

ADDING TO THE HAVOG MICROBIOLOGY & MANAGEMENT FOLLOWING NATURAL DISASTERS



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Adding to the havoc: microbiology and management following natural disasters

Guest Editors: İpek Kurtböke, Candan Çiçek and Ian Macreadie

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Cover image: Top image: Brisbane River inundating Southbank walkway (see Blaskovich and Harris, pp. 176–180, image credit: M. A. T. Blaskovich). Bottom image: damage in the city of Hatay after the 7.8 magnitude earthquake that occurred in Turkey (image credit: Fatih Renkligil; CC BY-SA, see https://commons.wikimedia.org/wiki/File:After_the_7.8_magnitude_ earthquake_Hatay_Province_in_Turkey,_on_August_6,_2023.jpg).



Vertical Transmission



Mark Schembri President of ASM

As we close in on the end of 2023, it's a good opportunity to reflect on some of the things that have happened in the ASM this year. Our leadership team has undergone significant change with the appointments of Hayley Newton (VP Scientific Affairs), Martina Sanderson-Smith (VP Corporate Affairs) and Sam Manna (VP Communications), each of whom have been serving in a VP-Elect position for the last 12 months and learning the role. It is a testament to our processes that this transition has been seamless, and I look forward to exciting times ahead working with our new team. On that note, I cannot let this moment pass without paying enormous thanks to our retiring Executive Committee VP members Anthony Baker, Kate Seib and Rebecca LeBard. Anthony, Kate and Rebecca served on the Executive Committee for the last 5 years and, together with our immediate-past President Dena Lyras, can take collective credit for placing the Society in such a strong position.

There are many ASM activities to highlight from this year. Our national meeting in Perth was a huge success, with excellent attendance and a fantastic mix of invited talks, symposium sessions, award lectures, student and Early Career Researcher award talks, networking sessions and interactive poster sessions. We introduced two new awards, the ASM Industry Engagement Award and the ASM Early Career Microbiology Educator Award, both of which will continue to be offered. Our CliniCon and EduCon meetings were also successful, with the CliniCon meeting for the first time running in parallel with the national conference and providing new interaction opportunities for our members and trade exhibitors. We launched our new Equity,

Diversity and Inclusion (EDI) Standing Committee, chaired by Dr Yogitha Srikhanta from Monash University.¹ You can read more about the EDI committee in this issue. We also kicked off an initiative to engage with politicians through a newly established Parliamentary Friends of Microbiology group, with a goal to increase the visibility of microbiology in Australia and present the ASM as an unbiased expert group able to give advice on all things microbiology. Finally, ASM Hour continues to thrive, and our State Branches and Special Interest Groups ran many engaging programs. I look forward to seeing all of this continue and progress in the new year.

In September, I had the opportunity to attend the ASM TriState meeting in Darwin. The meeting was chaired by Janessa Pickering and Justin Morgan from the Western Australian ASM Branch, with 47 delegates from across Australia in attendance. This was my first time at the meeting, and I thoroughly enjoyed the engaging program, fantastic talks and networking opportunities. The venue and relaxed setting made for a great conference, and I strongly encourage you to consider putting this meeting on your calendar in the future. I also attended the South Australian ASM Branch AGM last month. It was fun to catch up with everyone in Adelaide and talk microbiology. This was also an opportunity to begin planning for the 2025 ASM National Conference, which will be held at the Adelaide Convention Centre. Stay tuned for more news next year.

As this is my last VT for 2023, I wish you all a safe and happy festive period and a fantastic New Year. There is still plenty to do in the next few weeks, but once we do wind down, I hope you get the opportunity to spend some quality time with your family and friends, and use the holiday break to relax and refresh.

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MICrobiology

Adding to the havoc: microbiology and management following natural disasters

İpek Kurtböke, Candan Çiçek and Ian Macreadie

This issue is dedicated to the memory of the victims of natural disasters

Following the successful special issue in 2014, jointly published with the Microbiology Societies of Australia, Türkiye and New Zealand,¹ the Microbiology Society of Australia has decided to publish another special issue with the Turkish Society of Microbiology as both countries have faced natural disasters simultaneously ranging from floods to earthquakes.

It is well documented that natural disasters can result in outbreaks of microbial diseases and the discipline of microbiology plays a significant role in surveillance, prevention and control. Post-natural disaster destruction of critical infrastructure and interruption to daily services can create a disease conducive environment where microorganisms thrive. Flooding, tornadoes, earthquakes, fires, volcanic eruptions, droughts, hurricanes and tsunamis can have a devastating effect on the local populations. Power shortages and lack of refrigeration can also facilitate microbial breeding. Over crowded living conditions in shelters, lack of sanitation and water supply as well as lack of vaccines and antibiotics can increase the severity of disease. Infections can also happen when injuries happen, and subsequent infections can occur. Emergency workers can also be affected along with the natural disaster victims. This special issue focuses on microbial diseases of post-disaster environments. Guest Editor, İpek Kurtböke, remembers her experiences of the devastating 1966 Varto earthquake in Türkiye as an elementary school child and fellow Guest Editor, Ian Macreadie, recalls the vulnerability of the emergency workers as he aided flood victims as an Emergency Services volunteer with the Australian Red Cross.

From Australia, Mark Blaskovich and Patrick Harris cover bugs in floods² and Timothy Ralf and Tsuyoshi Kobayashi discuss the impacts of floods on soil microbiology.³ Food safety is also another important risk factor in disaster-stricken areas and SP Singh provides an overview on how flooding adversely affects fresh produce safety.⁴ Heike Neumeister-Kemp, Lara M. Kemp and Natalie Tijsen provide information on mould contamination of dwellings after flooding,⁵ which can be an important health hazard in tropical regions.

From Türkiye, Fahri Yüce Ayhan emphasises the importance of the management in clinical laboratories and blood banks.⁶ Yeşim Beşli and Banu Sancak provide an overview on gastrointestinal infections after the earthquake⁷ and Fadile Yıldız Zeyrek, Salim Yakut and Metin Korkmaz discuss vector-borne parasitic infections after the earthquake.⁸ Seyfi Durmaz, Gönül Aslan, Raika Durusoy and Candan Çiçek share their experiences on the 2020 İzmir earthquake and its impact on COVID-19 cases.⁹

The Turkish Society of Microbiology (TMC) was established in 1931. Prof. Candan Cicek is currently the President of the Society (Türk Mikrobiyoloji Cemiyeti, see https:// www.tmc-online.org/). It has 18 Special Interest Groups, ranging from antibiotic resistance to anaerobes to Tularemia to Virology. After the publication of the first special issue in 2014, ASM President Prof. Paul Young, Microbiology Australia Editor-in-Chief Prof. Ian Macreadie and Microbiology Australia Editorial Board Chair Ipek Kurtböke attended the TMC-2014 Conference in Antalya, Türkiye, by the invitation of the TMC. This was reciprocated by the invited visit of Prof. Ahmet Başustaoğlu in 2015 to the annual conference of the ASM in Canberra, Australia. Both societies continue to work for the same missions that is peace and harmony contributed with microbial power for sustainable futures and look forward to future joint publications.

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Bugs in floods

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ABSTRACT

Floods are natural disasters that affect millions of people every year, with escalating impact due to a combination of factors that include increasing urbanisation of previously uninhabited land, deforestation, and climate change. Floods do not discriminate between lower-middle income countries (LMICs) and high-income countries, though the types of damage can differ. As a 'fire or flood' country, Australia is no exception. Apart from the obvious physical damage to infrastructure and direct impact on human health due to injury and drowning, there is a more insidious danger lurking in floodwaters – a range of microbial pathogens that can opportunistically cause additional morbidity and mortality. These health effects can be both acute, and longer term. This review focuses on bacterial infections that can be attributed to floods, divided into sections that summarise opportunistic infections by commonly seen human pathogens, versus infections caused by more unusual microbes that are normally not encountered until they are released by floods.

Keywords: Burkholderia, disaster management climate, flood pathogens, infectious disease, Leptospirosis, Vibrio.

Australia has a long history of both fire and floods (Fig. 1) – and the two are not unrelated, as wildfires strip the land of water-retaining vegetation and create a water-repellant soil surface, increasing run-off and the likelihood of floods. A 2022 report¹ by the UN Environment Programme (UNEP) and GRID-Arendal predicts climate change will lead to a global increase of extreme fires of up to 50% by the end of the century, and this will be accompanied by increased flood events. An analysis of data captured between 1900 and 2019 by the Institute for Economics and Peace found flooding is the most common natural disaster since 1990, with floods accounting for 42% of 9924 natural disasters recorded from 1990 to 2019.²

The immediate physical threat of floods to both human health and infrastructure is obvious, but floods also carry a more insidious hidden threat: a range of disease-causing pathogens that lead to infection and illness after the waters have subsided and clean-up begins.^{3,4} Their impact is exacerbated by cuts and injuries and accidental ingestion sustained during the flood event or during clean-up activities,⁵ potentially further aggravated by compromised immune systems resulting from the stress of dealing with injury or displacement.⁶ Although viruses, parasites and fungi also play an important role in flood-related infections, this article focuses on bacterial threats (Fig. 2). Other infecting species and potential treatments for both bacterial and non-bacterial infections are nicely summarised in a 2015 'field manual' developed for responding providers who are engaged in care after a flooding event.⁷

One obvious effect of floods is environmental contamination due to the spread of animal and human waste containing reasonably common bacteria that are normally of little concern as they are properly contained and controlled. Sewage lines and plants are inundated releasing large quantities of raw sewage, while animal waste from farms and feedlots is swept up by the floodwaters and widely distributed. The main culprit, particularly in resource-rich areas, is *Escherichia coli*. Accidental ingestion of floodwaters or contaminated drinking water supplies can lead to gastrointestinal illnesses, including vomiting, diarrhoea, stomach pains and fever, with dehydration in young children and the elderly a particular associated risk. These effects can be persistent, with elevated levels of *E. coli* (and, concerningly, associated antibiotic resistance genes) found in river water samples 6 months after Hurricane Harvey flooding in Houston, Texas.⁸ Another gastrointestinal concern are *Salmonella enterica* serotypes, which also spread by water contaminated with faeces of infected humans and animals. Flood events in rural settings

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Fig. 1. Urban floodwater in Brisbane in February 2021: local park in Bardon, during and after floods (note person walking through floodwater, circled in yellow); Brisbane River inundating Southbank walkway (images: M. A. T. Blaskovich).

have consistently led to the detection of antibiotic-resistant strains of *Salmonella*, such as in water samples collected in North Carolina after Hurricane Florence.⁹ *Campylobacter* spp. and *Arcobacter* are additional animal-associated pathogens causing gastrointestinal infections that have been found in floodwaters, such as in North Carolina (a region highly dense in facilities that produce food animals, particularly swine and poultry) after Hurricane Florence in 2018.¹⁰

Other common human pathogens that lead to increased infections as a result of floods are *Staphylococcus aureus* and *Streptococcus pyogenes*. These bacteria can lead to skin infections, including cellulitis and impetigo. *S. pyogenes* can also lead to respiratory infections by colonisation of the throat (strep throat). The most severe manifestation of *S. pyogenes* infection includes necrotising fasciitis and toxic shock syndrome, which are associated with high risk of mortality and severe morbidity (e.g. need for limb amputation). When flood victims have aspirated water during neardrowning, pneumonia is highly likely, with a range of pathogens possible.¹¹ These cases are often polymicrobial and complicated by abscess formation or empyema. Although some reports have identified acute respiratory infections (cough, sore throat, fatigue, aches and chest or nasal congestion) as the most common infectious disease after flooding, the vast majority are likely due to viral infections.¹²

Another zoonotic infection spread by floods is leptospirosis, caused by the corkscrew-shaped obligate aerobic spirochaete Gram-negative bacteria *Leptospira* spp. (including *L. interrogans* and *L. borgpetersenii*) with symptoms including muscle pain, fever and headaches. These bacteria are spread through the urine of infected animals, including rodents, livestock and domestic pets.¹³ A meta-analysis of observational studies suggests that flooding is associated with the risk of occurrence of leptospirosis in endemic countries.¹⁴ North Queensland has one of the highest incidences of leptospirosis in the world.¹⁵ There was a 65% upswing in cases in South-East Queensland in the weeks after the 2011 floods¹⁶; in



Vibrio cholera

Vibrio vulnificus

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Mycobacterium chelonae
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Fig. 2. A range of bacteria are involved in flood infections (images: Adobe Stock).

