

PRELIMINARY STUDY OF VARIANT K ALLELE - MEROZOITE SURFACE PROTEIN 1 OF PLASMODIUM FALCIPARUM AMONG PATIENTS IN YENAGOA, BAYELSA STATE

Pughikumo Dibo Tabot ^{1*}, Peter Erigbali ¹, Tolulope Alade ², Pughikumo Ogho Crosdale ³, Amos Grace Preye ¹

1. Department of Human Physiology, Niger Delta University, Nigeria.

2. Department of Medical Laboratory Sciences, Niger Delta University, Nigeria.

3. Department of Haematology and Oncology, Niger Delta University, Nigeria.

ABSTRACT

Genetic polymorphism imposes a huge challenge in quest for effective vaccines, and enhanced malaria control. This research aimed at detecting frequency of the K allele - msp-1 gene in malaria infected patients. A total of 25 samples from children (52% males and 48% females) from ages 5 and below was used. Malaria parasites identification was carried out using rapid diagnostic test (RDT) technique. Genotyping of Plasmodium specie was done by Polymerase Chain reaction (PCR). Results from RDT showed 48% of the samples were infected with plasmodium falciparum, 24% in both males and females respectively. PCR showed that the Msp variant k is more prevalent in males than females with the percentage of 20% and 16% respectively. Molecular diagnostic test is more precise and accurate. Further research should be made on the prevalence of the Msp variant k, for enhanced malaria control.

Key Words: Plasmodium Falciparum, Genetic polymorphism, Msp variant k, Malaria.

INTRODUCTION

Malaria, despite huge controlling strides that has been made is still burdensome especially in Africa [37]. Pregnant women and their unborn children are particularly vulnerable to the disease, which causes anemia, low birth weight, premature birth, and infant deaths.

Attention is now on vaccine [21]. To develop a vaccine, it is imperative to understand protective immune mechanisms, identify antigenic targets, and establish robust and reliable assays measuring correlates of protection. Persons who live in regions where malaria is endemic naturally acquire immunity against the disease with increasing numbers of survived infections. This sought of protection is majorly mediated by serum antibodies which control levels of blood-stage parasites [12].

Studies have shown various adversities towards attaining absolute control against the menace. [68], [60], [31]. Molecular characterization of *P. falciparum* enables the investigation of the genetic diversity of its infection within alignment with various factors, such as disease phenotype, age and host immunity [32]. In tandem with current focus, molecular investigations garners support globally [3], [25], [30]. However, dearth of information exists in Bayelsa state, Nigeria .

MATERIALS AND METHODS

Current research ensued at Nucleometrix Research Laboratory, within ultra-modern Tobis clinic, Yenagoa, Bayelsa state. The State is cosmopolitan in nature and located in the southern part of Nigeria, geopolitically located within Latitude 4°15 North, 5°23 South, Longitude 5°22 West and 6°45 East. It has an area of 706km.

In cross section investigation, random samples were selected following ethical committee approval, and statistical package, SPSS was used for analysis of the data. The research was done using Rapid Diagnosis test and molecular diagnosis (PCR technique) methods. The Rapid Diagnosis test is a simple, quick, and cost-effective test used to determine the presence of malaria parasites and utilizes the principle of immuno-chromatography. It has the test strip coated with monoclonal Anti - HRP - II (Test line Pf) which is specific to the histidine-rich protein II of *Plasmodium falciparum*. The result is read 20 minutes after the sample is applied to the test strip. The appearance of lines or colors gives the test result.

The PCR technique involved extraction of the DNA by a Chemical Method and the extracted DNA quantified using Nanodrop 1000 spectrophotometer.

MSP 1 was carried out using forward and reverse primers; MSP1-OF: 5'-

CTAGAAGCTTTAGAAGATGCAGTATTG -3' and MSP1-OR: 5'-

CTTAAATAGTATTCTAATTCAAGTGGATCA-3' respectively on a ABI 9700 Applied Biosystems thermal cycler at a final volume of 30 microlitres for 25 cycles. The PCR then primes below.

