

IS MALARIA AN ENTIRELY PREVENTABLE AND TREATABLE

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ABSTRACT

Malaria keeps on killing more than three-times the same number of individuals as every outfitted clash; in 2015, there were an expected 438,000 — 631,000 passings coming about from Malaria, contrasted and an expected 167,000 passings because of outfitted conflicts. In territories of nonstop transmission of malaria, youngsters <5 years old furthermore, the babies of contaminated pregnant ladies experience the most bleakness and mortality from the ailment. Malaria stays a significant weight to individuals living in asset restricted regions in Africa, Asia and Focal and South America. An assessed 214 million cases of Malaria happened in 2015. Africa bears the brunt of the weight, with 88% of the cases, trailed by Southeast Asia (10%), the eastern Mediterranean district (2%) and Focal and South America (<1%).

Keywords: Malaria Vaccine, drug discovery, K13, Artemisinin.

I. INTRODUCTION

Malaria is an illness of tropical and subtropical locales, having been annihilated from calm nations consistently in the course of the most recent 100 years. It is communicated by the nibble of the female Anopheles mosquito (1,2). Illness occurrence depends on ecological reasonableness for neighborhood vectors in wording of elevation, atmosphere, vegetation, and execution of control measures, and subsequently is inseparably connected to destitution, cataclysmic events, and war. More uncommon transmission courses are from mother to youngster, or by means of blood bonding, an uncommon event in non-endemic nations because of blood giver screening systems,(3,4) however a noteworthy hazard in asset poor settings. Expectations as with the impact of environmental change on worldwide Malaria dispersion later on change, yet have proposed the populace in danger of Malaria will increment, specifically in tropical good country territories (5).

II. MALARIA PARASITE AND ITS LIFE CYCLE

Malaria is a vector-borne parasitic tropical ailment found in 91 nations worldwide. There are more than 120 Plasmodium species contaminating warm blooded creatures, winged animals, and reptiles, just six are known to contaminate people Normally (6,7). Plasmodium falciparum delivers significant levels of blood-stage parasites that sequester in basic organs in all age gatherings and cause serious iron deficiency in African youngsters, in whom by far most of Malaria passings happen. Plasmodium vivax ordinarily creates milder ailment, yet can be extreme, and repetitive scenes bring critical related horribleness (8, 9,10). Plasmodium malariae, what's more, the morphologically unclear sympatric species Plasmodium ovale curtisi and Plasmodium ovale wallikeri are understudied, however seriousness of disease is by and large like simple vivax malaria. Plasmodium is a principally zoonotic contamination experienced in southeast Asia that can cause intestinal sickness (11,12).

The mosquito vector sends the Plasmodium spp. parasite in the sporozoite stage to the host during a blood dinner. Inside 30–an hour, sporozoites attack liver cells, where they reproduce and partition as merozoites (13,14). The contaminated liver cell bursts, delivering the merozoites into the circulatory system, where they attack red blood cells and start the abiogenetic conceptive stage, which is the suggestive phase of the infection. Manifestations create 4–8 days after the underlying red platelet attack

(15.16). The replication pattern of the merozoites inside the red platelets endures 36–72 hours (from red platelet attack to haemolysis). Subsequently, in coordinated contaminations (diseases that start from a solitary irresistible chomp), fever happens each 36–72 hours, when the contaminated red platelets lyse and discharge endotoxins (17,18).

Plasmodium vivax and Plasmodium ovale can likewise enter a lethargic state in the liver, the hypnozoite. Merozoites delivered from red platelets can attack other red platelets and keep on recreating, or at times, they separate into male or then again female gametocytes (19, 20, 21). The record factor AP2-G (not appeared) has been appeared to direct the promise to gametocytogenesis. Gametocytes move in skin vessels and are then taken up by the mosquito vector in another blood feast. In the gut of the mosquito, every male gametocyte produces eight microgametes after three rounds of mitosis; the female gametocyte develops into a macrogamete. Male microgametes are motile structures with flagellae and look for the female macrogamete (22, 23). The male and female gametocytes combine, framing a diploid zygote, which stretches into an ookinete; this motile structure exits from the lumen of the gut over the epithelium as an oocyst. Oocysts go through patterns of replication furthermore, structure sporozoites, which move from the mid-region of the mosquito to the salivary organs. Subsequently, 7–10 days after the mosquito benefits from blood containing gametocytes, it might be 'furnished' and ready to taint another human with Plasmodium spp. with her chomp (24,25,26). Medications that forestall Plasmodium spp. attack or expansion in the liver have prophylactic action, drugs that obstruct the red platelet stage are required for the treatment of the indicative period of the illness, and mixes that repress the arrangement of gametocytes or their advancement in the mosquito (counting drugs that execute mosquitoes benefiting from blood) are transmission-blocking specialists (27,28,29).

