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NEWS AND VIEWS

Issue 12, October 2021

Upcoming Event

Lecture Series on Infectious Diseases
Lecture 05 - Prof D. Kwiatkowski
Wellcome Sanger Institute, UK
25th October, 2021

Malaria News: First WHO-approved malaria vaccine

NIMR Activities

1. Virtual Poster Competition

2. Vector Bionomics and Control Workshop

3. Distinguished Lecture
Prof Elizabeth Winzeler

4. Lecture Series on Infectious Diseases
Lecture 04 - Prof A. Dondorp

Editorial

Interviews

1. Dr Saman Habib
Chief Scientist
CSIR-CDRI

2. Dr Ajeet K Mohanty
Assistant Research Scientist &
Officer-in-Charge
ICMR-NIMR FU Goa

Research in Spotlight

Editorial

Dear readers,

MERA-India team brings to you the twelfth issue of our newsletter.

In a major breakthrough in the fight against malaria, WHO recently approved the first malaria vaccine for children under-5years. We have highlighted this important development in this issue.

A number of activities/trainings were organized at ICMR-NIMR during September 2021. MERA-India organized a Virtual Poster Competition for the PhD students, postdocs and project staff working at NIMR, Delhi and the field units. The second lecture of the "Distinguished Lecture Series" was delivered by Professor Elizabeth Ann Winzeler, from the University of California & the Director of the Malaria Drug Accelerator (MalDA), on the topic "Phenotypic screens, genetics, genomics, and the hunt for Next-Generation medicines for Malaria elimination". The fourth lecture of the "Lecture Series on Infectious Diseases'" was delivered by Professor Arjen Dondorp from Mahidol Oxford Tropical Research Unit, Thailand, on the topic "Multidrug resistant *falciparum* malaria and how to treat it". MERA-India also organized three different training workshops for MERA-India fellows and the project staff. The details of these activities are provided in this issue.

For the 'Malaria Scientists to Watch' section, we interviewed Dr Saman Habib (Chief Scientist, CSIR-CDRI, Lucknow) and Dr Ajeet K. Mohanty (Assistant Research Scientist and Officer-in-Charge, ICMR-NIMR Field Unit - Goa).

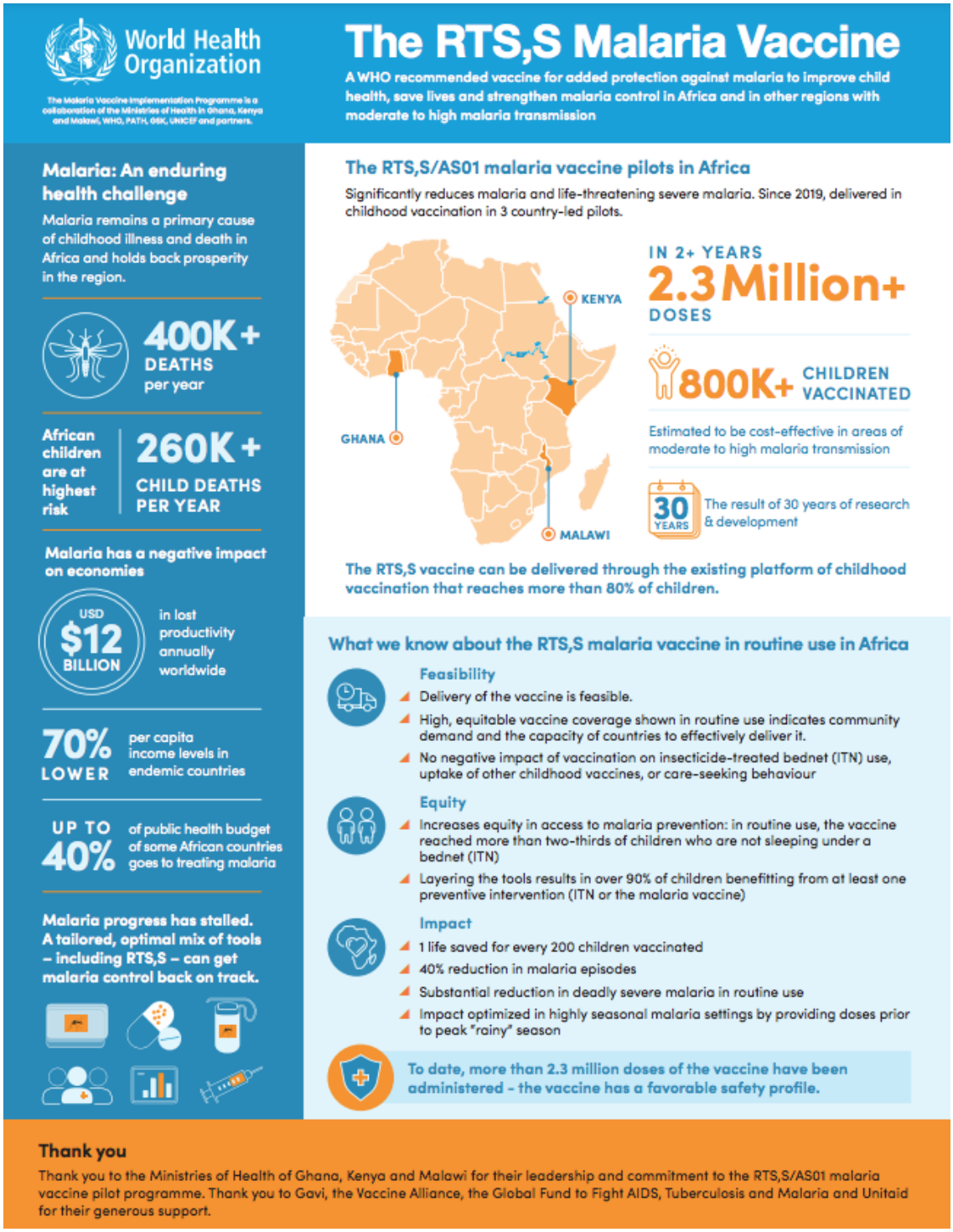
In the 'Research in Spotlight' section, four recent malaria research articles have been highlighted. In the study by Balikagala B. *et al.,* published in NEJM, the authors have provided evidence of artemisinin-resistance in Africa. In the study by Feleke S M. *et al.,* published in Nat Microbiol., the authors have reported the false-negative cases of *P. falciparum* infection detection using RDTs in Ethiopia due to *pfhrp2*/*pfhrp3* deletion in the malaria parasite. In the study by Molina-Cruz A. *et al.*, published in Communications Biol., the authors have proposed a genotyping assay to determine the geographical origin and transmission potential of the malaria parasites. In the study published by Rajvanshi H. *et al.,* in Malar J., the authors have assessed the impact of communication strategies used in the Malaria Elimination Demonstration Project in Mandla district of Madhya Pradesh in India, to spread knowledge and awareness about malaria in community.

