RESEARCH Open Access



The presence of *Plasmodium malariae* and *Plasmodium knowlesi* in near malaria elimination setting in western Indonesia

Irbah Rea Alvieda Nainggolan¹, Rycha Dwi Syafutri¹, Monica Nadya Sinambela¹, Clara Devina², Handayani², Beby Syofiani Hasibuan², Sriwipa Chuangchaiya³, Paul C. S. Divis⁴, Zulkarnain Md Idris⁵, Ranti Permatasari⁶ and Inke Nadia Diniyanti Lubis^{2*}

Abstract

Background: Indonesia is progressing towards malaria elimination. To achieve this goal, intervention measures must be addressed to cover all *Plasmodium* species. Comprehensive control measures and surveillance programmes must be intensified. This study aims to determine the prevalence of microscopic and submicroscopic malaria in Langkat district, North Sumatera Province, Indonesia.

Methods: A cross-sectional survey was conducted in six villages in Langkat district, North Sumatera Province in June 2019. Data were recorded using a standardized questionnaire. Finger pricked blood samples were obtained for malaria examination using rapid diagnostic test, thick and thin blood smears, and polymerase chain reaction.

Results: A total of 342 individuals were included in the study. Of them, one (0.3%) had a microscopic *Plasmodium malariae* infection, no positive RDT examination, and three (0.9%) were positive for *P. malariae* (n = 1) and *Plasmodium knowlesi* (n = 2). The distribution of bed net ownership was owned by 40% of the study participants. The participants had a house within a radius of 100–500 m from the forest (86.3%) and had the housing material of cement floor (56.1%), a tin roof (82.2%), wooden wall (35.7%), bamboo wall (28.1%), and brick wall (21.6%).

Conclusion: Malaria incidence has substantially decreased in Langkat, North Sumatera, Indonesia. However, submicroscopic infection remains in the population and may contribute to further transmission. Surveillance should include the detection of microscopic undetected parasites, to enable the achievement of malaria elimination.

Keywords: Malaria, Indonesia, North Sumatera, Elimination, P. knowlesi, P. malariae

Background

Indonesia has shown significant progress towards a malaria-free zone within the last decade with a reduction in 50% of cases and 66% of deaths due to malaria [1]. Aggressive efforts in scaling up diagnostic and treatment measures with a tailored intervention for each district of

the country are essential to achieve malaria-free by 2030 [2, 3]. Nevertheless, despite the effort to scale up control measures by the government, there were still an estimated 784,854 cases and 1443 deaths due to malaria in 2020 [4]. Furthermore, in 2020, Indonesia is one of two countries in Southeast Asia failing to achieve the WHO Global Technical Strategy with 40% reduction of cases and deaths compared to 2015 [5].

Microscopic examination is currently the gold standard for malaria diagnosis, however, misdiagnosis occurs in cases of low parasitaemia as well as incorrect species

Full list of author information is available at the end of the article



© The Author(s) 2022. **Open Access** This article is licensed under a Creative Commons Attribution 4.0 International License, which permits use, sharing, adaptation, distribution and reproduction in any medium or format, as long as you give appropriate credit to the original author(s) and the source, provide a link to the Creative Commons licence, and indicate if changes were made. The images or other third party material in this article are included in the article's Creative Commons licence, unless indicated otherwise in a credit line to the material. If material is not included in the article's Creative Commons licence and your intended use is not permitted by statutory regulation or exceeds the permitted use, you will need to obtain permission directly from the copyright holder. To view a copy of this licence, visit http://creativeccommons.org/licenses/by/4.0/. The Creative Commons Public Domain Dedication waiver (http://creativecommons.org/publicdomain/zero/1.0/) applies to the data made available in this article, unless otherwise stated in a credit line to the data.

^{*}Correspondence: inke.nadia@usu.ac.id

² Department of Paediatrics, Faculty of Medicine, Universitas Sumatera Utara, Medan 20155, Indonesia

identification [6]. Rapid diagnostic test (RDT) is commonly used to diagnose malaria in remote areas where expertise are not available [7], and for lower density infections, polymerase chain reaction (PCR) has higher sensitivity and is used extensively for malaria surveillance and research, yet it has limitations as a routine diagnostic method [8].

