Contribution of *Plasmodium knowlesi* to multi-species human malaria infections in North Sumatera, Indonesia

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Running Title: Multi-species malaria in North Sumatera

40-word summary:

Indonesia is aiming for malaria elimination by 2030. A parasitological survey of 3,731 individuals in North Sumatera province identified 1,169 parasitaemic individuals by PCR. Highly specific amplification of *sicavar* genes was used to identify *Plasmodium knowlesi* infection in 377 people.

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ABSTRACT

Background

As Indonesia works towards the goal of malaria elimination, information is lacking on malaria epidemiology from some western provinces. As a basis for studies of antimalarial efficacy, we set out to survey parasite carriage in three communities in North Sumatera Province.

Methods

A combination of active and passive detection of infection was carried out among communities in Batubara, Langkat and South Nias regencies. Finger-prick blood samples from consenting individuals of all ages provided blood films for microscopic examination and blood spots on filter paper. Plasmodium species were identified by nested PCR of rRNA genes, and a novel assay which amplifies a conserved sequence specific for the *sicavar* gene family of *P. knowlesi*.

Results

614 of 3,731 participants (16.5%) were positive for malaria parasites by microscopy. PCR detected parasite DNA in samples from 1,169 individuals (31.3%). In total, 377 participants (11.8%) harboured *P. knowlesi*. Also present were *P. vivax* (14.3%), *P. falciparum* (10.5%) and *P. malariae* (3.4%).

Conclusions

Amplification of *sicavar* is a specific and sensitive test for the presence of *P. knowlesi* DNA in humans. Subpatent and asymptomatic multi-species parasitaemia is relatively common in North Sumatera, and so PCR-based surveillance is required to support control and elimination activities.

Keywords:

Malaria;   Indonesia;   Plasmodium knowlesi