III. HOW PARASITE ENTERS INTO RED BLOOD CELLS

Intrusion happens through a multistep cycle. During pre-intrusion, low-partiality contacts are framed with the red platelet layer (30). Reorientation of the merozoite is important to empower close contact between parasite ligands and host cell receptors, and this is then trailed by close intersection arrangement. In Plasmodium falciparum, a forward hereditary screen has indicated that supplement rot quickening factor (not appeared) on the host red platelet is fundamental for the intrusion of all P. falciparum strains (31,32). The association of a complex of P. falciparum proteins (PfRH5), PfRH5-connecting protein and cysteine-rich defensive antigen (PfCyRPA)) on the red platelet surface is additionally basic for the intrusion in all strains 261,262. PfRH5 has been concentrated as a potential immunization applicant, and antibodies against basigin have been considered as a likely remedial methodology. During the PfRH5–PfRipr–PfCyRPA–basigin restricting advance, an initial structures between the parasite and the red platelet, and this triggers Ca²⁺ discharge and empowers parasite-delivered proteins to be embedded into the red platelet film (33,34,35). These proteins are emitted from the micronemes (the little secretory organelles that bunch at the apical finish of the merozoite) and from the neck of the rhoptries, and incorporate rhoptry neck protein 2 (PfRON2). Official among PfRON2 and apical film antigen 1 (PfAMA1) on the merozoite surface is required to intervene tight intersection arrangement before the disguise cycle,(36,37) and PfAMA1 is additionally being assessed as an immunization applicant. Parasite replication inside the red platelet requires the combination of DNA, which can be obstructed by a few antimalarials: pyrimethamine (PYR), P218 and cycloquanil target P. falciparum dihydrofolate reductase (PfDHFR)266, and atovaquone (ATO) squares pyrimidine biosynthesis by restraining the outflow of the mitochondrial quality pfcytb (which encodes P. falciparum cytochrome b) (38,39,40) and by forestalling the development of oxidized coenzyme Q, which is expected to empower the pyrimidine biosynthetic protein dihydroorotate dehydrogenase (PfDHODH) to play out its response inside the mitochondria. The stage II clinical competitor DSM likewise squares pyrimidine biosynthesis by straightforwardly restraining PfDHODH1(41,42,43). Notwithstanding DNA blend, different cycles can be focused by antimalarial drugs (44). Chloroquine (CHQ) represses haem polymerization in the food vacuole however can be removed from this compartment by the P. falciparum chloroquine-opposition carrier (PfCRT)(45,46,47). The stage II clinical up-and-comer KAE609 and the

preclinical applicant SJ(557)733 both restrain P. falciparum p-type ATPase 4 (PfATP4), which is required for Na⁺ homeostasis during supplement acquisition(48,49,50). The stage I clinical up-and-comer MMV(390)048 (REF. 191) represses P. falciparum phosphatidylinositol 4-kinase (PfPI(4)K), which is required for the age of transport vesicles that are expected to advance layer modifications during ingress (51-55).

IV. DRUG DISCOVERY AND MALARIA TREATMENT

Medicines for malaria are not generally curative.67–70 Treatment disappointment normally presents as a repeat of manifestations with perceivable parasitaemia(56,57) .Two month and a half after an evidently effective treatment and isn't generally due to sedate opposition. Elective clarifications incorporate high parasite densities (especially in non-invulnerable people), helpless medication bioavailability, non-adherence to treatment, and adulterated or unsatisfactory antimalarials.(58,59,60).