In near to elimination settings, there are several challenges to approach its elimination goal. There is a shift in the trend of malaria infection with a decrease of Plasmodium falciparum infection prevalence to an increase of non-P. falciparum infection prevalence. This is a concern as the current malaria elimination strategies are focusing on P. falciparum and Plasmodium vivax infections [9], and the current control measures might not be suitable to reduce other non-falciparum and non-vivax infections. Furthermore, the submicroscopic infection is a major malaria elimination challenge that is manifested without any symptoms but remains as a source of transmission for malaria infection [10]. In low transmission areas, microscopic examination misses a considerable proportion of parasites due to submicroscopic infections that persist longer because of the absence of proper treatment [10, 11].

The prevalence of submicroscopic malaria infection in Langkat was 33.5% with falciparum malaria infection being the most common type of malaria infection in that area [12]. This study aims to describe the prevalence of malaria infection both by microscopic and

submicroscopic examination. The results of this study can inform the stakeholders of the importance of molecular surveillance in the regions where malaria is almost eliminated.

Methods

Ethics statement

The study was conducted in accordance with the Declaration of Helsinki and was approved by the Ethics Committee of the Faculty of Medicine, Universitas Sumatera Utara (No. 179/TGL/KEPK FK-USU-RSUPHAM/2019). Survey subjects were informed by the local health district personnel of the purpose and procedures of the study, and a written informed consent was obtained from each adult participant at study registration. In the case of individuals < 18 years, written informed consents were sought from their parents or legal guardians.

Study sites and sample collection

A cross-sectional study was conducted in six villages (i.e. Garunggang, Telagah, Bunga Rinte, Parit Bindu, Adin Tengah and Pajok) in Langkat district, North Sumatera Province, Indonesia in June 2019 (Fig. 1). Langkat has an area of 6263.29 km² with an altitude of 4–105 m above sea level. The population of Langkat was estimated 1,041,775 inhabitants in 2019 [13]. All villages have the same environmental characteristics with their location on the forest fringes. Farming is the major economic



Nainggolan et al. Malaria Journal (2022) 21:316

activity for the villagers with major crops including rice and vegetables.

The sample size for study participants was calculated using the following Cochran's formula: $N = z^2 p (1 - p)$ e2, where z is the confidence interval which is set at 95% (z-value of 1.96); (p) is the expected prevalence of malaria infections of 34% from a previous study [12] and (e) is the allowed error margin which is set to 5%. In addition, contingencies were adjusted by adding another 10% of individuals, giving a minimum of 334 participants to be sampled. A convenience sampling strategy was used in this study. The village leaders and household heads were informed about the objectives and procedures of the study, and were asked to invite residents and family members to come to the selected survey point to participate. The inclusion criteria were individuals aged over 6 months old, had been living in the area for at least 6 months and consented to participate in the study. Meanwhile, the exclusion criteria were physically or mentally unfit individuals and incomplete examination data. A standardized questionnaire was used to collect sociodemographic information from each participant.

Field and laboratory methods

Blood sample was collected from finger pricked and spotted on glass slides for thick and thin blood film, onto malaria RDT (CareStart[™] Malaria HRP2/pLDH [Pf/ PAN], AccessBio Inc, USA), onto the Whatman 3MM filter paper (Whatman International, UK) for molecular screening, and onto a microcuvette for Hb examination using the HemoCue® Hb 301 (HemoCue, Sweden). The malaria RDT kit and Hb examination were performed according to the manufacturer's instructions and read on site. Similarly, thin and thick blood films were prepared on site, stored in slide boxes and transported to the Parasitology Laboratory, at the Faculty of Medicine, Universitas Sumatera Utara. Thin blood films were fixed with methanol and all films were stained with 3% Giemsa solution (Sigma-Aldrich, Germany) for 30 min and examined under oil immersion ($10 \times 100 \times$ magnification) by experienced microscopists. Blood films were defined as negative if no parasites were found after examining 1000 × high power microscopy fields. For any positive samples, malaria species were identified and asexual parasite forms were counted against 200 leukocytes. Gametocytes counts were separately recorded. Parasite density was estimated from parasite counts, assuming that there were 8000 leukocytes per µl of blood. All slides were independently re-examined by two experienced microscopists blinded to the first microscopy reading results. Discrepancies between the two readings were resolved by a third experienced microscopist.

