Background The West Africa Ebola virus disease (EVD) outbreak between 2015 and 2016 accelerated the need for safe and effective vaccines. Among candidate vaccines in clinical development, the recombinant Vesicular stomatitis virus (VSV) vectored with the Ebola virus (EBOV) glycoprotein (rVSV-ZEBOV-GP) vaccine showed acceptable safety and promising immunogenicity results across diverse settings.

Baseline screening data from the phase I trial of this vaccine in Lambaréné, Gabon, established that prior to vaccination about 21% (33/155) and 8% (12/155) of adults had naturally acquired antibodies to infectious ZEBOV particle and ZEBOV-GP, respectively. In participants with prior ZEBOV(-GP) antibodies, post-vaccination antibodies titres were significantly higher 56 days following vaccination with doses of 3×10⁶, 3×10⁵, and 3×10⁴ PFU compared to those without.

Our study seeks to investigate rVSV vector non-specific boosting of naturally acquired antibodies to other viral infections (dengue virus 1–4, and yellow fever virus).

Methods We measured antibodies titres to Dengue (serotypes 1–4) and yellow fever infection at baseline, 28 and 56 days after injection in a total of 155 serum samples from vaccinees receiving various doses of rVSV-ZEBOV-GP using ELISA technique.

Results Preliminary results were presented at the meeting.

Conclusion Our results confirm rVSV vector non-specific replication on non ZEBOV-GP circulating antibodies in Lambaréné vaccinees and potential boosting action on naturally acquired dengue virus (serotypes 1–4) and yellow fever virus antibodies.

Background As malaria transmission intensity declines, the heterogeneity in infectious burden becomes pronounced. There is thus the need for more sensitive tools to identify micro-geographic areas of higher risk for targeted interventions. We sought to evaluate several immunogenic peptides of *P. falciparum*, secreted ookinete and sporozoite proteins (PSOP24) and possibly validate specific short sequence immunogenic peptides as an infectious bite marker for assessing malaria transmission intensity and dynamics.

Methods We conducted four cross-sectional serological and parasitological surveys within one peri-urban and one rural community about 3 km apart, in South-western Ghana. The field surveys were conducted from November 2012 to July 2014 across dry and rainy seasons. Several bioinformatics models were used to predict the immunogenic epitopes of PSOP24 peptides. Total IgG antibody response were determined for three most promising peptides (PSOP24-374, PSOP24-375 and PSOP24-377), together with MSP1, CSP and salivary gland antigen. Alongside we determined parasite prevalence and density as well as the entomological inoculation rates.

Results Peptide PSOP24-377 showed seasonal variation with a twofold increase in IgG response in the high-transmission rainy season. This collaborates with the twofold increase in IgG response to the mosquito salivary antigen gSG6-P1. Also, PSOP24-377 was able to show a subtle difference from Ayeigbekorpe to Odumase during the dry season and a high sero-prevalence between the two communities during the rainy season. This was in contrast with gSG6-P1 because while PSOP24-377 measures sero-response to infectious bites, gSG6-P1 measure responses to only vector exposure. The immune response variation determined by PSOP24-377 correlated with parasite prevalence and the entomological inoculation rates.

Conclusion The preliminary data points to the potential of PSOP24-377 as an infectious bite marker. This may be exploited as a routine surveillance tool for monitoring malaria transmission at the community level.