

Infectious Diseases Associated with and Causing Disaster

Subjects: Allergy

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In 2019, 396 natural disasters were recorded in the Emergency Events Database (EM-DAT), with 11,755 deaths, 95 million people affected, and USD 103 billion in economic losses worldwide. This burden was not shared equally since Asia suffered the highest impact, accounting for 40% of disaster events, 45% of deaths and 74% of the total affected. During disasters, a lack of safe water access and inadequate sanitation facilities allow the transmission of water-borne and food-borne pathogens. Diarrheal diseases such as cholera, typhoid fever, and shigellosis cause epidemics with high mortality rates. Malaria and other vector-borne diseases in risk areas include arboviruses, such as dengue, yellow fever, Japanese encephalitis, Rift Valley fever, and tick-borne illnesses, including Crimean–Congo hemorrhagic fever and typhus. Diseases associated with overcrowding, such as measles in unvaccinated areas and tuberculosis, can occur after natural disasters.

Keywords: disaster ; infectious diseases ; leptospirosis ; tuberculosis ; dengue ; POCT ; COVID-19

1. Introduction

In 2019, 396 natural disasters were recorded in the Emergency Events Database (EM-DAT), with 11,755 deaths, 95 million people affected, and USD 103 billion in economic losses worldwide. This burden was not shared equally since Asia suffered the highest impact, accounting for 40% of disaster events, 45% of deaths and 74% of the total affected ^[1]. Japan has historically suffered from large-scale natural disasters. Hojoki, one of the oldest essays in Japan, describes a great fire (A.D. 1177), a tornado followed by the relocation of the capital (A.D. 1180), a famine (A.D. 1181–2), and an earthquake (A.D. 1185). Recently, Japan endured the Great East Japan Earthquake and Tsunami (GEJET) of 11 March 2011—a magnitude-9 earthquake that attacked Sendai and neighboring cities, leaving 20,000 people missing. This area was attacked by a tsunami (Jogan) on 13 July 869, indicating that large-scale tsunamis occur within a 1000-year interval ^[2]. The Nankai Trough mega-earthquake (NTME) is anticipated as the next major earthquake in Japan, involving the Shizuoka prefecture. It is anticipated to cause approximately 323,000 deaths and approximately USD 1.5 trillion in direct impact, with a production and service decline amounting to approximately USD 0.4 trillion ^[3]. Sharing researchers' knowledge of the disaster is one way to initiate effective measures against these disasters. For this purpose, researchers decided to share their knowledge with annual seminars about infectious diseases that may occur due to disasters. The participants were from the International Research Institute of Disaster Science (IRIDeS) at Tohoku University in Sendai who suffered from GEJET, and those involved in disaster countermeasures and medical treatment in the Shizuoka prefecture since 2014. It is important to enhance the resilience of national health systems for disaster risk reduction. Some approaches include integrating disaster risk management into primary, secondary, and tertiary healthcare (especially at the local level), developing health workers' understanding of disaster risks, applying and implementing disaster risk reduction approaches to healthcare, promoting and enhancing training in the field of disaster medicine, and training community health groups in disaster risk reduction through health programs in collaboration with other sectors ^[4]. During disasters, a lack of safe water access and inadequate sanitation facilities allow the transmission of water-borne and food-borne pathogens. Diarrheal diseases such as cholera, typhoid fever, and shigellosis cause epidemics with high mortality rates. Malaria and other vector-borne diseases in risk areas include arboviruses, such as dengue, yellow fever, Japanese encephalitis, Rift Valley fever, and tick-borne illnesses, including Crimean–Congo hemorrhagic fever and typhus. Diseases associated with overcrowding, such as measles in unvaccinated areas and tuberculosis, can occur after natural disasters. During the seminars, researchers discussed infectious diseases associated with disasters, such as leptospirosis ^[5], dengue virus infection ^[6], and tuberculosis ^{[7][8]}. Researchers also discussed biomarkers for these diseases that reflect disease severity ^[9], and a point-of-care test (POCT) to detect pathogens, including loop-mediated thermal amplification (LAMP) in tuberculosis ^[10], single-tag hybridization chromatographic-printed array (STH-PAS) ^[11], and a nanopore technology-based sequencer called MinION ^[12]. Researchers proposed that acquired immune deficiency syndrome (AIDS) co-infected with tuberculosis (TB) (AIDS/TB) constitutes a natural disaster because the deaths caused by AIDS/TB account for 47% of all deaths in South Africa ^[13]. Severe acute respiratory syndrome coronavirus 2 (SARS-

CoV-2) [14] caused a pandemic in 2019 (COVID-19) with more than 286 million cases and 5,429,617 deaths by the end of 2021 (<https://coronavirus.jhu.edu/>) (accessed on 30 December 2021). The expansion of the pandemic severely damaged society. Therefore, the last two seminars were held exclusively on SARS-CoV-2 infections. In this entry, researchers introduce 10 seminars on measures against disaster-related infectious diseases and propose the role seminars play in combating infectious diseases associated with disasters.

