## PA-364 KNOWLEDGE AND REPORTING OF ADVERSE EVENTS FOLLOWING CHILDHOOD IMMUNIZATION AMONG HEALTH WORKERS AND CAREGIVERS AT MENGO HOSPITAL, KAMPALA

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**Background** Although all vaccines used in National Immunization Programmes are safe and effective, no vaccine is completely risk-free and adverse events occasionally occur after an immunization. Failure to report adverse events following immunization (AEFI) can lead to death and misconceptions about vaccine safety hence vaccine hesitancy. Alleged vaccine quality and safety issues must be dealt with rapidly and effectively. This study assessed level of knowledge and reporting of AEFI among healthcare workers and caregivers at Mengo Hospital, Kampala.

**Methods** A health facility-based mixed-methods cross-sectional study design was used. Eligible participants were caregivers of children and healthcare workers. Qualitative data were collected through self-administered questionnaires. Focus group discussions (FGDs) among caregivers and Key informant interviews (KII) among healthcare workers collected data on knowledge and reporting procedures of AEFIs. Level of knowledge of AEFI was assessed using the Likert scale and logistic regression was used to analyse the association of different factors with reporting of AEFI. Qualitative data were analysed manually into themes.

**Results** A total of 388 participants enrolled with mean age (SD) of 28.75 (5.65) years and 51.8% were female. Over two-thirds (61.3%) had poor knowledge about AEFIs. Less than half (41.8%) had ever reported an AEFI to the hospital. Unemployment (OR= 1.628), good knowledge of AEFI (OR=1.572), and parity less than four (OR= 2.070) were found to increase odds of reporting of AEFIs. From the 7 KII and 6 FGDs, we found that most healthcare workers and caregivers had good knowledge of AEFIs but the majority had never reported nor knew the procedure for reporting of AEFI.

**Conclusion** The reporting of AEFIs was low among caregivers in Kampala. There is need to sensitize caregivers about the necessity to report AEFIs.

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## PA-367 PROFILE OF MOLECULAR MARKERS OF PLASMODIUM FALCIPARUM RESISTANCE TO SULFADOXINE-PYRIMETHAMINE IN SOUTHERN BRAZZAVILLE AND BEYOND, IN THE REPUBLIC OF CONGO

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**Background** Growing resistance of Plasmodium falciparum to Sulfadoxine-Pyrimethamine threatens the effectiveness of the intermittent preventive treatment during pregnancy with Sulfadoxine-Pyrimethamine (IPTp-SP) in malaria endemic areas. WHO recommends discontinuation in case of ineffectiveness as determined by over 95% and 10% prevalence of K540E and A581G mutants respectively. The objective of this study was to determine the prevalence of molecular markers of P.falciparum resistance to SP in the parasite population circulating in the south of Brazzaville and beyond, in the Republic of Congo.

**Methods** Two parallel surveys including hospital and community based cross sectional studies were carried out in the south of Brazzaville and beyond (urban, rural areas) between February 2021 and September 2022, to characterize the molecular markers of P.falciparum resistance to SP (dhfr and dhps). Restriction Fragment Length Polymorphism was used for the detection of single nucleotide mutation within the dhfr and dhps genes of the parasite, and detected mutations were further confirmed using Oxford nanopore sequencing platform.

**Results** High prevalence of mutations was reported for dhfr gene: N51I (100%), C59R (79.9%), S108N (100%), N164L (0.9%), and dhps gene: A437G (89.5%), K540E (42.4%), A581G (42.1%). The prevalence of the quintuple mutant (N51I+ C59R + S108N + A437G + K540E) and sextuple mutant (N51I+ C59R + S108N + A437G + K540E + A581G) were reported for 32.9% (111/337) and 20.8% (70/337) of the participants respectively while all the seven investigated mutations were reported in only one participant (0.3%). dhfr and dhps mutations were more prevalent in rural compared to the urban areas.

**Conclusion** These results indicate high prevalence of mutations within the dhfr and dhps genes of P. falciparum in south of Brazzaville and beyond in the Republic of Congo, which might threaten the effectiveness of IPT-SP in this area.

## PA-372 EVALUATION OF THE PREVENTION OF MOTHER-TO-CHILD TRANSMISSION OF HIV PROGRAMS AT THE SECOND IMMUNIZATION VISIT IN BURKINA FASO AND ZAMBIA, COUNTRIES WITH DIFFERENT HIV EPIDEMICS

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**Background** Monitoring indicators for prevention of mother-to-child transmission of HIV programs (PMTCT) is key to assessing the progress toward elimination of mother-to-child transmission (MTCT) of HIV. Using a patient-orientated innovative strategy based on the second visit in the expanded program on immunization (EPI-2) visit at 6–8 weeks, we assessed PMTCT indicators in Burkina Faso and Zambia.

**Methods** From December 2019 to September 2021, the PROMISE-EPI study (Clinical Trial: NCT03870438) assessed women attending EPI-2 at primary health care facilities in Burkina Faso and Zambia with their children about their exposure to PMTCT interventions. Women living with HIV

viral load was measured using GeneXpert® HIV RNA, and their children were tested for HIV using GeneXpert® HIV Qual.