MSP1 K genes were amplified using the MSP1 K F: 5'-AATGAAGAAGAAATTACTACAAAAGGTGC-3' and MSP1 K R: 5'-GCTTGCATCAGCTGGAGGGCTTGCACCAGA-3' as forward and reverse primers respectively on the ABI 9700 Applied Biosystems thermal cycler at a final volume of 30 microlitres for 35 cycles.

RESULTS

Twenty-five samples (aged range one to five) were obtained from male and female patients in the ultra-modern, Tobis clinic,. Five was from one year olds, seven samples from age 2, three samples from age 3, five from age 4, and five from age 5.

Table1: Distribution of patients' age and gender.

Age	Male	Female	Total
1	2	3	5
2	4	3	7
3	1	2	3
4	3	2	5
5	3	2	5
Total	13	12	25
Percentage	52%	48%	100%

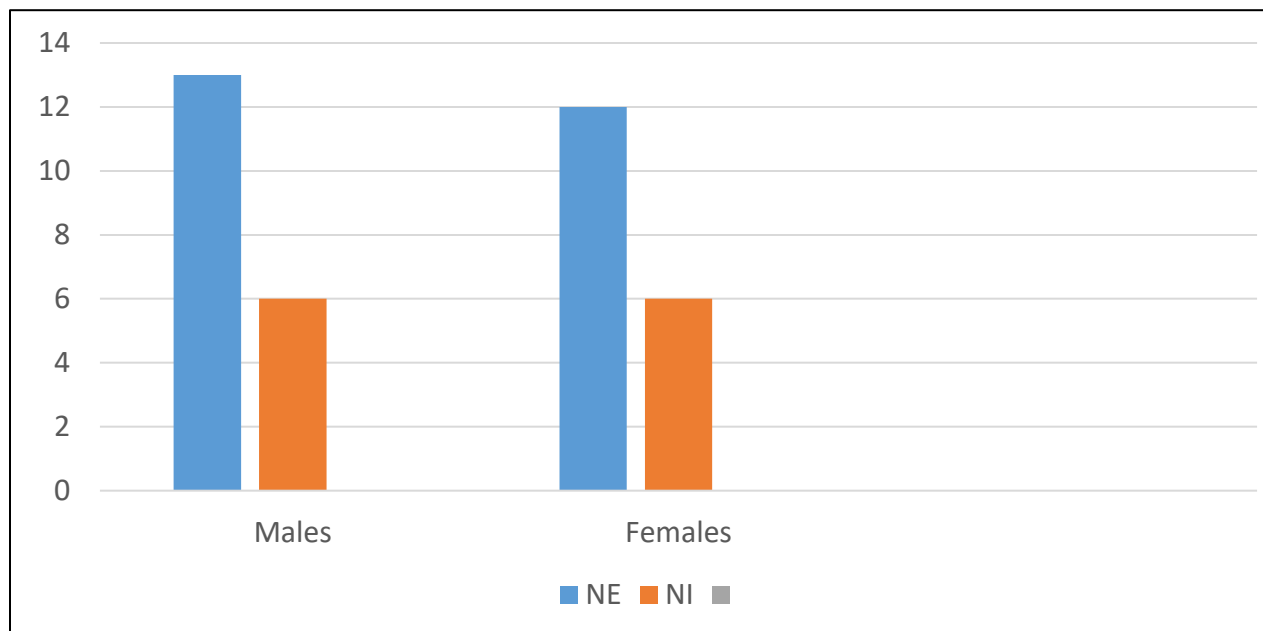
The table below shows the results of malaria tests using the Rapid Diagnosis test method indicating the patients' age and gender. Where; NE= persons assessed , NI= persons Infected

