Results: The mGFT increased sensitivity from 38% to 100% and maintained 100% specificity. MERS-CoV scored 40 points of a total 54 points (likelihood: 74%) using GFT, and 40 points of a total 60 points (likelihood: 67%) using the mGFT, both indicating a high likelihood that human MERS-CoV outbreak in Saudi Arabia may be of unnatural origin.

Conclusion: Using an accepted tool, the GFT, and the mGFT which was modified for improved sensitivity, the MERS-CoV outbreak in Saudi Arabia scored in the range of high likelihood of an unnatural origin. Whilst tools such as the GFT are not definitive in proving biowarfare, they provide a systematic and scientific method of risk analysis, which can flag unusual epidemics which warrant further investigation.

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0611

Spatial time series analysis of ongoing Dengue outbreaks in the Philippines

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Background: Dengue fever is a tropical disease spread by mosquitoes. Dengue, a mosquito–borne viral infection found in tropical countries worldwide, can lead to hemorrhaging and organ failure in severe cases and there is no specific treatment for the illness.

Methods and materials: Spatial-temporal analyses of disease outbreaks are versatile tools for studying and understanding transmission and spread of a disease. It is useful in the different frontiers of its upsurge, possibility of its containment or eradication. The present study fit a spatial time series model to the ongoing Dengue outbreaks in the Philippines.

Results: Between 1 January and 21 September 2019, Philippines, 322,693 dengue cases including 1,272 deaths were reported through the DOH (Department of Health) routine surveillance system, with a CFR of 0.39%. Calabarzon accounted for the highest number of dengue cases with 49,661 included the 152 death cases followed by Western Visayas with 49,068 withthe highest number of deaths with 214

Conclusion: In reaction to the outbreak, the health department has intensified its dengue prevention campaign, destroying mosquito breeding sites and ensuring adequate blood supply in hospitals. Reducing mosquito populations by cleaning water sources like wells and water storage containers is essential to preventing further spikes in dengue cases, but higher temperatures and longer rainy seasons contribute to the scale of the outbreak, as can a change in the type of dengue virus.

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0612

Establish a standard inactivation protocol for virus research in a high containment laboratory

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Background: Emerging and re-emerging infections caused by viruses continue to threaten us. Over the past decades, Singapore has faced threats caused by the SARS Coronavirus, Influenza, Dengue, and Chikungunya viruses, just to name a few. To understand the viral pathogenicity as well as control and prevention of the infections, a high containment has been applied for the research of high biorisk pathogens. Here, a standard precaution has been established to remove an inactivated virus samples to low biosafety environment as a business continuous strategy. An inactivate protocol is divided into two parts, inactivation and validation. Inactivation is a strategy completely remove the virus infectivity, included physical and chemical methods, e.g. heat and methanol. Validation shall be a solid method to reveal inactivation part was sufficient to inactivate virus and the samples still able to carry out for downstream experiments.

Methods and materials: Stability of virus was performed in different temperatures. The virus cultures were aliquot into 200 uL and incubated from 5 mins up to 2 weeks in -80 °C, 4 °C, room temperature, 37 °C, and 95 °C. Cell lines infected by virus was fixed by 100% cold methanol for 15 mins, then washed and harvested for validation. To extract viral genome, an infected cells or virus cultures was treated by lysis buffer containing guanidine isothiocyanate. All treated samples were used to cultivate for at least 3 days to validate it has no virus CPE. For safety precaution, a witness is required to monitor the inactivation process.

Results: By an in-principle approval protocol, the Mayaro virus (MAYV), for example, was certified to inactivate by using 95 °C for 5 mins, 100% cold methanol for 15 mins, and lysis buffer containing guanidine isothiocyanate for 5 mins. However, the infectivity of MAYV was started dropping after 24 hrs in 37 °C and 7 days in room temperature. It was no infectivity after 72 hrs in 37 °C.

Conclusion: In conclusion, to remove a high biorisk samples to low biosafety environment for downstream experiments may expose to the risk and to cause laboratory-acquired infections. A proper guideline, procedure, and training shall be in place for prevention and control.

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0613

The role of the clinical diagnosis of dengue during an outbreak: A qualitative study of how dengue is triaged and managed at a Malaysian hospital

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Background: Dengue is estimated to pose a risk to half of the world's population and represents a significant global economic burden. In Malaysia, dengue is a major cause of morbidity and infectious disease mortality, with an annual upward trend in nationally reported cases. The identification of dengue patients upon presentation, specifically, the diagnosis, classification and management of cases, can be challenging due to the wide spectrum of disease manifestation. Current case definitions and classifications of dengue can be difficult to apply in practice. Often, clinicians in low and middle income countries must rely on a clinical diagnosis due to the absence or delay of obtaining reliable laboratory test results. Although many studies have assessed the application of the 1997 and 2009 WHO dengue case management guidelines to manage dengue, there is limited qualitative research exploring how cli-

nicians identify and triage dengue cases during an outbreak in a hospital setting.