Progress towards Malaria disposal is uneven. Indigenous cases in Europe, focal Asia, Sri Lanka, and a few nations in Latin America are presently amazingly uncommon (61). Nonetheless, in numerous subSaharan African nations, where transmission is most elevated, killing Malariahas demonstrated more troublesome what's more, there are signs that progress toward this path has stalled.1,6,137Areas with common disturbance have encountered generous increments in jungle fever, exemplified by Venezuela (62,63,64). Pilot investigations of mass medication organization (MDA) of ACT with single-portion primaquine to quicken end of medication safe jungle fever in southeast Asia have occurred and early reports propose it is viable The most exhaustive antimalarial revelation portfolio has been created by the not-revenue driven item advancement organization Meds for Malaria Adventure (MMV) as a team with its accomplices in both scholarly world and the pharmaceutical business, with help from benefactors (primarily government offices what's more, generous establishments)(66-70). Promising compound arrangement have been distinguished from three methodologies: speculation driven structure to create options to advertised mixes (for instance, manufactured peroxides, for example, ozonides); target-based screening and levelheaded plan (for instance, screening of inhibitors of P. falciparum dihydroorotate dehydrogenase and phenotypic screening(71-75). Phenotypic screening has been the best way to deal with date,in terms of conveying preclinical up-and-comers and recognizing — through the sequencing of safe freaks — novel sub-atomic targets. Notwithstanding, with propels in the comprehension of parasite science and in sub-atomic science innovation, target-based methodologies will most likely have a considerable job in coming years (76,77,78).Malaria subunit immunizations are intended to give invulnerability against proteins uncovered at basic phases of the lifecycle. Focusing on sporozoite stages by means of one of the surface proteins that intervene homing to the liver and host cell crossing or intrusion plans to decrease recurrence of contamination (79,80,81). The RTS,S/AS01 antibody dependent on P falciparum circumsporozoite protein is the most contemplated immunization (82,83,84).

V. CONCLUSIONS

Over 130 years have gone since the protozoan reason for malaria was found. The advancement towards end in certain nations shows that current devices can be sufficient to dispense with malaria if the correct conditions are set up: political responsibility, admittance to social insurance, and sufficient human furthermore, monetary assets. There is proof that admittance to great ACTs is still excessively low (<25%) in a few areas. The spread of pyrethroid opposition among Anopheles vectors and expanding reports of ACT disappointments in southeast Asia signal that the fateful opening to wipe out malaria with existing apparatuses may be shutting (85,86,87). Expanded assets for ailment control typically as it were come in the midst of emergency, yet a purposeful exertion presently could exploit ongoing additions and quicken progress towards disposal. The antibody isn't viewed as an 'enchantment slug' against intestinal sickness yet is a significant structure hinder towards the advancement of future malaria vaccines (88,89,90).The immunization works by keeping the malaria parasite from entering the liver where it can develop furthermore, increase to cause sickness symptoms. In mid-2015 the world's first malaria immunization Mosquirix (otherwise called RTS,S) was given the green light for use against Plasmodium

falciparum intestinal sickness in Africa. The immunization works by keeping the malaria parasite from entering the liver where it can develop and duplicate to cause ailment indications(91-95).

Despite the fact that the drawn out assurance gave by the immunization has still not been resolved, the best assurance has been seen when the immunization is given to kids matured five to year and a half in three dosages given a month separated, trailed by a sponsor portion following 20 months(96-99).

On the off chance that an malaria parasite gets impervious to an antimalarial tranquilize, the medication takes more time to kill all the parasites in the body and it takes more time for the patient to quit having the manifestations of malaria.

The issue of medication opposition is additionally entangled by a cycle called cross-obstruction. This is when protection from one medication likewise empowers the parasite to be impervious to another medication that works by a comparative system.