For the detection by molecular screening, blood spotted filter papers were air-dried thoroughly at ambient temperature before sealed in individual zipped plastic bags and stored at the $-20\,^{\circ}$ C. The molecular analysis was performed at the laboratory in the Faculty of Medicine, Universitas Sumatera Utara, Medan. DNA was extracted using Chelex method [14], and PCR amplification for *Plasmodium* spp. identification was conducted following previously published methods targeting the 18S rRNA, and confirmation of *P. knowlesi* infection was done using PCR targeting the *sicavar* genes [12, 15, 16].

Statistical analysis

The data collected were double entered into Microsoft Excel (version 2016) spreadsheets and cross-checked for errors. Then, the data were processed and analysed using SPSS software (IBM, version 25). The data were presented as a frequency distribution table and analysed with Fisher's exact test ($P \le 0.05$) to identify the risk factors of submicroscopic malaria as well the correlation with related variables evaluated.

Results

Characteristic of respondents

A total of 342 participants were enrolled in this study (Table 1). The majority of participants were female (68.4%), aged > 18 years (75.4%) with a median age 39 years old, and belong to Batak Karo ethnicity (97.7%). Over half of the participants (59.4%) had an occupation related to the forest, 75.7% had a history of going to the forest, but a very small numbers (4.4%) had to spend the night at the forest. Roughly about 40% also admitted to use the bed net while sleeping (Table 2). Most of the participants (86.3%) had a house within a radius of 500 m from the forest, and the houses mostly constructed with wooden wall (35.7%), cement floor (56.1%) and corrugated iron roofs (82.2%). None of the previously reported risk factors [17–19] to malaria was associated with submicroscopic malaria infection.

Prevalence of malaria infection

The prevalence of malaria by microscopy, RDT and PCR is shown in Table 3. Only one individual (0.3%) was positive for *P. malariae* by microscopy, with asexual and sexual parasite densities of 1160 and 2320 parasites μ/L of blood, respectively (Fig. 2). No positive result from RDT examination. Using molecular analysis, three additional submicroscopic infections were detected. Although the *P. malariae* detected by microscopy came up undetected molecularly (DNA concentration of 31.050 ng/μl). None of the common human malaria parasites were detected, while *P. knowlesi* and *P. malariae* infections contributing to 1.2% positivity. All of the infections occurred in

Nainggolan et al. Malaria Journal (2022) 21:316 Page 4 of 7

Table 1 Demographic characteristic of participants

| Demographic charateristic | n | % |
|---------------------------|-----|------|
| Total | 342 | 100 |
| Gender | | |
| Male | 108 | 31.6 |
| Female | 234 | 68.4 |
| Age group | | |
| 0–5 | 28 | 8.2 |
| 6–18 | 56 | 16.4 |
| >18 | 258 | 75.4 |
| Study village | | |
| Garunggang | 67 | 19.6 |
| Telagah | 53 | 15.5 |
| Bunga Rinte | 51 | 14.9 |
| Parit Bindu | 73 | 21.3 |
| Adin Tengah | 25 | 7.3 |
| Pajok | 73 | 21.3 |
| Ethnicity | | |
| Batak Karo | 334 | 97.7 |
| Others (Jawa, Malay) | 8 | 2.3 |
| Occupation | | |
| Forested occupation | 213 | 59.4 |
| Non-forested occupation | 113 | 33.0 |
| Housewives | 26 | 7.6 |
| Anemia (Hb<11 g/dl) | 28 | 8.2 |
| Fever | 2 | 0.5 |

Table 2 Risk factors to malaria infection

| Risk factors | n | % |
|--|-----|------|
| House construction | | |
| Floor | | |
| Cement | 192 | 56.1 |
| Soil | 68 | 19.9 |
| Other | 82 | 24 |
| Roof | | |
| Corrugated iron | 281 | 82.2 |
| Thatch | 39 | 11.4 |
| Other | 22 | 6.4 |
| Wall | | |
| Wooden | 122 | 35.7 |
| Bamboo | 96 | 28.1 |
| Brick | 74 | 21.6 |
| Other | 50 | 14.6 |
| House and forest within 500 m radius | 295 | 86.3 |
| Occupation related to the forest | 203 | 59.4 |
| History going to the forest | 259 | 75.7 |
| History of spend the night at the forest | 15 | 4.4 |
| Bed net ownership | 144 | 42.1 |

