



Predicting risk zones of Nipah virus from foraging utilization of Lyle's flying fox (*Pteropus lylei*) in eastern Thailand

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Abstract

Flying foxes (*Pteropus* spp.) play a key role in forest regeneration as seed dispersers and are major reservoirs for the Nipah virus (NiV). Lyle's flying fox (LFF) is the dominant reservoir host species capable of transmitting NiV to humans due to its population size and distribution and its habitat being located closer to humans compared to the other flying fox species in Thailand. Predicting and identifying landscape features that influence risk to NiV spillover would be helpful in preventing emergence in human populations. The role of vegetation cover, environmental factors, a livestock factor, an anthropogenic factor and foraging locations of LFF from high-resolution global position system telemetry were investigated to qualitatively evaluate the potential risk factors that may contribute to the spread of NiV. The consideration was based on expert opinion to identify a probabilistic surface of zoonotic transmission potential of NiV across the study area. The results predicted that the area with the highest risk for NiV covered 449 km² (3.06% of the total study area) inhabited by 1,481,789 people and 599,780 households, with particular focus on Plaeng Yao and Bang Phra sub-districts. The results presented can be utilized to create early warning system management strategies for public health and conservation policies that simultaneously protect LFF.

Introduction

Lyle's flying fox (*Pteropus lylei*) is classified as Vulnerable on the IUCN Red List due to substantial population decline (Bumrungsri et al., 2008). It is also listed in Appendix II of the CITES (CITES, 2015). LFF belongs to the Old-World fruit bat family, Pteropodidae. LFF is found in colonies of 100–1,000 individuals in Thailand, Cambodia and Vietnam, and in small, distinct areas in southern China (Bumrungsri et al., 2008). This species is present only on the mainland of lower central and eastern Thailand (Boonkird and Wanghongsa, 2004; Duengkae et al., 2015).

Malaysia in 1998. It has been frequently reported in Bangladesh since 2001 and occasionally in neighboring India; it causes severe febrile encephalitis resulting in death in 40% to 75% of human cases (Hsu et al., 2004; Chadha et al., 2006; Epstein et al., 2006; Gurley et al., 2007; Luby, 2013). In Thailand, there has been no evidence of NiV in domestic animals, but NiV has been found in wildlife. LFF is the only species in which NiV is found in both the saliva and urine. Two NiV strains previously identified as circulating in Malaysia and Bangladesh were found in the bat's urine (Wacharapluesadee et al., 2010)



Risk mapping created from distributions of wildlife reservoirs for human pathogens has been most successful in predicting the risk of directly transmitted zoonoses (Ostfeld et al., 2005). Mapping risk may help in identifying previously undocumented NiV outbreak locations (Hahn et al., 2014a), and prevent zoonotic transmission of NiV by highlighting areas of suitable habitat for LFF where there have been no reported human cases. Understanding which habitats are utilized by LFF can provide information for risk area management strategies. From the foraging location and characterization of the ecological narrative linking bat habitat utilization with human and livestock activity, it is possible to spatially predict the risk zones.

Materials and Methods

This study covered three provinces (Prachinburi, Chachoengsao and Chonburi) in eastern Thailand covering 14,365 km², with eight LFF roosting sites, ranging from 618 to 7,991 individuals/site (Chaiyes et al., 2017). In total, 348 presence points were generated from 19 individual LFF foraging points recorded using high-resolution global position system (GPS) loggers. These presence points were then ground truth-checked as actual foraging point data.

This investigation aimed to forecast the risk of NiV spillover in eastern of Thailand as a function of foraging utilization, the predicted distribution of LFF and environmental factors. Risk was mapped in the study area using two approaches. The first approach mapped the foraging utilization suitability of LFF as a predictor of NiV spillover to humans, while the second mapped the risk zones of NiV transmission based on expert opinion. Species distribution modelling (Peterson, 2014) was used to identify the key factors that influence foraging utilization of LFF populations. The maximum entropy (MaxEnt) modelling technique (Phillips et al., 2006) was used to model the presence data at 30 m resolution based on exploratory environmental factors: vegetation cover (17 LFF food types), elevation, aspect, slope, precipitation, temperature and distance to main streams. The vegetation cover map was produced by Thailand's Land Development Department. Elevation, aspect, slope and stream data were provided by the Department of National Parks, Wildlife and Plant Conservation. Precipitation and temperature data were obtained from the Thai Meteorological Department. Model performance was evaluated based on the area under the curve (AUC). The potential risk map of NiV in Thailand was developed using expert opinion in probabilistic risk analysis. The use of five experts was employed to assess emerging NiV in bats and to assess the risk of the spread of NiV in this study. The environmental risk response factors for potential risk modelling consisted of: 1) environmental data; land use types (Daszak et al., 2013); 2) livestock data, specifically pig density (Luby et al., 2009); 3) LFF data: distance to roosting site, density of LFF, areas where bats are hunted and a foraging utilization map modelled using MaxEnt (Daszak et al., 2013; Hahn et al., 2014a; Hahn et al., 2014a; Hahn et al., 2014b; Walsh, 2015); and 4) anthropogenic data: density of population and location of villages (Luby, 2013; Hahn et al., 2014a; Hahn et al., 2014b). This study applied all known environmental risk factors from countries with previous NiV outbreaks to map potential NiV risk. The potential surface analysis method ranks spatial factors according to their importance using difference weightings (Nakya et al., 2010). Initial rating and weighting scores were assigned to factors with values ranging from 0 to 10 (no risk to highest risk). All factors were quantified by the experts, and overlays were then developed into risk maps. After overlaying and analysis, the environmental risk factors were used to create a potential risk map of NiV in Thailand. Risk scores were classified based on the quantile approach commonly used as a pragmatic criterion to define low, medium and high risk of exposure.

