.5, 0.5 to 1 and 1. The reproduction number was calculated by multiplying the attack rate with the number of household contacts of each index case.

To identify factors associated with household contacts becoming infected with SARS-CoV-2, χ^2 tests and a univariate regression analysis with mixed effects were used to select potential variables for the multivariable analysis. Variables with $P<0.1$ in the univariate analysis were eligible for the multivariable mixed effects regression analysis, whereas variables with $P<0.05$ were considered significant factors associated with COVID-19 infection among household members.

The effectiveness of vaccination against COVID-19 was assessed by comparing vaccinated household members with those who had not been vaccinated. Stata 16 was used for both descriptive and analytical statistics (StataCorp, College Station, TX, USA).

Fig. 1. **Epidemic curve of students and household members with COVID-19 infection, by date of sampling, in Ha Nam, Phu Tho and Thanh Hoa provinces, Viet Nam, September to December 2021**



RESULTS

Confirmed cases

There were a total of 157 confirmed COVID-19 cases in the school outbreaks in the three provinces. Ha Nam reported its first case from the affected school on 20 September 2021. Case numbers increased the next day. High numbers of household members tested positive for COVID-19 on 21 and 24 September. The outbreak in Phu Tho was reported on 16 October 2021, with cases rapidly increasing on 17 October. Thanh Hoa reported its first confirmed case on 14 October, and from 14 to 25 October, several household members were affected (**Fig. 1**).

The median (interquartile range [IQR]) age for cases at each school in Ha Nam was 13 years (13 to 13 years; only seventh grade students were infected), in Phu Tho it was 13 years (13 to 14 years) and in Thanh Hoa it was 8 years (8 to 11 years). There were more female than male cases in Phu Tho (53% [48/91] and 47% [43/91], respectively), but male cases outnumbered female cases in both Ha Nam (65% [15/23] and 35% [8/23], respectively) and Thanh Hoa (58% [25/43] and 42% [18/43], respectively). The proportion of cases with Ct values <20 was 74% (17/23) in Ha Nam, 31% (28/91) in Phu Tho and 35% (15/43) in Thanh Hoa. The proportion of cases that were symptomatic was 70% (16/23) in Ha Nam, 53% (48/91) in Phu Tho and 14% (6/43) in Thanh Hoa. Fever was the most common symptom reported by confirmed cases: 61% (14/23) in Ha Nam, 42% (38/91) in Phu Tho and 12% (5/43) in Thanh Hoa. In Ha Nam, 48% (11/23) of cases reported having a loss of taste or smell; for Phu Tho, the proportion was 4% (4/91) and for Thanh Hoa, it was 0% (0/43) (**Table 1**).

Household contacts

There were 540 household contacts included in this study. Of these, 133 were positive for COVID-19, giving an overall attack rate among all household contacts of 24.6%. The attack rate was highest in Ha Nam at 37% (32/87), followed by 24% (83/347) in Phu Tho and 17% (18/106) in Thanh Hoa. The median (IQR) Ct values among household members who tested positive for COVID-19 were 16.6 (13.3 to 26.7) in Ha Nam, 20 (17 to 27) in Phu Tho and 21.9 (19.1 to 31.4) in Thanh Hoa. Confirmed cases had an overall reproduction number of 0.85.

Table 1. **Characteristics of COVID-19-positive students in Ha Nam, Phu Tho and Thanh Hoa provinces, Viet Nam, September to December 2021**

Factor	Province[a]		
	Phu Tho	Ha Nam	Thanh Hoa
Total	91	23	43
Age group (years)			
Preschool (0–5)	0 (0)	0 (0)	1 (2)
Primary school (6–10)	0 (0)	0 (0)	31 (72)
Secondary school (11–14)	81 (89)	23 (100)	2 (5)
High school (15–18)	10 (11)	0 (0)	9 (21)
Median (IQR)	13 (13–14)	13 (13–13)	8 (8–11)
Sex			
Male	43 (47)	15 (65)	25 (58)
Female	48 (53)	8 (35)	18 (42)
Ct value of infected students			
<20	28 (31)	17 (74)	15 (35)
20 to <25	26 (29)	3 (13)	13 (30)
25 to <30	16 (18)	2 (9)	6 (14)
≥30	21 (23)	1 (4)	9 (21)
Median (IQR)	23.0 (19.0–29.0)	15.3 (12.2–20.5)	22.2 (17.5–29.8)
Any symptom at time of testing			
No	43 (47)	7 (30)	37 (86)
Yes	48 (53)	16 (70)	6 (14)
Fever			
No	53 (58)	9 (39)	38 (88)
Yes	38 (42)	14 (61)	5 (12)
Cough			
No	78 (86)	17 (74)	40 (93)
Yes	13 (14)	6 (26)	3 (7)
Sneeze			
No	90 (99)	19 (83)	40 (93)
Yes	1 (1)	4 (17)	3 (7)
Fatigue			
No	91 (100)	17 (74)	38 (88)
Yes	0 (0)	6 (26)	5 (12)
Headache or abdominal pain			
No	90 (99)	22 (96)	43 (100)
Yes	1 (1)	1 (4)	0 (0)
Loss of taste or smell			
No	87 (96)	12 (52)	43 (100)
Yes	4 (4)	11 (48)	0 (0)
Trouble breathing			
No	90 (99)	23 (100)	43 (100)
Yes	1 (1)	0 (0)	0 (0)
Household contacts			
Median no. (IQR)	4 (3–4)	4 (3–4)	2 (2–3)
Attack rate in household			

Factor	Province[a]		
	Phu Tho	Ha Nam	Thanh Hoa
0	34 (37)	11 (48)	33 (77)
>0 to <0.5	40 (44)	0 (0)	2 (5)
0.5 to <1	11 (12)	7 (30)	1 (2)
1	6 (7)	5 (22)	7 (16)
Median (IQR)	0.2 (0–0.33)	0.5 (0–0.75)	0 (0–0)

Ct: cycle threshold value; IQR: interquartile range.

[a] Values are *n* (%) unless other wise indicated.

In Ha Nam and Phu Tho, almost half of household members who tested positive for COVID-19 were aged ≥40 years (47% [15/32] and 42% [35/83], respectively). In Thanh Hoa, 28% (5/18) were aged ≥40 years, with more than half (67% [12/18]) aged 19–39 years. The proportion of household members with COVID-19 who were female was 50% (16/32) in Ha Nam, 60% (50/83) in Phu Tho and 67% (12/18) in Thanh Hoa (**Table 2**).

Regarding vaccination status, 14% (12/83) of household contacts in Phu Tho who tested positive were fully vaccinated, compared with 6% (2/32) of those who tested positive in Ha Nam and 0% in Thanh Hoa (**Table 2**). Higher proportions of household contacts who tested positive were unvaccinated in Ha Nam and Thanh Hoa (62% [20/32] and 94% [17/18], respectively). The majority of vaccinated household members who had COVID-19 had received only the AstraZeneca vaccine: 28% (9/32) in Ha Nam, 22% (18/83) in Phu Tho and 6% (1/18) in Thanh Hoa.

The relationship between confirmed cases and household contacts who tested positive for COVID-19 was also investigated, with 44% (14/32) in Ha Nam, 72% (60/83) in Phu Tho and 67% (12/18) in Thanh Hoa being parents of a confirmed case. The proportions of household members testing positive for COVID-19 who had other family relationships with the case were much lower (**Table 2**).

Factors associated with COVID-19 infection of household contacts

When comparing household members who tested positive for COVID-19 with household members who were negative for COVID-19 in the multivariable analysis, the risk of being positive for COVID-19 was greater among household contacts aged 19–39 years (adjusted risk ratio [aRR]: 2.51, 95% CI: 1.50–4.21). Household contacts who were fully vaccinated and those who lived with a confirmed case aged 6–10 years had a lower risk of becoming a COVID-19 case (for contacts who were fully vaccinated – aRR: 0.46, 95% CI: 0.26–0.84; for contacts who lived with a confirmed case aged 6–10 years – aRR: 0.15, 95% CI: 0.02–0.93). All other variables were not significant in the multivariable analysis (**Table 3**).

