PA-034

PLASMODIUM FALCIPARUM MEROZOITE SURFACE PROTEIN-1 GENETIC DIVERSITY AND MULTIPLICITY OF INFECTION IN ISOLATES FROM CONGOLESE CHILDREN CONSULTING IN A PAEDIATRIC HOSPITAL IN BRAZZAVILLE

Nerly Gampio Gueye,¹ Christevy Vouvougui,¹ Felix Koukouikila-Koussounda,¹ Simon Kobawila,² Francine Ntoumi¹. ¹FCRM, Republic of Congo; ²University Marien Ngouabi, Republic of Congo

10.1136/bmjgh-2016-000260.70

Background As in many countries in sub-Saharan Africa, the burden of malaria has been reduced in the Republic of Congo as a result of massive deployment of insecticide-treated nets and availability of artemisinin combination therapies.

However, limited data are available on the impact of these interventions on parasite populations. In this study, we investigated the *P. falciparum* genetic diversity and multiplicity of infection in isolates from Congolese young patients and we compared the results to previous studies conducted before the introduction of ACTs.

Methods A total of 229 children were enrolled at the paediatric hospital located in Northern part of Brazzaville. Inclusion criterion was fever ($T^{\circ} \geq 37.5^{\circ}\text{C}$); then thick and thin blood smears were done to detect malaria parasites and determine parasite density as well as plasmodial species. In order to identify sub-microscopic infection, *P. falciparum msp1* gene was used as molecular marker. The genetic diversity and the multiplicity of infection (MOI) were determined.

Results We found 22 children with positive blood smear, therefore diagnosed with uncomplicated malaria (UM, 9.6%). Among the 216 microscopy-negative children, using *msp1* marker, 57 were shown to harbour submicroscopic malaria infection (27,5%). In the age group 1–5 years, MOI was 1.4 and 2.4 in submicroscopic and UM children, respectively while in the age group ≥ 5 years, MOI was 1.7 and 3 in submicroscopic and UM children, respectively. The number of *msp1* alleles in isolates was 15 and 18 in SM and UM group, respectively. We observed that new alleles were detected only in isolates from UM children. Data are further analysed to investigate any association with age, living area, haemoglobin type carriage, and haemoglobin rate.

Conclusions This study shows no change either in *P. falciparum* genetic diversity or in MOI 10 years after the introduction of ACTs.