Central Queensland nine cases were identified in the 3 months following the floods, compared to nine confirmed cases in the 7 years prior to the flood.¹⁷

The second broad category of flood-associated infections result from microorganisms that live in the environment. One of the best known is Clostridium tetani, a common spore-forming Gram-positive motile, anaerobic soil bacterium that is the cause of tetanus. Tetanus immunisation programs normally provide protection, but in areas where immunisation is low, the combination of C. tetani released by flooding and skin abrasion or cuts due to physical damage can lead to a significant number of cases. The 2004 tsunami in Indonesia led to 106 cases of tetanus in Aceh province, of which 18.9% were fatal.¹⁸ Of particular concern to Australia is Burkholderia pseudomallei, another soil-dwelling bacterium that is endemic in tropical regions such as northern Australia and Southeast Asia, though it has also been reported along the Gulf Coast of Mississippi in the United States (US Centers for Disease Control and Prevention, see www.cdc.gov/ melioidosis/index.html, accessed 20 July 2023). Infections by this Gram-negative, bipolar, aerobic, non-spore-forming, motile, rod-shaped bacterium cause the clinical syndrome of melioidosis, often presenting with severe pneumonia, sepsis and bloodstream infection, visceral abscesses or with involvement of the central nervous system. The disease can affect multiple organs, or cause localised infections in the skin. Chronic respiratory, cutaneous or visceral disease may also present less acutely and mimic other conditions such as tuberculosis or malignancy (Queensland Government, see http:// conditions.health.qld.gov.au/HealthCondition/condition/14/ 33/455/melioidosis, accessed 20 July 2023). Treatment requires extended antibiotic therapy for over 3 months. Case clusters of melioidosis in the Northern Territory of Australia are associated with extreme weather events.¹⁹ A study of melioidosis in the remote Katherine region of northern Australia identified 128 patients from 1989 to 2021, with nine attributed to the flooding of the Katherine River in 1998.²⁰ Flooding in Townsville, Qld, in 2019 affected more than 3000 properties and led to more than 10 cases of melioidosis, with one death.²¹ Melioidosis can often be deadly - a cluster of 10 cases in eastern Sri Lanka identified in the 2 months following an extreme weather event in 2015 had a mortality rate of 40%.²²

Other environmental bacteria live in the water. Many natural disasters, including floods, lead to outbreaks of potentially lethal cholera, particularly in poorly resourced countries. Cholera is caused by highly virulent *Vibrio* cholerae (e.g. serogroups O1 or O139), a comma-shaped Gram-negative, facultative anaerobe which colonises the small intestine. It then releases large quantities of a toxin (cholera toxin, CT or CTX), a protein complex formed from six subunits that activates the CFTR ion channel, releasing chloride ions that draws water into the intestine (World Health Organization, see www.who.int/news-room/factsheets/detail/cholera, accessed 20 July 2023). Cholera can be easily treated through oral rehydration solution or intravenous fluids. Antibiotics are not recommended to stop outbreaks, but vaccination is an effective preventative strategy (see www.who.int/news-room/fact-sheets/detail/cholera). Floods in Nigeria in 2022 led to more than 6000 suspected cases and a 4–5% case fatality ratio,²³ while monsoon floods in Pakistan in 2022 led to nearly 2000 confirmed cases of cholera across all four provinces.²⁴ V. cholerae is halotolerant and is naturally found in brackish and estuarine environments.²⁵ Other Vibrio spp. infections are associated with saltwater exposure resulting from storm surges: Hurricane Katrina in 2005 led to 22 identified cases of Vibrio illness and five deaths, mainly due to wound infections caused by V. vulnificus or V. parahaemolyticus, with five deaths reported.²⁶

Aeromonas species are Gram-negative, rod-shaped facultatively anaerobic bacteria found in fresh or brackish water, and have been shown to form biofilms on various biotic and abiotic surfaces.²⁷ The species considered to be potential human pathogens include A. hydrophila, A. caviae and A. veronii biovar sobria.²⁸ They predominantly cause gastrointestinal tract disorders, but are also associated with infections in wounds, soft tissues, and other sites. A study of a subset of hospitalised patients from the 2004 tsunami in Thailand found 515 of 777 had skin and soft-tissue infections: 22% of cultured isolates were Aeromonas spp.²⁹ An Australian study of bacterial pathogens in 5 consecutive years (2015-2019) from 375 842 stool samples of patients with gastroenteritis found Aeromonas species were the third most common bacterial pathogens, following Campylobacter and Salmonella, though no flood association was noted.³⁰

A range of other Gram-negative bacteria that may lead to soft-tissue infections after water exposure include facultatively anaerobic motile Shewanella spp., a normal component of the surface flora of fish. Shewanella putrefaciens, S. algae, S. haliotis and S. xiamenensis all cause rare cases of human infection^{31,32}; though most literature cases do not appear to be specifically associated with flood exposure, a news report describes a North Carolina case of S. putrefaciens after Hurricane Florence in 2018.33 Leclercia adecarboxylata is a facultative-anaerobic motile bacillus of the Enterobacteriaceae family recognised as an emerging opportunistic pathogen, with rare infections generally found in immunocompromised patients.³⁴ A polymicrobial infection including L. adecarboxylata was identified in a man in his 80s who had cleaned up floodwater in his basement after Hurricane Irene in the US in 2011.35 Chromobacterium violaceum is a facultatively anaerobic coccobacillus that usually inhabits soil and stagnant water; it produces a unique violacein pigment when cultured. Skin infections can rapidly progress to sepsis, with mortality rates of 48–64%.³⁶

Non-tuberculous mycobacteria (NTM) are ubiquitous in the environment and may also cause infections after exposure

to floodwater, particularly rapid growing *Mycobacterium* species such as *M. fortuitum*, *M. chelonae* and *M. abscessus*.³⁷ In an analysis of NTM infections in Missouri (USA), risk of geographical case clustering was significantly higher in counties with > 5 flooding events per year *v*. no flooding (rate ratio 2.82, 95% CI 1.90–4.19).³⁸ Typically, NTM can cause indolent skin and soft tissue infections in healthy individuals, which may fail to respond to first-line antibiotics, but can also cause more aggressive or disseminated disease in immuno-compromised hosts. Specific laboratory techniques may be required to isolate and identify mycobacteria from clinical samples, so close liaison with the laboratory is essential in suspected cases.

In summary, bacterial infections resulting from exposure to contaminated water during floods present a significant health risk. Physicians should be aware of the potential for unusually rare cases in the months following severe weather events, and patients with infection symptoms should remember to inform their doctors if they have been exposed to floodwaters. Simple precautions by the general population, such as avoiding entry into floodwaters and wearing protective equipment during cleanup, can substantially alleviate the threat.

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resistant bacteria and the use of randomised trials to define optimal management for ESBL- and AmpC-producing Enterobacterales, and was lead author for the influential MERINO trial published in JAMA in 2018. He has also been the clinical lead for the Queensland Genomics infection program, aiming to introduce the routine application of microbial genomics to infection control practice.

MICrobiology 3

Impact of inundation on soil microbiology

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***Correspondence to:** Tsuyoshi Kobayashi Science, Economics and Insights Division, NSW Department of Planning and Environment, Lidcombe, NSW 2141, Australia Email: yoshi.kobayashi@environment.nsw.gov.au ABSTRACT

Genetic sequencing as well as culture-based studies have revealed diverse aerobic and anaerobic microbes across a range of aquatic environments in floodplain wetlands. Hydrological conditions related to riverine inundation are a predominant factor determining the structure and function of soil bacterial communities in floodplain wetlands. Despite their complex mosaics of topography, landforms and aquatic habitats, some consistent response patterns are observed among soil bacterial communities with changing inundation patterns and history. Considering hydrological events and changes as a form of disturbance, Connell's 'intermediate disturbance hypothesis' has been used to explain the observed bell-shaped response of soil microbial communities with varying hydrological conditions. Further application and testing of general ecological theories and hypotheses may help advance our understanding and predictive modelling capability for the dynamics of floodplain soil bacterial communities with changing with changing hydrological conditions.

Keywords: Actinobacteria, Cyanobacteria, flooding, floodplain microbes, floodplain wetlands, fluvial geomorphology, hydrological regimes, Proteobacteria, relative abundances, taxonomic and functional diversity.

Introduction

Based on 16S rRNA gene sequencing and other molecular methods, as well as culturebased techniques, diverse aerobic and anaerobic microbes are known to inhabit wetland ecosystems.^{1–5} They contribute to essential metabolic and biogeochemical processes, such as the mineralisation of organic compounds and the cycling of carbon, nitrogen, phosphorus, sulfur, iron and other elements.^{2,3,5–7} In inland floodplain wetlands that receive water primarily from riverine flows and flooding, including those in Australia, soil microbial communities may be typically dominated by members of the phyla Proteobacteria,^{2,3,8,9} Acidobacteria,^{2,3,9,10} Actinobacteria,^{2,3,8-10} Bacteroidetes,² Verrucomicrobia² and Firmicutes.⁸ Proteobacteria is also known to be the most abundant in natural as well as constructed wetlands.¹¹ Floodplain soil microbes are subject to varying wet and dry conditions.^{4,9} Observational and experimental studies have been conducted to understand the association of the microbial community structure and function with varying wet and dry conditions in floodplain wetlands.^{2,6,8,12,13} Hydrological conditions (including a gradient of hydrological connectivity, water depth fluctuations and inundation frequency) are considered critically important in determining the microbial community structure and function in floodplain wetlands.^{6,8,9,12} In this article, we briefly review the recent studies on the relationships of soil bacteria with hydrological conditions in floodplain wetlands including those in Australia, with a focus on the bacterial relative abundances, taxonomic diversity and functional diversity.

Relative abundances

There are studies that explicitly report the relationships between relative abundances of soil bacteria and hydrological conditions in floodplain wetlands^{2,8} including those in semi-arid Australia.⁹ Although these studies were conducted in different geographical regions and have dealt with different aspects of hydrological conditions, the soil bacteria show consistent taxon-specific patterns in terms of how their relative abundances change with increasing wet (or dry) conditions. They can be categorised into positive, negative and neutral (independent) groups in terms of their relative abundances in communities increasing with increasing wet conditions.⁹ For example, the positive-response group of bacteria includes Bacteroidetes,⁸ Chloroflexi,⁸ Euryarchaeota,⁸ Firmicutes⁸ and

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Fig. 1. Examples of dry aquatic environments in floodplain wetlands of the Macquarie Marshes, Australia (*a*), with associated elevation (*b*), inundation frequency (*c*) and logit-transformed relative abundances of the floodplain Proteobacteria (*d*), Actinobacteria (*e*) and Cyanobacteria (*f*) against inundation frequency from the period 1979–2006.³⁷ Fitted regression lines for Proteobacteria and Actinobacteria (*d*, *e*) are significant at P = 0.05.⁹

Proteobacteria.^{8,9} The negative-response group of bacteria includes Acidobacteria,^{2,8} Actinobacteria^{2,3,8,9} and Plancto-mycetes.⁸ The neutral-response group of bacteria includes Cyanobacteria.⁹

Increased wet conditions are likely to lead to more anaerobic conditions than aerobic conditions in floodplain soils, favouring anaerobic taxa over aerobic taxa in microbial communities.^{2,8} In the positive-response group, Bacteroides is obligately anaerobic.¹⁴ Many members of the Proteobacteria and Chloroflexi are obligately or facultatively anaerobic,^{15,16} although the members of Euryarchaeota and Firmicutes may be more heterogeneous in terms of oxygen preference.^{17,18} In the negative-response group, many members of Actinobacteria, Acidobacteria and Planctomycetes are aerobic.^{19–21} In the neutral-response group, Cyanobacteria are capable of anoxic, anoxygenic photosynthesis^{22,23} and are likely to grow even in increased wet conditions. In addition, Cyanobacteria can exist in the form of dormant cells, such as akinetes, during dry times.^{24,25} Such physiological adaptations by Cyanobacteria may render the presence of Cyanobacteria independent of hydrological conditions (e.g. inundation frequency) in floodplain soils, relative to other members of the microbes (Fig. 1).⁹

Because floodplain wetlands are comprised of a suite of landforms that are geomorphologically dynamic and underpin a mosaic of aquatic habitats,^{26,27} small, spatial heterogeneity in hydrological conditions (e.g. due to elevational differences within <1-km distance) can produce taxon-specific effects on their relative abundances of soil bacteria in floodplain wetlands.^{4,9}

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Taxonomic diversity

The fluctuations in hydrological conditions are known to affect the diversity of floodplain soil bacteria. For example, Peralta et al.²⁸ have shown that bacterial communities originating from fluctuating hydrological conditions were more diverse and capable of greater changes in community composition in response to changes in soil moisture than bacterial communities shaped by stable, less dynamic, hydrological conditions (i.e. more permanently wet or dry conditions). Shen et al.⁴ also reported that the diversity of soil bacteria was high at middle elevation sites (corresponding to sites of intermediate flooding duration), relative to high and low elevation sites. They stated that the observed curvilinear relationship between the soil bacterial diversity and flooding disturbance can be explained by Connell's 'intermediate disturbance hypothesis'.²⁹ Flooding or inundation is thought to be a reasonably common and important disturbance type in floodplain wetlands including those in semi-arid Australia.^{11,30,31} Interestingly, Rayburg et al.³¹ have shown that semi-arid floodplain sites subject to an intermediate level of flood disturbance also have a greater level of diversity in soil properties than those sites subject to frequent flood disturbances.

Functional diversity

Changes in hydrological conditions also influence the functional diversity of floodplain soil bacteria, by affecting soil redox, nutrient and carbon environments as well as grain size distributions in topsoil.^{32,33} For example, they may allow the coexistence of nitrifying and denitrifying bacteria in floodplains following inundation, with additional functional pathways of nitrogen cycling.^{32,34,35} In terms of carbon cycling, Limpert *et al.*³ reported the changes in the rates of carbon dioxide (CO₂) and methane (CH₄) emissions in a semi-arid Australian floodplain wetland before, during and after inundation. Overall, the total carbon emissions in the form of CO₂ and CH₄ are reduced during and after wetting due to increasing vegetative growth and subsequent CO₂ sequestration.

By using Biolog EcoPlates (Biolog, Inc., Hayward, CA, USA), Wilson et al.¹² measured the diversity of carbon substrate use by Australian floodplain soil bacteria. They reported that initially following flooding, a diverse range of carbon substrates was used by floodplain soil bacteria. However, after 24 days there was no significant difference between the carbon substrates used in flooded and nonflooded samples. They suggest that the initial rapid increase in substrate utilisation is due to opportunistic growth of *r*-selected species responding to a change in their immediate environmental condition, which was followed by growth of K-selected species. Similarly, using Ecoplates, Rana et al.¹³ investigated the intensity and diversity of carbon substrate use by soil bacterial communities in areas exposed to different historical inundation frequencies (moderate, low and very low areas) in semi-arid Australia. They detected the highest microbial activity from the soil bacteria community in a very low inundation frequency area. The diversity of carbon substrates used also differed among communities initially following inundation but became similar diversity levels after ~ 1 week of inundation.

Conclusion

The structure and function of soil bacteria are intrinsically related to hydrological conditions in floodplain wetlands. There are consistent response patterns among soil bacterial communities with changing hydrological conditions in floodplain wetlands, despite their complex topography, landscape and aquatic habitats. Considering hydrological changes as a form of disturbance, Connell's 'intermediate disturbance hypothesis' has been used to explain the observed bellshaped response of soil microbial communities with varying hydrological conditions.²⁹ There is inherent difficulty in clearly defining what is meant by an 'intermediate' disturbance due to ecosystem-specific reference conditions such as average, minimum and maximum values.³⁶ Nevertheless, further application and testing of general ecological theories and hypotheses may help advance our understanding and predictive modelling capability for the dynamics of floodplain soil bacterial communities with changing hydrological conditions.