In the 'Upcoming Event' section, there are details about the fifth lecture of the "Lecture Series on Infectious Diseases" by Professor Dominic Kwiatkowski, Wellcome Sanger Institute UK, on 25th October 2021, on the topic "Uncovering host-parasite genetic interactions in malaria".

We hope you will this issue enjoyable and informative to read. For any feedback or suggestions towards the content of the newsletter, please write to us at meranewsletter@gmail.com.

With best wishes
MERA-India team

Malaria News: First WHO-approved malaria vaccine



(Source: https://www.who.int/multi-media/details/the-rts-s-malaria-vaccinev2)

In a major step towards preventing malaria-deaths, WHO has recommended the first malaria vaccine, RTS,S/AS01, for children at risk of *P. falciparum* infection

(https://www.who.int/news/item/06-10-2021-who-recommends-groundbreaking-malaria-vaccine-for-children-at-risk). In 2019, children under 5-years accounted for 67% of worldwide malaria deaths, thus this vaccine could save millions of young lives. We congratulate all the scientists and researchers involved in this ground breaking research.

NIMR Activities:
Virtual Poster Competition for NIMR PhD students

MERA-India organized a Virtual Poster Competition in September 2021 for the PhD students, postdocs and project staff working at NIMR, Delhi and the field units. The participants were invited to submit their abstracts/ posters under three malaria-research based themes: Parasite-Host Biology, Vector Biology and Epidemiology. There were a total of sixteen participants. Each participant was given 10 minutes to present their poster, followed by questions from the judges and audience. Dr Manju Rahi (Scientist-F/ Deputy-Director General (SG), ICMR) and Dr Ruchi Singh (Scientist-E, ICMR-National Institute of Pathology) were the invited judges for the competition.

Based on the scores from the judges, the following poster presenters were adjudged as the winners of the competition:

- **First Prize** (Cash prize of 3100₹, a pen drive and a certificate)**:** Mr Debattam Mazumdar (ICMR-NIMR Field Unit, Goa) - "Seasonal prevalence and spatial distribution of mosquito species (Diptera: Culicidae) in the Western part of India".
- **Second Prize** (Cash prize of 2100₹, one pen drive and a certificate)**:** Mr Loick P. Kojom Foko (ICMR-NIMR, Delhi) - "Non-falciparum species, asymptomatic malaria and submicroscopic parasitemia: Three rising threats to malaria control efforts in Cameroon".
- **Third Prize** (Cash prize of 1100₹, one pen drive and a certificate)**:** Dr Vandana (ICMR-NIMR, Delhi) - "*Plasmodium falciparum* Metacaspase-2 capture its natural substrate in a non-canonical way".

All the winners and participants were awarded with prizes and certificates of participation in a ceremony held at NIMR, Delhi by Dr Amit Sharma (Director, ICMR-NIMR).

Workshops for MERA-India Fellows and staff

MERA-India organized training workshops at ICMR-NIMR, Delhi for the Principal Investigators (PIs)/co- investigators (co-Is), and the associated project staff in three of the MERA-India funded project themes as below:

