PLOS | NEGLECTED TROPICAL DISEASES

RESEARCH ARTICLE

Estimating Geographical Variation in the Risk of Zoonotic *Plasmodium knowlesi* Infection in Countries Eliminating Malaria

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Abstract

Background

Infection by the simian malaria parasite, *Plasmodium knowlesi*, can lead to severe and fatal disease in humans, and is the most common cause of malaria in parts of Malaysia. Despite being a serious public health concern, the geographical distribution of *P*. *knowlesi* malaria risk is poorly understood because the parasite is often misidentified as one of the human malarias. Human cases have been confirmed in at least nine Southeast Asian countries, many of which are making progress towards eliminating the human malarias. Understanding the geographical distribution of *P*. *knowlesi* is important for identifying areas where malaria transmission will continue after the human malarias have been eliminated.

Methodology/Principal Findings

A total of 439 records of *P*. *knowlesi* infections in humans, macaque reservoir and vector species were collated. To predict spatial variation in disease risk, a model was fitted using records from countries where the infection data coverage is high. Predictions were then made throughout Southeast Asia, including regions where infection data are sparse. The resulting map predicts areas of high risk for *P*. *knowlesi* infection in a number of countries that are forecast to be malaria-free by 2025 (Malaysia, Cambodia, Thailand and Vietnam)

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