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Flooding adversely affects fresh produce safety

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ABSTRACT

Flooding is the most recurring and common natural disaster affecting society, food security and the environment. Floodwater is known to be a carrier of biological, chemical and physical hazards affecting food safety during primary production and processing of fresh horticultural produce. Runoff from livestock, industrial, residential and sewage treatment areas into waterways and their overflow can contaminate agricultural water sources, production fields and post-harvest processing facilities. A transient increase in the population of faecal indicators such as *Escherichia coli* and the detection of environmental pathogens such as *Listeria monocytogenes* and *Salmonella* in produce, water, soil and processing facility are the short-term and most notable impacts of flooding, leading to a significant amount of food losses due to microbial contamination and potentially a rise in the foodborne illnesses among produce consumers. However, the long-term impacts of recurring flooding are far more severe and damaging due to the survival and persistence of microbial pathogens in soils, water sources and processing environments. This article focuses on how flooding can exacerbate the microbial food safety risks in the primary production and processing of fresh produce and briefly describes the management strategies.

Keywords: floodwater, foodborne pathogens, food safety, fresh produce, irrigation, natural disaster, post-harvest processing, soil and water contamination.

Flooding events have been a recurring natural disaster in Australia, causing significant economic damage to infrastructure, communities and the environment. With a reduction in average annual rainfall, the intensity and frequency of heavy rainfall in Australia is predicted to increase, leading to extreme weather events such as floods, cyclones, drought and temperature extremes.¹ In 2022, 47 flooding events were declared natural disasters as per the Australian disaster database (Australian Government Department of Home Affairs, see https://www.disasterassist.gov.au/find-a-disaster/australian-disasters, accessed 19 August 2023). The total costs of natural disasters in Australia in 2017 were estimated to be A\$18 billion per year and forecasted to rise to \$39 billion per year by 2050.² Flooding has been the most damaging natural disaster costing on an average \$8.8 billion per year, which is approximately half the total costs of all natural disasters such as cyclone, hail, storm and bushfires. In addition to direct economic losses, flooding events can have significant effects on the food security and the occurrence and spread of foodborne diseases in the communities, whose economic impacts are currently unknown.

Extreme weather events such as flooding have been linked with foodborne and waterborne gastrointestinal illness outbreaks.³ Fresh horticultural produce, generally grown in open fields, is more prone to extreme weather events, natural disasters and associated food safety risks. In Australia, dust storms were associated with *Listeria monocytogenes* outbreak caused by rockmelons in 2018. Similarly, flooding or runoff was speculated to be responsible for introducing toxic weed (*Datura stramonium*) seeds into spinach production field, leading to a large-scale intoxication outbreak in December 2022 caused by the contamination of bagged spinach leaves with weed leaves.⁴ The increase in foodborne illness outbreaks related to fresh produce is a global concern with frequent implications of microbial contaminants such as Shiga-toxin *Escherichia coli* (STEC), *Salmonella* species and *L. monocytogenes* in these outbreaks. Natural disasters such as flooding can aggravate the distribution and transmission of microbial contaminants in agricultural production and processing systems.

Flooding events and associated hazards

Flooding can be broadly categorised into two types. The first type is linked to heavy rainfall leading to water accumulation in production fields and can affect microbial

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contamination of fresh produce through overland flows and splash transfer of pathogens from the soil onto the crops during rainfall.⁵ In Finland, a *Cryptosporidium parvum* outbreak in 2012 was speculated to be caused by contaminated water splash from heavy rains onto frisee salad in the fields.⁶ An increase in the detection of foodborne bacterial pathogens on fresh produce has been observed after heavy rainfall events in Australia (S. P. Singh, unpubl. data).

The second type of flooding, which is experienced as a natural disaster, is severe and involves large runoff and overflow from surface waters such as rivers, creeks, lakes and dams and enters into production fields and post-harvest processing facilities.⁷ Floodwater can carry physical (e.g. wood, metal and glass), chemical (e.g. chemical residues, heavy metals, toxins, petroleum products) and biological (e.g. bacteria, viruses and parasites) hazards and transfer them into water sources, production fields and processing facilities (Fig. 1). The risks of contamination associated with flooding are significant when these operations are adjacent to livestock, industrial and residential areas. Floodwater mobilises pathogens from the environment such as sewage or septic overflow, runoff from livestock operations and compost yards, and industrial areas.

Flooding-induced microbial contamination during primary production and processing of fresh produce

The contamination of water sources poses a serious threat to the introduction and transmission of foodborne illness causing pathogens.⁸ Agricultural water has been implicated in several foodborne illness outbreaks related to fresh produce, including *E. coli* O157:H7 outbreaks linked to romaine lettuce,⁹ enterohemorrhagic *E. coli* in salad¹⁰ and *Salmonella* Newport in tomatoes.¹¹ Floodwater carrying foodborne bacterial and viral pathogens and parasites can introduce these contaminants in water sources, growing crops, soils and processing facilities. The contamination of water sources, both surface and underground, can have short-term and long-term impacts on the pathogen transmission and persistence in the agricultural production and processing environments.⁷

Studies have shown that high faecal indicator pathogen loads are often detected in floodwater¹² and can contaminate agricultural water used for irrigation, foliar sprays and post-harvest operations.⁸ Under normal circumstances, microbial quality of surface water varies considerably according to the season and location. For example, the *E. coli* population in the Australian Murray River water

Fig. I. Floodwater as a source and route of microbial contamination in fresh horticultural produce adjacent to livestock, industrial and residential areas.

Fig. 2. Escherichia coli population in the Murray River water samples collected from multiple locations between June 2022 and June 2023 (Data source: Lower Murray Water, Victoria, Australia, see https://www.lmw.vic.gov.au/water-supply-and-services/water-quality-and-treatment/e-coli-river-water-reports/). The flooding events occurred between October and December 2022. MPN, most probable number.

samples collected from multiple locations in the Lower Murray region varied considerably between June 2022 and June 2023 (Fig. 2). The flooding in the region between October 2022 and January 2023 inconsistently increased the *E. coli* population at several locations. The highest *E. coli* population was recorded during April 2023 from Piangil, Kerang and Swan Hill locations, coinciding with the receding of floodwater (Fig. 2).

Microbial pathogens capable of forming biofilms and oocytes can persist in agricultural waters for weeks, increasing likelihood of their transmission.¹³ Further to it, the contamination of agricultural water distribution systems (e.g. pumps, pipelines and sprinklers) can become a source of cross-contamination when water is used for irrigation, foliar application and post-harvest processing. The survival and persistence of these pathogens could be affected by several environmental factors such as solar radiation, organic load, as die off rates of these pathogens are highly variable and influenced by plethora of factors. In addition to microbial risks, high nutrient load in surface water sources (e.g. rivers, lakes and ponds) can also lead to the growth and multiplication of blue-green algae and thus production of associated toxins, making the water unfit for agricultural purposes.¹⁴ These toxins can be absorbed or translocated in the plant system, rendering the fresh produce unsafe for human consumption. Therefore, the impact of flooding on microbial quality of agricultural water can have direct and indirect impacts ranging from short- to long-term.

Floodwater has strong potential to introduce bacterial and viral pathogens and parasites in production field soils. The persistence and survival of these pathogens varies considerably depending upon factors such as such as temperature, rainfall, solar radiation, soil pH, soil type, moisture, agronomic practices, nutrient availability, as well as soil biological interactions.¹⁵ For example, abundance of the Salmonella Typhimurium in soils was reduced to the detection limit between 40 and 180 days, most of the Salmonella did not survive in soil for more than 90 days. Flooding and soil texture (content of sand) promote the decline rate of Salmonella in soils.¹⁵ Similarly, foodborne viral pathogens get readily adsorbed on to fine-textured soils compared to coarse-textured soils. Sandy soils are relatively poor adsorbents of enteric viruses, whereas soils with clay content of 30–100% are excellent adsorbents.¹⁶ The broader understanding and knowledge of die off rates of various microbial contaminants under variable conditions are unknown which limit the scientific basis of advice to growers regarding the post-flooding microbial hazards presents in the soil. Microbiological testing of soil for various target pathogen is thus the most reliable risk assessment method.

Floodwaters can contaminate agricultural equipment, packaging and storage facilities, and transportation vehicles. If these contaminated surfaces come into contact with fresh produce, cross-contamination can occur, leading to the spread of pathogens or chemicals from the floodwaters to the produce. This can happen during harvesting, processing, packing or transportation stages. Environmental pathogens such as *L. monocytogenes* and *Salmonella* can enter the processing facilities with produce itself, workers shoes, equipment and machinery. Contamination of produce-contact (e.g. conveyor belts, brushes) and non-contact surfaces (e.g. floors, walls) can lead to persistent contamination risks if their anchorage and harbourage remains unnoticed.

After a flood event, water used for post-harvest activities, such as washing, rinsing and cooling of fresh produce, can become contaminated. If this contaminated water is used during these processes, it can introduce pathogens or chemicals onto the produce, compromising its safety. Flooding can also lead to a loss of quality and reduced shelf life of fresh produce. Excessive moisture and prolonged exposure to water can cause physical damage, such as bruising, decay or mould growth, making the produce unsuitable for consumption.

Floodwater impacts on fresh produce safety – case studies

Spain

A study in Spain showed that irrigation water, soil and lettuce samples showed the presence of coliforms and *E. coli* when sampled 1 week after flooding.⁷ However, bacterial population drastically decreased 3 weeks after the flooding. All three major foodborne bacterial pathogens (e.g. *Salmonella*, STEC and *L. monocytogenes*) were detected in lettuce samples after flooding. Salmonella was also detected in irrigation water and soil samples 1 week after the flooding. Similarly, another study in a greenhouse grown tomato crop, the presence of *E. coli* and *Salmonella* Newport was demonstrated in tomato samples during and after a flooding event in Mexico.¹⁷

Australia

After October to December 2022 floods in Victoria, a total of 86 samples (18 produce samples and 15 soil drags from production fields and 53 environmental samples from post-harvest processing facility) were collected from a fresh-produce farm located near Mildura, which was partially affected by flooding (S. P. Singh, unpubl. data). STEC was detected in a soil drag sample and on a produce sample from the flood-affected zone of the farm. Similarly, STEC was also detected on harvest bins and drains in the fruit receival area of processing facility, indicating the potential transmission of STEC from soil to produce to harvest bins to drains in the packing facility. Salmonella and L. monocytogenes were also detected on the non-contact produce surfaces (e.g. floors and drains) of the processing facility. In previous years (2021 and 2022) of food safety monitoring, no foodborne bacterial pathogens were detected on produce and environmental samples collected from this farm (S. P. Singh, unpubl. data). This case study highlights the potential of flooding events in introducing microbial contamination in the production fields and their transmission from field to processing facilities along with produce, harvesting and post-harvest equipment.

Management options

Post-flooding response

Educating growers and farm workers about flood-related risks and appropriate handling practices should be part of the preparedness for natural disasters. The flood-affected zones of the farm should be clearly identified and marked to restrict the potential transfer of microbial pathogens and produce from the affected zone to the clean zone. Once a flooding event has occurred, clear guidelines should be followed such as the United States Food and Drug Administration (US FDA) guidance on evaluating the safety of flood-affected food crops. 18

Produce that has come in contact with flood water is considered adulterated and cannot be sold for human or animal consumption. If the crop comes in proximity to or is exposed to a lesser degree, a thorough risk-assessment should be conducted involving factors such as the floodwater hazards, type and stage of crop growth, degree and duration of crop exposure to floodwater and related conditions and likelihood for crops to absorb or internalise potential contaminants. Microbiological testing for faecal indicators and foodborne microbial pathogens should be the objective and integral part of food safety risk assessments.

Preharvest water should be subjected to microbial reduction strategies when the microbial load is intermediate (100–1000 colony-forming units per 100 mL). Electrolysis, ozone, UV and photocatalysis hold promise, either as single treatments with pre-treatments that remove suspended material or as combined treatments, with another chemical or physical treatment methods.¹⁹

Flood-affected fields should not be replanted for at least 30–60 days after the water recedes.¹⁸ The waiting period for replanting are based on the known die off rates of pathogens and other factors such as temperature weather and soil type. Replanting with fresh produce crops such as leafy vegetables, herbs, melons and strawberries is not recommended. Crops with edible parts away from the soil and likely to be consumed after cooking or processing are more suitable for replanting.

The US FDA recommends the segregation of flood-affected crops from non-affected crops with a 30-foot (\sim 9.1 m) buffer zone to prevent cross contamination between the flooded and non-flooded fields.¹⁸ Conducting thorough risk assessments of flood-prone areas and implementing appropriate mitigation strategies are important strategies to manage flooding risks. Improving water and flood management systems, such as proper drainage and irrigation practices are critical. Enhancing hygiene practices during harvesting, processing and transportation of fresh produce along with regular testing and monitoring of water sources used in preharvest and postharvest operation are among the practical management options.

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Biography

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Disaster management in clinical laboratories and blood banks

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ABSTRACT

The challenge of disaster management in healthcare facilities is dealing with the incident's consequences and maintaining regular operations. Diagnostic and clinical microbiology laboratories have a critical role in the early diagnosis of causative agents of infectious diseases that could spread rapidly in the community and lead to outbreaks. Blood banks are also crucial to maintain the blood supply chain and to cope with the raised demand for blood components because of disaster-related injuries. It is thus necessary to prepare emergency plans, including step-by-step action plans for various disaster scenarios. Even though inconvenient conditions exist during disasters, biosafety and biosecurity precautions still apply, as well as quality control requirements in diagnostic and clinical laboratories and blood banks.

Keywords: blood bank, diagnostic and clinical laboratory, disaster management, disaster preparedness, emergency plan.

