Results The pre-treatment prevalence of *Pfmdr*1 (N86 and D1246Y) in the RCT phase varied significantly between the sites. *Pfmdr*1 *NYD* haplotype was significantly higher in Uganda while haplotype *YYD* was higher in the Democratic Republic of Congo, ($p<0.001$). Comparison between pre-treatment and post-treatment adequate clinical and parasitological response (ACPR) or PCR-adjusted treatment failure did not indicate increased selection of *Pfmdr*1 N86, D1246 and Y184 in either AL or ASAQ arm in the pre-RCT, RCT and post-RCT phases. The relative risk (RR) of treatment failure (TF) in patients harbouring *Pfmdr*1 N86 did not significantly increase in patients treated with AL (RR=0.2, 95% CI: 0.11–1.05, p=0.061) or ASAQ (RR=1.03, 95% CI: 0.47–2.26, p=0.94).

Conclusions Our findings suggest the limited impact of treatment and re-treatment with AL or ASAQ on selection for *Pfmdr1* variants and haplotypes associated with resistance to partner drugs. These findings support the recent WHO recommendation to use ACTs as alternative rescue therapy for *P. falciparum* malaria. However, enhanced resistance monitoring is warranted to maintain the drug's effectiveness in endemic settings.

PA-005 LIMITED IMPACT OF TREATMENT AND RE-TREATMENT WITH ARTEMETHER-LUMEFANTRINE AND ARTESUNATE-AMODIAQUINE ON THE SELECTION OF *PLASMODIUM FALCIPARUM* MULTIDRUG RESISTANCE-1 ALLELES

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Background The emergence of resistance against artemisinin combination treatment (ACTs) is a major concern for malaria control. ACTs are recommended as rescue treatment; however, there is limited evidence on the impact of treatment and re-treatment with ACTs on selection for drug-resistant parasites. We aimed to investigate the impact of treatment and re-treatment using artesunate-amodiaquine (ASAQ) and artemether-lumefantrine (AL) on the selection of *Plasmodium falciparum* multidrug resistance-1 (Pfmdr1) alleles.

Methods A total of 776 isolates were collected in 28-days follow-up involving children aged 0–59 months in a clinical trial in the Democratic Republic of Congo and Uganda. Nested PCR and RPFL was used to detect *Pfmdr1* single-nucleotide polymorphisms at codons N86Y, F184Y, and D1246Y. The analysis compared *Pfmdr*1 alleles in the pre-randomisation (pre-RCT), randomisation (RCT) and post-randomisation (post-RCT) phases of the trial.