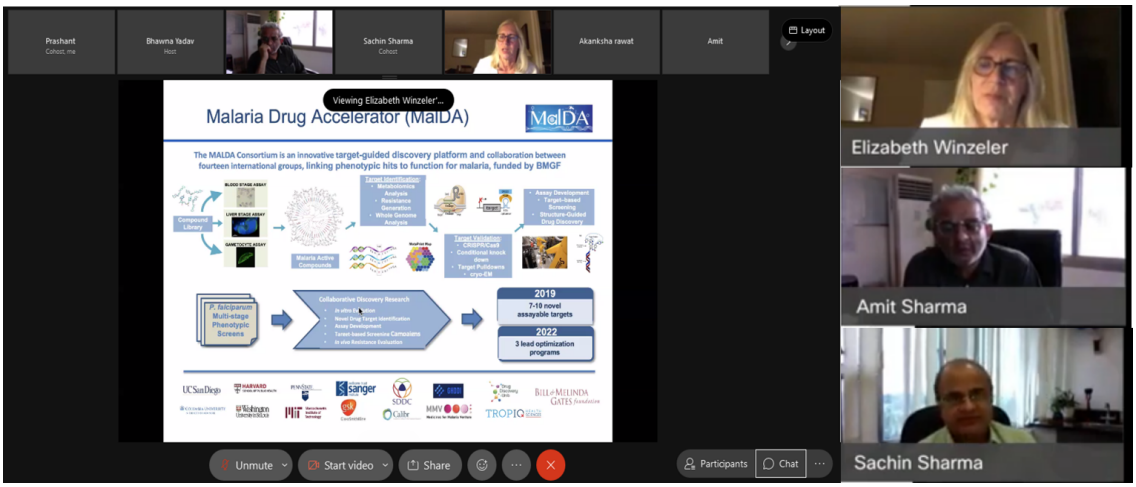
1. Vector Bionomics & Control
2. Low-Density Infection Detection
3. Community Behaviour

During the workshops, experts and mentors were invited to provide hands-on training (wherever possible), and guidance to the participants on different aspects of the specific themes. The workshops were highly interactive in nature and included lectures, demonstrations, field trips and group exercises. In the group discussion rounds at the end of the workshops, queries related to projects were discussed and potential solutions were suggested by experts.

The Vector Bionomics & Control Workshop was organized between 14th – 16th September 2021 under the guidance of Dr P. Jambulingam (Former Director, ICMR-VCRC, Puducherry); Dr K. Gunasekaran (Sr. Consultant & Formerly Scientist G, ICMR-VCRC, Puducherry), and Dr K. Raghavendra (Sr. Consultant & Formerly Scientist G, ICMR-NIMR, Delhi). The participants were taught about the vector life cycle and behaviour, vector bionomics and vectorial capacity, vector surveillance and sampling, insecticide resistance monitoring and management in vectors, principles of vector control and personal protection, and planning entomological surveys. Dr Arun K. Sharma (Director, ICMR-NIIRNCD, Jodhpur) gave an online lecture on the use of GIS for vector surveillance and answered the queries related to this topic. Field trips were also organized to train the participants in trap setting and outdoor/indoor/resting mosquito collections. The field exercises were followed by identification, data compilation and group presentations based on the mosquito samples collected.

In the future newsletter issues, we will provide the glimpses from the other two workshops on Low-Density Infection Detection and Community Behavior.

Distinguished Lecture by Professor Elizabeth Ann Winzeler



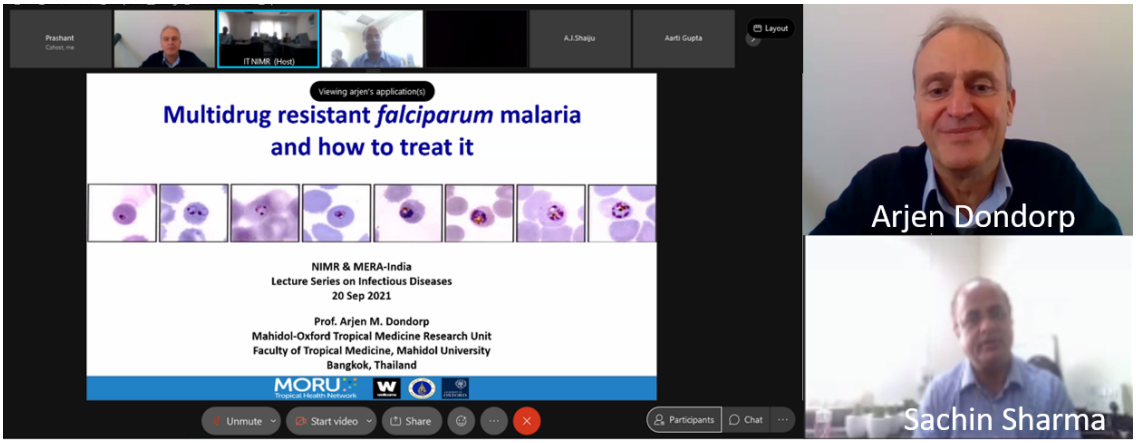
The second lecture in the series of the "Distinguished Lecture" was delivered on 24th September 2021 by Professor Elizabeth Ann Winzeler from the School of Medicine, University of California, San Diego, and the Director of the Malaria Drug Accelerator (MalDA), on the topic "Phenotypic screens, genetics, genomics, and the hunt for Next-Generation medicines for Malaria elimination". Dr Amit Sharma (Director, ICMR-NIMR), welcomed Professor Winzeler, and Dr Sachin Sharma (Chief Consultant, MERA-India) introduced the speaker.

Professor Winzeler talked about the need to develop new drugs which could prevent malaria and also block its transmission, particularly owing to the evolving drug resistance. She then presented some of the work done by her group to identify potent antimalarial compounds using different approaches, including high throughput assays and phenotypic screening, and assess their activity/efficacy against different forms of malaria parasites (blood-stage, liver-stage, gametocytes). She also described the target-based drug discovery approach to identify compounds against a particular target using *in-vitro* evolution assays. Further, she talked about the collaborative approach adopted by Malaria Drug Accelerator (MalDA) to identify, test and validate novel and potent anti-malarial molecules.

