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A Sensitive, Colorimetric, High-Throughput Loop-Mediated Isothermal Amplification Assay for the Detection of Plasmodium knowlesi

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Abstract. The simian parasite Plasmodium knowlesi is now the commonest cause of malaria in Malaysia and can rapidly cause severe and fatal malaria. However, microscopic misdiagnosis of Plasmodium species is common, rapid antigen detection tests remain insufficiently sensitive and confirmation of P. knowlesi requires polymerase chain reaction (PCR). Thus available point-of-care diagnostic tests are inadequate. This study reports the development of a simple, sensitive, colorimetric, high-throughput loop-mediated isothermal amplification assay (HiLAMP) diagnostic test using novel primers for the detection of P. knowlesi. This assay is able to detect 0.2 parasites/μL, and compared with PCR has a sensitivity of 96% for the detection of P. knowlesi, making it a potentially field-applicable point-of-care diagnostic tool.

Human infection with the simian malarial parasite, Plasmodium knowlesi results from transmission from long-tailed and pig-tailed macaques, via the Anopheles leucocryptus mosquito vector,1 and has been documented in all countries of southeast Asia, except Laos and Timor Leste. In Sabah, Malaysia, while the total number of reported malaria cases has decreased since 1992, the absolute number and proportion due to P. knowlesi have increased significantly such that in 2013, 62% of malaria cases were due to P. knowlesi, making it the most common cause of malaria in this region.2

Plasmodium knowlesi malaria is difficult to diagnose by conventional microscopy. Ring and trophozoite stages of P. knowlesi appear morphologically very similar to both Plasmodium falciparum and Plasmodium malariae.3 Microscopy has been found to be unreliable for diagnosing P. knowlesi in regions where it coexists with P. falciparum and Plasmodium vivax.3,4 resulting in inappropriate or delayed administration of anti-malarial treatment. Although high parasitaemia has been found to predict severe disease, symptomatic disease frequently occurs at low parasitism.5,6 There are currently no P. knowlesi-specific rapid diagnostic tests (RDTs), and those based on parasite lactate dehydrogenase (pLDH) and aldolase have been shown to be inadequately sensitive for clinical diagnosis.4,7 Of concern, Grigg and others reported that for the 31% of P. knowlesi malaria patients with parasitaemia < 1,000 parasites/μL, pLDH-based RDTs had a sensitivity of only 12%.7

Currently, definitive diagnosis of P. knowlesi infection relies on polymerase chain reaction (PCR) performed retrospectively in reference laboratories. Tests that have been reported include nested PCR assays targeting either the 18S ribosomal small subunit8 or the cytochrome b mitochondrial gene.9 Assays have been configured as single-step PCR,10 real-time PCR,11 multiplex PCR,12 or semi-nested multiplex PCR.13 However, due to its cost and requirements for infrastructure and technical expertise, PCR remains a reference laboratory confirmation tool and is generally inaccessible in regional health-care facilities, making it unsuitable as a point-of-care diagnostic tool. Of the alternative molecular technologies, loop-mediated isothermal amplification (LAMP) offers much potential as a field-applicable molecular diagnostic tool. Of the two published P. knowlesi-specific LAMP assays, primers targeting the beta tubulin gene using a Loopamp kit (Eiken Chemical Co. Ltd., Tokyo, Japan) are yet to be validated in human clinical samples.14 A LAMP assay targeting the P. knowlesi apical membrane antigen-1 reported a sensitivity of 100% and specificity of 98% in 74 clinical samples.15 However, it required post-amplification addition of SYBR (Invitrogen, Carlsbad, CA) which risks contamination. Although it has been recommended that LAMP be reserved for surveillance rather than point-of-care diagnostics, in view of the difficulties associated with the identification of P. knowlesi using microscopy and RDTs, there is a pressing need for developing point-of-care diagnostic alternatives for the diagnosis of P. knowlesi infection.

This report describes a sensitive, high-throughput, colorimetric, field-applicable LAMP assay targeting a mitochondrion gene that can detect P. knowlesi infection at low parasitemia.

Novel LAMP primers (Pk101) targeting a Plasmodium mitochondrial gene (Table 1) were designed based on modification of previously designed P. vivax LAMP primers.10 Dried blood spot (DBS) samples from patients with PCR-confirmed malaria caused by P. knowlesi (N = 25; median parasitemia 1,541 parasites/μL; range 75–95,456), P. vivax (N = 15; median parasitemia 4,630 parasites/μL; range 441–110,460), mixed P. knowlesi/P. vivax (N = 1; parasitemia 5,767 parasites/μL), P. falciparum (N = 4; median parasitemia 92,938 parasites/μL; range 11,024–362,420), and P. malariae (N = 1; parasitemia 3,354 parasites/μL) were used to validate the primes. These patients (N = 46) were a subset of patients enrolled in prospective clinical studies, with ethics approval granted by the Malaysian Medical Research Ethics Committee and Menzies School of Health Research, Australia, conducted in Kota Marudu district, Sabah, Malaysia.6,17 Approximately 20 μL DBS were prepared from symptomatic patients presenting to the district hospital with a diagnosis of malaria infection by microscopy. Multiplex PCR was performed as described8 on DNA extracted using the Qiagen® DNA mini kit (Qiagen, Australia) from clinical samples to identify Plasmodium genus and human-only species (P. falciparum, P. vivax, Plasmodium ovale, and P. malariae), and nested PCR as described8 was used for identifying P. knowlesi. High-throughput loop-mediated isothermal amplification assay (HiLAMP) was performed on DNA extracted from DBS using a modified chelex

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protocol. Briefly, 6 mm DBS samples were incubated in 1 mL of 0.5% saponin in phosphate buffered saline (PBS) for 2 hours at 37°C, centrifuged, washed in PBS, heated at 98°C for 30 minutes in 150 μL of 6% chelex, and centrifuged at 4,000 rpm for 3 minutes. The resultant 100 μL supernatant was stored at −20°C.

