on neutrophils is poorly described. We assessed the effect of high dose vit.D3 in vitro on activation and microbial killing capacities of neutrophils and monocytes under near-physiological conditions using fresh whole blood from adult healthy donors.

Methods Whole blood was exposed to Mycobacterium bovis Bacille Calmette-Guérin (BCG) and Lipopolysaccharide (LPS) post treatment with 100 nM vit.D3 for 2hr, 6hr, and 24hr. Cellular phenotyping by flow cytometry was performed to quantify expression of neutrophil (CD16bri14low) and monocyte (CD14bri16low) activation markers (CD11b, CD62L), bacterial phagocytic capacity, and reactive oxygen species (ROS) production. Interleukin 8 (IL-8) and myeloperoxidase serum levels were quantified using ELISA, and correlated with intracellular killing capacities by performing colony forming unit (CFU) analysis.

Results Vit. D3 had no significant direct effect on CD11b/62L expression, phagocytic capacity, ROS production, inflammatory marker expression (IL-8, MPO) and killing efficacy independent of the pre-treatment durations. This may reflect differences in vit.D3 concentrations used and kinetics of vit.D3 mediated response patterns in the cells studied when compared to previous reports. Although these results cannot be extrapolated onto in vivo conditions as vit.D3 effects under physiological conditions can be more complex, the whole blood assay proves a valuable tool to analyse host responses ex vivo in patient cohorts. This assay is employed in our ongoing EDCTP funded 96-week randomized placebo-controlled clinical trial (VITALITY) involving high-dose vit.D3 supplementation (20,000 IU/week) in HIV positive adolescents to assess effects on neutrophil and monocyte antimicrobial responses.

Conclusion An interplay of background effects of HIV and other comorbidities need to be considered as they may influence overall benefits of vit.D3 in this population.

PA-803 INSTITUTIONALIZATION OF RESEARCH AND KNOWLEDGE TRANSLATION IN ZAMBIA: ADVANCING EVIDENCE-BASED DECISION-MAKING FOR IMPROVED HEALTH OUTCOMES

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Background The National Health Research Authority (NHRA) is implementing a program under the name institutionalization of research and knowledge translation (KT) in Zambia as a means to enhance evidence-based decision-making and ultimately improve health outcomes. The institutionalization of research and KT involves the integration of systematic research processes and the effective translation of research findings into policies and practices within the national health system. NHRA recognizes the critical role that research plays in informing health policies, programs, and interventions.

Methods In order to actualize this program, the NHRA utilized a multi-faceted methodology. This involved carrying out a needs assessment of the ten (10) provinces in Zambia to identify the research and knowledge translation gaps for key personnel. Consequently, the NHRA conducted a research priority setting for each of the ten (10) provinces, through stakeholder engagements, to identify and prioritize research topics/areas aligned with Zambia's health needs and policy priorities. NHRA also developed a robust frameworks to assess the impact of research and knowledge translation activities in the provinces.

Results The NHRA has since created Terms of References (TORs) and facilitated the appointment of Research and Knowledge Translation Focal Point Persons (R&KT FPPs) in all the ten (10) provinces to spearhead research and knowledge translation activities within respective provinces. Consequently, with support from CDC foundation, NHRA has engaged the R&KT FPPs in its research and knowledge translation training and KT mentorship programs. The R&KT FPPs have been trained in Research Methods and Scientific Writing, as well as a KT mentorship course dubbed as Data to Policy.

Conclusion With greater funding and partnership, it is hoped that the program will cascade to the lower levels (district, facility and community) within the Ministry of Health for better health outcomes. Undoubtedly, this initiative represents a crucial and timely step towards evidence-based decision-making and improved health outcomes.

PA-806 A COMPOSITE CYTOKINE MODEL TO MONITOR TUBERCULOSIS TREATMENT RESPONSE. A PILOT STUDY

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Background There is an urgent need for biomarkers that predict TB treatment response in clinical practice and research. Despite its poor specificity and sensitivity, sputum microscopy and culture conversion 8 weeks following treatment initiation remains the recommended surrogate for TB treatment response. A blood-based biomarker with the ability to predict TB treatment response will significantly improve research into TB treatment-shortening trials, trials testing new anti-TB therapy and clinical practice where it can potentially aid in early identification of patients at risk of poor treatment outcomes.

Methods We conducted a pilot, nested case-control study to identify potential biomarkers to predict TB treatment response. All participants completed the PredictTB treatment-shortening clinical trial. All available confirmed relapses at the time of this pilot study (17) and one treatment failure participant were included and 54 controls were randomly selected. Multiplex immunoassays were used to measure serum expression of 50 cytokines at baseline, weeks 04, 08 and 16 and 24. In addition, demographic and symptom data, clinical examination parameters and laboratory results were collected.

Results Using baseline and week 8 parameters, we derived a model that discriminated between relapses and controls with an AUC of 0.81, sensitivity of 0.78 and a specificity of 0.85. Parameters that were most useful in discriminating between relapses and controls were changes from baseline to week 8 in TNF-alpha, sIL2R-alpha, IL 12p70, sVEFFR3, sVEGFR1, E-selectin, and MIP-1. In addition to chest pain and diastolic blood pressure; baseline Apo A1, IL-1beta, and Apo C3 also contributed to the model. Our data also validated a previously published treatment response signature.

Conclusion Our results indicate that a multivariable model may be better at predicting TB treatment response compared to current measures. This work is preliminary and will be combined with a larger cohort.