The terms disaster, crisis and emergency have distinct definitions. Disaster is the term used to define situations that refer to malfunctioning the community and leading to the losses or injuries of humans, economic demolition and environmental destruction. It is almost impossible to cope with a disaster using the resources of the affected community. By contrast, an emergency is an unpredictable circumstance that entails setting aside usual procedures to save lives and protect the environment. A crisis is a sudden change that makes it difficult to cope with an emergent condition in ordinary work or life.^{1–3}

Dealing with an emergency, crisis or disaster requires an action plan that includes pre-, peri- and post-event activities and interventions. The first stage of an action plan is the mitigation phase, which minimises the impact of a potential incident and reduces its subsequent disruptive effects. The second is the preparedness phase, involving the prediction of the exposure, the assessment of the risks and vulnerabilities, and the implementation of the actions. Next is the response phase, which includes coping with the incident's aftermath. The final stage is the recovery phase to resume work and restore the facilities' abilities.³

These two aspects mentioned above of the disaster are challenging for the diagnostic and clinical laboratory and blood bank. Although the facility should serve the community during or after the emergency, the tragedy would also affect it. Therefore, the action plan must consist of operations for both distinct aspects. After assessing potential vulnerabilities, designing intended actions comes next. Structural and non-structural vulnerabilities, plus organisational and administrative vulnerabilities, should be evaluated distinctively.

An action plan should (1) clearly define the difference between emergency plans for disaster and daily routine work. (2) Define essential requirements to continue the facility's operations. (3) List these requirements in the emergency plans. (4) Prioritise important operations and the staff responsible for them, emergency communication, critical goods, equipment, and data protection are necessary to maintain any facility's functions during and after a disaster. (5) State the evacuation routes, assembly points, shutdown procedures, restoring backup data, closure period and alternative laboratories for the damaged facilities. Developing emergency plans is beneficial for helping people suffering from a disaster and preventing significant damages for those involved in the incident.^{3–5}

During a disaster, the aim of the microbiology laboratories is early and accurate diagnosis of the causative agents of infections. However, besides diagnosing individual patients, identifying the pathogens that might potentially cause outbreaks would be the primary task for medical microbiologists.⁶

In a disaster, consider deploying portable, mobile, temporary-stationary, or fixed laboratory facilities for laboratory service. Portable laboratories are helpful for

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Fig. 1. Mobile laboratory servicing at the disaster area after the earthquake hit Turkey in 2023 (reproduced with the permission of DHA-Demiroren News Agency).

small-scale testing, e.g. water analysis for epidemiological surveys. Mobile laboratories are flexible for both medical diagnostic testing and epidemiological surveys (Fig. 1).

Temporary stationary laboratories can serve in vehicles, carriers, tents, or fixed buildings. Fixed laboratories in existing buildings would be preferable to provide a system for pre-analytical, analytical and post-analytical requirements besides biosafety and biosecurity precautions. Although point-of-care testing may be an efficient alternative for the disaster period, quality assurance remains essential.^{6,7}

Laboratory conditions are significant for determining the Hospital Safety Index (HSI), a universal assessment tool for health services. Laboratory safety ratings are critical parameters for estimating HSI listed in the World Health Organization (WHO) guidelines. Safety is rated low if laboratory equipment is in poor condition and breached biosafety. If the equipment is in good condition and the laboratory has well-established biosafety precautions with appropriate measures for protection and security, the safety rating is high.⁸

In case of emergency, besides considering the biosafety precautions, biosecurity also has to be taken notice in clinical microbiology laboratories. A laboratory response network for biothreats designed by the American Society of Microbiology stipulated the establishment of sentinel laboratories with the capability of surveillance of emerging microorganisms and pandemics.⁹

All disasters affect the functioning of blood banks and transfusion services in a particular manner. Natural disasters (e.g. earthquakes, floods, tsunamis, landslides) may disrupt the blood supply chain by damaging the transportation infrastructure and keeping healthcare facilities inoperative. Pandemics challenge blood inventory management by reducing blood donations and paring back the workforce of blood establishments. Mass casualty incidents may disable the blood banks because of the high demand for blood donations.^{5,10}

Using mock scenarios or computer simulations to predict blood product requirements during a disaster is advisable. Furthermore, *Tabu Search*, a metaheuristic problem-solving approach by mathematical modeling, is suggested to determine post-disaster temporary blood bank locations.^{5,11,12}

Although it is improper to transfuse untested blood even in emergencies, the 'Walking Blood Bank' concept is for the troublesome absence of blood products in particular situations leading to mass casualties such as war or terrorist attacks. The term describes the practice of transfusion of whole blood taken from typed donors for blood group and screened for infectious disease markers in previous donations.¹³

As constituent parts of the health care system, diagnostic and clinical laboratories, and blood banks are utilities that would have crucial roles in minimising the health impacts of the disaster. Early diagnosis of infectious diseases, offering essential tests used in caring for the disaster victims and providing safe blood components for transfusion are significant tasks assigned to such laboratories.¹⁴

In conclusion, management requires a holistic approach, which includes vulnerability assessment, mitigation strategies and preventive measures, and rapid response to the incident without any concession from the quality requirements.

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Gastrointestinal infections after earthquake

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ABSTRACT

Natural disasters such as earthquakes resulting in infrastructural damage in affected areas can also result in outbreaks of infectious diseases, with infections usually beginning within 4 days of the initial impact. Gastrointestinal diseases are prevalent due to the lack of food and water supplies. The rates of diarrheal illnesses following natural disasters are mainly influenced by the (i) endemicity of intestinal pathogens before the disaster, (ii) the availability of safe water and sanitation facilities, (iii) the severity of the disaster, (iv) the degree of crowding and (v) the availability of healthcare resources. Among the causative agents of gastroenteritis, viral infections are the most common ones, followed by bacterial and parasitic infections. Maintenance of sanitation and availability of primary healthcare are critical for early diagnosis, treatment and prevention of infectious disease outbreaks following natural disasters.

Keywords: diarrhoeal illness, diarrhoea in resource-limited settings, earthquake, enteric pathogens, gastroenteritis, gastrointestinal illness, natural disaster, outbreak, public health.

Introduction

Earthquakes are the second most documented natural disasters and the most recorded geophysical catastrophe, particularly in regions of high seismic activity.¹ The devastation of an earthquake can create a potential for infectious disease outbreaks because of prevailing circumstances, such as the socioeconomic conditions of the affected area.^{1,2} Research demonstrates that infectious diseases occur not only after destructive earthquakes that cause mortality and morbidity but also following earthquakes that severely affect structural elements with limited immediate impact on human life. Infections can manifest within 4 days and up to 4 weeks after the initial impact of the earthquake. However, symptoms and clinical signs may appear up to 4 weeks after the disaster if a pathogen can cause latent infection or has a longer incubation period. In addition, conditions such as water source contamination or over-crowded communal living increase the risk of infectious diseases.³ A significant increase in the incidence of infectious diseases in the postearthquake period compared to the pre-earthquake period for gastrointestinal infections (163.4 per 100 000 people) was reported.⁴ Infectious disease outbreaks are thus one of the most significant factors that can exacerbate the effects of a disaster and delay recovery. Accordingly, a comprehensive understanding of natural disaster characteristics and risk factors of post-disaster outbreaks can enable better preparedness, response, and surveillance and strengthen region-specific disaster risk reduction in the future.⁵

Risk factors

The primary risk factors include displacement, poor access to safe drinking water and poor hygiene. If flooding occurs this can also result in the breakdown of sanitation, leading to outbreaks of waterborne illnesses such as leptospirosis, cholera, and dysentery. Additionally, following extensive damage to infrastructure, overcrowding due to inadequate or temporary shelters, and camps are more likely to occur, with subsequent displacement where young females and children constitute the most affected category.⁵ Other factors that affect the likelihood of outbreaks of infectious diseases include the scale and intensity of the earthquake, the prevalence of aftershock effects, the demographic and epidemiological characteristics of the region, the socioeconomic aspects and living conditions of the community, and the damage to public health infrastructure and facilities.³

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The sudden appearance of unexpectedly large numbers of dead bodies can raise concerns about disease outbreaks.⁴ However, most pathogens do not survive for long in the post-mortem body, exceptions being deaths due to cholera or haemorrhagic fever related. Interestingly, there is no documented evidence that corpses pose a risk of triggering an epidemic following natural disasters.⁶

Actiology and epidemiology reference

Post-earthquake infectious disease rates are well documented, with gastrointestinal, skin, and respiratory infections being the most reported ones.^{3,7} The intensity of the earthquake, its location, tsunami and other possible events that might occur afterwards may play an essential role in infectious diseases. The incidence of post-earthquake gastrointestinal tract infections was reported to be as high as 456.6 cases for 100 000 for viral hepatitis and 56.8 cases for 100 000 for diarrhoeal diseases.⁷

Shigella

Following a natural disaster, *Shigella* infections represent a significant threat for children under 5 years of age in endemic regions where climatic conditions and lack of water supply create a conducive setting. Antibiotics are essential in limiting the impact of severe illness, death and transmission of causative agents in small and large outbreaks as a result of natural disasters; thus their supply can be critical.⁸

Salmonellae

An outbreak of *Salmonella enterica* among Italian children was reported 4 years after the great earthquake of 6 April 2009, and the underlying factor of this outbreak was reported to be contamination of natural spring water due to geological processes.^{3,9} There is no Centers for Disease Control and Prevention (CDC) recommendation for typhoid vaccination when responding to disasters within the USA, as the likelihood of exposure in the region is low.¹⁰ Current typhoid vaccines are not recommended for mass vaccination campaigns,¹¹ however, such recommendation can be reviewed based on regional epidemiology and risk assessments.^{11–13}

Cholera

Vibrio cholerae can be transmitted by consuming contaminated food and water. Fomites and insects may additionally be involved. Specific characteristics of the causative agent such as the ability to remain infectious for up to 24 h after faecal excretion and its ability to grow in liquid environments at 30°C, with a salinity of 1–2% and a pH of 8.5, are the factors that can facilitate the spread of the pathogen and the emergence of an epidemic.¹⁴

After a 7.0-magnitude earthquake struck Haiti in 2010, cholera quickly spread across the country caused by *V. cholerae*, Ogawa biotype, serogroup O1. Notably, most affected patients had previously consumed contaminated water from a nearby river.¹⁵ Similarly, following the 2015 Gorkha earthquake, Kathmandu, Nepal's capital and largest

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city, encountered cholera outbreaks. Twenty-nine people contracted cholera from *V. cholerae* serogroup O1 serotype Ogawa after consuming contaminated water in heavily populated areas of the region.¹⁶

Since the first cholera case was documented in Syria on 10 September 2022, more than 50 000 suspected cases were reported in Idlib and Aleppo governorates. By mid-February 2023, the reported cases decreased by 63%. Continuous surveillance resumed, and in Syria, 1784 new cases were reported by the end of February 2023.¹⁷ Yet, no cases of cholera were officially documented in Türkiye following the earthquake. On 4 March 2023, the Turkish Ministry of Health announced that health screenings did not identify any infectious disease epidemics.¹⁸

The CDC have no recommendation for a cholera vaccine when responding to disasters in the USA, primarily because the likelihood of exposure in the region is low.¹⁸ The WHO and UNICEF launched a cholera vaccination campaign in north-western Syria in response to the devastating earthquakes of 6 February 2023 near the epicentre Kahramanmaraş in Türkiye.¹⁷

Tularaemia

In 2005, the first cases of tularaemia were detected in the Gölcük district of Kocaeli province in Türkiye. The underlying cause of the outbreak was contaminated water, consumed by individuals in a newly formed settlement.¹⁹ Further research aimed at preventing tularaemia infections or epidemics is essential for public health in an event of a natural disaster or earthquake in regions where *Francisella tularensis*, a highly virulent as well as a recognised bioterrorism agent, is endemic.

Rotavirus

Earthquake damage that leads to widespread contamination of drinking water sources, such as the 2005 Kashmir earthquake, can result in rotavirus outbreaks, which are globally prevalent and cause diarrhoea in children under 5 years of age. Insufficient living conditions, inadequate water supplies, and poor hygiene contribute to mortality.^{3,20} For this reason, irrespective of the region in which the earthquakes strike, improvement of the existing conditions and increasing vaccination rates are important precautions to prevent outbreaks of rotavirus and other pathogens among vulnerable populations.

Hepatitis A and E

After the earthquakes in İzmit and Düzce, which struck Türkiye's north-west region twice in less than 3 months in 1999, the occurrence of Hepatitis A (HAV) and E (HEV) in children residing in temporary camps was 68.8 and 44.4% in Gölyaka and 17.2 and 4.7% in Düzce respectively.^{2,21}

The CDC recommends two doses of HAV vaccine, given at least 6 months apart for children aged 10 who are exposed to natural disasters if immunisation records are unavailable.¹⁰ Yet, the WHO's recommendations for preventing outbreaks of HAV in disaster areas do not include vaccination.¹¹

Giardia

Giardiasis is associated with poverty and unsafe water. Approximately 2 years after a severe earthquake in the Armenia region of Colombia on 25 January 1999, giardiasis was the most common parasitic infection, spread by shared toilets and water from municipal sewers.²² Similarly, two earthquakes in north-western Türkiye in 1999 destroyed 80% of the houses and schools in Düzce.²³ A comparison of two groups of children living and studying in different socioeconomic conditions after the earthquake demonstrated a significant increase in the prevalence of giardiasis in children still living and studying in temporary settlements years after the earthquake.²³

Role of microbiology laboratory and diagnostic approaches

The normalisation, maintenance and provision of essential laboratory services are urgently required after a natural disaster.² In addition to disaster-related events, laboratory support should continue for routine services such as maternal and child health and other ongoing disease control interventions. A multi-level laboratory system can be adopted to operate laboratory services effectively (see Fahri Yüce Ayhan article in this issue²⁴). The central and subordinate laboratories in the affected area need to be identified. Procedures such as routine laboratory services and sampling should be initiated at the site level.²⁵

Pre-diagnosis of potentially epidemic infectious diseases, such as cholera and rotavirus, can be achieved using field immunochromatography and lateral flow devices. As part of the post-disaster response, simple environmental tests, such as ortho-toluidine testing to monitor effective chlorination, can be used at the field level to maintain the use of water resources. Rapid diagnostic tests used in the field and primary care are essential for the early detection of increases in infectious agents, clusters of infections and even outbreaks. For laboratory confirmation of an infection or outbreak, samples should be sent to a next-level laboratory for retesting or further laboratory analysis.^{2,25}

Preventive measures and preparedness

An uninterrupted supply of safe drinking water, sanitation and site planning are essential. Chlorine can be used as an effective and inexpensive disinfectant against waterborne pathogens. In addition, settlement planning must meet water and sanitation requirements and the number and size of shelters should be follow international guidelines. Access to primary health care is crucial for the prevention, early diagnosis, and treatment of various diseases. It also provides a triage step to secondary and tertiary healthcare. The following interventions are recommended to reduce the impact of infectious diseases: early diagnosis and treatment of diarrhoea, use of treatment protocols for infectious diseases, availability of medicines such as oral rehydration, and distribution of health education messages.²⁵ Finally, good hand hygiene practices, safe food preparation techniques, boiling or chlorinating water, early interventions for fever, and insecticide-treated bed nets can help prevent infectious diseases. Public awareness of basic health measures is essential to reduce the risk of infectious diseases following natural disasters.^{2,25}

Conclusions

The main cause of mortality and morbidity during and after earthquakes and many natural disasters is the traumatic impact at the time of the event. By contrast, post-disaster health care for survivors determines the depth and duration of the effects of a disaster. The emergence of post-disaster epidemics is closely linked to the displaced population's size, health status and living conditions. Access to safe water resources is the main concern. Water and food-borne illnesses are prominent infections following an earthquake, with numerous gastrointestinal diseases, particularly diarrheal diseases. It is possible to reduce disaster-related infections and epidemics, including those of the gastrointestinal tract, through improved and more systematic disaster response and preparedness planning. The prevention of infections can significantly contribute to the post-disaster recovery and normalisation of affected communities.^{2,26} Understanding the connection between earthquakes and infectious agents (particularly V. cholerae, Salmonella spp., Shigella spp., F. tularensis, rotavirus and hepatitis A and E viruses), along with the identification of the causative agents, and efficient surveillance will be pivotal prevention and control.

