Title of project:

PREDICT 2: Surveillance for emerging zoonotic disease threats and behavioral risk characterization in high-risk communities in Cambodia

Coordination: Duong Veasna

Partners: Wildlife Conservation Society, University California Davis, Ministry of Agriculture Laos, National Veterinary Research Institute (NaVRI)

Background

Anthropogenic activities, such as wildlife trade and land conversion for agriculture, are recognized as drivers of zoonotic disease emergence. Cambodia is a key source, conduit, and consumer of wildlife. In the past decade, the country has seen economic development accompanied by large scale land-use change and increasing human-wildlife-domestic animal contact, which may increase opportunities for pathogen spillover from animals to people.

Objectives

Emerging infectious diseases pose a significant burden on human and animal health and global economies. Conventional approaches to epidemic control have most often been reactive. However, explosive human population growth, dramatic changes in land use, and increased global trade and travel require a shift toward a proactive, predictive approach. The PREDICT project aims to prevent, detect, and rapidly respond to the spillover of novel infectious pathogens from wildlife to humans. The goal of the PREDICT project in Cambodia was to build local capacity to conduct surveillance and diagnostics for zoonotic pathogens in wildlife.

Core of the project

Anthropogenic activities, such as wildlife trade and land conversion for agriculture, are recognised as drivers of zoonotic disease emergence. Cambodia is a key source, conduit, and consumer of wildlife. In the past decade, the country has seen economic development accompanied by large scale land-use change and increasing human-wildlife-domestic animal contact. The PREDICT project aims to prevent, detect, and rapidly respond to the spillover of novel infectious pathogens

from wildlife to humans. The goal of the PREDICT project in Cambodia was to build local capacity to conduct surveillance and diagnostics for zoonotic pathogens in wildlife.

In PREDICT 1, a total of 3,887 animals were sampled (300 nonhuman primates, 552 rodents, and 2,503 bats). Polymerase Chain Reaction (PCR) screening for 16 viral families and additional pathogens of regional concern was conducted at IPC. The following viral families were targeted for testing: arenaviruses, alphaviruses, astroviruses, bocaviruses, bunyaviruses, coronaviruses, enteroviruses, filoviruses, flaviviruses, influenza viruses, hantaviruses, henipaviruses, herpesviruses, orthopoxviruses, paramyxoviruses, rhabdoviruses, lyssaviruses, retroviruses (Lentivirus genus), simian foamy viruses, and seadornaviruses.

The success of PREDICT 1 has led to further funding from USAID for the PREDICT 2 project (5 years) where IPC has the lead role in carrying out the project in Cambodia. While PREDICT 1 studied only wildlife at the interface with humans (hunting, restaurant, wildlife market, etc), phase 2 of PREDICT will focus at the interface of wildlife, livestock and humans. The project started in October 2014 and focused on surveillance and interventions at the source of pathogen emergence, amplification, and spread in human populations and to forecast risk from viruses before they emerge, through: (1) expanded characterisation of pathogens of known epidemic and unknown pandemic potential and their dynamics among hosts; (2) documenting pathogen sharing between wildlife, domestic animals, and people at high-risk interfaces for disease emergence; (3) target surveillance at high-risk pathways for disease emergence, spillover, and spread in order to identify social and ecological drivers of (i.e. factors influencing) pathogen emergence and transmission and determine appropriate targets for intervention; (4) build on global One Health initiatives for effective collaboration across disciplines and geographic borders.

Three sites presenting interface between human, wildlife and livestock were identified: 1) bat farming site for guano, 2) cross border rodents trade for consumption to Vietnam and 3) land concession area with different landscape changes due to deforestation. Molecular assays will be used to screen for 10 virus families.

Prospective

HTS sequencing is being conducted on selected CoV positive samples from PREDICT 1 in Cambodia. The whole genome sequences generated by HTS will help us characterise the genome of these different CoV in bats and study their host specificity in transmission. Further characterisation of different viruses detected in PREDICT1 are being explored.

Recent publications (2013-2016)

1. Mey C, Metlin A, Duong V, Ong S, In S, Horwood PF, Reynes JM, Bourhy H, Tarantola A, Buchy P. Evidence of two distinct phylogenetic lineages of dog rabies virus circulating in Cambodia. Infection, Genetics and Evolution. 2016 Mar;38:55-61. doi: 10.1016/j.meegid.2015.12.011.

2. Cosson JF, Picardeau M, Mielcarek M, Tatard C, Chaval Y, Suputtamongkol Y, Buchy P, Jittapalapong S, Herbreteau V, Morand S. Epidemiology of leptospira transmitted by rodents in southeast Asia. PLoS Negl Trop Dis. 2014 Jun 5;8(6):e2902. doi: 10.1371/journal.pntd.0002902.