**Results** Overall, 25093 were enrolled from Burkina Faso and 8961 women from Zambia. Almost, all women attended at least one antenatal care visit, the median number of visits was 4 (IQR: 3–5) in both countries. Among Women diagnosed with HIV at EPI-2, 4.5% and 1.7% were not aware of their HIV status, in Burkina Faso and Zambia, respectively. Among those aware of their HIV positive status, 95.8% and 99.2% were on ART in Burkina Faso and Zambia respectively. Among WLHIV on ART, 75% and 79.2% achieved a viral load suppression (Viral load < 1000 copies/mL) in Burkina Faso and Zambia respectively. Infant postnatal prophylaxis was administered from birth until EPI-2 to 60.9% and 89.7% of HIV exposed children in Burkina Faso and Zambia, respectively. In Burkina Faso, only 60/192 (31.3%) of HIV exposed children were sampled for early infant diagnosis and 3 (1.6%) received a result by EPI-2. In Zambia, these figures were 879/1465 (64.0%) and 9.9% (145/1465) respectively.

**Conclusion** This evaluation strategy could strengthen program monitoring and help identifying gaps to be addressed on the last mile towards elimination of MTCT of HIV.

## PA-375 FEASIBILITY OF A PROGRAMMATIC MASS DRUG ADMINISTRATION CAMPAIGN FOR MALARIA IN SOUTHERN MOZAMBIQUE

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**Background** Malaria Mass Drug Administration (MDA) is recommended to reduce malaria in low transmission settings, with a target coverage of ≥80%. This study assesses the feasibility of a programmatic MDA (pMDA) pilot implementation in southern Mozambique.

**Methods** The National Malaria Control Programme implemented pMDA in Chidenguele (Gaza Province), where the estimated population is 59,271. Two rounds of door-to-door distribution (using satellite maps with previously enumerated households (Reveal® platform)) with fixed points were conducted between December 2022 and February 2023. Household coverage was estimated with both district census data and satellite number of expected households. All eligible individuals ≥6 months received a full therapeutic 3-day-course of dihydroartemisinin-piperaquine. Individual data collection was conducted during round 1 (R1), which was changed to aggregated data at the household level in round 2 (R2). Community engagement and human resources were also strengthened between the two rounds. The target number of households to be reached by team/day was 25/30 in R1 and 15 in R2.

**Results** When using census data, household coverage (households reached over targeted) increased from 59.4% (8799/14818) in R1 to 94.3% (13972/14818) in R2, while with the satellite estimates, it increased from 62.5% (8799/14075) to 99.3% (13972/14075). Population programmatic coverage (individuals treated over total population) increased from 40.9% (24237/59271) to 69.8% (41347/59271). Treatment rate among present individuals (operational coverage) decreased from 91.3% (24237/26541) to 85.1% (41347/48588).

**Conclusion** Collecting aggregated data, decreasing the household target per day per team and using fixed-points at the end as a recovery strategy helped improve operational performance. However, reaching an 80% programmatic coverage is challenging even with high rates of household visitation and operational coverage, mainly due to absences and exclusions.

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## PA-376 SALIVA AS A TOOL FOR SARS-COV-2 GENOMIC AND IMMUNOLOGICAL SURVEILLANCE IN THE REPUBLIC OF CONGO

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**Background** The design of this study was intended to evaluate the use of saliva as a reliable non-invasive tool for the genomic and immunological surveillance of SARS-CoV-2 infection in the Republic of Congo.

**Methods** During this cross-sectional study, the active infection was determined by detecting SARS-CoV-2 RNA using RT-PCR in 220 paired saliva and oropharyngeal samples (OPS), and by sequencing SARS-CoV-2 genome using the Oxford nanopore technology. The detection of anti-SARS-CoV-2 IgG antibody was done in 148 pair saliva and plasma samples using an in-house developed ELISA, and the reproductivity of the assay based on Saliva were assessed in two independent laboratories.

**Results** Overall, saliva (22/220) and OPS (23/220) showed similar rates of viral detection (p= 1.00). The sensitivity and specificity of detecting SARS-COV-2 active infection in saliva were 95.7% (95%CI: 79.0–99.8%) and 100% (95%CI: 98.1–100%) respectively, with the mean cycle threshold values similar to those of oropharyngeal samples (p>0.05). The genome sequencing revealed a mean coverage of 95.5 ± 2.8%, finding omicron as the main variant. The anti-SARS-COV-2 antibody detection in saliva showed a sensitivity of 92.0% (95%CI: 85.0–96.0%) and specificity of 93.3% (95%CI: 78.0–99.2%) compared to plasma. There was a high agreement in antibody detection results between FCRM and ITM laboratories (Cohen's kappa 0,94; p = 0.0001).

**Conclusion** These findings demonstrate that saliva can be used as a surrogate to Oropharyngeal or plasma for surveillance of SARS-COV-2 infection in the Republic of Congo.