2. Disaster-Related Infectious Diseases

2.1. Leptospirosis

Leptospirosis is zoonotic, often occurs after floods, and is mainly endemic to subtropical or tropical countries. It has not been reported since 2009 in the Tohoku region (northern Japan). However, four patients with leptospirosis were found in the region between 2012 and 2014. These cases imply that leptospirosis has reemerged in the region, probably due to global warming [15]. In the Philippines, leptospirosis occurs after floods caused by typhoons or heavy rainfall. The main pathogens consist of numerous serovars (>250). The case fatality rate is 10–20%, and the majority of patients, about 85%, are young males. In addition to rats, its main reservoirs are animals such as wild rodents, herbivores, livestock, and pets, which transmit leptospires through *Leptospira*-colonized water with urinary excretion in the environment [16][17]. Dominant *Leptospira* serovars with high virulence include *L. interrogans* serovar Manilae, *L. interrogans* serovar Losbanos, *L. interrogans* serovar Ratnapura, and *L. borgpetersenii*. After a storm surge during the super typhoon Haiyan (Yolanda), pathogenic *Leptospira* survived in coastal soil in Leyte. Meteorological factors showed that leptospirosis occurrence is associated with floods following monsoons in Manila. Besides rainfall, leptospirosis is also associated with relative humidity and temperature in the Philippines. The peak occurrence of leptospirosis preceded DF by only one month, despite occurring 2–3 months later than the peak occurrence of dengue in Thailand [6].

Researchers conducted a biomarker analysis of leptospirosis using two representative matricellular proteins, OPN and Gal-9, in plasma. Both the full-length Gal-9 (FL-Gal9) and OPN (FL-OPN) had increased levels of leptospirosis. Compared to other infectious diseases, pFL-Gal-9 levels showed an inverse correlation with pFL-OPN levels ($r = -0.24$, $p < 0.05$), but no correlation with other markers. By contrast, pFL-OPN levels correlated significantly with other markers of kidney injury, indicating that FL-OPN levels reflect kidney injury in leptospirosis. N-gal was associated with tubular dysfunction in AKI [18].

2.2. Tick-Borne Disorders

Scrub typhus or “Tsutsugamushi disease” was recognized in Japan as a Japanese flood fever with high mortality [19]. A recent study in Laos suggested that *O. tsutsugamushi* infection is an important cause of central nervous system infections in Laos [20]. Global warming causes changes to all living things on earth. Tick-borne Lyme disease is increasing annually in the United States and Canada [21], and tick-borne encephalitis (TBE), Lyme borreliosis (LB), and emerging borrelial relapsing fever are widespread in Russia [22][23]. The increased number and distribution of ticks, vulnerability to rain, and increased wild animals, which are sources of blood-sucking for ticks, are involved. Tick and tick-borne pathogen surveillance efforts improve researchers' understanding of geographic variation in risk factors for tick-borne diseases, and efforts to build such programs have increased in recent years [24].

2.3. Mosquito-Borne Disorders

Disasters change the behaviors of vectors and increase the incidence of vector-borne diseases, including malaria and DF [25]. Unlike the immediate impacts of flooding, malaria epidemics emerge after the acute phase of the crisis has passed. Heavy precipitation is thought to flush established larval habitats; however, malaria vectors rapidly reestablish, and a surge in disease may occur months after the disaster. Chemo-prevention is useful for reducing the excess disease burden associated with a severe flood [26]. It has also been suggested that DF cases in Manila are influenced by monsoon occurrence, contemporaneous with high temperature, high relative humidity, and heavy rainfall. Heavy rainfall precedes the occurrence of DF cases by two months. This timing can be attributed to the life-cycle of mosquitoes and an adequate number of cases for transmission, which is affected by population density [6]. An epidemic from imported DF occurred in Japan in 2014 and 200 cases were diagnosed. According to the analysis of virus strains, it was found that a single strain may have caused Dengue virus (DENV) cases in Tokyo. It should be noted that the plasma levels of Gal-9 are elevated in both DF and malaria. In malaria, Gal-9 levels were higher at day 0 compared with day 7 and day 28 ($p < 0.0001$). Gal-9 levels were significantly higher in severe malaria (SM) cases than uncomplicated (UM) cases on days 0 and 7. Therefore, Gal-9 is released during acute malaria and reflects its severity in malaria infections [27]. In DENV infection, Gal-9 levels in the critical phase were significantly higher in DENV-infected patients compared with healthy patients or those with non-dengue febrile illness. The highest Gal-9 levels were observed in dengue hemorrhagic fever (DHF) patients. Gal-9 levels