Table 3 Prevalence of malaria infections among the population (N=342) living in Langkat district, North Sumatera Province, Indonesia

| Malaria diagnosis methods | Prevalence, n (%) | Species |
|------------------------------|-------------------|-------------|
| Microscopy | 1 (0.3) | P. malariae |
| RDT | 0 | 0 |
| PCR | | |
| 18sRNA | 1 (0.3) | P. malariae |
| sicavar | 2 (0.6) | P. knowlesi |

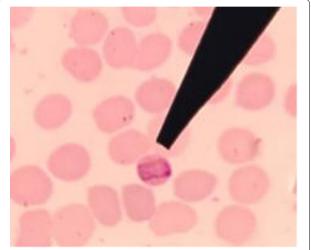


Fig. 2 Microscopic examination shows band form of *Plasmodium malariae*

women aged > 18 years with asymptomatic clinical manifestation and one respondent had an anaemia (Hb level was 8.7~g/dl).

Discussion

This study was done as a follow-up study conducted at the same study sites in 2015. A significant decline was observed in the prevalence of microscopic malaria in the area from 16.5% to 0.3%. The dramatic reduction was also seen in the submicroscopic infection [11]. This suggested a successful control efforts in the near elimination settings in North Sumatera province, Indonesia. The absence of the most common human malaria infections, *P. falciparum* and *P. vivax*, indicating the control interventions for these species are effective.

The malaria control programme named "Gebrak Malaria" was started in 2009 with several control measures, such as active and passive case finding, mass blood surveys and malariometric surveys, effective drug administration, vector control and surveillance. These interventions were conducted to reduced malaria burden and

accelerate the target of Indonesia being malaria-free by 2030 [20].

Both microscopic and submicroscopic examination in this study found non-falciparum malaria. Previously, a significant reduction of falciparum malaria infection in the population has been associated with an increased in the prevalence of *P. malariae* and *P. ovale* by 2 and 6 times, respectively [9]. *Plasmodium malariae* infection causes prolonged infection, but also reactivation after decades, and remain in the body as asymptomatic infection [21]. Further, its 72-h intra-erythrocytic cycle may cause this species to evade anti-malarial exposure [22]. Studies in Ghana, Uganda and Indonesia have reported *P. malariae* recurrences after 3-days treatment with ACT, suggesting that the universal treatment for malaria might not be appropriate enough to support human malaria elimination particularly for *P. malariae* [23–25].

The continuing trends of decreased incidence in human-only malaria in Sabah, and an increased in knowlesi malaria explains that the current control measures are mainly addressing human-malaria only. *P. knowlesi* has more complex factors contributing in its life cycle, involving humans, the mosquito vectors and the macaque hosts. Environmental factors such as deforestation and land-use change contributed to more competent vectors, increased breeding sites which in favour to an increase in knowlesi transmission [18, 26, 27]. Hence, the standard malaria prevention is not sufficient, and there is a need of *P. knowlesi* specific control measures.

There were several limitations in this study. First, all malaria infections detected occurred in females. The participants were screened for only one day in each survey area, and screening was done between 9 am and 4 pm. The study sites were located in the middle of the forest, and most of the male residents work in the forest and return to the village at dawn. This may have increased female participation (68%) and caused a sampling bias in this study. Although a low proportion of P. knowlesi infection was detected among females, knowlesi malaria is mostly found in men [28], who have more exposure to forestry and agricultural activities [17]. Plasmodium knowlesi infection is also more common in adults and usually among older individuals compared to falciparum and vivax malaria [28]. The presence of asymptomatic infections in these individuals could be due to the immunity to the malaria parasite [17].

A very low prevalence of malaria was found in this study. Surprisingly, the only parasite detected by microscopy resulted in a negative PCR. One of the possibilities was DNA degradation due to improper collection and storage of the filter papers [6, 8]. Filter paper stored at 30 °C with 60% humidity reduced the

sensitivity by 100 times than the whole blood samples on PCR detection of malaria parasites [29]. The study sites are located in remote villages in Langkat district with a long journey to the preferred research laboratory. The storage of the samples were at room temperature before being transported for examination, and might have affected the quality of the samples. Furthermore, the utility of an RNA-preserving medium to store blood samples in areas distant to a laboratory, the use of more sensitive RNA extraction protocol and PCR assay using different gene targets and methods may increase the sensitivity of malaria detection, and may exclude a possible false-negative finding in this study [30, 31].