Table 2: Result of Rapid Diagnosis test

Age	Male		Female		Total	
	NE	NI	NE	NI	NE	NI
1	2	1	3	2	5	3
2	4	2	3	1	7	3
3	1	1	2	2	3	3
4	3	1	2	1	5	2
5	3	1	2	0	5	1
Total	13	6	12	6	25	12
Percentage %	52%	24%	48%	24%	100%	48%

Table 3: Distribution table showing the results of molecular diagnosis

Age	Male		Female		Total	
	NE	NI	NE	NI	NE	NI
1	2	1	3	1	5	1
2	4	1	3	0	7	3
3	1	1	2	2	3	3
4	3	2	2	1	5	2
5	3	0	2	0	5	0
Total	13	5	12	4	25	9
Percentage %	52%	20%	48%	16%	100%	36%

**Figure 1: Chart showing results from RDT.**

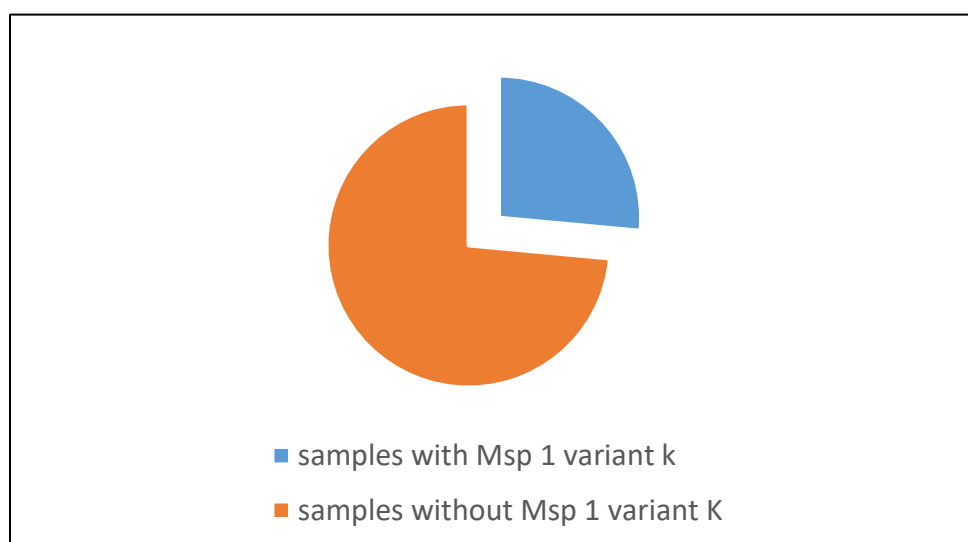


Figure2: Pie chart showing the presence or absence of the Msp variant K.

DISCUSSION

In operation, most RDTs target a *P. falciparum*-specific protein, such as histidine-rich protein II (HRP-II) or lactate dehydrogenase (LDH). Some tests detect both *P. falciparum*-specific and pan-malarial antigens (e.g., aldolase or pan-malaria pLDH), allowing them to differentiate malaria illnesses [38], [35].

The RDT kit used in this study specifically targets HRP-II. A total of 25 samples were tested, and the results (Table 2) indicate that 12 (48%) samples were infected with *P. falciparum*. The distribution by age shows that three samples (12%) were from individuals aged 1, 2, and 3 years, two samples (8%) from age 4, and one sample (4%) from age 5, with infections occurring in both genders.

Diversified genetics awareness is relevant in regulating drug- or vaccine-resistant parasites [70],[26],[69]. The availability of polymorphic genetic markers, combined with the ease of characterizing them through sensitive PCR amplification from field-collected samples [43], [58], [64],[20],[65][20],[71], has facilitated such investigations; and nested PCR, has garnered preference for investigations in spite of its sophistication [65],[7].