VI. REFERENCES

- [1] WHO, World Malaria Report 2014. 2014, WHO: Geneva.
- [2] Fairhurst, R.M., et al., Artemisinin-resistant malaria: research challenges, opportunities, and public health implications. *The American journal of tropical medicine and hygiene*, 2012. 87(2): p. 231-241.
- [3] Siddiqui FA. Malaria Control and Elimination: How Far we are: An Opinion Article. *Journal of Biometrics & Biostatistics* 2016. DOI: 10.4172/2155-6180.1000321
- [4] Wangdahl, A., et al., Severity of Plasmodium falciparum and Non-falciparum Malaria in Travelers and Migrants: A Nationwide Observational Study Over 2 Decades in Sweden. *J Infect Dis*, 2019. 220(8): p. 1335-1345.
- [5] Brashear AM, Roobsoong W, Siddiqui FA, Nguitrangool W, Sattabongkot J, López-Urbe MM, et al. (2019) A glance of the blood stage transcriptome of a Southeast Asian Plasmodium ovale isolate. *PLoS Negl Trop Dis* 13(11): e0007850. <https://doi.org/10.1371/journal.pntd.0007850>
- [6] Draper, S.J., et al., Malaria Vaccines: Recent Advances and New Horizons. *Cell Host Microbe*, 2018. 24(1): p. 43-56.
- [7] Pandey AK, Reddy KS, Sahar T, Gupta S, Singh H, Reddy EJ, Asad M, Siddiqui FA, Gupta P, Singh B, More KR, Mohammed A, Chitnis CE, Chauhan VS, Gaur D. 2013. Identification of a potent combination of key Plasmodium falciparum merozoite antigens that elicit strain transcending parasite-neutralizing antibodies. *Infect. Immun.* 81:441-451. doi:10.1128/IAI.01107-12
- [8] Siddiqui FA, Dhawan S, Singh S, Singh B, Gupta P, Pandey A, Mohammed A, Gaur D, Chitnis CE. 2013. A thrombospondin structural repeat containing rhoptry protein from Plasmodium falciparum mediates erythrocyte invasion. *Cell Microbiol* 15:1341-1356. <https://doi.org/10.1111/cmi.12118>
- [9] White, N.J., Antimalarial drug resistance. *The Journal of clinical investigation*, 2004. 113(8): p. 1084-1092.
- [10] WHO, Global Report on Antimalarial Efficacy and Drug Resistance: 2000-2010. 2010, WHO: Geneva. p. 9-10.
- [11] Yeung, S., et al., Antimalarial drug resistance, artemisinin-based combination therapy, and the contribution of modeling to elucidating policy choices. *The American journal of tropical medicine and hygiene*, 2004. 71(2 suppl): p. 179-186.
- [12] Klayman, D.L., Qinghaosu (artemisinin): an antimalarial drug from China. *Science*, 1985. 228(4703): p. 1049-1055.
- [13] White, N.J., Qinghaosu (artemisinin): the price of success. *Science*, 2008. 320(5874): p. 330-334.
- [14] Ye, R., et al., Distinctive origin of artemisinin-resistant Plasmodium falciparum on the China-Myanmar border. *Scientific reports*, 2016. 6.
- [15] Davis, T., H.A. Karunajeewa, and K.F. Ilett, Artemisinin-based combination therapies for uncomplicated malaria. *Med J Aust*, 2005. 182(4): p. 181-5.
- [16] Fairhurst, R.M. and A.M. Dondorp, Artemisinin-resistant Plasmodium falciparum malaria. *Microbiology spectrum*, 2016. 4(3).

- [17] Straimer, J., et al., K13-propeller mutations confer artemisinin resistance in Plasmodium falciparum clinical isolates. *Science*, 2015. 347(6220): p. 428-431.
- [18] Golenser, J., et al., Current perspectives on the mechanism of action of artemisinins. *International journal for parasitology*, 2006. 36(14): p. 1427-1441.
- [19] O'Neill, P.M., et al., Enantiomeric 1, 2, 4-Trioxanes Display Equivalent in vitro Antimalarial Activity Versus Plasmodium falciparum Malaria Parasites: Implications for the Molecular Mechanism of Action of the Artemisinins. *ChemBioChem*, 2005. 6(11): p. 2048-2054.
- [20] O'Neill, P.M. and G.H. Posner, A medicinal chemistry perspective on artemisinin and related endoperoxides. *Journal of medicinal chemistry*, 2004. 47(12): p. 2945-2964.
- [21] Ashley, E.A., et al., Spread of artemisinin resistance in Plasmodium falciparum malaria. *New England Journal of Medicine*, 2014. 371(5): p. 411-423.
- [22] Hott, A., et al., Artemisinin-resistant Plasmodium falciparum parasites exhibit altered patterns of development in infected erythrocytes. *Antimicrobial agents and chemotherapy*, 2015. 59(6): p. 3156-3167.
- [23] White, N., et al., Averting a malaria disaster. *The Lancet*, 1999. 353(9168): p. 1965-1967.
- [24] von Seidlein, L., et al., Treatment of African children with uncomplicated falciparum malaria with a new antimalarial drug, CGP 56697. *Journal of infectious diseases*, 1997. 176(4): p. 1113-1116.
- [25] Tjitra, E., et al., Therapy of uncomplicated falciparum malaria: a randomized trial comparing artesunate plus sulfadoxine-pyrimethamine versus sulfadoxine-pyrimethamine alone in Irian Jaya, Indonesia. *The American journal of tropical medicine and hygiene*, 2001. 65(4): p. 309-317.
- [26] Adjuik, M., et al., Amodiaquine-artesunate versus amodiaquine for uncomplicated Plasmodium falciparum malaria in African children: a randomised, multicentre trial. *The Lancet*, 2002. 359(9315): p. 1365-1372.
- [27] Barennes, H., et al., A randomized trial of amodiaquine and artesunate alone and in combination for the treatment of uncomplicated falciparum malaria in children from Burkina Faso. *Tropical Medicine & International Health*, 2004. 9(4): p. 438-444.
- [28] Staedke, S.G., et al., Combination treatments for uncomplicated falciparum malaria in Kampala, Uganda: randomised clinical trial. *The Lancet*, 2004. 364(9449): p. 1950-1957.
- [29] Awab, G.R., et al., Clinical trials of artesunate plus sulfadoxine-pyrimethamine for Plasmodium falciparum malaria in Afghanistan: maintained efficacy a decade after introduction. *Malaria journal*, 2016. 15(1): p. 1.
- [30] Dondorp, A.M., et al., Artemisinin resistance in Plasmodium falciparum malaria. *New England Journal of Medicine*, 2009. 361(5): p. 455-467.
- [31] WHO, Status report on artemisinin and ACT resistance - September 2015. 2015 WHO: Geneva.
- [32] Duru, V., et al., Plasmodium falciparum dihydroartemisinin-piperaquine failures in Cambodia are associated with mutant K13 parasites presenting high survival rates in novel piperaquine in vitro assays: retrospective and prospective investigations. *BMC medicine*, 2015. 13(1): p. 1.
- [33] Wang, Z., et al., Prevalence of K13-propeller polymorphisms in Plasmodium falciparum from China-Myanmar border in 2007–2012. *Malaria journal*, 2015. 14(1): p. 1.
- [34] Escobar, C., et al., Polymorphisms in Plasmodium falciparum K13-Propeller in Angola and Mozambique after the Introduction of the ACTs. *PLoS One*, 2015. 10(3): p. e0119215.
- [35] Liu, H., et al., Investigation and control of a Plasmodium falciparum malaria outbreak in Shan Special Region II of Myanmar along the China-Myanmar Border from June to December 2014. *Infectious diseases of poverty*, 2016. 5(1): p. 1.
- [36] Arie, F., et al., A molecular marker of artemisinin-resistant Plasmodium falciparum malaria. *Nature*, 2014. 505(7481): p. 50-55.
- [37] Tun, K.M., et al., Parasite clearance rates in Upper Myanmar indicate a distinctive artemisinin resistance phenotype: a therapeutic efficacy study. *Malaria journal*, 2016. 15(1): p. 1.
- [38] Amaratunga, C., et al., Artemisinin-resistant Plasmodium falciparum in Pursat province, western Cambodia: a parasite clearance rate study. *The Lancet infectious diseases*, 2012. 12(11): p. 1.