Despite the limitations of this study, the possibility of successful malaria control resulting in significant decline of malaria burden in these areas was could not completely ruled out. The incidence of microscopic and submicroscopic malaria in the same study areas in 2015 were 33.5% and 13.6%, respectively. Four *Plasmodium* species except *P. ovale* were detected [12]. In contrast, the malaria prevalence by microscopy and PCR were already at a very low level. Only one sample was positive by microscopy, and none of the common human malaria was detected. This supported the hypothesis that the malaria control measures have been successful in this study sites. Furthermore, malaria transmission is very sensitive to weather changes with the transmission peak at the end of the rainy season [32]. This study was conducted during the dry season, while the samples collection in the 2015 study was during the rainy season [12, 13], therefore further decrease in malaria prevalence may occur. The use of serological detection may explain the trend of malaria transmission in the study areas.

Conclusion

Indonesia aims to become malaria free area by 2030. Follow-up survey in Langkat district, North Sumatera province showed a substantial decrease of malaria prevalence to 1.2%. Submicroscopic infection contributed to 75% of these malaria cases. *Plasmodium malariae* and *P. knowlesi* were the only malaria species detected suggesting the control efforts for human malaria may be effective in reducing the malaria burden in the area. Additional strategies are still needed to accelerate malaria elimination by intensification of vector control, targeting the submicroscopic malaria, and the interruption of the non-human malaria parasite transmission, thus Indonesia can achieve its target to be malaria free.

Nainggolan et al. Malaria Journal (2022) 21:316 Page 6 of 7

Abbreviations

ACD: Active case detection; MBS: Mass blood survey; PCR: Polymerase chain reaction; RDT: Rapid diagnostic test; RBM: Roll Back Malaria; SDGs: Sustainable Development Goals.

Acknowledgements

We would like to thank the study populations, village leaders, and local midwives for their support and assistance during the study. We are grateful to all members of the research team. We are grateful to Dinas Kesehatan Provinsi Sumatera Utara (Provincial Health Office) for providing the RDT to the study.

Author contributions

INDL, ZMI, PCSD, SC, BSH, RP and IRAN conceived and designed the study. IRAN, RDS, MN and INDL performed the fieldwork. IRAN, RP and INDL performed data cleaning and analysed the data. IRAN, BSH, RP and INDL interpreted the data. IRAN wrote the first draft of the manuscript. INDL, BSH, RP, ZMI, PCSD and SC provided critical revision on the manuscript for important intellectual content. All authors read and approved the final manuscript.

Funding

This study was supported by Talenta Funding from Universitas Sumatera Utara (250/UN5.2.3.1/PPM/SPP-TALENTA USU/2020, 352/UN5.2.3.1/PPM/SPP-TALENTA USU/2020) and ASEAN Science Technology and Innovation Fund (ASTIF) (FF-2019-124) from the ASEAN Secretariat.

Availability of data and materials

The dataset used and/or analysed during the current study are available from the corresponding author upon request.

Declarations

Consent for publication

All authors approved the final draft for journal submission.

Competing interests

The authors declare no competing financial interests.

Author details

¹Faculty of Medicine, Universitas Sumatera Utara, Medan 20155, Indonesia. ²Department of Paediatrics, Faculty of Medicine, Universitas Sumatera Utara, Medan 20155, Indonesia. ³Department of Community Health, Faculty of Public Health, Kasetsart University, Chalermphrakiat Sakon Nakhon Province Campus, 47000 Sakon Nakhon, Thailand. ⁴Malaria Research Centre, Faculty of Medicine and Health Sciences, Universiti Malaysia Sarawak, 94300 Kota Samarahan, Sarawak, Malaysia. ⁵Department of Parasitology and Medical Entomology, Faculty of Medicine, Universiti Kebangsaan Malaysia, 56000 Cheras, Kuala Lumpur, Malaysia. ⁶Department of Clinical Pathology, Faculty of Medicine, Universitas Sumatera Utara, Medan 20155, Indonesia.