After the lecture, Professor Winzeler answered the questions from the audience. Dr Sachin Sharma thanked the speaker and the attendees, and concluded the session.

The recording of this lecture is available on the MERA-India website (https://www.meraindia.org.in/lecture-series).

Lecture 04 of Lecture Series on Infectious Diseases



The fourth lecture of the NIMR & MERA-India “Lecture Series on Infectious Diseases” (June 2021-May, 2022), was delivered by Professor Arjen Dondorp, Deputy Director and Head of Malaria Research at Mahidol Oxford Tropical Medicine Research Unit, Thailand on the topic “Multidrug resistant *falciparum* malaria and how to treat it”. Dr Sachin Sharma, Chief Consultant, MERA-India introduced the speaker.

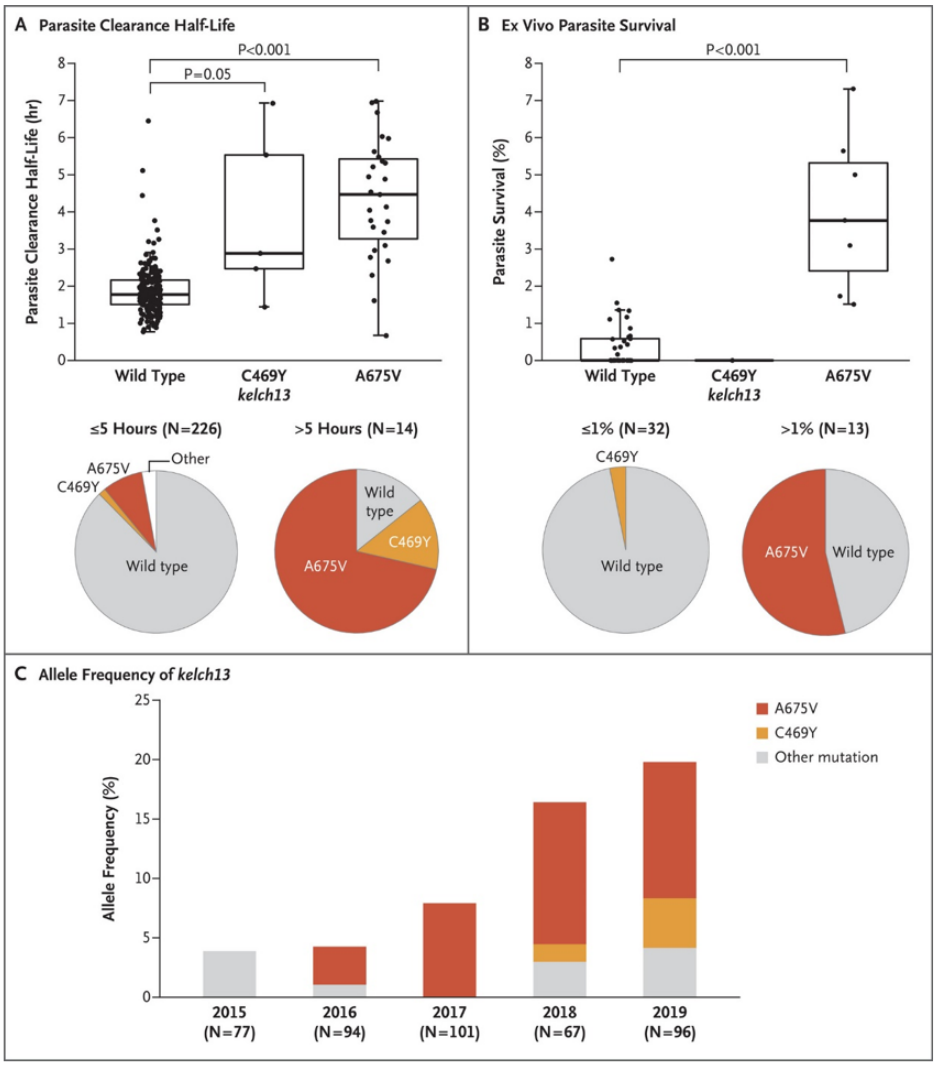
In his lecture, Professor Dondorp talked about the evolving multidrug resistance against artemisinin and ACT partner drugs in *Plasmodium falciparum*. He described how the antimalarial drug resistance first emerges in low-transmission settings, and how the use of Artemisinin-based Combination Therapies (ACT) as the frontline treatment, contributed to the decline in malaria burden when the resistance to the previously used drugs (quinine, chloroquine, sulfadoxine-pyrimethamine and mefloquine) emerged. However, the decline in potency of ACT therapy was gradually observed first in Cambodia and then in other regions of Greater Mekong Sub region and now in Africa as well. The artemisinin resistant parasites displayed slow clearance after treatment. Several SNPs in *kelch*13 contributing to the artemisinin resistance have been identified and validated as molecular markers for resistance surveillance. Additionally, artemisinin resistant parasites have been observed to have a higher chance to develop resistance to partner drugs used in ACT therapy. He further talked about the new drugs under development and the treatment options in regions with antimalarial drug resistance.

The lecture was followed by answers to the audience questions. The event concluded with a note of thanks from Dr Sachin Sharma to the speaker and the attendees.

The recording of this lecture is available on the MERA-India website (https://www.meraindia.org.in/lecture-series).