In this study (Table 3), PCR analysis of 25 samples revealed that 36% carried the Msp variant K, with 20% of cases occurring in males and 16% in females, all within the 1–5 age group. Specifically, one sample (4%) at age 1, three samples (12%) each at ages 2 and 3, and two samples (8%) at age 4 tested positive for Msp variant K, while no cases were detected at age 5. These results align with findings that PCR is more sensitive than QBC and some RDTs [57]. PCR has demonstrated higher sensitivity and

specificity compared to conventional microscopic examination of stained peripheral blood smears and is now considered the most reliable method for malaria diagnosis [39].

CONCLUSION

The Molecular diagnosis test is more precise and accurate than the Rapid Diagnostic test. From the result above, 48% of samples are infected with *Plasmodium falciparum* and 36% showed the presence of MSP variant K, there's thus a possibility that the Msp variant K is prevalent in Yenagoa, Bayelsa state.

CONTRIBUTION TO KNOWLEDGE

The findings contribute to the understanding of the distribution and epidemiology of Msp variant K, which can inform future disease control and prevention efforts. The study highlights the importance of utilizing multiple diagnostic approaches to gain a more complete understanding of the distribution and prevalence of specific malaria parasite variants. It is thus recommended that further research should be made in the state on the prevalence of the Msp variant k, to ensure rapid control and elimination of the infection. Also, Molecular diagnostic tools should be provided by the government to health sectors to ensure accurate and precise results in molecular testing.

REFERENCES

- [1] Adeoye GO, Nga IC. Comparison of Quantitative Buffy Coat technique (QBC) with Giemsa-stained Thick Film (GTF) for diagnosis of malaria. *Parasitol Int.* 2007; 56:308–12.
- [2] Aonuma H, Suzuki M, Iseki H, Perera N, Nelson B, Igarashi I, et al. Rapid identification of *Plasmodium*-carrying mosquitoes using loop-mediated isothermal amplification. *BiochemBiophys Res Commun.* 2008; 376:671–6.
- [3] Bakhiat AMA, Abdel-muhsin AA, Elzaki SG, Al-Hashami Z, Albarwani HS, Alqamashoui BA, et al. *Plasmodium falciparum* population structure in Sudan post artemisinin-based combination therapy. *Acta Trop.* 2015; 148:97–104.
- [4] Baer K, Klotz C, Kappe SH, et al. Release of hepatic *Plasmodium yoelii* merozoites into the pulmonary microvasculature. *PLoS Pathog.* 2007;3(11): e171.
- [5] Blackman MJ, Heidrich HG, Donachie S, McBride JS, Holder AA. A single fragment of a malaria merozoite surface protein remains on the parasite during red cell invasion and is the target of invasion-inhibiting antibodies. *J Exp Med.* 1990;172(1):379–82.
- [6] Bhandari PL, Raghuveer CV, Rajeev A, Bhandari PD. Comparative study of peripheral blood smear, quantitative buffy coat and modified centrifuged blood smear in malaria diagnosis. *Indian J PatholMicrobiol.* 2008; 51:108–12.

