Since January 2020 Elsevier has created a COVID-19 resource centre with free information in English and Mandarin on the novel coronavirus COVID-19. The COVID-19 resource centre is hosted on Elsevier Connect, the company's public news and information website.

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Results: In total, 53 specimens were tested between August 2019 and December 2019, including 36 environmental samples (cooling towers, fountains, wastewater) and 17 patient specimens. Lp1 DNA was detected in 8 patient specimens and Lp1 was cultured from 6 of 8 specimens. Lp1 was detected and isolated from 4 environmental samples. The IDEXX method was essential in the isolation of Lp1 from 2 clinical and 2 environmental samples. WGS analysis results demonstrated that 4 of the clinical isolates were closely related to each other and to an environmental sample (2-5 SNP differences). All other environmental isolates were not related.

Conclusion: The efficient testing algorithm used by WC was instrumental in the isolation of Lp1 in this investigation. The combined use of molecular methods, various culture techniques including the IDEXX platform, and WGS analysis confirmed the source of the outbreak, helping to prevent any further cases.

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Meshing Biosurveillance and Climate Data to inform Chikungunya Disease Surveillance
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Purpose: Vector-borne and zoonotic pathogens comprise a substantial portion of the global disease burden causing ∼1.4 million deaths annually, and account for approximately 17% of the entire disease burden due to infectious diseases. Current Public Health and Department of Defense surveillance systems track individual infectious disease cases to report disease trends across populations, but these are retrospective and do not provide predictive information that could identify high-risk areas to better protect public health as well as deploying military personnel.

Methods & Materials: We have built an integrated system which ingests (1) historical outbreak data from ProMED, PAHO and other sources; (2) global climate data sourced from NOAA and NASA including rainfall, land surface temperature etc; (3) Population data from the Socioeconomic Data and Applications Center (SEDAC) at Columbia University, and (4) Chikungunya vectors (Aedes aegypti and Aedes albopictus) location data from VectorMap (WRBU) and VectorBase (NIADD-BRC). We employ Machine Learning techniques to assess the relationship between locations of chikungunya outbreaks, climate variables and ancillary data. The Random Forested model was selected as the best performing model and used in deriving current and forecast risk maps globally.

Results: We derive both current and forecast risk maps at admin level 2 globally. Validation results for 2019, indicate that 80% of reported locations with chikungunya activity were predicted to be at risk by the current risk maps and ∼70% of reported locations with chikungunya activity were predicted to be at risk by the forecast risk maps. This information can be visualized in CHIKRisk App at https://vbd.usra.edu/ and is updated on a monthly basis.

Conclusion: Global Chikungunya Monitoring and Forecasting System (CHIKRisk App) presents progress towards monitoring and forecasting on vector-borne diseases by utilizing publicly available climate and outbreak data. This system is now being utilized by the Armed Forces Health Surveillance Division - Global Emerging Infections Surveillance Branch to inform Force Health Protection (FHP) decisions and by PAHO for public health surveillance. We hope to use this framework to build other next generation early warning systems for vector-borne diseases of global public health significance.

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Severe Acute Respiratory Infection Collaborative surveillance and monitoring outbreak, Viet Nam
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Purpose: Lack of understanding of the circulation, emergence of avian influenza new strain viruses, and risk of transmission from animal to human were big challenges causing heavy losses in human life and socio-economic. SARI collaborative surveillance has been set up and operated to fill the gaps in the border province of Vietnam - Cambodia.

Methods & Materials: Clinical, epidemiological data and outcomes of SARI patients were collected in provincial hospital. Samples were performed by PCR technique for influenza and non-influenza viruses included Coronavirus, Paramyxoviruses, Filoviruses, and Flaviviruses. Positive influenza samples were isolated and characterized. Information sharing and risk analysis were conducted between animal health and public health sectors

Results: SARI patient per year was 14.4% (3016/20956) among hospitalized and incident rate was 534.4/10000 population. Annual death caused by SARI ranged from 6.6 - 12.5%. Most SARI patients were neonatal (55.4% - 529/95)). Among 20.1% (955/4771) represented SARI patients were tested, respiratory and influenza virus-positive samples were 70.4% (673/955) and 24.9% (238/955) respectively. Influenza A/H1N1pdm09 virus was dominant (50.9%) and RSV accounted for 16.6% (159/955) and mostly in children <5. Coronavirus and paramyxoviruses were detected. Coinfected respiratory viruses was 25.6% (245/955). H5N1, H9, and H5N6 viruses have been detected in domestic poultry and pig.

Conclusion: Collaborative surveillance fundamentally contributed to monitoring the evolution, showed risk of transmission of avian influenza viruses to human exists considerably high, and strengthened the pandemic preparedness capacity of public health and animal health sectors. Intensive studies and wider expansion to multi-sector coordination and across-national borders are needed.

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