- 851-858.
- [39] Tripura, R., et al., Persistent Plasmodium falciparum and Plasmodium vivax infections in a western Cambodian population: implications for prevention, treatment and elimination strategies. *Malaria journal*, 2016. 15(1): p. 1.
- [40] Takala-Harrison, S., et al., Genetic loci associated with delayed clearance of Plasmodium falciparum following artemisinin treatment in Southeast Asia. *Proceedings of the National Academy of Sciences*, 2013. 110(1): p. 240-245.
- [41] O'Brien, C., et al., Recent clinical and molecular insights into emerging artemisinin resistance in Plasmodium falciparum. *Current opinion in infectious diseases*, 2011. 24(6): p. 570.
- [42] Bosman, P., et al., Plasmodium prevalence and artemisinin-resistant falciparum malaria in Preah Vihear Province, Cambodia: a cross-sectional population-based study. *Malaria journal*, 2014. 13(1): p. 1.
- [43] Cheeseman, I.H., et al., A major genome region underlying artemisinin resistance in malaria. *Science*, 2012. 336(6077): p. 79-82.
- [44] Mita, T., et al., Little polymorphism at the K13 propeller locus in worldwide Plasmodium falciparum populations prior to the introduction of artemisinin combination therapies. *Antimicrobial agents and chemotherapy*, 2016. 60(6): p. 3340-3347.
- [45] Feng, J., et al., Evaluation of antimalarial resistance marker polymorphism in returned migrant workers in china. *Antimicrobial agents and chemotherapy*, 2015 a. 59(1): p. 326-330.
- [46] Hawkes, M., et al., Slow clearance of Plasmodium falciparum in severe pediatric Malaria, Uganda, 2011–2013. *Emerging infectious diseases*, 2015. 21(7): p. 1237.
- [47] Kite, W.A., et al., Alternative methods for the Plasmodium falciparum artemisinin ring-stage survival assay with increased simplicity and parasite stage-specificity. *Malaria journal*, 2016. 15(1): p. 1.
- [48] Alareqi, L.M., et al., Molecular markers associated with resistance to commonly used antimalarial drugs among Plasmodium falciparum isolates from a malaria-endemic area in Taiz governorate—Yemen during the transmission season. *Acta Tropica*, 2016. 162: p. 174-179.
- [49] Chenet, S.M., et al., Independent emergence of the Plasmodium falciparum kelch propeller domain mutant allele C580Y in Guyana. *Journal of Infectious Diseases*, 2015: p. jiv752.
- [50] Mbengue, A., et al., A molecular mechanism of artemisinin resistance in Plasmodium falciparum malaria. *Nature*, 2015. 520(7549): p. 683-687.
- [51] Feng, J., et al., Amplification of pfmdr1, pfcr1, pvmdr1, and K13 propeller polymorphisms associated with Plasmodium falciparum and Plasmodium vivax isolates from the China-Myanmar border. *Antimicrobial agents and chemotherapy*, 2015 b. 59(5): p. 2554-2559.
- [52] Ghorbal, M., et al., Genome editing in the human malaria parasite Plasmodium falciparum using the CRISPR-Cas9 system. *Nature biotechnology*, 2014. 32(8): p. 819-821.
- [53] Chatterjee, M., et al., No polymorphism in Plasmodium falciparum K13 propeller gene in clinical isolates from Kolkata, India. *Journal of pathogens*, 2015. 2015.
- [54] Huang, B., et al., Polymorphisms of the artemisinin resistant marker (K13) in Plasmodium falciparum parasite populations of Grande Comore Island 10 years after artemisinin combination therapy. *Parasites & vectors*, 2015. 8(1): p. 1.
- [55] Tanabe, K., et al., Spontaneous mutations in the Plasmodium falciparum sarcoplasmic/endoplasmic reticulum Ca²⁺-ATPase (PfATP6) gene among geographically widespread parasite populations unexposed to artemisinin-based combination therapies. *Antimicrobial agents and chemotherapy*, 2011. 55(1): p. 94-100.
- [56] Edwards, H.M., et al., Novel cross-border approaches to optimise identification of asymptomatic and artemisinin-resistant Plasmodium infection in mobile populations crossing Cambodian borders. *PloS one*, 2015. 10(9): p. e0124300.
- [57] Torrentino-Madamet, M., et al., K13-propeller polymorphisms in Plasmodium falciparum isolates from patients in Mayotte in 2013 and 2014. *Antimicrobial agents and chemotherapy*, 2015. 59(12):