- [7] Bottius E, Guanzirolli A, Trape JF, Rogier C, Konate L, Druilhe P. Malaria: even more chronic in nature than previously thought; evidence for subpatentparasitaemia detectable by the polymerase chain reaction. *Trans R Soc Trop Med Hyg.* 1996; 90:15–9.
- [8] Briggs C, Costa AD, Freeman L, Aucamp I, Ngubeni B, Machin SJ. Development of an automated malaria discriminant factor using VCS technology. *Am J ClinPathol.* 2006; 126:691–8.
- [9] Bharti AR, Patra KP, Chuquiyauri R, Kosek M, Gilman RH, Llanos-Cuentas A, et al. Polymerase chain reaction detection of *Plasmodium vivax* and *Plasmodium falciparum* DNA from stored serum samples: implications for retrospective diagnosis of malaria. *Am J Trop Med Hyg.* 2007; 77:444–6.
- [10] Bell D, Wongsrichanalai C, Barnwell JW. Ensuring quality and access for malaria diagnosis: how can it be achieved? *Nat Rev Microbiol.* 2006;4:S7–S20.
- [11] Beeson JG, Drew DR, Boyle MJ, Feng G, Fowkes FJ, Richards JS. Surface proteins in red blood cell invasion, immunity and vaccines against malaria. *FEMS Microbiol Rev.* 2016;40(3):343–72.
- [12] Cohen S, McGregor IA, Carrington S. Gamma-globulin and acquired immunity to human malaria. *Nature.* 1961; 192:733–7.
- [13] Centers for Disease Control and Prevention (CDC). Malaria. Atlanta, GA: CDC; 2023.
- [14] Chotivanich K, Silamut K, Day NPJ. Laboratory diagnosis of malaria infection—a short review of methods. *Aust J Med Sci.* 2006; 27:11–5.
- [15] Clendennen TE, Long GW, Baird KJ. QBC and Giemsa-stained thick blood films: diagnostic performance of laboratory technologists. *Trans R Soc Trop Med Hyg.* 1995; 89:183–4.
- [16] Doderer C, Heschung A, Guntz P, Cazenave JP, Hansmann Y, Senegas A, et al. A new ELISA kit which uses a combination of *Plasmodium falciparum* extract and recombinant *Plasmodium vivax* antigens as an alternative to IFAT for detection of malaria antibodies. *Malar J.* 2007; 6:19.
- [17] Doolan DL, Mu Y, Unal B, Sundaresh S, Hirst S, Valdez C, et al. Profiling humoral immune responses to *P. falciparum* infection with protein microarrays. *Proteomics.* 2008; 8:4680–94.
- [18] Erdman LK, Kain KC. Molecular diagnostic and surveillance tools for global malaria control. *Travel Med Infect Dis.* 2008; 6:82–99.
- [19] Fleck SL, Birdsall B, Babon J, Dluzewski AR, Martin SR, Morgan WD, et al. Suramin and suramin analogues inhibit merozoite surface protein-1 secondary processing and erythrocyte invasion by *Plasmodium falciparum*. *J Biol Chem.* 2003;278(48):47670–7.
- [20] Felger I, Tavul L, Beck HP. *Plasmodium falciparum*: a rapid technique for genotyping the merozoite surface protein 2. *ExpParasitol.* 1993; 77:372–5.

