

## **Exposure and infection to Plasmodium knowlesi in case study communities in Northern Sabah, Malaysia and Palawan, The Philippines**

### **ABSTRACT**

Primarily impacting poor, rural populations, the zoonotic malaria *Plasmodium knowlesi* is now the main cause of human malaria within Malaysian Borneo. While data is increasingly available on symptomatic cases, little is known about community-level patterns of exposure and infection. Understanding the true burden of disease and associated risk factors within endemic communities is critical for informing evidence-based control measures. We conducted comprehensive surveys in three areas where *P. knowlesi* transmission is reported: Limbuak, Pulau Banggi and Matunggung, Kudat, Sabah, Malaysia and Bacungan, Palawan, the Philippines. Infection prevalence was low with parasites detected by PCR in only 0.2% (4/2503) of the population. *P. knowlesi* PkSERA3 ag1 antibody responses were detected in 7.1% (95% CI: 6.2±8.2%) of the population, compared with 16.1% (14.6±17.7%) and 12.6% (11.2±14.1%) for *P. falciparum* and *P. vivax*. Sero-prevalence was low in individuals <10 years old for *P. falciparum* and *P. vivax* consistent with decreased transmission of non-zoonotic malaria species. Results indicated marked heterogeneity in transmission intensity between sites and *P. knowlesi* exposure was associated with agricultural work (OR 1.63; 95% CI 1.07±2.48) and higher levels of forest cover (OR 2.40; 95% CI 1.29±4.46) and clearing (OR 2.14; 95% CI 1.35±3.40) around houses. Spatial patterns of *P. knowlesi* exposure differed from exposure to non-zoonotic malaria and *P. knowlesi* exposed individuals were younger on average than individuals exposed to non-zoonotic malaria. This is the first study to describe serological exposure to *P. knowlesi* and associated risk factors within endemic communities. Results indicate community-level patterns of infection and exposure differ markedly from demographics of reported cases, with higher levels of exposure among women and children. Further work is needed to understand these variations in risk across a wider population and spatial scale.