Vaccine effectiveness for household contacts

The vaccine effectiveness for fully vaccinated household contacts was 39% (95% CI: -1–63; **Table 4**). For male household contacts, vaccine effectiveness was 52% (95% CI: -25–82) and for females it was 34% (95% CI: -19–63), although this was not statistically significant. The vaccine effectiveness for household contacts differed by age group: 23% (95% CI: -40–58) among those aged 19–39 years and 65% (95% CI: 17–85) among those aged >40 years. Vaccine effectiveness was not applicable to children aged 0–18 years because they were not eligible for vaccination in Viet Nam when this study was conducted.

DISCUSSION

This study assessed the within-household risk of transmission of SARS-CoV-2 from schoolchildren to household members during three school outbreaks in northern Viet Nam occurring between September and December 2021. The overall attack rate for household members of confirmed cases from the schools was 24.6%, lower than in studies from the Republic of Korea

Table 2. **Demographic information for household members living with schoolchild who tested positive for COVID-19 in Ha Nam, Phu Tho and Thanh Hoa provinces, Viet Nam, September to December 2021**

Demographic information	Province[a]								
	Phu Tho			Ha Nam			Thanh Hoa		
Factor[b]	Positive	Negative	Total	Positive	Negative	Total	Positive	Negative	Total
SARS-CoV-2	83	264	347	32	55	87	18	93	106
Age group (years)									
0–18	14 (17)	88 (33)	102 (29)	9 (28)	17 (31)	26 (30)	1 (6)	21 (24)	22 (21)
19–39	34 (41)	57 (22)	91 (26)	8 (25)	12 (22)	20 (23)	12 (67)	32 (36)	44 (42)
≥40	35 (42)	115 (44)	150 (43)	15 (47)	26 (47)	41 (47)	5 (28)	34 (39)	39 (37)
Median (IQR)	38 (15–49)			39 (16–46)			34.5 (24–47)		
Sex									
Male	33 (40)	136 (52)	169 (49)	16 (50)	28 (51)	44 (51)	6 (33)	51 (58)	57 (54)
Female	50 (60)	128 (48)	178 (51)	16 (50)	27 (49)	43 (49)	12 (67)	37 (42)	49 (46)
Fully vaccinated (received at least two doses)									
No	71 (86)	198 (75)	269 (78)	30 (94)	48 (87)	78 (90)	18 (100)	88 (100)	106 (100)
Yes	12 (14)	66 (25)	78 (22)	2 (6)	7 (13)	9 (10)	0 (0)	0 (0)	0 (0)
Type of vaccine									
None	33 (40)	131 (50)	164 (47)	20 (62)	27 (49)	47 (54)	17 (94)	87 (99)	104 (98)
Only AstraZeneca	18 (22)	34 (13)	52 (15)	9 (28)	22 (40)	31 (36)	1 (6)	1 (1)	2 (2)
Only Moderna or Pfizer–BioNTech (mRNA vaccine)	7 (8)	31 (12)	38 (11)	2 (6)	6 (11)	8 (9)	0 (0)	0 (0)	0 (0)
Only Sinovac Life Sciences (vero cell vaccine)	22 (27)	49 (19)	71 (20)	0 (0)	3 (5)	0 (0)	0 (0)	0 (0)	0 (0)
Mixed vaccine types	2 (2)	11 (4)	13 (4)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)
Relationship to confirmed case									
Parent	60 (72)	0 (0)	60 (17)	14 (44)	23 (42)	37 (43)	12 (67)	46 (52)	58 (55)
Sibling	16 (19)	2 (1)	18 (5)	12 (38)	15 (27)	27 (31)	2 (11)	23 (26)	25 (24)
Grandparent/uncle	7 (8)	1 (<1)	8 (2)	6 (19)	17 (31)	23 (26)	4 (22)	19 (22)	23 (22)
Ct value									
<20	40 (48)	–	40 (48)	16 (50)	–	16 (50)	6 (33)	–	6 (6)
20 to <25	16 (19)	–	16 (19)	2 (6)	–	2 (6)	6 (33)	–	6 (6)
25 to <30	13 (16)	–	13 (16)	6 (19)	–	6 (19)	0 (0)	–	0 (0)
≥30	13 (16)	–	13 (16)	3 (9)	–	3 (9)	5 (28)	–	5 (5)
Median (IQR)	20 (17–27)			16.6 (13.3–26.7)			21.91 (19.14–31.43)		
Any symptom at time of testing?									
No	28 (34)	2 (1)	30 (9)	–	–	–	–	–	–
Yes	54 (65)	16 (6)	70 (20)	–	–	–	–	–	–

Ct: cycle threshold value; IQR: interquartile range.

[a] Values are *n* (%) unless otherwise indicated; – indicates data are not applicable.

[b] Some factors do not add up to the total due to missing data.

and Thailand.[11,12] This disparity could be attributed to the study period, the circulating variant, and differences in countries and populations. Moreover, prior research has also found that the Delta variant had a lower attack rate than the Omicron variant.[11]

The secondary attack rate for schoolchildren was 37% in Ha Nam, 24% in Phu Tho and 17% in Thanh Hoa. The median age of confirmed cases among schoolchildren was 13 years in Ha Nam, 13 years in Phu Tho and 8 years in Thanh Hoa. The discrepancy in median age among provinces may account for the lower secondary attack rate in Thanh Hoa, as older children (10–19 years) reportedly had a higher transmission rate than younger children (<10 years).[13] Research by Madewell et al. also found that the secondary attack rate increased for households with more than three people.[14] Consequently, the data support our conclusion that the attack rate was higher in Ha Nam and Phu Tho, where the average number of household members per family was four, than in Thanh Hoa, where it was two. Phu Tho and Thanh Hoa had lower secondary attack rates than similar clusters in Peru (53%)[15] and China (32.4%).[16] The secondary attack rate among household members found recently in China, the Republic of Korea and the United States of America ranged from 4.6% to 17%.[17–19] These discrepancies may be due to each study's sample size, the social distancing that was in place and different quarantine measures among the countries at the time of investigation. Our results showed that factors directly related to the infection rate among household contacts were their sex, age, vaccination status and age of the index case.

Our findings suggest that female household contacts might be more susceptible to contracting infection, although this finding did not reach statistical significance in our data. Our results differ from studies conducted in Norway and Pakistan, where male household members had a higher incidence of infection.[20,21] However, our findings are consistent with those of researchers in Malaysia and Türkiye who also found that female household contacts had a significantly increased risk for COVID-19.[22,23] This contrast may result from cultural and social differences between the Vietnamese population and those in other countries.

This study showed that household contacts who were positive for COVID-19 were more likely to be aged 19–39 years, compared with those who were negative for COVID-19. This is consistent with studies from China, Japan, Malaysia and Pakistan.[20,22,24,25] A survey conducted in Bosnia and Herzegovina also found that household contacts aged 18–49 years were nearly five times more likely than those aged 0–17 years to become infected.[26]

Fully vaccinated household members had a lower risk of becoming ill with COVID-19, consistent with a previous Norwegian study that indicated full COVID-19 vaccination was a protective factor among household contacts.[21] Our findings demonstrated a vaccine effectiveness rate of 39% against SARS-CoV-2 infection among household members. This was a lower vaccine effectiveness rate than reported in Singapore (56.4%),[27] which may be because only mRNA vaccines were authorized for use in Singapore at the time.