Research in Spotlight

Balikagala B. *et al.*, *NEJM*, 2021: Evidence of Artemisinin-Resistant Malaria in Africa

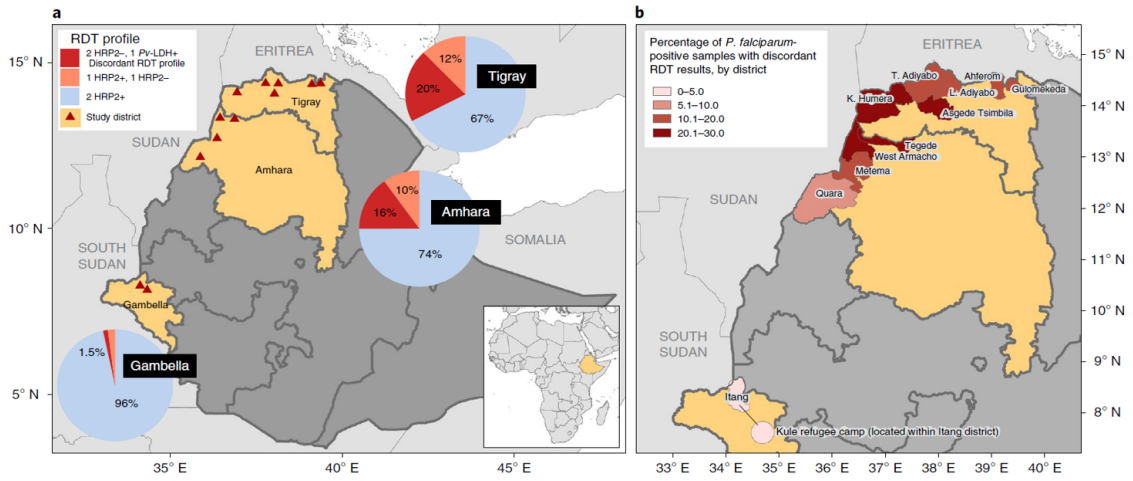


Source: https://pubmed.ncbi.nlm.nih.gov/34551228/

Antimalarial drug-resistance is an emerging threat to malaria elimination in endemic regions. Previous studies in different regions of the world have shown the evidence of artemisinin resistance in *P. falciparum*, and mutations in *pfkelch*13 gene have been identified and validated as markers for resistance by WHO. In this study, the authors have looked for the artemisinin treatment efficacy between 2017 and 2019 in northern Uganda by assessing for parasite clearance half-life (a 5 hours cutoff was considered to confirm resistance), ex-vivo ring-stage survival assay, and genotyping to look for association

between artemisinin resistance and mutations in *kelch*13 gene. Out of the 247 patients assessed after ACT and artemisinin monotherapy, gametocytes were detected in 7 patients. Of the remaining 240 patients, 14 patients (5.8%) showed parasite clearance half-life of more than 5 hours, suggesting artemisinin resistance. In 38 out of these 240 patients (15.8%), mutations in *kelch*13 gene were observed. A675V mutation was the most common mutation and was detected in 27 patients, while C469Y mutation was detected in 5 patients. Both of these mutations were associated with an increase in parasite clearance half-life, as compared to the wild type alleles. These mutations have also been linked with artemisinin resistance in southeast Asia. SNP haplotype analysis of *kelch*13 flanking regions in A675V mutants from Uganda and southeast Asia showed that the isolates had emerged independently in Africa and southeast Asia. Ex-vivo ring-stage survival assays were performed successfully for 45 patients, out of which 13 patients (28.9%) showed more than 1% parasite survival. The findings of this study thus provide an evidence of artemisinin resistance parasites emerging in Africa, which is quite concerning considering that Africa contributes to close to 90% of worldwide malaria cases and deaths.

Feleke S M. *et al.*, *Nat Microbiol.*, 2021: *Plasmodium falciparum* is evolving to escape malaria rapid diagnostic tests in Ethiopia

