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.

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