Report on the meeting:

Some of the sessions that were important and more focused and relevant to the direction on which I am interested are presented below in categories.

- The differential adaptation of parasites to a declining transmission intensity which is not an immediate response and proved to be established and maintained response was presented by Bozdech Z using elegant transcriptomics works of Rono and colleagues. Alternative hypothesis were presented on the balance between investment on reproduction and growth when the parasite is exposed to reduced transmission intensity and the transmission becomes an important bottle neck. Thus, in addition to investing more on reproduction, as indicated in the above work, resistant parasites for instance, may derive both reproduction and growth. One of the important theories mentioned in quite few presentations was the analogue of the lock and key theory that drug resistant parasites infect more mosquitoes. The other important concept presented was the sterilizing effect of artemisinins on male gametocytes, instead of their total clearance from the circulation. This was proved by the dual gametocyte formation assay. Toure Dinkorma Ouoluguem and colleagues from Mali presented their important finding on the identification of host immunological and plasmodium instrinsic factors that influence gametocyte infectivity to mosquitoes in the field. With a proteomic approach, using microarray assay, they detected important regulators of infectivity to mosquitoes that can in the future be used as targets of transmission blocking vaccine.
- One of the important sessions during oral and poster presentations was the utility of genotyping to trace and inform policy on residual infections in areas approaching elimination. Sara Volkman from Harvard University presented their elegant finding on the development of a panel of 22 SNP barcode to genotype *P. falciparum* parasites. This work is published by *Daniels et al., Malaria Journal 2018* and *Schafner et al., Malaria Journal 2018*.
- The fixation of *Pfmdr1* mutations and its role as a potential driver mutation in the development of resistance to the current first line treatments and the role of transcriptomics to dissect the acquisition of drug resistance; especially related with increased commitment to gametocytes and ultimately increased infectivity when under drug pressure was discussed. Lucy Okell presented an important finding on drivers of Artemisinin resistance in Africa; such as, dhps 540E, Pfcrt, 86Y and Pfmdr1. Okell and colleagues (*Okell, Reiter et al BMJ Global Health 2018*) indicated that there is difference in the west vs east of Africa regarding the fixation of these chloroquine resistance markers in *P. falciparum* that Pfmdr1 was selected against Artemisinin-lumefantrine and 86Y selected by Amodiaquine-Artesunate.
- The other important sessions were on *P. vivax* biology and radical cure. Camille Roesch and colleagues presented that amplification of PvDBP (*Roesch et al., Plos NTD 2018*) does not vary between settings (settings with differing duffy negativity) which indicated that it might PvDBP amplification might not be the reason behind vivax malaria infection in individuals with the duffy negative genotype. The hypothesis was that there might be an alternative pathway for vivax invasion. The candidate that was presented was PvDBP2/PvEBP which was found partially amplified in Madagascar than Cambodia but this requires further studies done before we can make conclusion on the subject. The radical cure meeting was interesting as unpublished and insightful data from ongoing trials on the comparison of 7 days and 14 days course of primaquine administration was presented that included Ethiopia. The study from different sites indicated that 7 days primaquine treatment was not inferior to 14 days dose in terms of preventing relapsing episodes within one year. No significant adverse events were reported in these studies.

Abstract

Substantial household level clustering and genetic relatedness of subpatent *Plasmodium falciparum* and *Plasmodium vivax* infections in a low-endemic setting aiming for elimination in Ethiopia

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Background: The heterogeneous distribution of infections in settings aiming for malaria elimination challenges finding and treating all relevant infections. Approaches that help find these infections may accelerate elimination efforts.

Methods: Family members and neighbors of patients with rapid diagnostic test (RDT)-confirmed *Plasmodium falciparum* (10 patients; 291 contacts), *P. vivax* (6 patients; 156 contracts) and mixed species infections (2 patients; 51 contacts) were screened for malaria clustering within households using RDT, quantitative PCR (qPCR) and genotyping approaches in Adama district, Ethiopia from October – December 2016. The same approach was used for controls attending clinics with (history of) fever but without malaria infections by RDT (18 controls; 453 contacts).

Results: In total, 77 *P. falciparum*, 103 *P. vivax* and 21 mixed infections were detected by qPCR. Family members who lived in households with ≥1 RDT-confirmed *P. falciparum* infected individual were more likely to have qPCR-detected *P. falciparum* infection (32.4%, 11/34) compared to individuals in households without RDT-detected infection (5.9%, 47/795; OR, 7.6; 95% CI, 3.5–16.5; *P*<.001). Similar findings were obtained for *P. vivax;* (25.0%, 17/68) vs (11.8%, 94/795; OR, 2.5; 95% CI, 1.4–4.5; *P*<.0045). Strong evidence for genetic relatedness (spatial and temporal) was detected between infections within households than infections detected between households whereby Index case infections were related each other. Infected individuals located around index cases had more complex and diverse infections than control cases.

Conclusion: The detection of within household and fine-scale focal transmission using genotyping tools supports the evidence that RCD-based detection can capture transmission related infections as opposed to those just related due to shared risk factors.

Key words: Clustering, Asymptomatic malaria, Malaria elimination, Reactive case detection, Parasite genotyping