- [21] Halbroth BR, Draper SJ. Recent developments in malaria vaccinology. *AdvParasitol.* 2015;88:1–49.
- [22] Hawkes M, Kain KC. Advance in malaria diagnosis. *Expert Rev Anti Infect Ther.* 2007;5:1–11.
- [23] Hanscheid T, Grobusch MP. How useful is PCR in the diagnosis of malaria? *Trends Parasitol.* 2002;18:395–8.
- [24] Hanscheid T, Melo-Cristino J, Pinto BG. Automated detection of malaria pigment in white blood cells for the diagnosis of malaria in Portugal. *Am J Trop Med Hyg.* 2001;64:290–2.
- [25] Hamid MMA, Mohammed SB, El-Hassan IM. Genetic diversity of *Plasmodium falciparum* field isolates in Central Sudan inferred by PCR genotyping of merozoite surface protein 1 and 2. *N Am J Med Sci.* 2013;5:95–101.
- [26] Gupta S, Day KP. A strain theory of malaria transmission. *Parasitol Today.* 1994;10:476–81.
- [27] Izumiyama S, Omura M, Takasaki T, Ohmae H, Asahi H. *Plasmodium falciparum*: development and validation of a measure of intraerythrocytic growth using SYBR Green I in a flow cytometer. *ExpParasitol.* 2009;121:144–50.
- [28] Kim SH, Nam MH, Roh KH, Park HC, Nam DH, Park GH, et al. Evaluation of a rapid diagnostic test specific for *Plasmodium vivax*. *Trop Med Int Health.* 2008;13:1495–500.
- [29] Kadekoppala M, Holder AA. Merozoite surface proteins of the malaria parasite: the MSP1 complex and the MSP7 family. *Int J Parasitol.* 2010;40(10):1155–61.
- [30] Lin CS, Uboldi AD, Epp C, Bujard H, Tsuboi T, Czabotar PE, et al. Multiple *Plasmodium falciparum* merozoite surface protein 1 complexes mediate merozoite binding to human erythrocytes. *J Biol Chem.* 2016; 291:7703–15.
- [31] Mohammed H, Kassa M, Mekete K, Assefa A, Taye G, Commons RJ. Genetic diversity of the *msh-1*, *msh-2*, and *glurp* genes of *Plasmodium falciparum* isolates in Northwest Ethiopia. *Malar J.* 2018;17:386.
- [32] Mahdi Abdel Hamid M, Elamin AF, Albsheer MMA, Abdalla AAA, Mahgoub NS, Mustafa SO, et al. Multiplicity of infection and genetic diversity of *Plasmodium falciparum* isolates from patients with uncomplicated and severe malaria in Gezira State, Sudan. *Parasit Vectors.* 2016;9:362.
- [33] Marsh K, Kinyanjui S. Immune effector mechanisms in malaria. *Parasite Immunol.* 2006;28:51–60. doi: 10.1111/j.1365-3024.2006.00808.x.
- [34] Moody A. Rapid diagnostic tests for malaria parasites. *ClinMicrobiol Rev.* 2002;15:66–78.
- [35] McCutchan TF, Piper RC, Makler MT. Use of malaria rapid diagnostic test to identify *Plasmodium knowlesi* infection. *Emerg Infect Dis.* 2008;14:1750–1752.

- [36] Murray CK, Bell D, Gasser RA, Wongsrichanalai C. Rapid diagnostic testing for malaria. *Trop Med Int Health*. 2003;8:876-883.
- [37] Murray CK, Gasser RA Jr, Magill AJ, Miller RS. Update on rapid diagnostic testing for malaria. *ClinMicrobiol Rev*. 2008;21:97-110.
- [38] Mungai M, Tegtmeier G, Chamberland M, Parise M. Transfusion-transmitted malaria in the United States from 1963 through 1999. *N Engl J Med*. 2001;344:1973-1978.
- [39] Morassin B, Fabre R, Berry A, Magnaval JF. One year's experience with the polymerase chain reaction as a routine method for the diagnosis of imported malaria. *Am J Trop Med Hyg*. 2002;66:503-508.
- [40] Mlambo G, Vasquez Y, LeBlanc R, Sullivan D, Kumar N. A filter paper method for the detection of *Plasmodium falciparum* gametocytes by reverse transcription polymerase chain reaction.
- [41] Mens PF, van Amerongen A, Sawa P, Kager PA, Schallig HD. Molecular diagnosis of malaria in the field: development of a novel 1-step nucleic acid lateral flow immunoassay for the detection of all 4 human *Plasmodium* spp. and its evaluation in Mbita, Kenya. *DiagnMicrobiol Infect Dis*. 2008;61:421-427.
- [42] Mendelow BV, Lyons C, Nhlangothi P, Tana M, Munster M, Wypkema E, Liebowitz L, Marshall L, Scott S, Coetzer TL. Automated malaria detection by depolarization of laser light. *Br J Haematol*. 1999;104:499-503.
- [43] Mercereau-Puijalon O, Fandeur T, Bonnefoy S, Jacquemot C, Sarthou JL. A study of the genomic diversity of *Plasmodium falciparum* in Senegal. Typing by the use of the polymerase chain reaction. *Acta Trop*. 1991;49:293-304.
- [44] National Malaria Elimination Programme, National Population Commission, The DHS Program. Nigeria Malaria Indicator Survey 2021 Final Report. Abuja, Nigeria, and Rockville, Maryland, USA; 2022.
- [45] Nguansangiam S, Day NP, Hien TT, Mai NT, Chaisri U, Riganti M, Dondorp AM, Lee SJ, Phu NH, Turner GD, White NJ, Ferguson DJ, Pongponratn E. A quantitative ultrastructural study of renal pathology in fatal *Plasmodium falciparum* malaria. *Trop Med Int Health*. 2007;12:1037-1050.
- [46] Ng OT, Ooi EE, Lee CC, Lee PJ, Ng LC, Pei SW, Tu TM, Loh JP, Leo YS. Naturally acquired human *Plasmodium knowlesi* infection, Singapore. *Emerg Infect Dis*. 2008;14:814-816.
- [47] Ohrt C, Purnomo, Sutamihardia MA, Tang D, Kain KC. Impact of microscopy error on estimates of protective efficacy in malaria prevention trials. *J Infect Dis*. 2002;186:540-546.