- p. 7878-7881.
- [58] Ménard, D., et al., A worldwide map of Plasmodium falciparum K13-propeller polymorphisms. *New England Journal of Medicine*, 2016. 374(25): p. 2453-2464.
- [59] Carter, T.E., et al., Artemisinin resistance-associated polymorphisms at the K13-propeller locus are absent in Plasmodium falciparum isolates from Haiti. *The American journal of tropical medicine and hygiene*, 2015. 92(3): p. 552-554.
- [60] Siddiqui FA, Boonhok R, Cabrera M, Mbenda HGN, Wang M, Min H, Liang X, Qin J, Zhu X, Miao J, Cao Y, Cui L. Role of Plasmodium falciparum Kelch 13 Protein Mutations in P. falciparum Populations from Northeastern Myanmar in Mediating Artemisinin Resistance. *Mbio*; 2020; 11:e01134-19. <https://doi.org/10.1128/mBio.01134-19> PMID:32098812
- [61] Tacoli, C., et al., Artemisinin Resistance-Associated K13 Polymorphisms of Plasmodium falciparum in Southern Rwanda, 2010-2015. *The American Journal of Tropical Medicine and Hygiene*, 2016: p. 16-0483.
- [62] Taylor, S.M., et al., Absence of putative artemisinin resistance mutations among Plasmodium falciparum in sub-Saharan Africa: a molecular epidemiologic study. *Journal of Infectious Diseases*, 2015. 211(5): p. 680-688.
- [63] Kamau, E., et al., K13-propeller polymorphisms in Plasmodium falciparum parasites from sub-Saharan Africa. *Journal of Infectious Diseases*, 2014: p. jiu608.
- [64] Cooper, R.A., et al., Lack of artemisinin resistance in Plasmodium falciparum in Uganda based on parasitological and molecular assays. *Antimicrobial agents and chemotherapy*, 2015. 59(8): p. 5061-5064.
- [65] Conrad, M.D., et al., Polymorphisms in K13 and falcipain-2 associated with artemisinin resistance are not prevalent in Plasmodium falciparum isolated from Ugandan children. *PloS one*, 2014. 9(8): p. e105690.
- [66] Muwanguzi, J., et al., Lack of K13 mutations in Plasmodium falciparum persisting after artemisinin combination therapy treatment of Kenyan children. *Malaria journal*, 2016. 15(1): p. 1.
- [67] Borrmann, S., et al., Genome-wide screen identifies new candidate genes associated with artemisinin susceptibility in Plasmodium falciparum in Kenya. *Scientific reports*, 2013. 3: p. 3318.
- [68] Bayih, A.G., et al., A Unique Plasmodium falciparum K13 Gene Mutation in Northwest Ethiopia. *The American journal of tropical medicine and hygiene*, 2016. 94(1): p. 132-135.
- [69] Heuchert, A., et al., Molecular markers of anti-malarial drug resistance in southwest Ethiopia over time: regional surveillance from 2006 to 2013. *Malaria journal*, 2015. 14(1): p. 1.
- [70] Boussaroque, A., et al., Emergence of Mutations in the K13 Propeller Gene of Plasmodium falciparum Isolates from Dakar, Senegal, in 2013-2014. *Antimicrobial agents and chemotherapy*, 2016. 60(1): p. 624-627.
- [71] Thriemer, K., et al., Delayed parasite clearance after treatment with dihydroartemisinin-piperaquine in Plasmodium falciparum malaria patients in central Vietnam. *Antimicrobial agents and chemotherapy*, 2014. 58(12): p. 7049-7055.
- [72] Mohon, A.N., et al., Mutations in Plasmodium falciparum K13 propeller gene from Bangladesh (2009-2013). *Malaria journal*, 2014. 13(1): p. 1.
- [73] Zhang J, Li N, Siddiqui FA, Xu S, Geng J, Zhang J, He X, Zhao L, Pi L, Zhang Y, Li C, Chen X, Wu Y, Miao J, Cao Y, Cui L, Yang Z. In vitro susceptibility of Plasmodium falciparum isolates from the China-Myanmar border area to artemisinins and correlation with K13 mutations. *2019 International Journal for Parasitology: Drugs and Drug Resistance*. DOI: 10.1016/j.ijpddr.2019.04.002
- [74] Mok, S., et al., Drug resistance. Population transcriptomics of human malaria parasites reveals the mechanism of artemisinin resistance. *Science*, 2015. 347(6220): p. 431-5.
- [75] Woodrow, C.J. and N.J. White, The clinical impact of artemisinin resistance in Southeast Asia and the potential for future spread. *FEMS Microbiology Reviews*, 2016: p. fuw037.
- [76] Adams, J., R. Kelso, and L. Cooley, The kelch repeat superfamily of proteins: propellers of cell