Our findings suggest that vaccine effectiveness may be lower in females than males; although this difference was not statistically significant in our analysis, it is similar to findings in a study in Angola.[28] However, the target population in the study in Angola was the general population, not household contacts. Sex differences in caregivers' duties and activities might also have played a role.[29] Additionally, antibody responses following COVID-19 immunization and their duration, as well as the type of vaccine, may impact the vaccine's effectiveness.[30,31] Therefore, further studies should be considered to clarify this difference. However, there was no statistically significant difference by sex when the analysis was adjusted for age.

There was a significant association between the confirmed case being aged 6–10 years and having household members who tested positive for COVID-19. A cohort study conducted in England found that children younger than 11 years had a lower rate of COVID-19 transmission.[32] Our results, however, found that young children (aged 0–5) are more likely to transmit SARS-CoV-2 than older ones, which is consistent with prior research.[32,33]

The risk of household transmission has been reported to be higher if the child index case is symptomatic, although this finding was not statistically significant.[34] Our findings indicate that household contacts of schoolchildren with cough at the time of

Table 3. **Univariate and multivariate analysis of selected factors related to transmission among students and household members, Viet Nam, September to December 2021**

Variable	SARS-CoV-2-positive[a]	SARS-CoV-2-negative[a]	Univariate			Multivariate[c]	
			aRR	*P*[b]	95% CI	aRR	95% CI
Household contacts							
Sex							
Male	55 (20.4)	215 (79.6)	1	0.022	–	1	–
Female	78 (28.9)	192 (71.1)	1.5		1.05–2.13	1.35	0.94–1.95
Fully vaccinated (received at least two vaccination doses)							
No	119 (26.3)	334 (73.7)	1	0.044	–	1	–
Yes	14 (16.1)	73 (83.9)	0.596		0.33–1.06	0.46	0.26–0.84
Age group (years)							
0–18	24 (16.0)	126 (84.0)	1	0.001	–	1	–
19–39	54 (34.8)	101 (65.2)	2.17		1.33–3.54	2.51	1.50–4.21
≥40	55 (23.9)	175 (76.1)	1.47		0.90–2.40	1.56	0.95–2.56
Confirmed cases (students)							
Any symptoms at time of testing							
No	57 (20.3)	224 (79.7)	1	0.053	–	1	–
Yes	76 (29.3)	183 (70.7)	1.49		0.99–2.22	1.02	0.50–2.06
Fever							
No	73 (21.7)	264 (78.3)	1	0.039	–	1	–
Yes	60 (29.6)	143 (70.4)	1.37		0.92–2.05	1.05	0.54–2.05
Cough							
No	103 (21.9)	367 (78.1)	1	<0.001	–	1	–
Yes	30 (42.9)	40 (57.1)	1.991		1.22–3.25	1.78	0.98–3.24
Sneezing							
No	73 (21.7)	264 (78.3)	1	0.001	–	1	–
Yes	14 (50.0)	14 (50.0)	2.268		1.12–4.60	1.77	0.68–4.61
Fatigue							
No	116 (23.0)	389 (77.0)	1	0.001	–	1	–
Yes	17 (48.6)	18 (51.4)	2.134		1.14–4.00	1.22	0.46–3.20
Age group (years)							
Preschool (0–5)	2 (100.0)	0 (0.0)	1	0.010	–	1	–
Primary school (6–10)	12 (15.4)	66 (84.6)	0.14		0.02–0.97	0.15	0.02–0.93
Secondary school (11–14)	108 (26.7)	296 (73.3)	0.258		0.041–1.62	0.38	0.07–2.21
High school (15–18)	11 (19.6)	45 (80.4)	0.176		0.03–1.23	0.28	0.04–1.82

95% CI: 95% confidence interval; aRR: adjusted risk ratio.

[a] Values are *n* (%) unless otherwise indicated; – indicates data are not applicable.

[b] *P* values were calculated using the χ^2 test.

[c] All variables with $P \leq 0.1$ in the univariate analysis were included in the multivariate analysis.

Table 4. **Effectiveness of COVID-19 vaccine among household contacts of schoolchildren who tested positive for COVID-19, Viet Nam, September to December 2021**

Factor	Vaccination doses						RR (95% CI)	Vaccine effectiveness[a] (95% CI)	*P*
	None or one			Two					
	Total	COVID-19-positive	Attack rate (a)	Total	COVID-19-positive	Attack rate (b)			
Total no.	453	119	0.26	87	14	0.16	0.61 (0.37–1.01)	39 (-1–63)	0.044
Age group (years)									
<18	148	24	0.16	2	0	0.00	–	–	–
18–39	123	45	0.37	32	9	0.28	0.77 (0.42–1.40)	23 (-40–58)	0.313
40–59	179	50	0.28	51	5	0.10	0.35 (0.15–0.83)	65 (17–85)	
Sex									
Male	232	51	0.22	38	4	0.11	0.48 (0.18–1.25)	52 (-25–82)	0.566
Female	221	68	0.31	49	10	0.20	0.66 (0.37–1.19)	34 (-19–63)	

95% CI: 95% confidence interval; RR: relative risk (b/a); – indicates that children <18 years were not vaccinated during the study period.

[a] Vaccine effectiveness is calculated as 1 - RR.

testing had a higher probability of testing positive for COVID-19. This result is consistent with previous studies that showed coughing by the index case was a significant risk[20,26] for transmission and an indicator of the index case's infectiousness.[35] Furthermore, according to Miller et al.,[32] index cases without respiratory symptoms had a lower risk of transmitting SARS-CoV-2, which is consistent with our finding that household contacts of students with sneeze or fatigue were at higher risk of becoming infected.

This study's strength lies in using outbreak data to assess factors associated with index cases and their household contacts that related to the role of children transmitting COVID-19 during school outbreaks. However, this study is not without its limitations. First, this study exclusively focused on cases associated with the Delta variant, which is no longer the predominant COVID-19 variant. However, the Delta variant has been reported to have the second-highest transmissibility after Omicron,[36] so the results still provide valuable insights for public health workers assessing potential similarities with future COVID-19 variants.

Second, this was an analysis of secondary data, and the routine nature of the data collected led to shortcomings in sampling and testing (e.g. symptoms at the time household contacts were tested may have been missing, as well as the date of symptom onset; serology data were lacking; data were missing about the exact date of testing for contacts). Otherwise, the World Health Organization's protocols for household transmission studies would have been applied.[37] Additionally, many household contacts were unvaccinated; therefore, it was impossible to analyse the protection rate of the vaccines by dose. We could not categorize the vaccination status variable by time because we did not have the date on which household contacts received their COVID-19 vaccine.

Third, this study collected data for many variables, but not data about household contacts' potential community exposure or self-protection measures. These data would have helped assess independent risk factors. At the time of our study, the three provinces did not have strict lockdowns in place, so we cannot rule out transmission occurring outside the households.

CONCLUSIONS

SARS-CoV-2 transmission from children to their household members was linked with variables associated with the primary case and their household contacts. We found that when the confirmed case was aged 6–10 years and household contacts were unvaccinated and aged 19–39 years, the household members were at lower risk of COVID-19 infection.

While the COVID-19 vaccines were primarily developed to reduce disease severity rather than transmission, this study found an overall vaccine effectiveness against infection of 39%. These results should be explored in future studies to improve the Viet Nam health system's preparedness and response capabilities for future pandemics. We strongly recommend that schoolchildren, a vulnerable population, should be prioritized for COVID-19 vaccination. Our attack rates may also provide guidance for future decision-making about school closures by policy-makers.

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Conflicts of interest

This research was conducted as part of the Master of Applied Epidemiology programme of the Australian National University in collaboration with the National Institute of Hygiene and Epidemiology, Viet Nam. TTV is a trainee in this programme and received a scholarship from the ASEAN–Australia Health Security Fellowship from the Australia Commonwealth Department of Foreign Affairs and Trade. The other authors have no conflicts of interest to declare.