To determine the limit of detection (LOD) of the assay, a PCR-confirmed P. knowlesi sample with a parasitemia determined by microscopy by two expert microscopists was diluted in Plasmodium-negative whole blood to produce a dilution series with parasitemia ranging from 2,000, 200, 20, 2, and 0.2 parasites/μL. The DNA from these samples was extracted using Qiagen® DNA mini kit (Qiagen, Australia) and tested in duplicate in the HiLAMP platform usingPk101 primers (HiLAMP-Pk) and published14,15 P. knowlesi primers (HiLAMP-Pk Iseki and HiLAMP-Pk Lau). HiLAMP-Pk was performed on clinical samples of P. knowlesi (N = 8), P. falciparum (N = 1), P. vivax (N = 2), and P. ovale (N = 1) to determine species specificity of the primers. HiLAMP reactions were performed in 25 μL total volume containing 1× buffer (20 mM Tris HCl pH 8.8, 10 mM KCl, 8 mM MgSO4, 10 mM (NH4)2SO4), 1.25 mM total volume containing 1× buffer (20 mM Tris HCl pH 8.8, 1 μL of forward outer primer/backward outer primer, 120 μM each deoxyribonucleoside triphosphate, 1.78 μM each of forward inner primer/backward inner primer, 0.8 μM each of loop forward primer/loop backward primer, 0.2 μM each of forward outer primer/backward outer primer), 120 μM hydroxynaphthol blue (Fluka, Sigma-Aldrich, Australia, CAS number 63451-35-4), 8 units Bst polymerase (New England Biolabs, Ipswich, MA), and 5 μL of DNA. The HiLAMP-Pk assay was done in a 96-well microtitre plate, incubated in a water bath at 65°C for 30 minutes, the resultant color change and precipitate recorded visually and confirmed using a portable photo spectrometer at 600 nm with a turnaround time of 6 hours, as previously described. A blue color change with a visible precipitate was a positive result, and purple color without a precipitate was a negative result. PCR was used as the gold standard to calculate the sensitivity and specificity of HiLAMP-Pk. The performance of HiLAMP in a resource-limited setting had previously been validated in a district hospital laboratory in Sabah. The HiLAMP-Pk assay had a LOD of 0.2 parasites/μL, compared with 200–2,000 parasites/μL for HiLAMP-Pk Iseki and 20–2,000 parasites/μL for HiLAMP-Pk Lau (Table 2). It is postulated that the HiLAMP-Pk primers are considerably more sensitive than the other published primers due to the high copy number of the target mitochondrial gene. The HiLAMP-Pk assay did not cross-react with P. falciparum, P. malariae, and P. ovale but did cross-react with P. vivax. However, the HiLAMP-Pk assay was more sensitive (96%, N = 25/26) for the detection of P. knowlesi compared with a cross-reacting P. vivax HiLAMP assay46 (sensitivity 42%, N = 11/26) and HiLAMP-Pk Iseki14 (sensitivity 81%, N = 21/26) for the detection of P. vivax and P. ovale and HiLAMP-Pk Lau (sensitivity 81%, N = 21/26) for the detection of P. ovale (Table 3). The HiLAMP assay, validated in a district hospital laboratory in Kota Marudu, Sabah, Malaysia, was able to be performed in a resource-limited setting with chelex-extracted DNA from DBS samples, using a water bath, centrifuge, and portable photospectrometer. The main limitation of the HiLAMP-Pk assay is the cross-reactivity with P. vivax, which resulted in a low species specificity. Given the 97% sequence identity between these species at this mitochondrial target, it may be challenging to further modify primer sets for this target site to improve species specificity. Although artemisinin combination therapy is an effective treatment for both of these Plasmodium species, P. vivax infection would need to be confirmed and glucose-6-phosphate dehydrogenase deficiency should be excluded before the administration of primaquine. Furthermore, the LOD of HiLAMP-Pk on chelex-extracted DNA is yet to be determined. The diagnostic sensitivity of the HiLAMP-Pk assay also requires further validation in a larger set of samples from both microscopy positive and negative, and symptomatic and asymptomatic patients with P. knowlesi malaria to establish a possible role for the assay as a test for detecting low level parasitemia in cross-sectional surveys. This is warranted due to evidence of significant asymptomatic, submicroscopic P. knowlesi carriage amongst household contacts of symptomatic patients. In addition, although the HiLAMP platform performed in a resource-limited laboratory setting demonstrated good diagnostic capability for identifying Plasmodium genus, P. falciparum,19 P. vivax,16 and P. knowlesi (using HiLAMP-Pk Iseki, data not shown), identification of P. knowlesi using the more analytically sensitive HiLAMP-Pk assay is yet to be similarly validated.

Nevertheless, it is well recognized that P. knowlesi parasitemia can rise rapidly and cause severe disease. Given the diagnostic limitations of currently available tests, there is a need to develop more sensitive diagnostic tools to facilitate early identification of infection with this parasite. Although microscopy may be the main stay of diagnosis for individual symptomatic patients, albeit without specificity, the HiLAMP-Pk assay offers a good analytical sensitivity, rapid turnaround time, capability of the platform to be performed in resource-limited settings, and potential for high throughput when multiple samples require testing. Therefore, with further refinement and validation, HiLAMP-Pk may have a potential role to
play as a diagnostic tool for early detection of *P. knowlesi* in resource-limited settings.

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**REFERENCES**