

Methods The cross-sectional, mixed methods design was employed. The study population was 785 health care workers and non-health workers working at University of Port-Harcourt Teaching Hospital (Nigeria). The purposive sampling was used for qualitative study while the stratified random sampling technique was utilised for the quantitative study. Qualitative data were collected from fifteen respondents while a total of 511 questionnaires were administered at the study site. The qualitative data was analysed using inductive thematic analysis. The quantitative data was analysed using structural equation modelling (SEM).

Results The qualitative study suggested that quality improvement was perceived as most useful in influencing all the tree sub-components of readiness. Training is perceived as most useful in building readiness while it is perceived to be moderately useful in influencing the sub-component of readiness. The OLS estimates indicates that QI/QA exert a positive and significant effect on motivation ($\beta=0.004$, $p<0.05$) and general capacity score ($\beta=0.28$ $p<0.05$) while it inversely but significantly exerts influence on innovation specific capacity ($\beta=-0.21\times 10^{-3}$, $p<0.05$). The SEM/pathway analysis shows the direct and indirect routes of interactions among predictors of readiness after adjusting for confounders. All the explanatory variables have significant effect on readiness except gender which was dropped from the final model.

Conclusion The strength of evidence of how an evidence-based system for innovation support can influence readiness was established. Though readiness is a rate-determining step in ensuring robust and effective implementation outcomes for epidemic containment, exploring innovation outcomes and their amplification through explicitly target readiness dynamics requires further investigation.

PO 8355 HOST GENETIC POLYMORPHISMS AND ASYMPTOMATIC MALARIA IN SOUTHERN GHANA

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Background Despite several interventions through malaria control programmes, asymptomatic malaria is a major barrier to control as asymptomatic individuals serve as reservoirs from which others are re-infected. The mechanism by which these individuals remain asymptomatic is not well understood. Much work has been done in relation to human genes and their association to severe, mild and uncomplicated malaria. However, there is limited knowledge regarding host genetic factors and asymptomatic malaria.

Method In this study, we investigated the association between host genetic polymorphisms of glucose-6-phosphate dehydrogenase gene (G6PD), mannose binding lectin (MBLG54A), tumor necrotic factor alpha (TNF-G308A) and nitric oxide synthase 2 (NOS2-G954C) and the outcome of asymptomatic *P. falciparum* malaria in 150 healthy individuals in southern Ghana.

Results We found a significant association between G6PDd and asymptomatic malaria with a prevalence of 9.6% ($p=0.035$, by chi-square test). All the individuals who were heterozygous and hemizygote deficient (5.3% and 4.3%) were found to be asymptomatic. Individuals homozygous (GG) for TNF (G308A) were found to be highly asymptomatic ($p=0.019$, by chi-square test). Regarding MBL (G54A) and

NOS (G954C), no significant association was found between these markers and asymptomatic malaria.

Conclusion Upon reviewing our data with other data from published work, we conclude that both heterozygous and hemizygous individuals with G6PD A- and homozygous individuals (GG) of TNF (G308A) polymorphisms could be predisposed genetically to asymptomatic malaria.

PO 8356 ANGIOGENIC AND ANGIOSTATIC FACTORS IN THE SALIVA OF MALARIA PATIENTS

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Background Malaria mortality is associated with exaggerated host responses to inflammatory factors such as C-X-C motif chemokine 10 (CXCL10) and host biomarkers such as angiopoietin 1 (Ang-1) and angiopoietin 2 (Ang-2). The aim of this study was to determine saliva levels of CXCL10, Ang-1 and Ang-2 and compare with plasma levels regarding their potential as biomarkers of malaria, which may be useful for further development of highly efficient non-invasive malaria detection methods.

Methods Case control study involving 213 subjects (119 with and 94 without malaria) aged 1–16 years. Haematological determination was done using Haematology Analyser. Plasmodium Lactate Dehydrogenase/Histidine Rich Protein-2 (pLDH/HRP-2) Antigen rapid diagnostic test (RDT) were performed. Plasma and saliva levels of CXCL10, Ang-1 and Ang-2 were measured using Elisa kit. Data was presented as mean \pm standard error or median and interquartile range (IQR). A p-value <0.001 was considered statistically significant.

Results There was decreased plasma levels of Ang-1 and increased plasma levels of CXCL10 and Ang-2 in individuals with malaria compared to those without malaria (Ang-1, $p<0.009$; Ang-2, $p<0.001$; CXCL10 $p<0.001$). Biomarker levels in both plasma and saliva in subjects with malaria and without malaria were correlated and a significant relationship was found between Ang -2 and CXCL10 which could be used to predict malaria severity ($p=0.001$ for Ang-2 and $p<0.01$ for CXCL10). Low Ang-1 and high Ang-2 in both plasma and saliva were significantly associated with increased risk of malaria severity: Ang-1, 2741.04 (1785.85–3582.68), $p<0.009$; Ang-2, 3508.82 (2139.61–5091.633.9), $p<0.001$ and Ang-1, 720.27 (439.82–1086.74); 16.98 (10.08–33.26), ($p<0.001$ for all). Finally, Ang-2 was informative when combined with CXCL10 to predict malaria severity.

Conclusion These results provide insight into the use of saliva for a non-invasive diagnostic method and demonstrate that Ang-2 combined with CXCL10 is a promising predictive biomarker of malaria severity.

PO 8369 BURULI ULCER: PATTERN OF PRESENTATION IN A NIGERIAN HOSPITAL

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