Ethics statement

This study was approved by the Human Ethics Committee at the Australian National University (identification number: 2022/380). This analysis was exempted from ethics review by the National Institute of Hygiene and Epidemiology, Viet Nam, as it was part of national COVID-19 outbreak investigation and response activities.

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Typhoid fever: the challenging diagnosis of a pseudo-outbreak in Benguet, Philippines

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Objective: The event-based surveillance and response report from the municipality of Buguias in the Philippines covering the period 1 January to 29 October 2022 indicated an unusual increase in the number of typhoid cases that surpassed the epidemic threshold for consecutive weeks. An investigation was conducted to confirm the existence of an outbreak, identify the source(s) of transmission and recommend prevention and control measures.

Methods: The investigation employed a descriptive design. Medical records were reviewed to verify diagnoses and to identify cases that met case definitions. Key informant interviews were conducted to identify possible sources of transmission and investigate the reporting of cases in the Philippine Integrated Disease Surveillance and Response (PIDSR) system.

Results: A total of 220 cases of typhoid fever were captured by the PIDSR system. Of the 208 suspected cases that were reviewed, only 15 (7.2%) met the case definition used in this investigation. Fourteen of these 15 verified cases were interviewed; five (35.7%) were farmers and 13 (92.8%) reported using springs as their main water source and source of drinking water. Reporting of cases in the PIDSR system was largely based on the final chart diagnosis or a positive Typhidot or Tubex rapid diagnostic test result. The PIDSR case definition was not followed in the reporting of cases.

Discussion: This study provides evidence of endemicity of typhoid fever in Buguias, Benguet, Philippines. However, from January to October 2022, cases were overreported by the surveillance system. Medical record reviews showed that most reported suspected cases did not meet case definition criteria. This finding emphasizes the need to improve typhoid guidelines with regards to diagnosis using rapid diagnostic tests and to investigate the cost-effectiveness of making confirmatory laboratory tests for typhoid available in the Philippines.

Between 1 January and 29 October 2022, the Philippine Integrated Disease Surveillance and Response (PIDSR) system reported a total of 9057 cases of typhoid fever.[1] This was a 121% increase in case numbers relative to the same period in 2021, when 4102 cases were reported. The Cordillera Administrative Region reported the highest number of cases, with Benguet Province being particularly affected. Benguet Province reported 1196 cases, accounting for 66% of all cases in the Cordillera region.[1]

Typhoid fever is caused by the bacterium *Salmonella typhi*, of which humans are the only reservoir. Other serotypes, such as *Salmonella paratyphi* (A, B, C), cause similar syndromes but are associated with less clinically significant disease and have an animal reservoir.[2] Salmonella is commonly found in poultry products, meats and chicken manure. Reusing chicken litter exacerbates contamination, especially with Salmonella.[3] Flies can also transmit typhoid, carrying bacteria and viruses in their vomit and excreta.[4] Inadequate sanitation and reliance on unsafe drinking water sources can also contribute to the spread of typhoid.[5]

According to a routine event-based surveillance and response report from the Buguias Municipal Health Office Epidemiology and Surveillance Unit (unpublished), in 2022, Buguias, a municipality in Benguet Province, experienced an unusual increase in the number of typhoid cases that surpassed the Philippines' standard epidemic threshold for several consecutive weeks. Buguias, with a total population of 44 877 (as of 2020),[6] is primarily an agricultural town known for its production of highland vegetables such as lettuce, cabbage, carrots and broccoli.[7] An outbreak investigation was conducted to confirm the existence of the outbreak and verify the cases, identify the source of transmission, and recommend prevention and control measures.

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METHODS

This study employed a retrospective case review design to investigate the increase in the number of typhoid fever cases reported to the surveillance system in Buguias, Benguet from 1 January to 29 October 2022 (epidemic weeks 1–43; the study could not encompass the entire year due to the limited length of the authors' training programme). Medical records of cases captured by the PIDSR system were obtained from local hospitals and reviewed to assess whether they met the PIDSR case definition and a slightly modified version of the PIDSR case definition. The modified version was used in this investigation to avoid missing cases that do not meet the stricter PIDSR definition, as not all symptoms were captured in the medical records and most cases could not be interviewed retrospectively. The PIDSR defined a suspected case as any person with an illness characterized by insidious onset of sustained fever, headache, malaise, anorexia, relative bradycardia, constipation or diarrhoea, and non-productive cough. The slightly modified version defined a suspected case as any resident of Buguias, Benguet who developed symptoms including fever, headache, malaise and any one or more of anorexia, constipation, diarrhoea, non-productive cough, vomiting, abdominal pain or dizziness, and who had a positive rapid diagnostic test result (Typhidot or Tubex) during the specified period.

Key informant interviews were conducted with Municipal Epidemiological Surveillance Unit staff and sanitary inspectors to identify possible sources of transmission and to discuss the management of the rise in cases of typhoid fever in the municipality. Hospital Epidemiology and Surveillance Unit staff were also interviewed as part of the investigation of the rise in case numbers reported by the PIDSR system. Informed consent was obtained from all respondents.

Suspected cases that met the modified case definition were interviewed using a structured questionnaire designed to collect information about water sources and treatment, as well as food preparation and storage practices. All cases gave their informed consent for the interview. In addition, the houses and immediate surroundings of each interviewed case were inspected and environmental samples (e.g. water, chicken manure, raw beef) were collected for laboratory testing. The latter was conducted using Salmonella Shigella Agar, a selective and differential medium for the isolation and enumeration of Salmonella and Shigella by means of the direct plating method. After inoculation of samples on the agar, plates were incubated for 48–72 hours before screening. Positive cultures showing black centre colonies were subjected to Phoenix automated identification and antibiotic sensitivity tests to confirm the presence of bacterial pathogens.

A profile of each suspected case was created and encoded in Microsoft Excel. Key characteristics of cases were summarized using descriptive statistics: categorical variables (such as sex) were described in terms of proportions, and continuous variables (such as age) were reported using measures of central tendency and dispersion (median and range). Weekly case numbers were compared with pre-defined alert and epidemic thresholds, which were derived from disease incidence data collected over the previous 5 years and calculated using the standard deviation method.

RESULTS

Medical records review

The PIDSR system recorded 220 suspected cases of typhoid fever during the period 1 January–29 October 2022 for the municipality of Buguias, of which 208 (94.5%) were reviewed using medical records to verify the diagnosis. Of the reviewed cases, 178 (85.6%) had less than four symptoms, and 29 (13.9%) had only one symptom. Only 15 (7.2%) cases met the modified case definition criteria used in this study, while none met the PIDSR case definition.