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In Prof. Sencak's biography, the sentence 'She is currently the Director of Microbiology Laboratory of the Medical School.' should be 'Her research interests are in areas of antimicrobial resistance, bacteriology and diagnostic microbiology.'

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Vector-borne parasitic infections after the earthquake

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ABSTRACT

The transmission of vector-borne infections after an earthquake is related to the changes in the environment caused by the earthquake. The displacement of thousands of people, especially in areas where vector-borne diseases are endemic, can significantly increase human exposure to mosquitoes and other vectors and the pathogens they may carry in overcrowded environments and inappropriate temporary shelters, leading to an increase in human infection cases. The devastating earthquakes in Türkiye on 6 February 2023 pose a risk of the spread and outbreaks of vector-borne infections such as cutaneous leishmaniasis (CL) and malaria, which are endemic in the region. Public health authorities should prioritise surveillance in all earthquake-affected areas. Immediate detection and identification of local vector species, monitor environmental conditions and potential breeding grounds, insecticide application and use of mosquito nets and development of interventions to prevent the emergence of vector-borne infections are essential. Case diagnosis and treatment follow-up, prophylaxis, training of the public and health personnel, improving temporary shelter conditions and facilitating access to clean drinking water and health services are essential to minimise the impact of vector-borne infections in post-earthquake situations.

Keywords: earthquake, malaria, parasites, Türkiye, vector-borne infection: leishmaniasis.

As stated by the WHO¹ and Chala and Hamde,² vector-borne infections, which are a significant public health issue worldwide, are infections that do not spread directly from person to person but are transmitted to humans through a vector. The most common vector-borne infections are transmitted by mosquitoes and ticks. Vector-borne infections can be caused by parasites, bacteria or viruses and annually, over 700 000 deaths are attributed to these infections, which represent more than 17% of all infectious diseases.^{1,2}

Host–environment interactions are key in vector-borne disease emergence. Favourable conditions for vector–host–climate–pathogen–human interactions increase transmission risk. Social and demographic factors also significantly contribute to the emergence of vector-borne infections.²

Earthquakes, which constitute 8% of natural disasters, can cause an increase in the incidence of infectious diseases.³ The transmission of vector-borne infections after an earthquake is related to the changes in the environment caused by the earthquake. The displacement of thousands of people, especially in areas where vector-borne infections are endemic, can significantly increase human exposure to mosquitoes and other vectors and the pathogens they may carry in overcrowded environments and inappropriate temporary shelters, which can lead to an increase in human infection cases.⁴

One of the most devastating earthquakes of the last century occurred in the southeastern region of Türkiye on 6 February 2023. The first earthquake, centred in the Pazarcık district of Kahramanmaraş, had a magnitude of 7.7 and occurred at 04:17 hours local time. Subsequently, at 13:24 hours, another earthquake with a magnitude of 7.6, centred in the Elbistan district of Kahramanmaraş, occurred. These earthquakes were felt in 11 provinces, including Gaziantep, Şanlıurfa, Diyarbakır and Hatay, and caused widespread building collapses and severe structural damage. The earthquakes resulted in the loss of more than 50 000 lives, with over 107 000 people injured (Fig. 1). An area of ~500 km in diameter was directly affected by the earthquake, affecting over 14 million people residing in the region. It was reported that more than half (50.52%) of the Syrian migrant population in Türkiye, lived in this region and were affected by

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Fig. 1. Provinces affected by the 2023 Turkey earthquake.

the earthquake. Due to the earthquakes, \sim 6 million people faced housing shortages, \sim 2 million people began living in temporary settlements, and \sim 4 million people migrated out of the earthquake-affected area. Access to clean drinking water and adequate sanitation facilities, including toilets and bathing, in tent camps was extremely limited.⁵

Additionally, on 15 March 2023, the earthquake-affected provinces of Şanlıurfa and Adıyaman experienced flooding. Twenty-one people lost their lives in this disaster. Because many of the temporary shelters were set up on unsuitable terrain, the living conditions of the local residents worsened after the flooding. Homeless earthquake victims were affected, and the floodwaters inundated many of the erected tents and containers, exacerbating the damage caused by the earthquake (see https://en.wikipedia.org/wiki/2023_Turkey_floods, accessed 29 October 2023).

Earthquakes and floods can affect vector-breeding sites and the transmission of diseases by these vectors. Although initial flooding can wash away existing mosquito breeding grounds, stagnant water caused by heavy rainfall, overflowing rivers or puddles created by earthquakes can create new breeding sites. This can lead to an increase in vector populations and disease transmission potential (typically with a delay of several weeks) depending on the local mosquito vector species and its preferred habitat.⁶

There are numerous examples demonstrating that earthquakes can lead to an increased incidence of vector-borne infections. In 1991, an earthquake in the Atlantic region of Costa Rica caused favourable changes in vector-breeding

habitats and resulted in a significant increase in malaria cases.7 In 2003, in the city of Bam, Iran, 124 malaria cases were reported within 2 months.⁸ During the same period, the incidence of cutaneous leishmaniasis (CL) gradually and then exponentially increased from 2004 to 2008. This earthquake in 2003 resulted in the formation of 10 million tons (~907 000 tonnes) of rubble, creating suitable conditions for the spread of sand-fly vectors. Since then, the epidemiology of CL has been changing, with the emergence of new foci and persistent clinical forms.⁹ After the 7.9-magnitude earthquake in China's Sichuan province on 12 May 2008, it was reported that it contributed to the spread of vector-borne infections, leading to outbreaks.⁴ Following the earthquake in Haiti in 2010, 76 out of 255 patients (29.8%) presenting with an unknown fever were diagnosed with falciparum malaria. Among other vector-borne infections, there were 13 cases of filariasis and 6 cases of dengue fever.¹⁰ In China, after the 2014 earthquake, there was an increase in vector populations, coupled with homelessness, resulting in significantly increased exposure to mosquito bites.¹¹

Leishmaniasis is a disease caused by protozoan parasites of the genus *Leishmania*. These parasites are transmitted to humans through the bite of infected female sandflies. The disease is still an important public health problem in Türkiye and is a notifiable disease (Fig. 2). CL is the most common form of the disease and exists in two main types in the Old World: zoonotic CL (ZCL), caused by *L. major* with rodents as the primary reservoir host, and anthroponotic CL (ACL), caused by *L. tropica* with humans as the reservoir host.⁹

Fig. 2. Cutaneous leishmaniasis lesion and distribution of cutaneous leishmaniasis cases.

A strong association between the number of earthquakes and an increased incidence of CL has been found and regions with frequent earthquakes have been considered as high-risk areas for CL.¹² According to a 2022 meta-analysis, there was a 1.5-fold increase in infectious diseases, including skin, respiratory, gastrointestinal, and central nervous system infections, in the post-earthquake period.¹³ When we look at vector-borne infections expected to occur in the postacute period after earthquakes (after the first month), it is observed that malaria is endemic in the region, and CL is one of the most common infections in the region.

ACL is endemic in the south-eastern Anatolia and Mediterranean regions. According to the Ministry of Health data, 96% of cases were reported from this region, with over half of them originating from Şanlıurfa. Although *L. tropica* remains the predominant causative agent in these cases, CL cases caused by *L. major* and *L. infantum* have also been reported in recent years.^{14–18} It is known that in the region, there are vectors such as *Phlebotomus sergenti* (the vector of *L. tropica*), *P. papatasi* (the vector of *L. major*) and *P. perfiliewi* (which could transmit *L. infantum*).^{19–21}

Leishmaniasis is linked to human behavioral patterns, urbanisation, and environmental changes caused by both human activities and natural disasters. The disease is wide-spread in weak healthcare systems and can lead to large outbreaks, especially in crowded conditions.²² The major earthquake in Iran, for instance, created new breeding potentials for vectors and had the most significant impact on CL incidence.⁹

Malaria, caused by *Plasmodium* species and transmitted by female *Anopheles* mosquitoes, includes five humaninfecting species: *P. falciparum*, *P. vivax*, *P. ovale*, *P. malariae* and *P. knowlesi*. In 2021, the World Health Organization reported 247 million new malaria cases in 84 endemic regions, with 619 000 malaria-related deaths. $^{\rm 23}$

For many years, Türkiye faced a significant public health challenge with chloroquine-sensitive *P. vivax* malaria. After long-standing efforts, it entered the pre-elimination stage in 2009 and since 2013, no new indigenous cases have been reported. Although imported malaria cases are observed, the WHO has not declared Türkiye as a malaria-free region.²³

In south and south-east Anatolia, malaria vectors, including 10 species such as *Anopheles sacharovi* and *A. superpictus*, are present.^{24–27} Identifying the vector species, environmental factors and breeding areas in the region is crucial for developing intervention activities and control measures against diseases transmitted by these vectors.

Factors such as an increase in infected and susceptible hosts following an earthquake, a weak public health infrastructure and interruptions in ongoing control programs are risk factors for the transmission of vector-borne infections. In public health emergencies like earthquakes, public health authorities should prioritise surveillance in all affected areas to reduce the emergence and spread of vector-borne infections. It is essential, especially in regions endemic to diseases such as malaria and CL, to promptly identify and characterise local vector species, environmental variables and breeding habitats. This is crucial for implementing control measures and preparing initiatives to prevent vector-borne infections. Key components of control measures include case diagnosis and treatment monitoring, prophylaxis, education of both the public and healthcare personnel, indoor application of insecticides for vector population control, the use of bed nets to reduce outdoor exposure, improvement of temporary housing conditions, and facilitating access to clean drinking water and healthcare services.

Considering the chaotic situation in the region, it is essential to begin implementing these measures as soon as possible. Following the earthquake in Haiti, the rapid diagnosis and treatment using fast tests played a vital role in controlling a potential malaria outbreak due to factors such as lack of coordination, logistical challenges, a mobile population, a constantly changing healthcare system and the absence of experienced microscopists.¹⁰ The use of pesticides has also been effective in preventing vector-borne infections from causing outbreaks after earthquakes.⁴

After an earthquake, the risk of transmission and spread of certain ectoparasitic infections may increase because of the environmental changes caused by the earthquake and the alteration of people's living conditions.² In areas with insufficient water, inadequate personal hygiene, and among those placed in temporary shelters or communal housing, scabies and pediculosis may pose significant problems.²

Scabies is a contagious skin infestation caused by the *Sarcoptes scabiei*. Infrequent bathing, not changing clothes regularly, sharing beds and incomplete treatment of entire families for scabies can increase the transmission risk. In the 2005 earthquake-affected Kaghan Valley of Pakistan, scabies was detected as the second most common infection among 22 122 patients, accounting for 17%.²⁸

Pediculosis is an infestation caused by louse. The notable lice are the head louse (*Pediculus humanus capitis*; head louse nit shown in Fig. 3), the body louse (*Pediculus humanus*)

Fig. 3. Nit of a head louse.

humanus) and the crab louse (*Phthirus pubis*). In overcrowded and poor hygiene conditions, there is an increased risk of lice transmission from person to person due to close physical contact. The prevention and control of the spread of pediculosis is aided by prompt diagnosis and effective treatment of infestations.²⁹

The Ministry of Health has established a network of outbreak investigation laboratories by setting up field laboratories in earthquake-affected areas with both active and nonfunctional existing laboratories 1 week after the earthquake. Through this network, in which the authors participated, active and passive surveillance has been carried out, and potential outbreak agents have been closely monitored. Despite sporadic cases of malaria and CL observed in these surveillance activities, there has been no imminent threat of an outbreak thus far. Although an outbreak is not expected in the near future due to the earthquake occurring in the winter months, the number of cases may increase in October– November as the vector–human and environmental conditions in the region have become more favourable for the development of vector-borne infections due to the earthquake.

Conclusion

After natural disasters, the placement of disaster survivors should be well-planned. The location of the shelter camps to

be established, their proximity to water sources, and the distance of mobile toilets and bathrooms to these water sources should be well planned. Additionally, it is crucial to ensure access to clean and safe water, establish proper sanitation conditions, deliver healthcare services, and collaborate with relevant institutions to ensure the collection and safe disposal of waste, garbage, toilets, and animal carcasses for environmental health protection. Measures such as rehabilitating vector-breeding sites, using appropriate pesticides, implementing interventions to reduce human–vector contact, and providing prophylaxis can reduce the risk of vector-borne infections.

In order to prevent the emergence of infectious diseases after an earthquake, it is crucial to assess potential outbreak risks and develop a scientific and reasonable monitoring and control plan that reduces economic and social damage.

