Tumour necrosis factor alpha (TNF-α) and Interferon gamma (IFNg), in the same set of spiked serum samples. Experiments on each platform were performed as recommended by the kit manufacturer. We assessed the concentration of each analyte detected by each platform Vs. the expected actual concentrations.

Results For samples with known low and high cytokine concentrations, all platforms were able to discriminate between low Vs. high expression, however, the actual concentration for each cytokine varied greatly amongst the three platforms. Our data revealed MSD as the most sensitive amongst the platforms compared, and Curiox as the most suitable for high-throughput multiplexing, when employed alongside a Luminex platform.

Conclusion Although quantitative differences were found between the platforms assessed, the relative concentrations detected were comparable, showing that all three platforms were suitable for analyzing trends in multiple cytokine profiles. Further studies, including comparison with ELISA are ongoing.

PA-320 OPTIMISATION OF RNA EXTRACTION METHODS FOR SMALL BLOOD VOLUMES FOR FUTURE USE IN TB HOST TRANSCRIPTOMIC BIOSIGNATURE APPLICATIONS

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Background Whole-blood-based transcriptomic methods have limitations, including in the amount of blood required for standard RNA blood collection tubes. This is particularly relevant to individuals with difficulty in providing large volumes of blood, such as children. Furthermore, the cold chain required for storing blood tubes is problematic in field applications and in remote settings. It is therefore important to optimise RNA extraction techniques to allow for the isolation of high quantity and quality RNA from small blood volumes, and samples that are easier to collect and store under field conditions. Thus, the aim was to evaluate the quantity and quality of RNA extracted from small volumes of whole blood including dried blood spots (DBS) using three commercial extraction kits, to determine suitability for future use in RT-PCR-based experiments.

Methods Total RNA was extracted from small blood volumes (500µl, 100µl, 50µl) and DBS samples using the GenElute™ Total RNA Purification, PureLink® RNA Mini, and Tempus™ Spin RNA Isolation Kits. The yield, purity and integrity of the resulting RNA was assessed with fluorometry, spectrophotometry and agarose gel electrophoresis respectively.

Results An average of 2321 ± 456.30 ng and 336.3 ± 113.6 ng RNA was obtained from 500 µl of blood with the Tempus™and PureLink® kits respectively. Overall, the RNA isolated with both kits were intact and of high quality. RNA isolated from lower blood volumes (100 µl, 50 µl and DBS) using all three kits, was not of sufficient quantity or quality.

Conclusion Preliminary findings indicate that the quantity and quality of RNA isolated from 500µl of blood using either the PureLink® or Tempus™ kits may be sufficient for downstream transcriptomic analysis. Upon completion, our findings may be valuable in future studies that are conducted in individuals with difficulty in providing large volumes of blood such as children.

PA-324 CYP2B6*6 HETEROZYGOSITY MEDIATES SLOW P. FALCIPARUM CLEARANCE IN MALARIA PATIENTS TREATED WITH ARTEMETHER-LUMEFANTRINE

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Background Emerging artemisinin resistance threatens the effort to eliminate malaria; artemisinin resistance investigation emphasizes parasites' genetic modification as the leading cause of treatment failure. But CYP2B6*6 is vital in determining Artemisinin pharmacokinetics hence treatment outcome. Inter-individual variability may mediate variable responses to artemisinin therapy among malaria patients.

Methods We recruited 100 symptomatic malaria patients aged five and above; who had P. falciparum infection and prescribed Artemether-Lumefantrine. We established their parasite load change during a 3-day treatment using the quantitative Polymerase Chain Reaction (qPCR) technique. We determined the prevalence of CYP2B6*6 Single Nucleotide Polymorphism among the patients and assessed the relationship with parasitological outcome.

Results 63% of patients had detectable parasites by qPCR, 54% had slow parasite load reduction, and 24% had parasite fold reduction of <100, while 5% of the individuals had > 10000 parasites/µL at day 3. Genotype frequency for CYP2B6*6 was 43% GG, 17%TT and 40% GT. Heterozygosity was associated with slow parasite clearance; P=0.02. The majority of the males were heterozygous.

Conclusion Most patients had delayed parasite reduction after Artemether-Lumefantrine therapy; this is more prevalent among CYP2B6*6 heterozygous individuals. Delayed parasite load reduction could be due to the slow activation of artemisinin to its active metabolite by CYP2B6*6 heterozygous patients. Such patients will have subtherapeutic levels of the active drug, unable to clear the parasite in the required treatment duration at the recommended dosage of artemisinin. The difference in treatment outcomes between different genotypes indicated that host genetic variability could determine treatment outcomes or confer selection pressure against artemisinin and the partner drug.

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PA-325 THE PEDIATRIC PRAZIQUANTEL CONSORTIUM: OUR DEVELOPMENT JOURNEY TO PROVIDE TREATMENT TO PRE-SCHOOL AGED CHILDREN

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Background Schistosomiasis, highly prevalent in tropical regions, affects over 240 million people. Praziquantel (PZQ) is considered the standard-of-care treatment. However, around 50 million preschool-aged children (PSAC) remain untreated