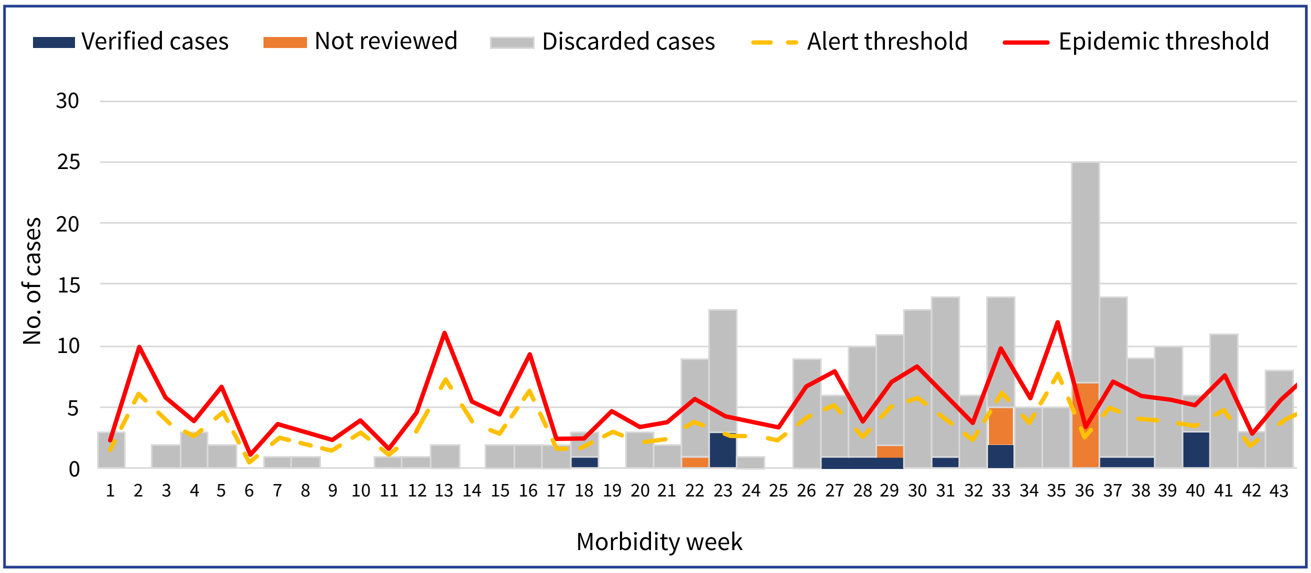
Of the 205 discarded cases (i.e. cases that did not meet the case definition criteria), 198 (96.6%) had a positive serological test result, either through Typhidot (*n* = 177, 86.3%) or Tubex (*n* = 21, 10.2%). About half (*n* = 104, 50.7%) had an additional diagnosis other than typhoid fever such as acute gastroenteritis (*n* = 31, 15.1%), respiratory tract infection (*n* = 30, 14.6%) or dengue (*n* = 27, 13.2%). In terms of the symptoms presented, 77 (37.6%) did not manifest fever, while 16 (7.8%) only had fever as a symptom (**Table 1**).

When the discarded cases were excluded, the number of typhoid cases breached the alert threshold only once (in morbidity week 23). In comparison, when all 220 recorded cases were considered, i.e. including the false positives that did not meet the modified case definition, the epidemic threshold was breached in

Table 1. **Characteristics of false positive typhoid cases reported to the surveillance system, Municipality of Buguias, the Philippines, 1 January–29 October 2022 (*N* = 205)**

Characteristics	No. of cases	% of total
Serological test		
Positive Typhidot	177	86.3
Positive Tubex	21	10.2
Negative	4	2.0
Not done	3	1.5
Final diagnosis in medical chart		
Typhoid fever only	89	43.4
Typhoid fever and acute gastroenteritis	31	15.1
Typhoid fever and upper/lower respiratory tract infection	30	14.6
Typhoid fever and dengue	27	13.2
Typhoid fever and other	16	7.8
None	12	5.9
Symptom profile		
No fever	77	37.6
Fever plus 2 other typhoid-like symptoms	45	22.0
Fever plus 1 other typhoid-like symptom	29	14.1
Fever plus cough only	22	10.7
Fever only	16	7.8
Fever plus vomiting only	9	4.4
Fever plus 3 other typhoid-like symptoms	7	3.4

Fig. 1. **Typhoid cases by morbidity week, Municipality of Buguias, the Philippines, 1 January–29 October 2022 (*N* = 220)**



Cases for which medical records could not be found were not reviewed. Discarded cases are suspected cases that did not meet the modified case definition used in this study.

15 out of the 43 morbidity weeks covered by this study (**Fig. 1**).

Profile of cases

Of the 15 verified cases, just over half were male ($n = 8$, 53.3%). Cases ranged in age from 14–66 years, with a median age of 31 years. The most common age group was 21–30 years ($n = 5$, 33.3%). Fourteen verified cases (93.3%) were interviewed. One third of the interviewed cases were farmers ($n = 5$, 35.7%); all 14 said that they lived within 50 m of a farm and 13 reported relying on springs as the main source of their drinking water (92.9%).

Seven cases (46.7%) reported that, in addition to fever, headache and malaise, they had experienced non-productive cough; five (33.3%) also experienced dizziness. Among the interviewed cases, all 14 reported that they normally wash their hands prior to handling food. Nine (64.3%) said that they sometimes ate raw vegetables. Most reported eating eggs at least once a month ($n = 9$, 64.3%), but none ate raw or soft-boiled eggs. Beef and chicken were seldom consumed by the majority of those interviewed ($n = 13$, 92.9%); only one person consumed beef and chicken regularly and none consumed raw meat. All 14 interviewed cases reported always seeing houseflies in their houses and self-reported that flies frequently land on their food.

Key informant interviews

According to the sanitary inspector, springs are the main source of water for many households living in and around Buguias. It is also the most common source of drinking water among farming communities. However, spring water is not always treated before use by some of the population as they believe it is clean and safe to drink. The sanitary inspector identified chicken manure as a possible source of water contamination, noting that compliance with an ordinance mandating that farmers who use chicken manure keep it in a storage area is not currently being adequately monitored.

Environmental investigation

Across the municipality, chicken manure is widely used as a fertilizer by farmers and thus flies are commonplace. Locally reared livestock products (beef, chicken and pork) are sold within the community, typically from open, uncovered displays, upon which flies are free to land.

Of the 12 water samples that were taken from domestic taps and water storage tanks and tested, two showed the presence of black colony formation. One out of six chicken manure samples showed the presence of black colony formation. One sample of raw beef taken from a beef store also showed the presence of black colony formation. Black colonies from a sample of chicken manure fertilizer were subjected to a confirmatory culture and sensitivity test and tested positive for *Leminorella grimontii*. No Salmonella species were detected. Confirmatory testing was negative for all other samples with black colony formation.

DISCUSSION

Although 220 suspected cases of typhoid fever were reported in the municipality of Buguias, Benguet between January and October 2022, this investigation showed that most of them did not meet the modified case definition. Moreover, the pattern of case reporting revealed that the disease reporting units relied heavily on the diagnosis recorded in the medical chart and the results of Typhidot and Tubex rapid diagnostic testing. While Typhidot is a sensitive test for early diagnosis of typhoid fever, it has low specificity, and positive results should be correlated with the clinical picture and other possible diagnoses. Other studies have demonstrated that cross-reactivity with other diseases can cause false positive results in some cases.[8] After verifying the reported diagnoses, we found that the number of cases was aligned with historical surveillance data and therefore we concluded that typhoid cases had been overreported and that the increase in case numbers in 2022 represented a pseudo-outbreak.

Although the number of verified cases was above the alert threshold in morbidity week 23, this increase is not inconsistent with, and generally follows, the endemic pattern. Routine surveillance has shown that there has been steady but low-level transmission of typhoid fever over a 5-year period and that known sources of transmission, including houseflies[4,9] and consumption of untreated drinking water,[5] are likely present in the municipality. It is notable that all the verified cases self-reported a constant presence of houseflies in their houses, and that their food was frequently exposed to flies. While this implies that the opportunity for flies to transmit the bacteria that cause typhoid fever does indeed exist in this community, the findings do not prove a causal relationship between houseflies and typhoid fever.

This investigation also revealed that a high proportion of the verified cases relied on untreated spring water as their main source of drinking water. The use of unsafe drinking water has been linked to an increased rate of typhoid fever in other studies,[5] and may be another possible contributory factor for disease transmission in the municipality. This observation highlights the need for proper water treatment and quality checks to ensure that the water supply is safe for consumption and to prevent the spread of waterborne diseases including typhoid.

The main limitation of this study is the lack of confirmatory laboratory tests, as it is not the standard to carry out these tests during clinical encounters in the Philippines, and we could not conduct them retrospectively. However, based on the clinical presentation of the suspected cases and the epidemiological context, we believe that the 205 cases we excluded were likely false positives.