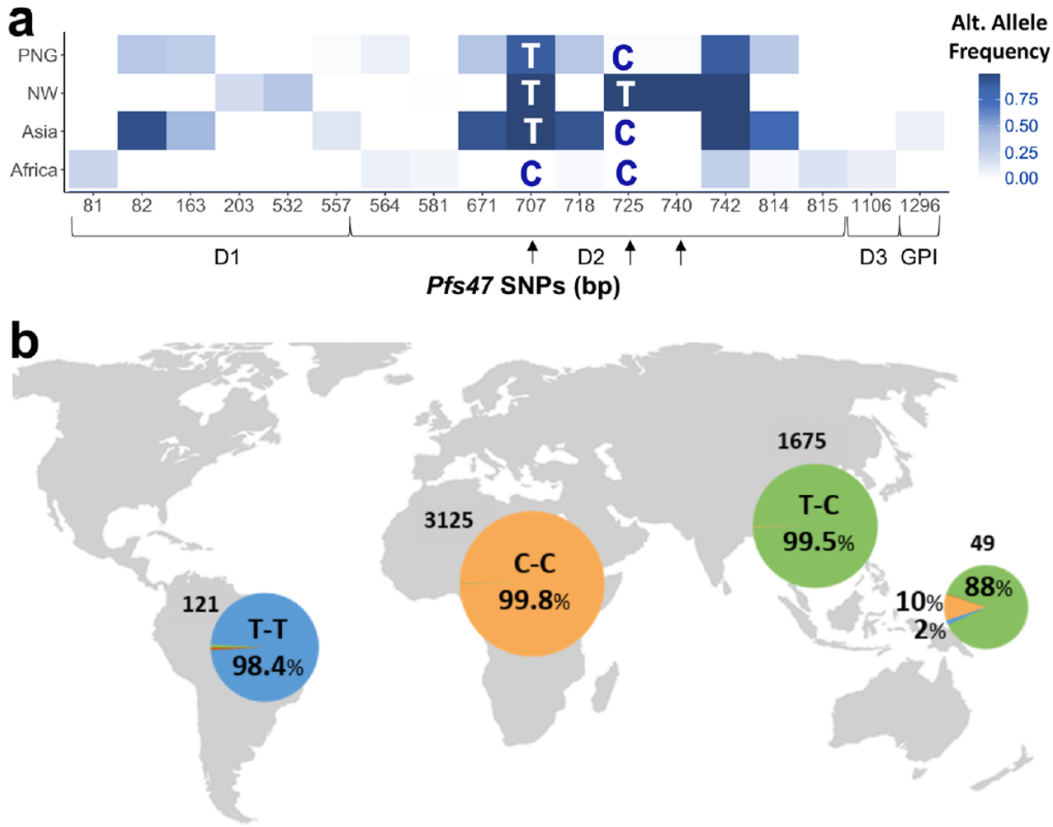


Source: https://pubmed.ncbi.nlm.nih.gov/34580442/

Rapid Diagnostic Tests (RDTs) diagnose malaria by detecting *P. falciparum* antigens *i.e.,* histidine-rich protein2 (HRP2) and 3 (HRP3). Prevalence of *pfhrp2/3*-deleted parasites that are undetected by the diagnostic tests threatens the malaria control and elimination. The authors of this article studied blood samples from a cohort of 12,572 participants across Ethiopia's borders with neighboring countries Eritrea, Sudan and South Sudan using RDTs, PCR, immunological assays, whole genome sequencing and/or molecular inversion probe (MIP) deep sequencing. They confirmed *pfhrp2/3* deletions and estimated 9.7% (95% CI 8.5-11.1) false-negative cases due to *Pfhrp2* deletion. They also suggested that the *pfhrp2/3*-deleted parasites evolve through *pfhrp3* deletion followed by selective pressures favoring the *pfhrp2* deletion. Though the study has few limitations, it strongly urges to

reconsider the existing diagnostic strategies in Ethiopia and improved surveillance for *pfhrp2* deletion.

Molina-Cruz A. *et al.*, *Communications Biol.*, 2021: A genotyping assay to determine geographic origin and transmission potential of *Plasmodium falciparum* malaria cases



Source: https://pubmed.ncbi.nlm.nih.gov/34593959/

In order to keep the resurgence of local malarial cases in check, a proper assessment of imported malaria instances is very crucial. The authors of this study developed High-Resolution Melting (HRM) assay to genotype *Pfs47* in order to decipher the possible geographical origin of *P. falciparum/vivax* and to assess the parasite compatibility with local mosquito vector population which in turn explains the possibility of transmission risk among the locals. Different compatible alleles of *Pfs47* at 707, 725, and 740 bp interact with the vector's *Pfs47* receptor which help the parasite to escape from immune response, survival, complete the development cycle in mosquito and transmission to the human host. It is noteworthy that in any continent, the "C-T" combination at 707 and 725 bp is under strong negative selection, thus the absence of detection of this combination suggests that it might be deleterious to the parasite. They also suggested that the *Pfs47* gene could be used as a marker to assess the continental origin of *P. vivax*. However, the present methodology has a limitation as it would not be reliable in cases where the patient is infected with parasites from multiple continents.

Rajvanshi H. *et al.*, *Malar J.*, 2021: Assessing community knowledge, attitude and practices to strengthen communication strategy for Malaria Elimination Demonstration Project in Mandla

Fig. 1 IEC BCC materials used by MEDP Mandla

Source: https://www.ncbi.nlm.nih.gov/pmc/articles/PMC8403442/

Malaria Elimination Demonstration Project (MEDP) is a unique and notable initiative established with government and public partnership to eliminate indigenous malaria transmission in Mandla, a tribal district in Madhya Pradesh state of India. The poor socio-economic status, hesitation to seek treatment, misconceptions about disease prevention and control, and the treatment by un-organized health care workers prevented the rapid diagnosis and accurate treatment of malaria in this district, along with the increased risk of transmission. One of the strategies adopted during the planning stage of MEDP to achieve its aim was to use Information, Education Communication (IEC) and Behaviour Change Communication (BCC). For this, communication and awareness strategies were built with the involvement of the community as well as the field staff. These included door-to-door/one-to-one communication using flip-books with information on malaria; calendars in local language with information about malaria prevention, treatment and control; spreading

awareness by storytelling through theatrics; clearing the misconceptions among children and teachers, and conducting quizzes, competitions and malaria-focused lectures in schools; and organizing IEC/T4 booths in weekly markets to track, diagnose and treat visitors with fever. After 18 months of the MEDP program implementation, a survey from 733 households across 1233 villages of Mandla district using clustered random sampling was conducted to assess the effectiveness of the MEDP communication strategy improvement in the awareness about malaria, including perceptions on malaria symptoms, transmission, control, prevention, diagnosis, treatment etc., and to assess the satisfaction levels in the community with the MEDP activities. The results from the survey provided in this study indicate that while the MEDP communication strategy has played a key role in the reduction in number of malaria cases, and in improving the knowledge and spreading awareness about malaria in the population, still more efforts are needed to improve the health literacy, address the knowledge gaps and remove the misconceptions.