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Mould contamination of dwellings after flooding

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ABSTRACT

Australia's sub-tropical coastline has been subjected to catastrophic flooding, congruent with a global trend of extreme weather events exacerbated by climate change. This study examined buildings post-flooding, to determine the impact of fungal contamination and evaluate remediation strategy success. Fungal species prevalence in association with wet building materials are outlined. Remediation methods found to be effective are highlighted. These findings support the necessity of establishing internationally recognised guidelines pertaining to mould contamination and remediation. This is particularly pertinent within the context of climate change. This research contributes to the scientific understanding of mycobiota in flood affected buildings, their health and safety implications and design of effective mitigation strategies.

Keywords: air cleaning, assurance program, climate change, climate disaster, education, exposure and health effects, extreme weather, flooding, mitigation (source control), mould, mycotoxin, policy, regulations, risk assessment, standards.

Background

Climate change has notably increased extreme weather events across the globe. Recently, Australia's sub-tropical coastline which is uniquely positioned on the country's Eastern-Shelf, has been subject to catastrophic atmospheric conditions, culminating in an extended 3-year La Niña phenomenon. This has led to several '1 in 100 years' floods due to anomalies referred to as 'rain-bombs' reflecting a global trend in unprecedented extreme weather events. Juxtaposed with each summer's prevailing bushfires, shock rainfall and mass flooding incidents into commercial and domestic buildings have devastated vast swaths of the country.¹ Many affected areas are highly remote and comprise suburban housing, roads, crops and central waterways engulfed in blackwater. This has rendered access inordinately difficult, with many buildings either partially or completely submerged for hours to weeks on end (Fig. 1). The high number of dwellings affected following from these extreme weather events often results in a delayed time-frame for the assessment and remediation of buildings.

There are many ways that water can ingress into a dwelling following a disaster; however, two pathways predominate. The first being rain or hail events affecting buildings from above, by roof egress, and from the sides by wall egress, or gutter overflow. Secondly, surface water from rivers or oversaturated ground – that is no longer able to absorb any additional rainfall – often overflows into buildings from below. A lesser known yet prolific secondary ingress pathway is caused by prolonged extremely high relative humidity. This typically occurs due to a lack of ventilation or climate control inside a building due to power outages, resulting in condensation build up. Additionally, in many buildings flooded from below and left closed, water migrated up through the air and walls to proliferate in the upper floors.

It is well known that blackwater from flooding events carries a multitude of waterborne microorganisms including bacteria and viruses.^{2,3} It is lesser known that once water subsides and buildings begin to dry, another large group of microorganisms emerge. Fungi and mould rapidly colonise the surfaces and penetrate deep into buildings; subsequent human exposure to these contaminated environments has a host of well documented associated health risks.^{1,4–7} Although bacteria and viruses require moisture to survive, fungal propagation remains viable long past the point that moisture has subsided.⁸

High humidity or direct water inundation leads to an elevated water activity (Aw) within building materials. Levels above 75% water activity in any given building material will enable mould proliferation. This surface mould will eventually become airborne,

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Fig. 1. Residential building wall mould growth above flood marked lines.

potentially cross contaminating all accessible areas of a built environment. Simultaneously, outdoor air concentrations of fungal spores rise, increasing the opportunity for mould to cross-colonise indoors. This is due to general post flood conditions, including high relative humidity, in combination with an extra nutritional load comprising of debris, vegetation, dead animals, wet surface soils and other displaced materials.

For the purpose of this study, only fungal contamination of buildings was considered. There is an increased risk of fungal infections after flooding, causing potential long term health effects in humans and animals such as respiratory and systemic infections. Additionally, poisoning from mycotoxins poses a notable risk, especially in already stressed or immunocompromised individuals, who may be suffering from displacement and psychological distress.⁹

Mycotoxicosis is a lesser-known term for poisoning associated with exposures to mycotoxins.¹⁰ Mycotoxins are poisonous substances produced by fungi or mould as a natural defence mechanism against other fungi in the competition for nutrition. They can be toxic for humans when they are eaten, absorbed into the skin or inhaled.¹¹ Even a small amount of mycotoxin can be damaging to human or animal health, and in extreme cases causing death. They have been linked with the development of neurodivergent disease.¹² Mycotoxins have the potential for both acute and chronic health effects, through entering the blood stream and lymphatic system. Nausea, gastrointestinal disturbances and vomiting symptoms have been reported in relation to mycotoxin exposure.^{11,13,14} The fungal genera *Aspergillus* and *Penicillium* are often found in water damaged buildings wherein humans are primarily exposed to them. They have the ability to produce ochratoxin A (OTA), which is a nephrotoxin, immunotoxin and carcinogenic mycotoxin. This chemical is produced by moulds in both the *Aspergillus* and *Penicillium* genera.¹⁵

Citrinin (dihydrocitrinone, DHC) is a mycotoxin produced by the same group of fungi, *Aspergillus, Penicillium* and *Monascus*. Citrinin exposure can lead to nephropathy, due to its ability to increase permeability of mitochondrial membranes in the kidneys.¹⁶ Studies have linked citrinin exposure to a suppression of the immune response, and gastrointestinal system.¹⁷

More common health problems associated with exposure to building moisture and subsequent biological agents, affect the allergenic, respiratory, and immune system responses in humans. Increased incidences of respiratory symptoms such as asthma¹⁸ and allergies including hay fever, allergic rhinitis, sinusitis and eczema have been well documented.^{13,14,19,20} In addition, negative effects on, and suppression of, the immune systems health, and resilience regularly occur.²¹ Illness may result from a combination of factors present in waterdamaged indoor environments, including, but not limited to, mould spores and hyphal fragments, mycotoxins, bacteria, bacterial endotoxins and cell-wall components.⁴ The mechanisms of illness include inflammation, oxidative stress, toxicity, infection, allergy and irritant effects of exposure. These effects have been linked to a heightened risk to the respiratory health of children.^{22,23}

According to the Institute of Medicine of the National Academies health effects can arise from exposure to mould by-products such as volatile and semi-volatile organic compounds, mycotoxins and other components.²⁴ Furthermore, substances produced by bacteria that grow in damp environments have been implicated in a range of biologic and health effects. These include inflammation of mucous membranes, respiratory effects, immunotoxicity, neurotoxicity, sensory irritation, skin toxicity and cancer-causing effects. There is evidence that some species of mould can lead to illnesses, such as hypersensitivity pneumonitis, allergic sinusitis, and allergic bronchopulmonary aspergillosis in susceptible individuals.²⁵

Ritchie Shoemaker was the first to associate exposure to mould and water damaged buildings with Chronic Inflammatory Response Syndrome (CIRS). He demonstrated that the immune systems of individuals with certain genes, could not react appropriately to biotoxins as they would in healthy individuals.²⁶ A recent study found negative effects on contextual memory, increased pain sensitivity and anxiety-like behaviour in mice when exposed to moulds found in water damaged buildings.²⁷

A recent parliament inquiry into biotoxin exposure by the Australian government, has shown a clear link between mould exposure and various symptoms, including CIRS.²⁸ Other studies on the long-term effects of mould and myco-toxin exposure suggest a link between mycotoxins and neurodegenerative diseases such as Alzheimer's Disease, Parkinson's Disease and Multiple Sclerosis.

As established, to avoid experiencing the negative health effects associated with mould exposure – as outlined in the

literature – exposure to mould should be avoided. Therefore, after flooding events, when risk of mould exposure is heightened, appropriate assessments should be conducted to ensure the safety of individuals and buildings.

The authors of this paper were commissioned by insurers to 'roll out' an Insurance Assurance program and independently validate mould contamination and remediation efforts after flooding and rain bombs. In Declared Catastrophic ('CAT') events, such as 'CAT 202', which occurred in Townsville, Queensland, in 2019, and 'CAT 781', which occurred in the Murray-Darling River Basin, South Australia, several hundred thousand dwellings were simultaneously affected. Pre-inspecting every single dwelling prior to remediation was not possible, because of the sheer volume of buildings and a lack of infrastructure and resources. Therefore, a generic remediation and scope of works for each CAT event was established and issued to builders and restorers. This was based on, and factored in parameters, such as the nature of water inundation, its duration, and the relevant climatic zone.

Each dwelling is an individual case, affected by building materials, age, geography and response speed of restorers. As such, it was of outmost importance to establish whether the proposed generic scope of works was sufficient for the removal and mitigation of mould contamination at each building.

Post Remediation Verification (PRV) testing was conducted after a 'strip out' and subsequent remediation of dwellings, to ensure the efficacy of the nominated process. If the process was found to be ineffective or incomplete remediation was repeated based on the PRV results.

A final Clearance Testing (CLT) after reinstatement of the dwelling was conducted as legal protection for builders and remediators in addition to providing 'peace of mind' for owners and occupiers. The data from both the PRV and CLT was then used in the process of re-insuring dwellings that had been disaster affected.

Methods

A 3-part risk assessment for mould exposure was produced based on existing literature and practice, this included mould, moisture and relative humidity testing. Methods for cultural and non-cultural fungal air and surface sampling were used, to determine the number and speciation of mould present. Simultaneously a visual and moisture assessment was conducted and Temperature (°C), CO₂ levels (ppm) and relative humidity (% RH) were measured.

Results

Results from the fungal analysis showed that *Penicillium chry-sogenum* and *Cladosporium cladosporioides* are the most common fungal species found in the air of dwellings after floods, followed by *Aspergillus versicolor* to a lesser degree.

The results demonstrated that *Chaetomium* spp., *Trichoderma* spp., *Acremonium* spp. and *Ulocladium* spp. are highly common on damp building materials after flooding.

Analyses revealed that associated mycobiota exist on different building materials, associations were found between:

- (i) Acremonium spp., Penicillium chrysogenum, Stachybotrys spp. and Ulocladium spp. with plasterboard and wallpaper.
- (ii) Aureobasidium pullulans, Cladosporium herbarum, Trichoderma spp. and yeasts with several types of wood (yellow-green tongue) and plywood.
- (iii) Aspergillus fumigatus, A. melleus, A. niger, A. ochraceus, Chaetomium spp., Mucor racemosus and M. spinosus with concrete and other floor-related materials.

These results (Table 1) can be used to develop new and resistant building materials and relevant allergen extracts and to help focus research on relevant mycotoxins, microbial volatile organic compounds, and microparticles released into the indoor environment.

Congruent with the recommendations of both The Australian Mould Guideline²³ and The Mould Workers Handbook,²⁹ the consistent success of remediators is attributed to the physical agitation of surfaces by high-efficiency particulate-absorbing (HEPA) filter vacuuming with horsehair brushes and wet wiping with a microfibre cloth. Use of either naturally brewed vinegar, alcohol or bio-enzymes had demonstratable positive outcomes as opposed to bleach, chlorine, oils, biocides and various branded 'organic' products that are demonstrated to be ineffective. Additional factors contributing to success include air scrubbing with a minimum of seven air changes throughout the remediation process followed by a gaseous treatment with hydrogen peroxide. Methods such as encapsulation with glues or paints, dry-ice blasting, fogging or spraying with various substances consistently failed PRV testing.

Conclusions

It can be concluded that there exists an associated mycobiota for different building materials much like there exists an associated mycobiota on different food types. The results presented can provide assistance to the building industry in the development, production and usage of materials that are less susceptible to fungal growth. Utilising glass fibre instead of wallpaper for example or manufacturing materials that consist of a non-toxic, fungus- or water-resistant composition such as coating plasterboards against Stachybotrys spp., would aid in limiting fungal growth within building after flooding events or prolonged relative humidity in turn decreasing the likelihood of mould exposure-related illnesses from occurring. With the notion of extreme changes in the world's climate, standards and guidelines are necessary for the development and assurance of future building materials, infrastructure and remediation to be able to combat fungal growth, henceforth, there is a pressing need for an internationally accepted and recognised guidelines. Currently, the World Health Organization has guidelines regarding indoor air quality²¹; however, these are not easily applicable for Australian ecologies, therefore, standards for the remediation and assessment of mould pertaining specifically to Australia are needed.^{29,30}

 Table I.
 Most common fungi found on contaminated building surfaces after flooding in Australia.

Acremonium sp.
Alternaria alternata
Ascomycetes
Aspergillus fumigatus
Aspergillus niger
Aspergillus flavus
Aspergillus restrictus
Aureobasidium sp.
Basidiomycetes
Botrytis sp.
Bipolaris sp.
Chaetomium sp.
Cladosporium cladosporioides
Curvularia sp.
Dreschlera sp.
Epicoccum sp.
Fusarium oxysporum
Fusarium solani
Geotrichum sp.
Monilia sp.
Monoascus spp.
Mucor spp.
Nigrospora sp.
Paecilomyces sp.
Penicillium corylophilum
Penicillium chrysogenum
Penicillium brevicompactum
Rhizopus sp.
Stachybotrys sp.
Stemphylium sp.
Sporobolomyces roseus
Trichoderma sp.
Ulocladium sp.
Yeast

The data obtained from this assurance program will form the base for research at the newly found RAC¹ Training Centre for Advanced Building Systems Against Airborne Infection Transmission at Queensland University of Technology (QUT) in Brisbane, Australia officially known as the THRIVE project.

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The 2020 İzmir earthquake and its effect on COVID-19 cases

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ABSTRACT

On 30 October 2020, an earthquake measuring 6.9 moment magnitude occurred between Kusadasi and Samos, Türkiye, with a significant impact on buildings in the Bornova–Bayraklı district of İzmir. Immediately afterwards, a comprehensive study was commenced to investigate the relationship between the earthquake that occurred during the SARS-CoV-2 (COVID-19) pandemic and case numbers at the Ege University, Faculty of Medicine's Hospital in Bornova, İzmir. This cross-sectional study was carried out based on the records of those admitted to the university hospital with suspicion of COVID-19 in the pre-earthquake and post-earthquake periods of the pandemic. The microbiology laboratory of the hospital used reverse transcription-polymerase chain reaction (RT-PCR) results as a dependent variable and compared with the time, age and gender as the independent variables, classified according to the timing of the earthquake. RT-PCR test results were positive in 11.60% of the whole study group; however, tests were 6.69% positive before the earthquake and increased to 23.42% afterwards (P < 0.001), which equated to an increase of 4.25 times (95% CI 4.04-4.47) when comparing pre- to post-earthquake RT-PCR positivity (P < 0.001). The positive COVID-19 RT-PCR detection rate among those aged 50 and over was greater by a factor of 1.15 (95% CI 1.06–1.23) compared to a younger age group (P < 0.001). There was no difference for the gender variable used in suspected case or contact tracing applications of COVID-19 PCR. However, when stratified by age and gender, in the female group, there was a 1.24-fold (95% CI 1.11-1.38) increase in the 50+ age group (26.2%) compared to the younger age group (22.2%) after the earthquake (P < 0.001). In the male group, the rate of laboratory diagnosis of COVID-19 before the earthquake was in the under-50 age group (7.6%) as compared to the >50 age group (5.2%; P < 0.001).