Reporting false positive cases can result in false outbreaks being declared and the misallocation of resources to unnecessary response efforts. To prevent this, it is crucial to enhance adherence to PIDSR protocols by providing disease surveillance officers with training in case assessment to ensure cases meet the case definition before they are included in the surveillance system report and by conducting regular evaluations of the surveillance system. Given the apparent reliance on rapid diagnostic test results for typhoid, we also recommend that diagnostic algorithms be used with clinical judgement and appropriate follow-up testing to ensure that fewer false positives are reported by the PIDSR system. Finally, this study emphasizes the need to improve typhoid guidelines with regards to diagnosis using rapid diagnostic tests and to investigate the cost-effectiveness of making confirmatory laboratory tests for typhoid available in the Philippines.

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Conflicts of interest

The authors have no conflicts of interest to declare.

Ethics statement

This study involved routine surveillance and response work conducted under Republic Act No. 11332, and the ethics of the study were taken into consideration. Consequently, approval for the study was deemed unnecessary.

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Large-scale salmonella outbreak associated with banh mi, Viet Nam, 2024

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Objective: To investigate the cause of a foodborne outbreak that occurred in Dong Nai province, Viet Nam, in 2024, and implement control measures.

Methods: An initial investigation was conducted to confirm the outbreak, which was followed by epidemiological and environmental investigations to find the plausible causative food item. Clinical specimens and food samples were tested to identify the pathogen.

Results: A total of 547 symptomatic cases were recorded, of whom two were in severe condition requiring extracorporeal membrane oxygenation and ventilation, one of whom died. Among 99 interviewed cases, the mean incubation time was 9 hours (range 2–24 hours), with the main symptoms being fever, abdominal pain, diarrhoea and vomiting. All patients had eaten banh mi from a local bakery. *Salmonella* spp. were identified in food samples and clinical specimens. The bakery halted production, and the outbreak ended after 1 week.

Discussion: All the patients were exposed to only one food in common, which facilitated the investigation process. This outbreak is a reminder to small retailers and take-away shops of the importance of food safety management in preventing similar future outbreaks. All food handlers must comply with food hygiene principles, especially in hot temperatures, which boosts bacterial growth.

Globally, *Salmonella* spp. are the most common causes of foodborne illness, leading to approximately 600 million cases and 420 000 deaths annually.[1] *Salmonella* spp. are the leading bacterial cause of foodborne illness in United States of America, with an annual average of 19 000 hospitalizations and 380 deaths.[2] *Salmonella* spp. are also the cause of 70–80% of bacterial foodborne illnesses in China, ranking as one of the country's top two diarrhoea-causing agents.[3]

Salmonellae are classified into two species that can cause human illness: *S. enterica* and *S. bongori*. Salmonellae are also further subdivided into serotypes, which differ in their natural reservoirs and ability to cause human infections.[4,5] However, only a small proportion of the over 2500 serotypes cause most human infections.[6] Poultry and poultry products, especially eggs, are commonly linked to *Salmonella* spp. Eggs may be infected via vertical (transovarian) transmission or horizontal (trans-shell) transmission.[7]

Salmonellae infection most commonly occurs when a person eats contaminated food, but it can also be spread by infected persons through the faecal-oral route. The infectious period ranges from several days to several weeks. A temporary carrier state occasionally continues for months, especially in infants. Approximately 1% of infected adults and 5% of children aged <5 years may excrete the organism for more than 1 year.[5,8]

In Viet Nam, foodborne illness affected 3711 individuals from March 2020 to August 2022.[9,10] Large-scale outbreaks related to *Salmonella* spp. have occurred in recent years.[11,12] In 2022, Khanh Hoa province reported 648 cases of school-related foodborne illness, with 211

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hospitalizations and one death.[11] Another outbreak in Khanh Hoa was reported in 2024, with 345 cases related to contaminated chicken rice at a restaurant.[12] In May 2024, a suspected foodborne outbreak occurred in Dong Nai province in southern Viet Nam. The Dong Nai Food Safety Department (FSD) cooperated with the Institute of Public Health in Ho Chi Minh City (IPH) in investigating the event to determine the cause of the outbreak and implement control measures.

METHODS

The investigation was conducted from 1 to 3 May 2024, in three stages: 1) an initial investigation to confirm the outbreak; 2) an epidemiological investigation to identify foods possibly implicated in the outbreak, including investigations at food facilities; and 3) a laboratory investigation to identify the pathogen. In the epidemiological investigation, the investigation team used only descriptive statistics because all patients had eaten banh mi bought from a local bakery, and therefore matching a control group for these cases was not possible. In addition, the bakery was a take-away shop and approaching all buyers would have been a challenge.

Initial investigation

A regional hospital in Dong Nai province admitted sporadic cases of gastrointestinal infections on the evening of 30 April 2024. As a foodborne outbreak was suspected, the hospital alerted Dong Nai FSD on 1 May. The same day, 201 other cases were hospitalized.

On the morning of 1 May, a rapid response team from Dong Nai FSD began investigating. Most patients shared similar symptoms, including diarrhoea, nausea, vomiting, abdominal pain and fever. All patients had eaten banh mi from the bakery in Long Khanh City. Based on initial information, the investigation team confirmed a foodborne outbreak and proposed to the local authority that the bakery be temporarily closed. The bakery immediately suspended its business.

Epidemiological investigation

First, a case definition should have been established, but because laboratory results were unavailable at this phase, it was not applied. The investigation team identified banh mi as a causative agent during this outbreak. The team focused on determining the incubation period and main symptoms for potential etiology. The suspected case definition was an inpatient who ate banh mi from the bakery on 30 April or 1 May 2024, and manifested at least three of four symptoms: abdominal pain, diarrhoea, vomiting and fever.

An adapted questionnaire was designed to collect information on hospitalized patients' characteristics, including name, sex, age, address, onset date and time, symptoms and food consumption history. The investigation team interviewed cases at the regional hospital to understand events and generate causal hypotheses. The hospital collected 23 patient faecal samples for testing at the IPH laboratory. The local authority also instructed hospitals and clinics to record all suspected patients involved in the event. Due to time and human resource shortages, the team selected 99 cases who met the case definition for interviewing. Descriptive statistics were applied to summarize information on patients, including frequency, percentage, median, mean and standard deviation.

Environmental investigation

The investigation team assessed the bakery. It was a take-away shop that only sold banh mi. All four vendors and food handlers were interviewed about food processing, routine selling activities and their history of illness. The team observed where the food was handled. The source of all materials was also recorded.

The team took two faecal and four pharyngeal samples from the bakery staff and six food samples (pate, pork, ham, pickled vegetables and two chicken eggs).

Laboratory investigation

Based on the symptoms and incubation time, the investigation team suspected the pathogen was a bacterium, specifically *Salmonella* spp., *Staphylococcus aureus*, Staphylococcal enterotoxins or *Bacillus cereus*. Thus, the laboratory was advised to prioritize these tests.

The IPH laboratory tested all samples using bacterial culture techniques and polymerase chain reaction (PCR) techniques. All 25 faecal samples were tested

Table 1. **Characteristics of recorded patients in foodborne outbreak in Dong Nai province, Viet Nam (N = 547)**

Characteristic	n	%
Sex		
Male	263	48.1
Female	284	51.9
Median age (years)	35	
Mean age (years) (mean ± SD)	34.4 ± 19	
Age group (years)		
<20	159	29.1
20–49	252	46.1
≥50	136	24.9
Hospital		
Regional	497	90.9
Other	50	9.1

SD: standard deviation.