Malaria Scientists to Watch

An interview with Dr Saman Habib

Dr Saman Habib

Chief Scientist

Division of Molecular and Structural Biology
CSIR- Central Drug Research Institute, Lucknow

1. *Please share with our readers your journey from being a young science student to your current role as Chief Scientist at CSIR- Central Drug Research Institute (CSIR-CDRI).*

In my early years as a science student I had wanted to study agriculture but decided to first get a degree in a basic science course. B.Sc. (Hons) in Botany from Miranda House and M.Sc. in Botany from Delhi University exposed me to fascinating new areas and I particularly enjoyed biochemistry, genetics and ecology. In 1991, I joined the National Institute of Immunology (NII), a new and modern institute at that time, where my work focused on understanding how certain viral DNA elements function as both origins of genome replication and transcriptional enhancers. NII had a vibrant scientific environment and the seven years I spent there working for my Ph.D. and later as research associate and INSA Young Scientist in Dr S.E. Hasnain's laboratory were foundational to my research training. Towards the end of my time at NII, I came across some fascinating work on the malaria parasite in which a new organelle (the apicoplast, a relict plastid) had just been discovered. I had wanted to continue working in India and applied for a position at CSRI-

CDRI which had advertised for independent research scientists. The history of malaria research at CDRI, particularly in aspects of drug discovery and development, and my own interest in pursuing work on the apicoplast was instrumental in that decision. It certainly helped that my husband had also been offered a similar position in another department of the institute and both of us were able to join CDRI within a few months of each other.

CDRI gave me the freedom to continue my INSA project as well as work on malaria. I practically learnt malaria together with my first students Divya and Sushma. The fascinating evolutionary origin of the organelle and the possibility of it being used to identify new pathways and proteins drove our work. In the early years, we faced some technical challenges. Our studies on understanding the mode of apicoplast genome replication required a lot of competitive PCR analyses, but we didn't have a PCR machine in the department when I joined. I mentioned this to Dr Pramod Upadhyay at NII and he generously gifted the PCR machine (ThermostarII) that he had designed and assembled. A simple device that worked on light and air, it could be plugged into the printer port of a PC. It sat in my home in Lucknow where I would run the reactions in the evening and do the analysis in the lab the next morning. The system worked beautifully and my students maintained that the machine worked better than the swanky Perkin Elmer thermal cycler we bought later! As my lab grew with funding from CSIR, ICMR, DBT, DST and the European Union, we were able to address several aspects of malaria organelle biology including DNA replication and genome organization, DNA repair, protein translation mechanisms, transcription, ribosome biogenesis, pathways for assembly of iron-sulfur clusters in the apicoplast and mitochondrion. My group also wanted to understand the role of human genetic polymorphisms in Indian populations with respect to susceptibility to severe malaria and such an opportunity came along with the launch of CSIR's Indian Genome Variation Consortium (IGVC), of which I was a member. Using IGVC data on polymorphisms in disease-related genes, we conducted case-control studies in collaboration with NIMR field stations, IGH-Rourkela, and KGMU-Lucknow with samples drawn from a malaria endemic (Odisha and Chhattisgarh) and non-endemic region (Uttar Pradesh) and found several significant associations between specific SNPs/repeats and haplotypes with susceptibility or resistance to *P. falciparum* malaria.

Being at CDRI also exposed me to the challenges of novel drug discovery and development and the importance of cohesive teamwork in that enterprise. I joined the institute 23 years ago and have seen many changes. The one thing that remains constant is the presence of cheerful students in the laboratory; when irked by bureaucratic red tape I can just step into my lab's world and everything seems all right.

2. *What motivated you to work in the field of malaria research?*

There isn't a single reason for the choice. As mentioned above, the discovery of the apicoplast was a trigger. I was quite aware of the immense cost of malaria on human health and had also suffered from severe disease resulting from a malaria and typhoid co-infection. Amitava Ghosh's novel "The Calcutta Chromosome" (based on events around the life of Sir Ronald Ross), interestingly placed in the "Genetics" section of the NII library, played a part too. When CDRI offered me a position, there was an opportunity to work on malaria which continued to be of great interest to the institute and there was expertise and animal infection models. In addition to the need for new drugs to counter malaria and the requirement of research effort in that direction, the malaria parasite is an intriguing

organism and provides many interesting challenges for exploratory research.

3. *If you were to pick one scientific discovery that has been crucial to our current understanding of malaria, which one would that be?*

Malaria is a complex disease with multiple parasite stages and diverse host-parasite interactions. A very large body of work has contributed to our current understanding of malaria. Apart from the immense impact of Laveran and Ross's work, I find it difficult to select merely one 'crucial' scientific discovery in the field.

4. *According to you, what is the biggest challenge for malaria elimination in India?*

There are several major challenges, but the one likely to have a maximal impact is district-level monitoring centres so that vector management and control, detection of malaria cases coming into the private health sector, disease surveillance for detection of asymptomatic cases, and assessment of drug resistance can be taken up in a coordinated manner. Strengthening of primary health care in remote areas is an obvious imperative.

5. *Apart from science and research, which other activities interest you?*

I am involved with a group that works on preserving cultural heritage and documentation of oral history. I enjoy literature and poetry and do illustrated and dramatised readings on stage. Two of our presentations- '*Lucknow in Letters: endeavours, achievements and tragedies*' and '*Aasmaan hilta hai jab gaate hain hum: readings from works of progressive writers*' have been performed in several festivals and colleges.