significantly declined from peak levels in DF and DHF patients in the recovery phase. Gal-9 levels tracked viral load and reflected the severity of DENV infection [9]. Finally, a dipstick DNA chromatography assay, a single-tag hybridization-printed array strip (STH-PAS), was evaluated for its efficacy in detecting DENV. PCR amplified reverse-transcribed DNA, and the amplified DNA was detected using the STH-PAS system. In clinical studies, the STH-PAS system showed 100% sensitivity with 88.9 and 86.6% specificities compared to Taqman RT-PCR and the SD Dengue Duo NS1 test, respectively. The STH-PAS system was found to have a superior sensitivity to the Taqman system [11].

3. COVID-19 Caused a Disaster

The COVID-19 outbreak is primarily a human tragedy, affecting countless people. Thus, many countries have undergone lockdowns, restricting their economic agents from mobilizing from one country to another, even nationally, due to the communicable COVID-19. The virus has had a growing impact on the global economy; unfortunately, the global health crisis has become a global economic crisis due to the cancellation of flights, restriction of labor mobility, volatility in stock markets, and so on. For vulnerable families, loss of income due to the outbreak translates to spikes in poverty, missed meals for children, and reduced access to healthcare beyond COVID-19 [28]. It also affects the education of surgeons in the medical community. Residents and young surgeons have shown a substantial decrease in clinical experience, affecting resident education and practice, and variable access to personal protective equipment (PPE). These wasteful efforts have resulted in emotional problems and burnout [29]. Internationally, governments have been enforcing travel bans, quarantine, isolation, and social distancing. Extended periods spent at home have resulted in reduced physical activity, changes in dietary intake with the potential to accelerate sarcopenia, deterioration of muscle mass and function (especially in older populations), as well as increases in body fat [30]. It was also revealed that SARS-CoV-2 has a lower mutation rate than other RNA viruses because it encodes proofreading enzyme genes. Nevertheless, ongoing rapid transmission between humans increases the genetic diversity of SARS-CoV-2 genomes, especially the Spike gene (or the receptor-binding domain, RBD); the latter is advantageous in virus infectivity, immune escape, and tolerance [31]. Interestingly, these globally occurring viral genetic changes display a convergent evolution of the SARS-CoV-2 genome worldwide [32]. Therefore, worldwide surveillance of the SARS-CoV-2 genome is important to understanding future epidemics and may help human control COVID-19. The historical background of mRNA-based vaccine development was also introduced during the seminar [33]. Furthermore, immunogenicity and BNT162b2, a lipid nanoparticle-formulated, nucleoside-modified RNA (modRNA) encoding the SARS-CoV-2 full-length spike, modified by two proline mutations that lock it in the prefusion conformation, were proven to be safe and effective [34]. Identifying risk factors for COVID-19 infection is critical to public health importance. Mosaic chromosomal alteration (mCA), a clonal expansion of leukocytes with somatic chromosomal abnormalities, is associated with an increased risk of many infectious diseases, including severe COVID-19 infection [35]. mCA is strongly associated with males and the elderly; however, the association was significant even after controlling for covariates such as age and sex. The presence of cancer enhanced this association. There was also a trend that the higher the patient's fraction of mCA, the higher the infection rate, suggesting that the expansion of cells with large mutations resulted in abnormal immune dysfunction. This mechanism is interesting; targeting abnormally expanded cells may present a new treatment for many infections, including COVID-19. It would be reasonable to stratify people by the presence or absence of mCA, carefully monitor the infections of those with mCA, and provide appropriate advice according to infection risk inferred from the presence or absence of mCA. SARS-CoV-2 RNA in concentrated and purified saliva specimens was detected 37 days after onset, using sugar chain-immobilized gold nanoparticles. It was suggested that early morning saliva specimens are more likely to show positive results than those obtained later in the day [36].

An intravenous administration of the anti-interleukin-6 receptor antibody tocilizumab (TCZ; 400 mg) effectively treated a patient with COVID-19 pneumonia and a kidney injury. An early administration of TCZ was proposed to prevent pneumonia and kidney injury caused by COVID-19 from progressing to hyperinflammatory syndrome [37]. Plasma levels of FL-Gal9 and FL-OPN and their truncated forms (Tr-Gal9, Ud-OPN, respectively) represent inflammatory biomarkers. For COVID-19 infection, Spearman's correlation analysis showed that Tr-Gal9, Ud-OPN, but not FL-Gal9 and FL-OPN, were significantly associated with laboratory markers for lung function, inflammation, coagulopathy, and kidney function in CP patients. It was proposed that the cleaved forms of OPN and Gal-9 can be used to monitor the severity of pathological inflammation and therapeutic effects of TCZ in CP patients [38].

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