Capacity development, training ans research uptake

PO - (8271) - PFHRP2 GENE DELETIONS IN PLASMODIUM FALCIPARUM AND SCHISTOSOMA MANSONI CO-INFECTIONS: AN EMERGING CHALLENGE FOR MALARIA RAPID DIAGNOSTIC TESTS

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Background: Malaria and schistosomiasis are infections that have a great impact in Sub Sahara Africa based on their high morbidity and mortality rates. We suggest the possibility that the microenvironment created from interactions between both parasites generates a pressure on the malaria parasite which could in turn favour the parasite’s adaptation or escape through Pfhrp2 gene deletions. Thus, this study aimed at determining the association between the co-infection with both parasites and false negative PfHRP2-based malaria rapid diagnostic tests which occur as a result of these deletions.

Method: This pilot study was conducted in a total of 149 children aged 7-17 years living in Yorro, located in the Mbam-Inoubou division of the Center region of Cameroon. We collected fresh stool samples from each participant to identify Schistosoma mansoni eggs by Kato Katz method and blood samples to identify the ring stages of Plasmodium falciparum by thick smear. Malaria rapid diagnostic and Pfhrp2 gene polymerase chain reaction were performed. The association between the co-infection with Sm/Pf and the false negative malaria RDTs was determined by the Fisher’s exact test. A p value < 0.05 was considered statistically significant.

Results: Our results showed that samples were singly infected with Sm, Pf, co-infected (Sm/Pf) and negative for both infections at frequencies of 12 %, 43 %, 30.2 % and 14.8% respectively. False negative PfHRP2-based RDTs were observed in 4.7% of the participants. A higher frequency (5/7) of the cases with false negative malaria RDTs were co-infected with Sm/Pf. A p value of 0.027 showed statistical significance in the association of Sm/Pf co-infection and false negative PfHRP2-based RDTs.

Conclusion: A significant association of Plasmodium falciparum and Schistosoma mansoni co-infection with false negative PfHRP2-based RDTs supports the case for a plausible implication in Pfhrp2 gene deletions and consequently in malaria rapid diagnostic testing.