Keywords: age, COVID-19, earthquake, epidemic curve, epidemiology, gender, İzmir, SARS-CoV-2, Türkiye.

Introduction

In Türkiye, most of the 60% of the population live in built-up areas where significant number of structures are vulnerable to earthquakes.¹ On 30 October 2020, an earthquake of 6.9 moment magnitude (Mw) occurred in the Aegean Sea, epicentre at Seferihisar, Türkiye. The earthquake caused extensive damage in İzmir; Türkiye's third largest city located \sim 70 km from the epicentre with a population of over 4.5 million. Damage was concentrated in Bornova and Bayraklı districts of İzmir, where the ground was soft and alluvial. The earthquake killed 117 people and injured more than 1000 others.²

The earthquake, which occurred during the SARS-CoV-2 2019 (COVID-19) pandemic, displaced more than 15 000 people. Most of these people were inhabitants of buildings that collapsed. Others forced to leave their homes after the earthquake also moved to temporary shelters. Temporary shelters were set up at various locations in İzmir. These shelters consisted of containers, tents, and other temporary structures.³ The number of people involved in rescue operations reached significant numbers and this led to population mobilisation subsequently increasing the risk of human-to-human contact. Simultaneously, the COVID-19 pandemic had a significant human and economic impact worldwide, including İzmir. The confluence of the earthquake and pandemic in İzmir may have increased vulnerability to infection due to the inability to maintain physical distancing and to comply with safety regulations, such as a lack of protective equipment.³

The Governor of İzmir, Mr Köşger, in a report published by the İzmir Medical Chamber, stated that all COVID-19 positive cases and their contacts ran out to the streets when the earthquake struck, encountering others. In the report, it was stated that COVID-19 positive cases and virus-related deaths thus increased 3-fold after the earthquake.⁴

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Microbiology Australia

The 2020 İzmir Earthquake was a major natural disaster during the COVID-19 pandemic. The earthquake caused significant damage and displacement and likely contributed to the spread of COVID-19. Thus, a need rose to investigate the relationship between the earthquake and the increase in COVID-19 cases and deaths in İzmir. This study, conducted at Ege University, Faculty of Medicine's Hospital in İzmir, aimed to examine whether there was a relationship between the earthquake during the pandemic and the rise in COVID-19 cases in the Ege University, Faculty of Medicine's Hospital in İzmir.

Methods

The Hospital started registering and testing all patients admitted with suspected COVID-19 as of 23 March 2020. Nasopharyngeal swabs of the applicants were taken in safe cabinets in outpatient clinics or wards where they were admitted and sent to the virology laboratory in viral nucleic acid buffer (Bio-Speedy vNAT Viral Nucleic Acid Buffer, Bioeksen, İstanbul, Türkiye). COVID-19 reverse transcription– polymerase chain reaction (RT-PCR) tests detected the causat ive agent in samples that were then sent to Ege University Medical Microbiology Laboratory. The tests used were approved by the Turkish Ministry of Health (Bio-Speedy SARS-CoV-2, Bioeksen; Diagnovital SARS-CoV-2 RT-PCR, RTA; and Coronex RT-qPCR, Gensutek, Türkiye). All amplification procedures and analyses were performed with Rotorgene (Qiagene, Luxembourg).

In this cross-sectional study, a case–time graph was created using the data from the positive test results reported in the Hospital's Microbiology Laboratory (Fig. 1, start time of the laboratory tests, 30 October 2020, *v*. the end of the peak of the pandemic, 21 December 2020). All data containing RT-PCR results up to the last date shown on the graph were included in this study (except for dates between 31 October and 1 November, as explained below). The Ministry of Health recommends testing for RT-PCR positivity for COVID-19 from the third day after contact.^{5,6} Therefore, considering the date of the earthquake, data from 31 October to 1 November 2020 were excluded from the study.

The data between 23 March 2020, when the testing started in the laboratory, and 30 October 2020, when the

earthquake occurred, were classified as 'pre-earthquake'. The period from the third day of the earthquake until 21 December 2020, when the peak in the graph ended, was considered 'post-earthquake'. The age parameter was used as a measurement variable and categorised (as <50 and ≥ 50). The gender parameter was used as the categorical variable.

Statistical analyses were performed using SPSS statistical software for Windows (ver. 25.0, SPSS, Chicago, IL, USA). The data were visualised using Excel 2016 (ver. 16.0.4266.1001, Microsoft Online) and S/R programming. The results are presented as numbers (n), frequencies (%), means and standard deviations. The Shapiro-Wilk test was used to test the normality of the age data. The difference between two independent samples was analysed using an independent twosample t-test for samples drawn from normally distributed populations. The Chi-Square test was used to examine whether there was a statistically significant relationship (difference) between the two categorical variables. Logistic regression was used for odds ratio (OR) calculation of variables that were found to be associated with positive RT-PCR results – a *P*-value ≤ 0.05 was considered significant for statistical tests.

Ethical issues

The study was approved by the institutional review board of Ege University Medical School (22-8.1T/55 on 25 August 2022).

Results

Between 23 March and 21 December 2020, 62 550 people were admitted to the Hospital with suspected COVID-19. From the data registered, 44 072 (70.7%) were admitted during the pre-earthquake period, and 18 263 (29.3%) were admitted during the post-earthquake period. After the earthquake, the number of cases reached its highest level (n = 188) in mid-November 2020 and completed its cycle (7 weeks) towards the end of December (n = 215, 0.3%) of the laboratory results from 2 days immediately after the earthquake were excluded from the study as described earlier).

The mean age of the individuals was 41.18 ± 20.92 , and 50.6% were male. The mean age of the applicants was

Fig. I. Daily new case-time plot (18 March 2020–28 February 2021).⁶

41.76 ± 21.64 years before the earthquake and 39.72 ± 18.96 years after the earthquake (P < 0.001). There was no statistically significant difference between the genders (P = 0.469). PCR positivity was 11.60% for all laboratory results. Although this rate was 6.69% before the earthquake, it was 23.42% after it (P < 0.001) (Table 1).

As seen in Table 2, the positivity of RT-PCR tests increased by 4.25 (95% CI 4.04–4.49) in those COVID-19 suspected cases after the earthquake compared to those who applied before the earthquake (P < 0.001). While there was no significant relationship between RT-PCR positive detection and gender, the significant association with age lost its significance in gender- and age-adjusted analyses (P = 0.151).

As seen in Table 3, in the pre-earthquake period, the rate of RT-PCR positive detection, which was 7.2% in the group under 50 years of age, was 5.8% in the group aged 50 years and older. In the older age group, RT-PCR positivity was 20.9% (95% CI 14.2–17.1) lower than that in the younger age group (P < 0.001). Post-earthquake, the RT-PCR positivity rate increased in both age groups and was 25.2% in the group aged \geq 50 years and 22.7% in the group aged < 50 years. Thus, the RT-PCR positive detection rate in the group aged 50 years and over was 1.15 times (95% CI 1.06–1.23) greater than the detection rate in the lower age group (P < 0.001).

In the female group, although there was no significant difference between the older age group (6.4%) and the younger group (6.8%) before the earthquake (P = 0.239), after the earthquake there was a 1.24-fold (95% CI 1.11–1.38) increase in the 50 years and older age group (26.2%) compared to the younger group (22.2%; P < 0.001).

In the male group, although there was a difference in the group under 50 years of age before the earthquake, the PCR positivity rate increased after the earthquake, and the difference between age groups disappeared. In the male group, the rate of COVID-19 diagnosis in the laboratory before the earthquake was 32.5% (95% CI 24.3–39.8) less in the over 50 years age group (5.2%) than in the under 50 years age group (7.6%; P < 0.001). After the earthquake, the rate was 24.3% in the group aged \geq 50 years and 23.2% in the group aged < 50 years, and there was no significant difference (P = 0.255) between the age groups.

Discussion

This study examined the temporal relationship between the earthquake of 30 October 2020, and the increase in COVID-19 cases in the hospital. No association was found between gender and the rise in COVID-19 cases before and after the earthquake. However, when evaluated according to age, COVID-19 cases before the earthquake were higher in the group under the 50 years of age.

It was observed that COVID-19 cases detected in İzmir increased more than four times in the peak period after the earthquake compared to the pre-earthquake period. Studies conducted in the past have revealed a significant increase in respiratory tract infections (RTIs) following earthquakes.^{7,8} RTIs resulting from earthquakes can manifest as acute and chronic consequences of natural disasters. During the immediate aftermath of an earthquake, RTIs may arise as a result

 Table 1.
 Comparison of the characteristics of individuals who applied to the laboratory due to suspicion of COVID-19 before and after the earthquake.

		Pre-earthquake (n = 44 072; 70.70%)		Post-earthquake (n = 18 263; 29.30%)			Total (n = 62 335; 100%)	
		n	%	n	%	Р	n	%
RT-PCR	Negative	41 123	93.31	13 986	76.58	<0.001	55 109	88.40
	Positive	2949	6.69	4277	23.42		7226	11.60
Gender	Female	21 735	49.32	9065	49.64	0.469	30 800	49.41
	Male	22 337	50.68	9198	50.36		31 535	50.59
Age	<50	28 60 1	64.90	13 142	71.96	<0.001	41 743	66.97
	≥50	15 471	35.10	5121	28.04		20 592	33.03
		Mean	s.d.	Mean	s.d.	Р	Mean	s.d.
Age		41.76	21.64	39.72	18.96	<0.001	41.18	20.92

Table 2. Evaluation of factors associated with RT-PCR positive detection by logistic regression.

					95% CI for OR		Р	Adjusted	95% CI for Adj. OR		Р
		n	%	OR	Lower	Upper		OR	Lower	Upper	
Earthquake	Post-eathquake	4277	23.42	4.26	4.05	4.49	<0.001	4.25	4.04	4.47	<0.001
	Pre-eathquake	2949	6.69	I				I			
Gender	Male	3677	11.62	1.01	0.96	1.06	0.758				
	Female	3566	11.54	I							
Age	≥50	2189	10.58	0.86	0.82	0.91	<0.001	0.96	0.91	1.02	0.151
	<50	5054	11.58	I				L			

						95% CI for EXP(B)		Р
			n	%	OR	Lower	Upper	
Total	Pre-earthquake	≥50	893	5.8	0.79	0.73	0.86	<0.001
		<50	2056	7.2				
	Post-earthquake	≥50	1290	25.2	1.15	1.06	1.23	<0.001
		<50	2987	22.7				
Female	Pre-earthquake	≥50	455	6.4	0.93	0.83	1.05	0.239
		<50	996	6.8				
	Post-earthquake	≥50	618	26.2	1.24	1.11	1.38	<0.001
		<50	1491	22.2				
Male	Pre-earthquake	≥50	438	5.2	0.67	0.60	0.76	<0.001
		<50	1060	7.6				
	Post-earthquake	≥50	672	24.3	1.06	0.96	1.18	0.255
		<50	1496	23.2				

Table 3. PCR positive results seen in age groups according to earthquake status and gender differences.

of inhaling tiny particles, smoke or other harmful fumes, as well as from ingesting water-based pathogens, chest injuries, living nearby in overpopulated makeshift camps or shelters over the extended course, and certain psychological impacts that can lead to weakened immunity.⁸ Overcrowded environments resulting from unplanned and crowded shelters after earthquake disasters, inadequate access to clean drinking or utility water, and malnutrition caused by limited transport leading to food shortages in the region can encourage the transmission of infectious agents among people. Such conditions increase the chance of common viral respiratory diseases in people living in proximity.⁸

After the earthquake of October 2020, due to the cold weather in November and December, people whose houses were destroyed or damaged were urgently placed in shelters. People aged over 50 who were not working at that time due to the pandemic had to come out of home isolation and were kept together under unfavourable conditions in crowded environments. This earthquake, which coincided with the 10th month of the COVID-19 pandemic, caused the COVID-19 cases to increase more than 4-fold. The Turkish Medical Association's first monthly report on the İzmir earthquake stated that there had been a significant increase in COVID-19 cases in the country.⁹

In studies conducted before the pandemic, increases in the incidence of acute respiratory infections were also reported after the 2005 Pakistan earthquake; as for the 2001 El Salvador earthquake, 30% of 594 affected people were reported to have RTIs. In Iran, 14% of 75 586 people who lost their homes due to the Bam earthquake 2003 were found to have RTIs.⁸

Since the beginning of the pandemic, young adult males were most frequently infected with COVID-19 in our region, while, after the earthquake, women aged over 50 were most often infected. In addition to coming out of home isolation prematurely, men and women aged over 50 also took part in the field to help their families and environment, regardless of gender. After the İzmir earthquake, many people from both domestic and foreign regions came to help, and the profile definition of people who were positive before the earthquake changed with the earthquake.⁴ Balbay *et al.* (2011) analysed tuberculosis patients' demographic and socioeconomic characteristics in three periods before, during and after the Düzce earthquake.¹⁰ The mean age of the patients was found to be significantly higher in the pre-earthquake period (50.50 ± 18.05) than in the earthquake period (36.26 ± 13.77) and post-earthquake period (41.34 ± 17.22). No significant difference was found between the groups in terms of gender.¹⁰

Conclusion

The highest number of cases in Türkiye since the beginning of the pandemic was recorded in early December 2020, which was \sim 1 month after the earthquake. The effect of the earthquake on these cases was thus investigated and results revealed a 4-fold increase after the earthquake. In addition, people aged over 50 who were in isolation before the earthquake had to break isolation prematurely and be exposed to earthquake-affected zones due to the loss of their homes as well as participating in post-earthquake relief activities. For this reason, the slight predominance of COVID-19 positivity among young men before the earthquake shifted to a postearthquake predominance of positivity in people aged over 50, with a slightly greater positivity rate in older women.