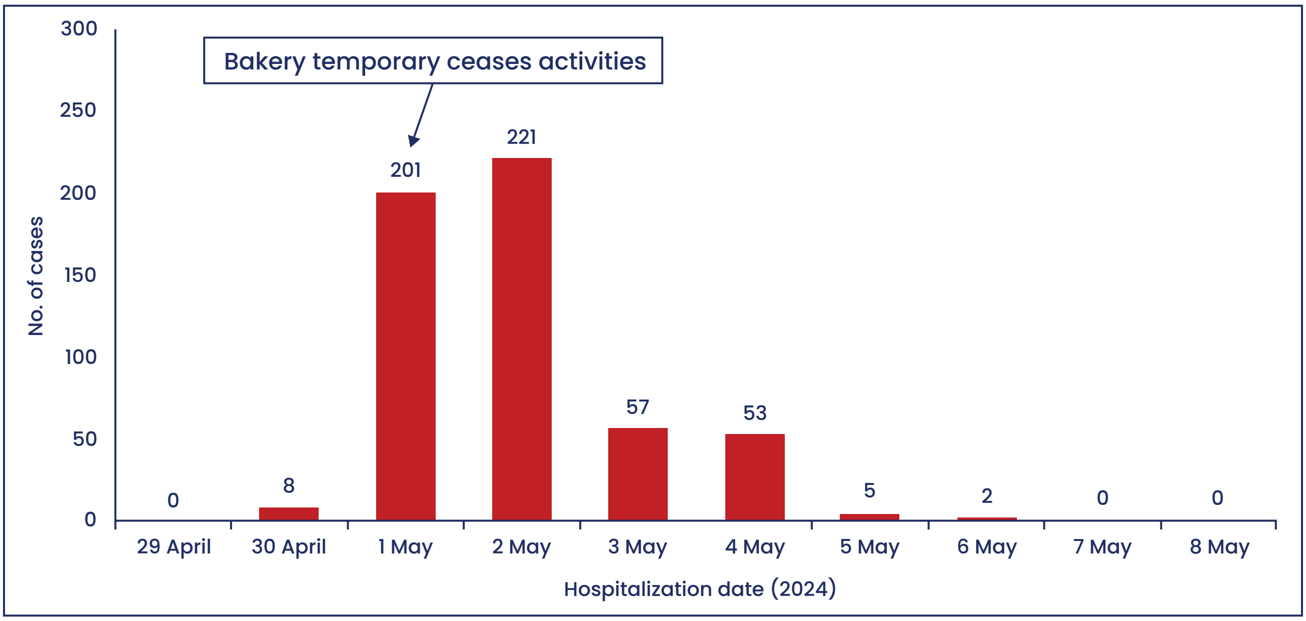
for *Salmonella* spp. (HD.PP.21-01/TT.VS). Five food samples (except one chicken egg sample) were tested for the presence of coliforms (AOAC 991.14), *Bacillus cereus* (AOAC 980.31), *Staphylococcus aureus* (AOAC 2003.07), *Salmonella* spp. (ISO 6579-1:2017), *Listeria monocytogenes* (ISO 11290-2:2017), *Clostridium perfringens* (AOAC 976.30) and Staphylococcal enterotoxins (ISO 19020:2017). The remaining chicken egg sample was only tested for *Salmonella* spp. The four pharyngeal samples were tested for the presence of coliforms (HD.PP.21-01/TT.VS), *Salmonella* spp. (HD.PP.21-01/TT.VS, HD.PP.10-05/TT.VS) and *S. aureus* (HD.PP.21-01/TT.VS). Results under 10 cfu/g were considered undetectable.

RESULTS

Epidemiological investigation

A total of 547 cases of foodborne illness were recorded from 30 April to 6 May 2024. Of those, 52% were female. The average age was 35.0 years, and the age distribution was 29% aged <20 years, 46% aged 20–49 years and 25% aged ≥50 years (**Table 1**). All patients resided in Long Khanh City. The regional hospital received 497 patients (90.9%, while six hospitals received the others (**Table 1**).

Fig. 1. **Epidemic curve of 547 foodborne illness cases in Dong Nai province, Viet Nam, 2024**



After temporarily ceasing the activities of the bakery on the morning of 1 May, the number of recorded cases peaked on 2 May and then sharply decreased in the following days, ending on 7 May (**Fig. 1**). Based on the epidemic curve, this was a point-source outbreak, lasting from 30 April to 7 May.

Among the 99 interviewed patients, the average age was 36.2 years, and cases appeared in all age groups.

Table 2. **Characteristics of interviewed patients in foodborne outbreak in Dong Nai province, Viet Nam (N = 99)**

Characteristic	n	%
Sex		
Male	41	41.4
Female	58	58.6
Median age (years)	35	
Mean age (years) (mean ± SD)	36.2 ± 20.0	
Age group (years)		
<20	27	27.3
20–49	43	43.4
≥50	29	29.3
Symptoms		
Diarrhoea	90	90.9
Abdominal pain	80	80.8
Fever	65	65.7
Vomiting	58	58.6
Nausea	6	6.1
Incubation time (hours)		
Mean ± SD	10.1 ± 5	
Median (range)	9.0 (2.0–24.0)	
Severe condition	2	2.0
Death	1	1.0

SD: standard deviation.

Environmental investigation

The bakery had sold banh mi for more than 20 years. Products were sold daily at 6:00–9:00 and 15:00–19:00, averaging about 1000 banh mi sales daily. The staff estimated that around 1500 banh mi were sold from 30 April to the morning of 1 May. Banh mi is a Vietnamese baguette sandwich filled with pate, Vietnamese pork roll, ham, pork and pickled vegetables. The bakery made the pate, pickled vegetables and sauces. The remaining foods were bought from a third-party supplier.

The investigation team observed that the bakery did not follow the one-way principle for food processing. All the processes overlapped in the cooking stages, and collisions or contact between raw and cooked foods could occur. The areas for preparing raw and cooked foods were next to each other, and there was no table or food storage shelf. The food and raw materials were put on the floor or in two cold stores. The team could not assess the temperature of the cold storage because they had been sealed by the police. All food processing utensils (knives, cutting boards, baskets and pots) were placed together, suggesting that they could be shared in the preparation of raw and cooked foods. However, the facility owner asserted that they cleaned and used all the instruments separately. Protective gloves were not used.

Table 3. **Laboratory results of clinical and food samples**

Type of sample	Positive results			
	Salmonella spp.	*Staphylococcus aureus*	Coliforms	*Bacillus cereus*
Faecal samples				
Patients (*n* = 23)	10 (43.5)	N/A	N/A	N/A
Staff (*n* = 2)	2 (100.0)	N/A	N/A	N/A
Pharyngeal samples				
Staff (*n* = 4)	0	2 (50.0)	2 (50.0)	N/A
Food samples (n = 6)[a]	4 (66.7)	2 (33.3)	3 (50.0)	1 (16.7)

N/A: not applicable.

[a] All food samples were also tested for *Listeria monocytogenes*, Staphylococcal enterotoxins and *Clostridium perfringens*, but the results were negative.

The most prevalent symptoms were diarrhoea (90/99, 90.9%), abdominal pain (80/99, 80.8%), fever (65/99, 65.7%) and vomiting (58/99, 58.6%). The average incubation time was 9 hours (**Table 2**). Two patients in severe condition required extracorporeal membrane oxygenation and ventilation. After a few weeks of treatment, one case recovered and the other died.

Laboratory results

Salmonella spp. were found in 12/25 faecal specimens (48.0%) and 4/6 food samples (66.7%). Noticeably, both faecal specimens from the staff were positive for *Salmonella* spp. Food samples were also contaminated with coliforms (3/6, 50.0%), *S. aureus* (2/6, 33.3%) and

B. cereus (1/6, 16.7%) (**Table 3**). Salmonellae in this outbreak were of serogroup OMA among both patients and staff.

DISCUSSION

Banh mi was the source of this community-based foodborne outbreak in Dong Nai province. The incubation time suggested a bacterial pathogen. *Salmonella* spp. were detected in both food and faecal samples. Fever, abdominal pain and diarrhoea are the most prevalent symptoms of salmonellosis, and the incubation period is 6–72 hours (usually 12–36 hours).[5,13] Thus, salmonellae was the most plausible agent of this outbreak.