Received: 21 June 2022 Accepted: 18 October 2022 Published online: 05 November 2022

References

- Sitohang V, Sariwati E, Fajariyani SB, Hwang D, Kurnia B, Hapsari RK, et al. Malaria elimination in Indonesia: halfway there. Lancet Glob Health. 2018;6:604–6.
- WHO. Global technical strategy for malaria 2016–2030. Geneva: World Health Organization; 2015. Accessed 28 Feb 2021.
- Siahaan L, Eyanoer P, Panggabean M. Optimization of diagnostic procedures in primary health services to detect asymptomatic malaria. Fam Med Primary Care Rev. 2018;20:67–70.
- 4. WHO. World malaria report 2021. Geneva: World Health Organization; 2021. Accessed 21 Jun 2022.
- WHO. Global technical strategy for malaria 2016–2030, 2021 update. Geneva: World Health Organization; 2021.
- Kang JM, Cho PY, Moe M, Lee J, Jun H, Lee HW, et al. Comparison of the diagnostic performance of microscopic examination with nested

- polymerase chain reaction for optimum malaria diagnosis in Upper Myanmar. Malar J. 2017;16:119.
- DÍallo MA, Diongue K, Ndiaye M, Gaye A, Deme A, Badiane AS, et al. Evaluation of CareStart™ Malaria HRP2/pLDH (Pf/pan) Combo Test in a malaria low transmission region of Senegal. Malar J. 2017;16:328.
- Li P, Zhao Z, Wang Y, Xing H, Parker DM, Yang Z, et al. Nested PCR detection of malaria directly using blood filter paper samples from epidemiological surveys. Malar J. 2014;13:75.
- Yman V, Wandell G, Mutemi DD, Miglar A, Asghar M, Hammar U, et al. Persistent transmission of *Plasmodium malariae* and *Plasmodium ovale* species in an area of declining *Plasmodium falciparum* transmission in eastern Tanzania. PLoS Neol Trop Dis. 2019;13: e0007414.
- Harris I, Sharrock WW, Bain LM, Gray KA, Bobogare A, Boaz L, et al. A large proportion of asymptomatic *Plasmodium* infections with low and sub-microscopic parasite densities in the low transmission setting of Temotu Province, Solomon Islands: challenges for malaria diagnostics in an elimination setting. Malar J. 2010;9:254.
- Okell LC, Ghani AC, Lyons E, Drakeley CJ. Submicroscopic infection in Plasmodium falciparum-endemic populations: a systematic review and meta-analysis. J Infect Dis. 2009;200:1509–17.
- 12. Lubis IN, Wijaya H, Lubis M, Lubis CP, Divis PC, Beshir K, et al. Contribution of *Plasmodium knowlesi* to multispecies human malaria infections in North Sumatera, Indonesia. J Infect Dis. 2017;215:1148–55.
- 13. Pemerintah kabupaten Langkat. Langkat: Kabupaten Langkat; 2014. Iklim dan wilayah; 2014; https://www.langkatkab.go.id/page/14/iklim-dan-wilayah. Accessed 23 Mei 2019.
- Plowe CV, Djimde A, Bouare M, Doumbo O, Wellems TE. Pyrimethamine and proguanil resistance-conferring mutations in *Plasmodium falciparum* dihydrofolate reductase: polymerase chain reaction methods for surveillance in Africa. Am J Trop Med Hyg. 1995;52:565–8.
- Singh B, Bobogare A, Cox-Singh J, Snounou G, Abdullah MS, Rahman HA. A genus- and species-specific nested polymerase chain reaction malaria detection assay for epidemiologic studies. Am J Trop Med Hyg. 1999;60:687–92.
- Imwong M, Madmanee W, Suwannasin K, Kunasol C, Peto TJ, Tripura R, et al. Asymptomatic natural human infections with the simian malaria parasites *Plasmodium cynomolgi* and *Plasmodium knowlesi*. J Infect Dis. 2019;219(5):695–702.
- Zhao Y, Zeng J, Zhao Y, Liu Q, He Y, Zhang J, et al. Risk factors for asymptomatic malaria infections from seasonal cross-sectional surveys along the China-Myanmar border. Malar J. 2018;17:247.
- Cooper DJ, Rajahram GS, William T, Jelip J, Mohammad R, Benedict J, et al. Plasmodium knowlesi malaria in Sabah, Malaysia, 2015–2017: ongoing increase in incidence despite near-elimination of the human-only Plasmodium species. Clin Infect Dis. 2020;70:361–7.
- WHO. Disease surveillance for malaria control: an operation manual. Geneva: World Health Organization; 2012. Accessed 22 Jul 2022.
- 20. Elyazar IR, Hay SI, Baird JK. Malaria distribution, prevalence, drug resistance and control in Indonesia. Adv Parasitol. 2011;74:44–175.
- Camargo-Ayala PA, Cubides JR, Niño CH, Camargo M, Rodríguez-Celis CA, Quiñones T, et al. High *Plasmodium malariae* prevalence in an endemic area of the Colombian Amazon Region. PLoS ONE. 2016;11: e0159968.
- Rutledge GG, Marr I, Huang GK, Auburn S, Marfurt J, Sanders M, et al. Genomic characterization of recrudescent *Plasmodium malariae* after treatment with artemether/lumefantrine. Emerg Infect Dis. 2017:23:1300–7.
- 23. Dinko B, Oguike MC, Larbi JA, Bousema T, Sutherland CJ. Persistent detection of *Plasmodium falciparum*, *P. malariae*, *P. ovale curtisi* and *P. ovale wallikeri* after ACT treatment of asymptomatic Ghanaian school-children. Int J Parasitol Drugs Drug Resist. 2013;3:45–50.
- Betson M, Sousa-Figueiredo JC, Atuhaire A, Arinaitwe M, Adriko M, Mwesigwa G, et al. Detection of persistent *Plasmodium* spp. infections in Ugandan children after artemether-lumefantrine treatment. Parasitology. 2014;141:1880–90.
- Lubis IN, Wijaya H, Lubis M, Lubis CP, Beshir KB, Staedke SG, et al. Recurrence of *Plasmodium malariae* and *P. falciparum* following treatment of uncomplicated malaria in North Sumatera with dihydroartemisinin-piperaquine or artemether-lumefantrine. Open Forum Infect Dis. 2020;7:ofaa116.