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Data availability. The data underpinning this study cannot be shared with the public on ethical or privacy grounds.

Conflicts of interest. The authors declare that they have no conflicts of interest.

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Biographies

Seyfi Durmaz is an Associate Professor of Public Health and worked in the Occupational Health and Safety Unit at Ege University Hospital during the pandemic period, actively tracking COVID-19 cases and high-risk contacts among healthcare workers. His research interests include health policy, tobacco control, infectious disease surveillance, occupational health, and medical education.

Dr Gönül Aslan is a Professor of Microbiology and the Head of the Department at Mersin University Faculty of Medicine. Her areas of interest include tuberculosis and immunology, and she has also served as the regional coordinator for COVID-19 diagnosis.

Raika Durusoy is a Professor of Public Health at Ege University, and she is the surveillance officer of the university hospital and responsible for the hospital's occupational health and safety unit, which actively continues to follow up on COVID-19 cases and contacts among the hospital staff since the beginning of the pandemic. Her research interests are communicable disease surveillance, tobacco control and environmental health.

Candan Çiçek is a Professor of Microbiology and an infectious diseases and clinical microbiology specialist with 30 years of experience in Ege University Medical School at the Department of Clinical Microbiology. Her academic and research interests include diagnostic microbiology, virology and healthcare-related infections. She is currently the President of the Turkish Society for Microbiology.

Future issues of Microbiology Australia

March 2024 – Challenges of the ongoing COVID-19 pandemic Guest Editors: Greg Walker and William Rawlinson

May 2024 – OneHealth and AMR Guest Editors: Darren Trott, Andrea McWhorter and Cheryl Power

ASM TriState meeting, 8-10 September 2023

Janessa Pickering and Justin Morgan (WA, meeting chairs)

For more than 30 years, TriState scientific meetings have been held to bring ASM to the 'Top End' of Australia, providing local and travelling colleagues opportunities to network and discuss microbiology matters that are particularly relevant to northern, central and remote Australia. The 2023 instalment was held at the Novotel CBD in Darwin, Northern Territory, in early September.

Organisers from the Western Australian ASM Branch welcomed 47 delegates from across Australia under the theme 'Technology in the Top End to Advance Health'. Research presentations of the highest calibre were delivered in an informal and relaxed setting and covered an array of topics spanning point-of-care technology, sexual health, outbreaks, tools for AMR, vaccination, microbiology in the community, tropical infections and virology. The atmosphere and smaller group size greatly facilitated networking opportunities, especially over welcome drinks held in the Novotel CBD foyer and at the conference dinner held at the PepperBerry restaurant.

In a timely address, Keynote speaker Prof. James Ward spoke of the effectiveness of health programs controlled by Aboriginal peoples in sexual health but also the extremely successful activities to prevent COVID-19 transmission in remote communities during the early pandemic. Prof. Ward reminded us that there is still health inequity in our Indigenous populations and solutions needed to integrated, tailored to the setting and have major coordination. He also provided strong evidence for why a Voice in parliament is important for Indigenous people. Assoc. Prof. Kalinda Griffiths complemented this messaging with an overview of data sovereignty, de-colonising practice, big data and epidemiological studies - all big concepts relevant to Aboriginal and Torres Strait Islander participants in research and in health systems. Kalinda highlighted the structures and frameworks in development which emphasised signs of transformative changes to come.

Delegates were delighted to hear from Nevio Sarmento, and the trials and tribulations of developing modern laboratory capacity in Timor-Leste (pictured with colleagues in Fig. 1). Nevio highlighted several ways he and his team applied innovative thinking in difficult circumstances to achieve laboratory diagnostics. We were particularly impressed with stories of team member contributions to blood agar – actions that go above and beyond! It also highlighted what we often take for granted in microbiology in Australia routine and regular

Fig. 1. From left to right: Ms Tessa Oakley, Mr Nevio Sarmento, Ms Carolina Maia and Ms Eurosia Cham working in the fully functional diagnostic laboratory in Timor-Leste.

supply of laboratory reagents. Additional researchers from the Menzies School of Health Research presented, including Prof. Heidi Smith Vaughan and Porsche Cahill. Together they showcased the pop up 'HealthLAB' laboratory and associated health promotion activities in remote Northern Territory communities, encompassing 10 years of co-design, education and community involvement.

We were fortunate to co-host the meeting with partners, the National Reference Laboratory (NRL). Wayne Dimech and Joe Vincini represented the NRL and ran a state-of-the art Quality Assurance Workshop to round up a productive and cohesive meeting. The next TriState is earmarked for 2025–26, and we pass the organising baton back to Northern Territory and South Australia branch committees. Thank you to all supporters and sponsors of this meeting. To read more about the meeting, find the full program and profile of speakers online: https://www.asmwabranch.com/events.

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MICrobiology

New committee to guide ASM's diversity and inclusion strategy

Yogitha Srikhanta (EDI Committee Chair)

The ASM would like to introduce the newly appointed members of ASM's inaugural Equity, Diversity, and Inclusion (EDI) Committee. The ASM is committed to supporting an inclusive, diverse and thriving microbiology sector, one in which all participants are valued and respected.

The EDI committee comprises seven members whose role will be to oversee ASM equity, diversity and inclusion strategies and will advise on what the ASM can do to create programs, events and a workplace that are fair, accessible, flexible, inclusive and in which unlawful discrimination, bullying, harassment or victimisation are not tolerated. The committee will ensure that our policies and practices enable inclusion toward positive and sustainable change in Australian microbiology and can be contacted directly at edicommittee@theasm.org.au.

Our committee members will strive to represent our diverse membership including people of different career stages, diverse genders, sexes and sexualities, indigeneity, those who are neurodiverse, those who have a disability, people of colour, those with different cultural, linguistic and religious backgrounds, and our rural ASM members.

Nuala Ellaby (she/her) is a Master of Medical Research candidate at the Institute for Glycomics, Griffith University. As the Queensland State Branch member of the EDI committee and a proud LGBTQIA + woman, she hopes to promote a diverse and inclusive environment within ASM at the state and national level.

Dr Zahra Islam (she/her) is an early-career postdoctoral researcher within the ARC Research Hub for Smart Fertilisers at The University of Melbourne and is the Victorian State Branch representative. She aims to bring her experience as a 2nd generation Australian, women of colour to help to foster an inclusive society of microbiologists as well as champion underrepresented communities.

August Mikucki (they/she) is a final year PhD candidate at the University of Western Australia and a research assistant at the Telethon Kids Institute and the Western Australian State Branch representative. They aim to use their own experience as a queer trans woman to help make microbiology in Australia a safe and rewarding place for people of all backgrounds and experiences.

Dr Gaofeng Ni (he/him) is a postdoctoral research fellow at the Greening Lab of the Biomedical Discovery Institute, Monash University. He aims to foster an inclusive society of microbiologists across various backgrounds and career stages, as well as to advocate for communities whose voices are

not heard, drawing strength from his experience as a man of colour, and a first-generation immigrant in Australia.

Dr Anahit (Ani) Penesyan (she/her) is a Research Fellow at the ARC Centre of Excellence in Synthetic Biology, Macquarie University and the New South Wales and Australian Capital Territory Branch representative. Ani firmly believes that promoting equity, diversity and inclusion in science is

essential for creating a more vibrant and equitable scientific community that can tackle complex challenges with a broader range of perspectives and talents.

Dr Yogitha (Yogi) Srikhanta (she/her) is a mid-career postdoctoral researcher based at the Biomedical Discovery Institute, Department of Microbiology, Monash University. As chair of the EDI committee, she aims to bring her experience as a woman of colour to build a more diverse microbiology community in Australia and ensure all voices are heard.

Meghan Zadow (she/her) is a postgraduate student in the Malaria and Toxoplasma Biology group at the University of Adelaide and is the South Australia and Northern Territory Branch representative. Having come into STEM through a 'non-traditional' pathway, she is passionate about equity and

accessibility in academia and the creation of environments where everyone has the tools and support they need to thrive.

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Veterinary Microbiology special interest group

Ala Mohan

The Veterinary Microbiology special interest group (SIG) recently organised a seminar series focusing on zoonotic pathogens.

Prof. Suresh V. Kuchupudi from the Penn State University gave a lecture on SARS-CoV2 in white-tailed deer in USA.

Prof. S. S. Vasan, Director of Health, WA spoke on lessons learned from the COVID-19 pandemic in Australia, under the zoonotic diseases umbrella.

Dr Samuel Phillips, research fellow at The Centre for Bioinnovation, University of the Sunshine Coast, and Honorary Fellow at the Murdoch Children's Research Institute (Infection and Immunity) and the Royal Women's Hospital (Centre for Women's Infectious Diseases) gave a presentation on the chlamydia vaccine for koalas and discussed their research.

Prof. Ruth Zadoks, Sydney School of Veterinary Science, spoke on strep B and mastitis in dairy cattle.

Nagendra Singanallur, Senior Research Scientist with the CSIRO Australian Centre for Disease Preparedness in Geelong, Australia, gave a lecture on systems approaches in studying host-pathogen interactions.

Our SIG also aims to cover antimicrobial resistance (AMR), the silent pandemic and zoonoses in the coming sessions in December 2023. We are finalising the speakers at the moment. We aim to continue to bring speakers from the field of food safety, and wastewater and AMR in the coming year's SIG seminars.

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Mycobacterium special interest group

Maria Globan

The Mycobacteria special interest group (MSIG) is a special interest group within the ASM community that serves to provide a forum for those members that have a particular interest in mycobacteria. The group attracts not only members that are employed within specialised state mycobacterial reference laboratories but also scientists who perform mycobacterial culture and microscopy within non-reference laboratories.

The MSIG hosts an annual 2-day meeting that is strategically held on or near World Tuberculosis (TB) Day, which is 24 March. The meeting location rotates through each Australian state, where it is hosted by each state reference laboratory, who also set the program. This has expanded to include the National Mycobacterium Reference Laboratory in Auckland, New Zealand, where the 2024 meeting is scheduled for 21-22 March. This meeting attracts a varied audience including diagnostic and research scientists, medical microbiologists and clinicians. Invitees are those who have registered with the MSIG convenor as a member or by word of mouth.

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Join the Bioinformatics special interest group

Brian Forde

We, the current members, are excited to announce the relaunch of the Bioinformatics Special Interest Group (SIG) within the ASM, and we invite you to become a part of this dynamic community.

About the Bioinformatics SIG

The Bioinformatics SIG is committed to advancing microbial genomics, transcriptomics and meta-omics through the development and application of computational approaches. Our primary goals are to foster collaboration and knowledge exchange microbial researchers, clinicians and allied health professionals with a shared interest in bioinformatics, computational biology and related fields. Through these activities, we aim to promote innovative research and discoveries that affect and advance scientific knowledge through to translational outcomes.

Why join?

Networking – connect with like-minded professionals in the field.

Knowledge sharing – stay updated on the latest bioinformatics advancements and best practices and contribute to the development of new bioinformatics software and workflows.

Collaboration – explore opportunities for research and project collaboration.

Professional development – enhance your skills and expertise.

Influence – contribute to the growth and impact of bioinformatics in the ASM community.

How to get involved

If you have a passion for bioinformatics or simply want to learn more about it, we encourage you to express your interest in joining our Bioinformatics SIG. Whether you are an ASM member or considering becoming one, your enthusiasm and ideas are welcome.

Please follow this link (see https://forms.gle/ z8BVfNRv7okVdpC39) and we will reach out to you with more details on how to become an active member of the SIG. If you have any questions or suggestions, feel free to reach out to us at b.forde@uq.edu.au.

We look forward to building a vibrant and engaged Bioinformatics SIG with your participation.

Microbiology Australia updates

Microbiology Australia (MA) continues to gain greater recognition globally, now being listed by the *Directory of Open Access Journals* (DOAJ), an online directory that indexes and provides access to high-quality, open access,

peer-reviewed journals. Inclusion in DOAJ has the benefits of raising visibility of MA content and, importantly, demonstrates best practice editorial and publishing standards (which also helps distinguish MA from the plethora of predatory open access journals out there). More information on the benefits of indexing in DOAJ can be found at: https://doaj.org/apply/why-index/#why-your-journal-should-be-indexed-in-doaj

Other databases listing MA include Scopus and Clarivate's Emerging Sources Citation Index (ESCI). MA is a member of COPE (Committee on Publication Ethics) and requires authors to list conflicts of interest and sources of funding.

Most importantly, MA aims to meets the needs of members of *The Australian Society for Microbiology*. Melinda and Tess (pictured here) were proud to receive the print copy of the most recent issue.

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Australian Journal of Primary Health The issues influencing community health services and primary health care

Australian Journal of Zoology Evolutionary, molecular and comparative zoology

Australian Mammalogy The journal of the Australian Mammal Society

Australian Systematic Botany Taxonomy, biogeography and evolution of plants

Crop & Pasture Science Plant sciences, sustainable farming systems and food quality

Environmental Chemistry Chemical approaches to environmental problems

Functional Plant Biology Plant function and evolutionary biology

Historical Records of Australian Science The history of science, pure and applied, in Australia and the southwest Pacific

International Journal of Wildland Fire The journal of the International Association of Wildland Fire

Invertebrate Systematics Systematics, phylogeny and biogeography

Journal of Primary Health Care

The journal of The Royal New Zealand College of General Practitioners

Journal of Southern Hemisphere Earth Systems Science

A journal for meteorology, climate, oceanography, hydrology and space weather focused on the southern hemisphere

Marine & Freshwater Research

Advances in the aquatic sciences

Microbiology Australia The journal of the Australian Society for Microbiology

Pacific Conservation Biology Conservation and wildlife management in the Pacific region

Proceedings of the Royal Society of Victoria Promotion and advancement of science

Reproduction, Fertility and Development Vertebrate reproductive science and technology

Sexual Health Publishing on sexual health from the widest perspective

Soil Research Soil, land care and environmental research

The APPEA Journal The journal of the Australian Petroleum Production & Exploration Association

The Rangeland Journal The journal of the Australian Rangeland Society

The South Pacific Journal of Natural and Applied Sciences

Research and review papers in the area of science, engineering and mathematics

Wildlife Research Ecology, management and conservation in natural and modified habitats

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