An interview with Dr Ajeet K Mohanty

Dr Ajeet Kumar Mohanty

Assistant Research Scientist & Officer-in-Charge

ICMR-National Institute of Malaria Research Field Unit - Goa

1. Please share with our readers your journey from being a young science student to your current role at ICMR-NIMR, Field Unit Goa.

My research career started in 2005 when I joined Dr R. K Hazra's lab at ICMR-Regional Medical Research Centre, Bhubaneswar for my master's dissertation research work. The topic of the research work was to study the role of *Wolbachia* bacteria on the development of *Brugia malayi* inside *Aedes aegypti* mosquito. During my dissertation research work, I learnt the basics of entomology from Dr Hazra, and vector biology, especially mosquitoes,

been my passion since.

After my post-graduation in Biotechnology (2005), I got an opportunity to work as an Assistant Research Scientist position at ICMR-NIMR Field Unit Goa, where I continue to work till now. At Goa University, I did my PhD in mosquito proteomics under the guidance of Dr Ashwani Kumar, Officer-in-Charge of the ICMR-NIMR Field Unit Goa from whom I learned about vector biology and malaria disease epidemiology. During my doctoral work, I got extensive training on sample preparations for quantitative proteomic analysis, mass spectrometry and proteomic data analysis at the Institute of Bioinformatics, Bengaluru under the guidance of Dr Keshav Prasad. I got an opportunity to interact and work with Dr Akhilesh Pandey, a renowned scientist in the field of mass spectrometry-based proteomics.

At Goa, in addition to working with mosquitoes, I also had the opportunity to establish the molecular biology laboratory. Now, the Goa field unit is one of the best field stations of NIMR, and has a fantastic set-up for infection experiments, cell culture and molecular biology facilities for vector and parasite research. In our field unit, we maintain laboratory colonies of *Anopheles stephensi*, *Culex quinquefasciatus* and *Aedes aegypti*.

During my 15 years' tenure at the Goa field unit, I have published 28 articles in national and international journals and have filed one patent application on "Novel peptides for developing anti-malarial vaccines and diagnostic kits". As Co-Investigator and Co-PI, I have handled several projects funded by WHOPES, SERB, DSTE (Goa) and NIH. As a site investigator, I oversee the research activities of the "Malaria evolution in South Asia" project funded by NIH, USA, ICMR-NIMR Field Unit Goa. From December 2020, I am the Officer-in-Charge of the ICMR-NIMR Field Unit Goa. Currently, my research focuses on vector bionomics, vector-*Plasmodium* compatibility and finding out the candidates for blocking disease transmission at the vector level. I closely work and provide support to the NVBDCP officials for the malaria elimination programme in Goa state.

2. *What has been your most surprising research finding?*

I was instrumental in establishing and standardizing the controlled *Anopheles-Plasmodium* interaction studies for the "Malaria Evolution at South Asia"- International Centers for Excellence in Malaria Research (MESA-ICEMR) program based at ICMR-NIMR Field Unit Goa. ICMR-NIMR Field Unit of Goa is one of the sites in India where *Plasmodium vivax* infection experiments are carried out. While exploring the *Plasmodium* susceptibility status of non-vector *Anopheles* species, I found that *An. jamesii*, considered to be a non-vector for human malaria parasites, can support the complete sporogonic cycle of *P. vivax* development. This will be the first study that shows *An. jamesii* can support the complete *Plasmodium* sporogonic cycle under laboratory conditions. Currently, this research article is under review.

3. If you were to pick one scientific discovery that has been crucial to our current understanding of malaria, which one would that be?

Rapid Diagnostic Tests (RDTs) are the backbone of the test-treat-track strategy in malaria endemic countries. RDTs are helpful for the quick detection of *Plasmodium falciparum* infected patients. Recently, researchers have identified genetic deletion of *pfhrp2* and *pfhrp3* gene in *P. falciparum* isolates leads to false-negative results, and may adversely

affect the progress made by the malaria control programmes, especially for the countries that have set their targets for malaria elimination. Therefore, there is an urgent need to identify and validate alternate target protein/s for RDT based *P. falciparum* detection.

4. According to you, what are the challenges for malaria vector surveillance in India?

Diverse ecosystems, high biodiversity of malaria vectors, variation in behaviour of different vector species, avoidance behaviour of vectors in response to interventions and impact of anthropogenic changes on mosquito ecological traits are some of the major challenges.

5. What significance do you see for MERA-India in achieving India's malaria elimination target?

MERA-India provides an opportunity for all the stakeholders in the community to participate and work together in a coordinated and combinatorial approach to eliminate malaria from India by 2030.

Upcoming Event

Lecture Series on Infectious Diseases: Lecture 05 by Professor Dominic Kwiatkowski

Professor Dominic Kwiatkowski, who leads the Malaria Genetics Group at the Wellcome Sanger Institute UK, would be the next speaker in the "Lecture Series on Infectious Diseases". He will be delivering the lecture entitled "Uncovering host-parasite genetic interactions in malaria" on 25th October 2021.

In the lecture, Professor Kwiatkowski will talk about the work that led to the discovery of common variants in the *Plasmodium falciparum* genome that enable the parasite to evade the protective effect of sickle haemoglobin.

To join this lecture, please click here: https://bit.ly/3vtt9rB

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