- function. Trends in cell biology, 2000. 10(1): p. 17-24.
- [77] Prag, S. and J.C. Adams, Molecular phylogeny of the kelch-repeat superfamily reveals an expansion of BTB/kelch proteins in animals. BMC bioinformatics, 2003. 4(1): p. 1.
- [78] Mitsuishi, Y., H. Motohashi, and M. Yamamoto, The Keap1-Nrf2 system in cancers: stress response and anabolic metabolism. Frontiers in oncology, 2011. 2: p. 200-200.
- [79] Velichkova, M. and T. Hasson, Keap1 regulates the oxidation-sensitive shuttling of Nrf2 into and out of the nucleus via a Crm1-dependent nuclear export mechanism. Molecular and cellular biology, 2005. 25(11): p. 4501-4513.
- [80] Villeneuve, N.F., A. Lau, and D.D. Zhang, Regulation of the Nrf2-Keap1 antioxidant response by the ubiquitin proteasome system: an insight into cullin-ring ubiquitin ligases. Antioxidants & redox signaling, 2010. 13(11): p. 1699-1712.
- [81] Dogovski, C., et al., Targeting the cell stress response of Plasmodium falciparum to overcome artemisinin resistance. PLoS Biol, 2015. 13(4): p. e1002132.
- [82] Mok, S., et al., Population transcriptomics of human malaria parasites reveals the mechanism of artemisinin resistance. Science, 2015. 347(6220): p. 431-435.
- [83] Mbenda HGN, Zeng W, Bai Y, Siddiqui FA, Yang Z, Cui L. Genetic diversity of the Plasmodium vivax phosphatidylinositol 3-kinase gene in two regions of the China-Myanmar border. Infect Genet Evol. 2018;61:45-52
- [84] Mbenda HGN, Wang M, Guo J, Siddiqui FA, Hu Y, Yang Z, Kittichai V, Sattabongkot J, Cao Y, Jiang L, Cui L. Evolution of the Plasmodium vivax multidrug resistance 1 gene in the Greater Mekong Subregion during malaria elimination. 2020. Parasites & vectors 13(1), 67.
- [85] Wang, M., Siddiqui, F.A., Fan, Q. et al. Limited genetic diversity in the PvK12 Kelch protein in Plasmodium vivax isolates from Southeast Asia. Malar J 15, 537 (2016). <https://doi.org/10.1186/s12936-016-1583-0>
- [86] Miotto, O., et al., Genetic architecture of artemisinin-resistant Plasmodium falciparum. Nature genetics, 2015. 47(3): p. 226-234.
- [87] Mukherjee, A., et al., Artemisinin resistance without pfkclh13 mutations in Plasmodium falciparum isolates from Cambodia. Malar J, 2017. 16(1): p. 195.
- [88] Siddiqui FA, Cabrera M, Wang M, Brashear A, Kemirembe K, Wang Z, Miao J, Chookajorn T, Yang Z, Cao Y, Dong G, Rosenthal PJ, Cui L. 2018. Plasmodium falciparum falcipain-2a polymorphisms in Southeast Asia and their association with artemisinin resistance. J Infect Dis 218:434 - 442. <https://doi.org/10.1093/infdis/jiy188>.
- [89] Zhao Y, Ziling Liu, Soe MT, Wang L, Soe TN, Wei H, Than A, Aung PL, Li Y, Zhang X, Hu Y, Wei H, Zhang Y, Burgess J, Siddiqui FA, Menezes L, Wang Q, Kyaw MP, Cao Y, Cui L. Genetic Variations Associated with Drug Resistance Markers in Asymptomatic Plasmodium falciparum Infections in Myanmar. 2019 Genes 10 (9), 692. DOI:10.3390/genes10090692
- [90] Pradhan, A., et al., Chemogenomic profiling of Plasmodium falciparum as a tool to aid antimalarial drug discovery. Scientific reports, 2015. 5.
- [91] Alam, M.M., et al., Phosphoproteomics reveals malaria parasite Protein Kinase G as a signalling hub regulating egress and invasion. Nat Commun, 2015. 6: p. 7285.
- [92] Dawn A, Singh S, More KR, Siddiqui FA, Pachikara N, Ramdani G, Langsley G, Chitnis CE. 2014. The central role of cAMP in regulating Plasmodium falciparum merozoite invasion of human erythrocytes. PLoS Pathog 10:e1004520 <https://doi.org/10.1371/journal.ppat.1004520>
- [93] Liang X, Hart KJ, Dong G, Siddiqui FA, Sebastian A, Li X, Albert I, Miao J, Lindner SE, Cui L. 2018. Puf3 participates in ribosomal biogenesis in malaria parasites. J Cell Sci 131:jcs212597. <https://doi.org/10.1242/jcs.212597>.
- [94] Balaich, J.N., et al., The Nonartemisinin Sesquiterpene Lactones Parthenin and Parthenolide Block Plasmodium falciparum Sexual Stage Transmission. Antimicrobial agents and chemotherapy, 2016. 60(4): p. 2108-2117.
- [95] Mott, B.T., et al., High-throughput matrix screening identifies synergistic and antagonistic