Results and Discussion

The AUC value for the predictions derived from the MaxEnt model of LFF presence was 98% indicating the model demonstrated excellent predictive skill of LFF utilization suitability. The model identified elevation, precipitation and vegetation cover as the main influential predictors in LFF utilization, accounting for 39%, 26%, and 21% relative contributions, respectively. The foraging suitability zones of

LFF were located on flat plains with an annual precipitation range of 100–120 mm. Most foraging areas of LFF were located in mixed orchard, mango and village types of land use. LFF highest utilization suitability presence was predicted extensively in the center of study area.

The predicted risk of NiV spillover as a spatial dependent function of the landscape features in the potential surface analysis based on expert opinion identified 449 km² (3.06% of the total study area) in the highest risk class containing 1,481,789 people and 599,780 households, encompassing the central and western parts of the study area and mainly in Plaeng Yao and Bang Phra sub-districts (Fig. 1). In addition, there have been reports of illegal hunting and consumption of bush meat in the area, which increase the chance of NiV spillover into humans. This study used ecological data to map potential NiV risk and provided a useful identification of priority areas.

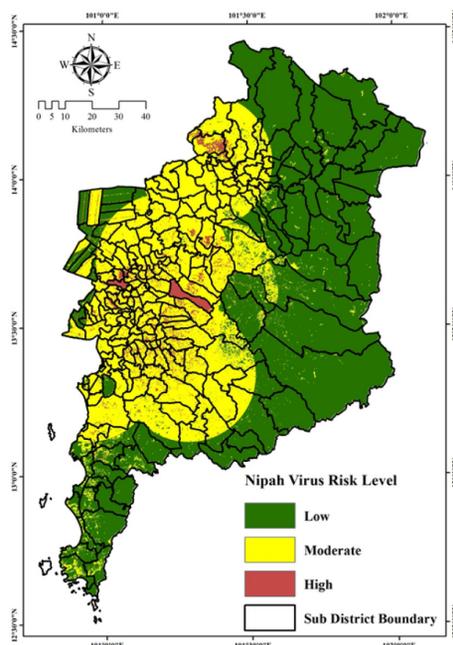


Fig. 1 Nipah virus risk level from foraging utilization of Lyle's flying fox (*Pteropus lylei*) in eastern Thailand

Risk mapping was used to identify risk zones of suitability for zoonotic transmission of NiV to humans by defining a set of data concerning the disease, the host or the environment that was characterized as suitable for infection. Disease data included the natural history of infection (including the latent, incubation and infectious periods) and surveillance data describing the distribution and spread of infection through space and time (Fraser et al., 2004). Knowledge of host demography is an essential component of any epidemiological analysis. Key demographic variables typically include the age and sex structure of the population, its density and spatial distribution and patterns of host movement for disease spread (Robinson et al., 2007; Tildesley et al., 2010). Environment is taken to refer to any factor that is not an attribute of the pathogen or the host(s). This encompasses a vast range of possible influences on disease dynamics, ranging from levels of hygiene in hospitals to land use and climate. Other drivers, such as human demography (population density, age structure, urbanization among others) have similar attributes (Woolhouse, 2011). At present, there is no known NiV outbreak in Thailand. The developed model used data from tracked LFF movements for disease spread. The knowledge of the importance of environment factors that may be applicable to Thailand remains limited. Factors associated with the risk of NiV spillover were based on data from countries that have had prior outbreaks (Luby et al., 2009; Daszak et al., 2013; Luby, 2013; Hahn et al., 2014a; Hahn et al., 2014b; Walsh, 2015).



Improving knowledge of LFF foraging utilization may provide further insight into the conditions leading to spillover of NiV into humans in Thailand. Building on the findings of this study, future assessment could utilize information on the dynamics of land cover mapping or the plant phenology of LFF food sources to precisely predict suitable domains for LFF roosting and foraging. This could aid in the prediction of annual human NiV outbreaks as well as help to define suitable foraging habitat, not just in Thailand, but throughout its range.

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