

**Environmental risk factors and exposure to the zoonotic malaria parasite *Plasmodium knowlesi* across northern Sabah, Malaysia: a population-based cross-sectional survey**

**ABSTRACT**

Background: Land use changes disrupt ecosystems, altering the transmission of vector-borne diseases. These changes have been associated with increasing incidence of zoonotic malaria caused by *Plasmodium knowlesi*; however, the population-level distributions of infection and exposure remain unknown. We aimed to measure prevalence of serological exposure to *P knowlesi* and assess associated risk factors. Methods: We did an environmentally stratified, population-based, cross-sectional survey across households in the Kudat, Kota Marudu, Pitas, and Ranau districts in northern Sabah, Malaysia, encompassing a range of ecologies. Using blood samples, the transmission intensity of *P knowlesi* and other malaria species was measured by specific antibody prevalence and infection detected using molecular methods. Proportions and configurations of land types were extracted from maps derived from satellite images; a data-mining approach was used to select variables. A Bayesian hierarchical model for *P knowlesi* seropositivity was developed, incorporating questionnaire data about individual and household-level risk factors with selected landscape factors. Findings: Between Sept 17, 2015, and Dec 12, 2015, 10 100 individuals with a median age of 25 years (range 3 months to 105 years) were sampled from 2849 households in 180 villages. 5·1% (95% CI 4·8–5·4) were seropositive for *P knowlesi*, and marked historical decreases were observed in the transmission of *Plasmodium falciparum* and *Plasmodium vivax*. Nine *Plasmodium* spp infections were detected. Age, male sex, contact with macaques, forest use, and raised house construction were positively associated with *P knowlesi* exposure, whereas residing at higher geographical elevations and use of insecticide were protective. Agricultural and forest variables, such as proportions and fragmentation of land cover types, predicted exposure at different spatial scales from households. Interpretation: Although few infections were detected, *P knowlesi* exposure was observed in all demographic groups and was associated with occupational factors. Results suggest that agricultural expansion and forest fragmentation affect *P knowlesi* exposure, supporting linkages between land use change and *P knowlesi* transmission.