- [48] Ochola LB, Vounatsou P, Smith T, Mabaso ML, Newton CR. The reliability of diagnostic techniques in diagnosis and management of malaria in absence of a gold standard. *Lancet Infect Dis.* 2006;6:582-588.
- [49] Oh JS, Kim JS, Lee CH, Nam DH, Kim SH, Park DW, Lee CK, Lim CS, Park GH. Evaluation of a malaria antibody enzyme immunoassay for use in blood screening. *Mem Inst Oswaldo Cruz.* 2008;103:75-78.
- [50] Patarakul K. Role of DNA microarray in infectious diseases. *Chula Med J.* 2008;52:147-153.
- [51] Palacios G, Quan PL, Jabado OJ, Conlan S, Hirschberg DL, Liu Y, Zhai J, Renwick N, Hui J, Hegyi H, Grolla A, Strong JE, Towner JS, Geisbert TW, Jahrling PB, Büchen-Osmond C, Ellerbrok H, Sanchez-Seco MP, Lussier Y, Formenty P, Nichol MS, Feldmann H, Briese T, Lipkin WI. Panmicrobial oligonucleotide array for diagnosis of infectious diseases. *Emerg Infect Dis.* 2007;13:73-81.
- [52] Padial MM, Subirats M, Puente S, Lago M, Crespo S, Palacios G, Baquero M. Sensitivity of laser light depolarization analysis for detection of malaria in blood samples. *J Med Microbiol.* 2005;54:449-452.
- [53] Park JW, Yoo SB, Oh JH, Yeom JS, Lee YH, Bahk YY, Kim YS, Lim KJ. Diagnosis of vivax malaria using an IgM capture ELISA is a sensitive method, even for low levels of parasitemia. *Parasitol Res.* 2008;103:625-631.
- [54] Prommano O, Chaisri U, Turner GD, Wilairatana P, Ferguson DJ, Viriyavejakul P, White NJ, Pongponratn E. A quantitative ultrastructural study of the liver and the spleen in fatal falciparum malaria. *Southeast Asian J Trop Med Public Health.* 2005;36:1359-1370.
- [55] Payne D. Use and limitations of light microscopy for diagnosing malaria at the primary health care level. *Bull World Health Organ.* 1988;66:621-628.
- [56] Poon LL, Wong BW, Ma EH, Chan KH, Chow LM, Abeyewickreme W, Tangpukdee N, Yuen KY, Guan Y, Looareesuwan S, Peiris JS. Sensitive and inexpensive molecular test for falciparum malaria: detecting *Plasmodium falciparum* DNA directly from heat-treated blood by loop-mediated isothermal amplification. *Clin Chem.* 2006;52:303-306.
- [57] Rakotonirina H, Barnadas C, Raherijafy R, Andrianantenaina H, Ratsimbaoa A, Randrianasolo L, Jahevitra M, Andriantsoanirina V, Ménard D. Accuracy and reliability of malaria diagnostic techniques for guiding febrile outpatient treatment in malaria-endemic countries. *Am J Trop Med Hyg.* 2008;78:217-221.
- [58] Ranford-Cartwright LC, Balfe P, Carter R, Walliker D. Genetic hybrids of *Plasmodium falciparum* identified by amplification of genomic DNA from single oocysts. *MolBiochemParasitol.* 1991;49:239-244.

