

effectively malaria free in 2011. However, there is still a high risk of re-emergence of malaria in the region.

Results: The mixed model with the best fit included the climatic variables minimum temperature and precipitation. The addition of non-climate factors, including political instability and the addition of malaria intervention activities in El Oro were also included in this model. By interacting the climate covariates with malaria intervention periods, we found the association between climate and malaria risk changed significantly following the interventions.

Conclusion: Distinct variation in spatially explicit random effects was found, which suggest that other environmental factors, such as land use change or area-specific intervention efforts should be explored to understand this variation. This study demonstrates that both environmental, socio-economic and political factors should be considered when developing predictive disease models, to understand the potential environmental suitability for re-emergence in the region, given a lapse in control efforts or periods of civil unrest.

<https://doi.org/10.1016/j.ijid.2018.11.084>

19.005

El Nino southern oscillation affects on influenza peak activity seasons: comparison of the effects between Korea and the USA with surveillance data from 2005 to 2018



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Purpose: Influenza affects about 10% of the population every year. In the temperate zone, influenza has a unique seasonal pattern with some variations, however, the factors affecting its seasonality and variations are still unclear. This study aimed to explore the effects of El Nino and La Nina events on the timing of influenza peak activity in both western and eastern side of the Pacific Ocean; Korea and the USA.

Methods & Materials: The weekly influenza surveillance data of Korea and the USA from September 2005 to July 2018 were taken from WHO FluNET site. The El Nino southern oscillation (ENSO) were retrieved from Korean Meteorological Administration. We used the definition of El Nino as the positive sea surface temperature anomalies ($\geq 0.5^\circ\text{C}$), while La Nina events are negative anomalies ($\leq -0.5^\circ\text{C}$) of 3 months moving average. The weeks with the highest activities of influenza A and B in each season were identified and compared according to the presence of the anomalies. The pandemic season of 2009/2010 was excluded from the analysis. We used the mid-p exact test for statistical significance.

Results: From 2005 to July 2018, there were 3 El Nino events and 5 La Nina events by the ENSO. The influenza A peak activity in study periods showed at $4.6(\pm 4.2)$ and $3.6(\pm 4.6)$ epidemic week in Korea and USA, respectively. However, in the season of La Nina, the peak activities of influenza A observed at $0.8(\pm 1.4)$ and $5.6(\pm 3.9)$ epidemic week in Korea and USA, respectively. The La Nina was associated with the early annual peak in Korea ($p=0.045$, mid-p exact test) and the El Nino was associated delayed the annual peak in USA ($p=0.09$, mid-p exact test). The peak activity of influenza B showed no statistical association with ENSO in both countries.

Conclusion: Both El Nino and La Nina affect the timing of influenza A peak activity, but the direction may be the opposite across the Pacific Ocean: ENSO associated the early emergency of

peak activities on the western part of the Ocean (Korea) but delay the peaks on the eastern part (USA) in northern hemisphere.

<https://doi.org/10.1016/j.ijid.2018.11.085>

19.007

Excretion dynamics of Henipa-related viruses in the Egyptian Rousette bat and triggers for potential spillover



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Purpose: Henipaviruses (Hendra and Nipah) are associated with zoonotic infectious diseases of bat origin responsible for high morbidity and mortality rates in humans. The recent 2018 outbreak of Nipah virus in Kerala State, India again emphasises the public health importance. Research previously reported on an expanded geographical and host range for these viruses to the African continent and resident bat species. This study investigated the presence of Henipa- and related viruses in the Egyptian Rousette bat in South Africa as well as determining potential excretion in urine over time.

Methods & Materials: From 2012–2018, 304 spleen and 58 urine samples were collected from individually captured bats. Additionally, a total of 255 pooled urine samples were collected longitudinally over 14 consecutive months (June 2017–July 2018) from sheets placed underneath the roost. An RT-PCR assay (Tong et al., 2008) was used for detection of viral nucleic acids. Five spleens (1.64%), two individual urine (3.45%) and 16 pooled urine samples (6.27%) tested positive for paramyxovirus RNA and were further characterised using DNA sequencing and Bayesian phylogenetic analysis. The dynamics of viral excretion was investigated using a Generalized Linear Model (GLM) with a binomial error and a logit link function. The “sampling month” was set as an explanatory variable and analyses were carried out using the R software package v.3.4.1.

Results: We detected, for the first time, henipavirus sequences in bat species in South Africa. A major peak in July characterised the excretion dynamic followed by a drastic decrease. Temporal excretion data were analysed in conjunction with information on the reproductive season of the bats as well as average weather data from the region over the past five years. The July peak coincides with the dry winter period as well as the waning of maternal antibodies in the bat population.

Conclusion: This study site is surrounded by rural housing and the presence of free-roaming livestock and domestic animals. The cave is also used in traditional practices by the local population creating a conducive interface for spill-over. Further studies will be required to determine the extent of exposure and the zoonotic potential of these viruses.

<https://doi.org/10.1016/j.ijid.2018.11.086>