Methods and materials: An ethnographic study conducted at an urban public hospital in Malaysia explored day-to-day dengue case management, with a focus on the triaging and diagnosis of dengue on the Emergency and Infectious Disease wards. The study employed ethnographic, qualitative methods, specifically direct observation, interviews and focus group discussions with doctors and nurses in two hospital departments. Fieldnotes and verbatim interview and focus group discussion transcripts were analysed using a modified thematic content analysis approach.

Results: Preliminary findings identified the challenges of identifying dengue in patients with atypical and typical presentations, with implications for patient morbidity and mortality. The diagnosis of dengue was complex; reliant on a detailed patient history, enhanced clinical assessment and where possible, laboratory diagnostic tests ranging in reliability. The uncertainty of dengue diagnostic tests, delays in receiving the results and the non-specific nature of dengue illness constituted challenges that clinicians faced when triaging, diagnosing and managing patients.

Conclusion: This study provides in-depth insights into how dengue cases are triaged and diagnosed at a hospital during an outbreak and the limitations of existing dengue case definitions. The findings from this research may be useful to other tertiary care settings in dengue endemic countries.

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0614

Sero-prevalence of Dengue infection in North India

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Background: Dengue is a vector–borne disease; however, non-vectorial transmission of dengue has been completely overlooked. As we know majority of Dengue infection is asymptomatic, however, during acute sub-clinical stage one might be infectious. One could also transmit the virus through blood transfusion at the time of acute asymptomatic stage during the early five days of viremia. We planned to estimate the burden of dengue in capital region of India.

Methods and materials: Seropositivity of Dengue for IgM Ab, NS1 Ag and IgG Ab were performed among the blood donors' samples to find out seroprevalance over three years.

Results: A total of 1558 healthy blood donors were screened for the study. On the basis of inclusion/exclusion criteria, we enrolled 1531 subjects for the study. Twenty seven donors were excluded from the study, out of which 6 were detected HIV +ve, 11 were positive for HBsAg and 10 were found positive for HCV. Mean age was 30.51 ± 7.75 years. Of 1531 subjects, 18 (1.18%) had a past history of typhoid fever, 28 (1.83%) chikungunya fever, 9 (0.59%) malaria and 43 subjects (2.81%) had a past history of symptomatic dengue infection. Regarding NS1 Ag seroposivity, 2.22% (34) of subjects were found positive for NS1 Ag with a peak point prevalence of 7.14% in October'18. IgM Ab was tested and seropositivity was detected in about 5.49% (84) subjects with a peak point prevalence of 14.29% in October'18. IgG seropositivity was detected in about 64.21% (983) subjects.

Conclusion: Blood samples in blood banks should be tested for dengue before transfusion to prevent transfusion transmitted dengue infection as we estimated 2.22% positivity of NS1 Ag in our study which indicates presence of dengue virus in blood donors' samples.

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0615

Descriptive epidemiology of Monkeypox outbreak in Bayelsa State South-South Nigeria, November 2017

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Background: Monkeypox is a rare zoonotic disease, caused by monkeypox virus which belongs to the Orthopoxvirus genus of the family, Poxviridae. Monkeypox was first discovered in 1958 among monkey colonies. In September 2017, Bayelsa State reported its first suspected outbreak. We confirmed the outbreak, characterized in time, place and person and instituted public health control measures.

Methods and materials: We conducted the investigation in Ogbia and Yenagoa Local Government Areas (LGA). We did a descriptive study of suspected cases of monkeypox from September to November 2017. We defined a suspected case of monkeypox as any person in Bayelsa State with a sudden history of fever, vesiculopustular rash occurring mostly on the face, palms and soles from April to November 2017, and a confirmed case as any suspected case with a laboratory confirmation by reverse transcription polymerase chain reaction (RT-PCR). We carried out active case search in affected communities and reviewed hospital records. We traced contacts of family members and health workers for a 21-day period, with daily visits and temperature monitoring. We collected blood samples for virology testing. We computed frequencies, proportions, attack rates and case fatality rates.

Results: Thirty patients were line listed, of which eleven were laboratory confirmed. 20 (66.7%) of patients were male. Median age was 31 years (Range: 1–43). No recorded deaths. Fourteen (47%) were aged 30–39years; and they all (100%) had rashes on one or more body parts.

The overall attack rate was 4.6/100,000. The epicurve demonstrated a continuous common source epidemic pattern.

Conclusion: Bayelsa State had a confirmed outbreak of monkeypox which predominantly affected individuals in the reproductive age group and who resided in Yenagoa LGA. We recommended community sensitization in affected communities and emphasized on enhanced monkeypox surveillance.

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