- [59] Raper C, Elhassan IM, Hviid L, Giha H, Richardson W, Babiker H, Satti GMH, Theander TG, Amot DE. Detection of very low level *Plasmodium falciparum* infections using the nested polymerase chain reaction and a reassessment of the epidemiology of unstable malaria in Sudan. *Am J Trop Med Hyg.* 1996;54:325-331.
- [60] Soe TN, Wu Y, Tun MW, Xu X, Hu Y, Ruan Y, et al. Genetic diversity of *Plasmodium falciparum* populations in Southeast and western Myanmar. *Parasit Vectors.* 2017;10:322.
- [61] Singh S, Chitnis CE. Molecular signaling involved in entry and exit of malaria parasites from host erythrocytes. *Cold Spring Harb Perspect Med.* 2017;7(10):a026815. doi: 10.1101/cshperspect.a026815.
- [62] She RC, Rawlins ML, Mohl R, Perkins SL, Hill HR, Litwin CM. Comparison of immunofluorescence antibody testing and two enzyme immunoassays in the serologic diagnosis of malaria. *J Travel Med.* 2007;14:105-111.
- [63] Sulzer AJ, Wilson M, Hall EC. Indirect fluorescent-antibody tests for parasitic diseases. An evaluation of a thick-smear antigen in the IFA test for malaria antibodies. *Am J Trop Med Hyg.* 1969;18:199-205.
- [64] Snewin VA, Herrera M, Sanchez G, Scherf A, Langsley G, Herrera S. Polymorphism of the alleles of the merozoite surface antigens MSA1 and MSA2 in *Plasmodium falciparum* wild isolates from Colombia. *Mol Biochem Parasitol.* 1991;49:265-275.
- [65] Snounou G, Viriyakosol S, Zhu X, Jarra W, Pinheiro LE, do Rosario VE, Thaithong S, Brown KN. High sensitivity of detection of human malaria parasites by the use of nested polymerase chain reaction. *Mol Biochem Parasitol.* 1993;61:315-320.
- [66] Sachanonta N, Medana IM, Roberts R, Jones M, Day NP, White NJ, Ferguson DJ, Turner GD, Pongponratn E. Host vascular endothelial growth factor is tropic for *Plasmodium falciparum*-infected red blood cells. *Asian Pac J Allergy Immunol.* 2008;26:37-45.
- [67] Scholl PF, Kongkasuriyachai D, Demirev PA, Feldman AB, Lin JS, Sullivan DJ Jr, Kumar N. Rapid detection of malaria infection in vivo by laser desorption mass spectrometry. *Am J Trop Med Hyg.* 2004;71:546-551.
- [68] Takala SL, Coulibaly D, Thera MA, Batchelor AH, Cummings MP, Escalante AA, et al. Extreme polymorphism in a vaccine antigen and risk of clinical malaria: implications for vaccine development. *Sci Transl Med.* 2010;1:2ra5.
- [69] Tibayrenc M. Beyond strain typing and molecular epidemiology: integrated genetic epidemiology of infectious diseases. *Parasitol Today.* 1998;14:323-329.
- [70] Tibayrenc M, Ayala FJ. Towards a population genetics of microorganisms: the clonal theory of parasitic protozoa. *Parasitol Today.* 1991;7:228-232.

- [71] Viriyakosol S, Siripoon N, Petcharapirat C, Petcharapi. *Plasmodium falciparum*: selective growth of subpopulations from field samples following in vitro culture, as detected by the polymerase chain reaction. *ExpParasitol*. 1994;79:517-525.