In search for the hotspots of Disease X: A biogeographic approach to mapping the predictive risk of WHO's blueprint priority diseases

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the period was conducted. Data was cleaned and analyzed for socio-demographic characteristics and signs and symptoms using Microsoft Office Excel version 2010. Counts, frequencies and proportions were determined.

Results: Of 370 suspected cases reported in 30 states, 165 (45.8%) were confirmed in 17 states. Five cases had both monkeypox and chickenpox. Males constituted 115 (70.1%) of cases with mean age of 29.3 + 11 years. Those most affected were 31–40 years old. 9 deaths were recorded (CFR-5.5%), 67% in known immune-compromised patients). Case reporting was highest within the first two months of the outbreak; but have continued to occur since then. Most common clinical presentations include rash (all cases), fever (n = 106, 64.8%) and headache (n = 78, 47.3%). Fever preceded rash in 59 (35.8%) of cases. Most common lesions include facial (n = 100, 60.6%), leg (n = 90, 54.5%), hand and thoracic (n = 84, 50.9%). Cases were mostly confined to the southern and central parts of the country.

Conclusion: Since the largest outbreak of monkeypox in 2017, sporadic cases have continue to occur in Nigeria pointing to endemicity of the disease. Unlike the central african clade cases are mostly seen in urban dwellers, especially among active young males.

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In search for the hotspots of Disease X: A biogeographic approach to mapping the predictive risk of WHO's blueprint priority diseases

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Background: Current trends of emerging infectious disease outbreaks (EIDs) forecast impending global epidemiological crises. Human-driven environmental changes, including climate change along with overpopulation and global travel, have been contributing to EIDs outbreaks in many developing countries. The subject has attracted increasing attention with the recent Ebola and Zika epidemics, which highlights the potential threats to human and animal health, social stability, and global trade and economy. The blueprint priority diseases (BPDs) is a list established by the World Health Organization of ten zoonotic diseases, which are in urgent need of research. We proposed mapping the predictive risk of the BPDs using spatial Bayesian models and species distribution modelling of the outbreaks following the year 2000. The aim is to provide a global perspective, measure predictive risks, and evaluate the use of biogeography on predicting diseases outbreaks. We also proposed disease biogeography as a tool for identifying the potential hotspots for Disease X listed in the BPDs.

Methods and materials: Data of the observed outbreaks (2000–2018) were obtained from promed mail and WHO archives. Bioclimatic covariates and altitude data were extracted from 'worldclim' (R package dismo) and the 2017 land cover data (MODIS satellite imagery). We constructed species distribution models including bioclim, maxent and Bayesian models with absence data generated to map the predictive risk of future outbreaks.

Results: Most of the predicted geographic risk extent estimated from the observed data of MERS, Marburg Virus Disease and Rift Valley fever were found to occur in arid and across the Middle East and Eastern regions of Africa. The predictive extent of Lassa fever and Ebola Virus Disease consisted of regions in the Western and Central Africa, predominated by humid rainforests. We found a significant correlation between the disease extent and the distribution of confirmed and suspected biological reservoirs and also with deforestation. The AUC of the generated models was maintained over 0.9 (average - 0.978).

Conclusion: Biogeography is a robust tool in forecasting hotspots of EIDs outbreaks. We will also complete the analysis by aggregating the common risk factors of the predicted EIDs to characterize hotspots for an unknown Disease X.

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Two years detection of respiratory syncytial virus subtypes A and B from children admitted to a General Hospital in Sri Lanka

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Background: Respiratory syncytial virus (RSV) associated acute respiratory tract infection (ARTI) is one of the most important causes of childhood morbidity and mortality**.** RSV consists of two major antigenic types - A and B. This study aims to identify the types of RSV circulating in the Kegalla district, Sri Lanka.

Methods and materials: We collected demographic and clinical data and nasopharyngeal aspirate (NPA) samples from 502 children with suspected ARTI admitted to the General Hospital, Kegalle, Sri Lanka from March 2016 to July 2018. The study sampled children less than 5 years of age with ≤4 days history of ARTI. Climatic data of the Kegalle region within the study period was obtained from the World Weather Online API (application programming interface). IFA (D3 UltraTM®, USA) was performed on NPA to detect seven viruses including RSV. Viral RNA was execrated (Qiagen, Germany) from RSV positive NPA samples and performed a real-time RT-PCR (Altona-Diagnostics EN) for typing.

Results: Of the 164 IFA positive children for RSV, 46 were infected with RSV A, 101 were infected with RSV B and 17 were co-infected with RSV A and B (RSV AB). RSV B was observed throughout the study period with peak incidences from March to June 2017 and April to June 2018. RSV A was detected from June to November 2016, March to November 2017 and May to July 2018. RSV AB was detected during time periods of RSV A and B co-circulation. Overall a male predominance was evident as 73.9% RSV A, 57.4% RSV B and 64.7% RSV AB positive patients were males. First-year of life appear to associate with RSV infection as 76% RSV A, 75.2% RSV B and 64.7% RSV AB positive patients were ≤1 year age. RSV activity positively correlated with rainfall, temperature, humidity and wind speed. Mild to moderate bronchiolitis, bronchopneumonia and unclassified lower respiratory tract infection were frequently diagnosed in RSV positive patients and RSV type did not appear to associate with disease severity.