- 26. Davidson G, Chua TH, Cook A, Speldewinde P, Weinstein P. The role of ecological linkage mechanisms in *Plasmodium knowlesi* transmission and spread. EcoHealth. 2019;16:594–610.
- Guerra CA, Snow RW, Hay SI. A global assessment of closed forests, deforestation and malaria risk. Ann Trop Med Parasitol. 2006;100:189–204.
- Daneshvar C, William T, Davis TM. Clinical features and management of Plasmodium knowlesi infections in humans. Parasitology. 2018;145:18–31.
- 29. Färnert A, Arez AP, Correia AT, Björkman A, Snounou G, Rosario VD. Sampling and storage of blood and the detection of malaria parasites by polymerase chain reaction. Trans R Soc Trop Med Hyg. 1999;93:50–3.
- Kucharski M, Tripathi J, Nayak S, Zhu L, Wirjanata G, Pluijm RW, et al. A
 comprehensive RNA handling and transcriptomics guide for highthroughput processing of *Plasmodium* blood-stage samples. Malar J.
 2020:19:363.
- 31. Grigg MJ, Lubis IN, Tetteh KK, Barber BE, William T, Rajahram GS, et al. *Plasmodium knowlesi* detection methods for human infections-diagnosis and surveillance. Adv Parasitol. 2021;113:77–130.
- 32. Ghinai I, Cook J, Hla TT, Htet HM, Hall T, Lubis IN, et al. Malaria epidemiology in central Myanmar: identification of a multi-species asymptomatic reservoir of infection. Malar J. 2017;16:16–25.

Publisher's Note

Springer Nature remains neutral with regard to jurisdictional claims in published maps and institutional affiliations.

Ready to submit your research? Choose BMC and benefit from:

- fast, convenient online submission
- $\bullet\,$ thorough peer review by experienced researchers in your field
- rapid publication on acceptance
- support for research data, including large and complex data types
- gold Open Access which fosters wider collaboration and increased citations
- maximum visibility for your research: over 100M website views per year

At BMC, research is always in progress.

Learn more biomedcentral.com/submissions

