

Human exposure to zoonotic malaria vectors in village, farm and forest habitats in Sabah, Malaysian Borneo

ABSTRACT

The zoonotic malaria parasite, *Plasmodium knowlesi*, is now a substantial public health problem in Malaysian Borneo. Current understanding of *P. knowlesi* vector bionomics and ecology in Sabah comes from a few studies near the epicentre of human cases in one district, Kudat. These have incriminated *Anopheles balabacensis* as the primary vector, and suggest that human exposure to vector biting is peri-domestic as well as in forest environments. To address the limited understanding of vector ecology and human exposure risk outside of Kudat, we performed wider scale surveillance across four districts in Sabah with confirmed transmission to investigate spatial heterogeneity in vector abundance, diversity and infection rate. Entomological surveillance was carried out six months after a cross-sectional survey of *P. knowlesi* prevalence in humans throughout the study area; providing an opportunity to investigate associations between entomological indicators and infection. Human-landing catches were performed in peri-domestic, farm and forest sites in 11 villages (3–4 per district) and paired with estimates of human *P. knowlesi* exposure based on seroprevalence. *Anopheles balabacensis* was present in all districts but only 6/11 villages. The mean density of *An. balabacensis* was relatively low, but significantly higher in farm (0.094/night) and forest (0.082/night) than peri-domestic areas (0.007/night). Only one *An. balabacensis* ($n = 32$) was infected with *P. knowlesi*. *Plasmodium knowlesi* sero-positivity in people was not associated with *An. balabacensis* density at the village-level however post hoc analyses indicated the study had limited power to detect a statistical association due low vector density. Wider scale sampling revealed substantial heterogeneity in vector density and distribution between villages and districts. Vector-habitat associations predicted from this larger-scale surveillance differed from those inferred from smaller-scale studies in Kudat; highlighting the importance of local ecological context. Findings highlight potential trade-offs between maximizing temporal versus spatial breadth when designing entomological surveillance; and provide baseline entomological and epidemiological data to inform future studies of entomological risk factors for human *P. knowlesi* infection.