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# Predicting the geographical distributions of the macaque hosts and mosquito vectors of *Plasmodium knowlesi* malaria in forested and non-forested areas

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## Abstract

**Background:** *Plasmodium knowlesi* is a zoonotic pathogen, transmitted among macaques and to humans by anopheline mosquitoes. Information on *P. knowlesi* malaria is lacking in most regions so the first step to understand the geographical distribution of disease risk is to define the distributions of the reservoir and vector species.

**Methods:** We used macaque and mosquito species presence data, background data that captured sampling bias in the presence data, a boosted regression tree model and environmental datasets, including annual data for land classes, to predict the distributions of each vector and host species. We then compared the predicted distribution of each species with cover of each land class.

**Results:** Fine-scale distribution maps were generated for three macaque host species (*Macaca fascicularis*, *M. nemestrina* and *M. leonina*) and two mosquito vector complexes (the Dirus Complex and the Leucosphyrus Complex). The Leucosphyrus Complex was predicted to occur in areas with disturbed, but not intact, forest cover (> 60 % tree cover) whereas the Dirus Complex was predicted to occur in areas with 10–100 % tree cover as well as vegetation mosaics and cropland. Of the macaque species, *M. nemestrina* was mainly predicted to occur in forested areas whereas *M. fascicularis* was predicted to occur in vegetation mosaics, cropland, wetland and urban areas in addition to forested areas.

**Conclusions:** The predicted *M. fascicularis* distribution encompassed a wide range of habitats where humans are found. This is of most significance in the northern part of its range where members of the Dirus Complex are the main *P. knowlesi* vectors because these mosquitoes were also predicted to occur in a wider range of habitats. Our results support the hypothesis that conversion of intact forest into disturbed forest (for example plantations or timber concessions), or the creation of vegetation mosaics, will increase the probability that members of the Leucosphyrus Complex occur at these locations, as well as bringing humans into these areas. An explicit analysis of disease risk itself using infection data is required to explore this further. The species distributions generated here can now be included in future analyses of *P. knowlesi* infection risk.

**Keywords:** Species distribution model, Deforestation

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