- antimalarial drug combinations. Scientific reports, 2015. 5.
- [96] Baragaña, B., et al., A novel multiple-stage antimalarial agent that inhibits protein synthesis. *Nature*, 2015. 522(7556): p. 315-320.
- [97] Hati S, Madurkar SM, Bathula C, Thulluri C, Agarwal R, Siddiqui FA, Dangi P, Adepally U, Singh A, Singh S, Sen S. Design, synthesis and biological evaluation of small molecules as potent glucosidase inhibitors. *Eur J Med Chem.* 2015; 100:188-196. <https://doi.org/10.1016/j.ejmech.2015.04.059> PMID:26087029
- [98] Li J, Zhang J, Li Q, Hu Y, Ruan Y, Tao Z, et al. (2020) Ex vivo susceptibilities of Plasmodium vivax isolates from the China-Myanmar border to antimalarial drugs and association with polymorphisms in Pvmdr1 and Pvcrt-o genes. *PLoS Negl Trop Dis* 14(6): e0008255. <https://doi.org/10.1371/journal.pntd.0008255>.
- [99] Li J, Zhang J, Li Q, Hu Y, Ruan Y, Tao Z, et al. (2020) Ex vivo susceptibilities of Plasmodium vivax isolates from the China-Myanmar border to antimalarial drugs and association with polymorphisms in Pvmdr1 and Pvcrt-o genes. *PLoS Negl Trop Dis* 14(6): e0008255. <https://doi.org/10.1371/journal.pntd.0008255>.