This salmonellosis outbreak had a considerable number of cases (547 hospitalizations), out of which two were severe and one died. The causative food was sold by a take-away bakery that, between 30 April and the morning of 1 May 2024, had sold an estimated 1500 portions, meaning up to 1500 people could have been infected. The 547 hospitalized cases accounted for 36.5% of this at-risk group. The hospitalization rate was in line with the 2022 European Centre for Disease Prevention and Control (ECDC) surveillance report of 39.3% out of 29 712 patients hospitalized.[14] The case fatality rate in this outbreak was 0.18% (1/547), which did not greatly differ from the ECDC report of 0.22%. However, the fatality rate in the United States was estimated to be higher at 1.6% (420 deaths among 26 500 hospitalizations annually).[15]

Most food samples (66.7%) were positive for *Salmonella* spp., indicating that all foods could be cross-contaminated due to poor hygiene practices. The results of the environmental investigation supported this assumption. The lack of a one-way approach to food processing and using the same utensils to process raw and cooked foods could be crucial reasons for cross-contamination.[16] The absence of a table or shelf for putting food and not wearing protective gloves could be additional reasons.

The time of year during the outbreak is the hottest in Dong Nai province, with daily average temperatures around 37–38°C. This is optimal for the growth of *Salmonella* spp.[17] Thus, inappropriate cooking and preserving practices carry a particularly high risk of foodborne outbreaks. Food standards do not allow for the presence of *Salmonella* spp., as a single organism could be enough to cause a foodborne event.[18]

Faecal specimens from the bakery staff were positive for *Salmonella* spp., and the serogroup (*Salmonella* OMA) was consistent with those of the patients. An asymptomatic carrier was possibly the cause of the outbreak. However, they could have been infected through the same sources as the patients. Thus, active surveillance of bakery staff is necessary for confirmation. Not all of the patients' faecal specimens were positive for *Salmonella* spp. because excretion of the organisms may be intermittent,[19] or patients could have taken medicines before hospital admission.

Symptoms of salmonellosis usually last for a few days, and most infections are self-limiting. Severe illness can occur, especially among children, older adults and persons with chronic diseases. In this outbreak, one severe case was a 7-year-old boy who was overweight (47 kg), with congenital deafness and muteness. He had symptoms on 30 April and was admitted on 1 May with diarrhoea and abdominal pain. He was in a serious condition the next day and needed a ventilator. After a few weeks of treatment, he recovered and was discharged.

The case who died was a 6-year-old boy who was hospitalized relatively late. Symptoms manifested on 30 April, and he was treated at home with over-the-counter medicines. He became comatose and experienced convulsions and cyanosis and was in cardiac arrest when admitted on 2 May. The boy died after 1 month of intensive treatment. Therefore, delayed presentation to hospital and inappropriate first aid, especially lack of rehydration for patients with diarrhoea,[20] can lead to more severe outcomes.

Although the outbreak was investigated and controlled promptly, the investigation team acknowledged certain limitations. Interviewing all patients was challenging due to the limited number of team members, and many patients with mild symptoms left the hospital before the investigation commenced. The team encountered difficulties collecting information from all individuals who consumed the contaminated banh mi because the bakery operated as a take-away shop. Consequently, a cohort study and attack rate calculation could not be performed.

In this outbreak, hospitals in Dong Nai responded well based on their available emergency response plans. They were adequately supplied with the tools and drugs to treat diarrhoeal infection, especially temporary toilets for use in overcrowded conditions to prevent cross-contamination.

Viet Nam lacks annual salmonellosis data due to the absence of a specific reporting system. Implementing such a system is crucial for rapid response but demands substantial resources, particularly financial. A sentinel surveillance system could serve as an effective alternative. This outbreak highlights the risk of foodborne illness from take-away facilities and small retailers. Local authorities should manage all food facilities well and raise awareness of proper food handling practices among vendors.

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Conflicts of interest

The authors have no conflicts of interest to declare.

Ethics approval

The activities conducted for this outbreak investigation were part of routine surveillance and response work, and standard procedures to protect personal information were taken. Therefore, ethics committee approval for the study was unnecessary.

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None.

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Tuberculosis in Solomon Islands: why declining case notifications may not reflect true incidence

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In a recent publication, Yanagawa et al. report that the decrease in tuberculosis (TB) case notifications between 2016 and 2022 in Solomon Islands represents a “major achievement” and may indicate an “actual reduction in TB incidence.”[1] We offer additional context to highlight major limitations in TB detection in Solomon Islands and advise caution in the interpretation of this result.

TB detection in Solomon Islands is difficult due to geographic and resource limitations. Solomon Islands is a Western Pacific nation consisting of nearly 1000 islands. Paved roads are almost non-existent outside of the capital, Honiara, which is home to the country’s only tertiary care centre. Although roughly 80% of Solomon Islanders live in rural areas, approximately 75% of doctors are based in the capital.[2] Prior research has highlighted under-reporting of TB cases and high rates of TB treatment failure in rural areas,[3] where people face logistical and cultural barriers to medical care.[4] Current diagnostic tools for TB in Solomon Islands include Xpert® MTB/RIF Ultra, which was introduced in 2023, sputum smear microscopy and chest X-ray. However, Xpert® MTB/RIF testing and X-ray are not available in all provinces.

Furthermore, in 2021, community-based contact tracing ceased due to workforce constraints. Due to disruptions related to the COVID-19 pandemic, contact tracing was only carried out for immediate family members who presented with the patient to the medical facility. Thus, other contacts – including children – who did not present with the patient to the facility were not evaluated. This change may have contributed to decreased case notifications in 2022. Although community-based contact tracing resumed in 2023, contacts are evaluated only once within 2 weeks of the patient’s presentation to a hospital. Given the potential delay of up to 12 weeks for tests of TB infection to turn positive, it is important to repeat testing.

Some findings reported by Yanagawa et al. suggest underdiagnosis of TB disease. The authors note a higher case notification rate among adult women than men. However, in most endemic settings, TB incidence is substantially higher among males.[5] As noted by Yanagawa et al., few members of high-risk populations, such as those with diabetes mellitus, were screened for TB.[1] Taken together with the 67% screening positivity in this group and the high incidence of diabetes mellitus in Solomon Islands, this finding suggests a high likelihood of TB underdetection in this population.

It is notable that the authors suggest that TB incidence may have decreased in Solomon Islands in recent years, despite most other countries reporting increased TB incidence following the pandemic due to reduced detection and increased community spread.[6] As previously mentioned, contact tracing was suspended during the pandemic in Solomon Islands. Moreover, in this country, where protocols mandate hospitalization during the intensive phase of TB treatment, the number of beds in TB units was reduced as they were reallocated to patients with suspected COVID-19. Consequently,

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patients with TB often remained in general medical or emergency wards, likely leading to increased nosocomial transmission.

The authors point to the "sustained population testing rate" over the surveillance period in combination with reduced case notifications as supportive of a reduction in TB incidence. However, according to the authors, only 0.13–0.18% of the population was evaluated each year.[1] This very small proportion is unlikely to be representative of the general population.

In summary, Yanagawa et al. have published an important paper on TB in Solomon Islands. Yet, given the high likelihood of TB underdetection, we advise caution in interpreting the decrease in TB notifications as reflecting a true reduction in incidence. We also urge further investment and research, which would strengthen active case-finding, more accurately capture TB incidence in Solomon Islands, improve effective TB diagnosis and treatment and reduce community transmission.

Conflicts of interest

The authors have no conflicts of interest to declare.

Ethics statement

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