Type: Poster Presentation

Final Abstract Number: 45.034 Session: Parasitology and Parasitic Infections Date: Thursday, April 3, 2014 Time: 12:45-14:15 Room: Ballroom

Antimalarial drug resistance polymorphims in South Eastern Nigeria: A preliminary report

U.M. Chukwuocha^{1,*}, C.P. Ekiyor², G.C. Nwakwuo¹, I.N. Dozie¹, A.C. Okpanma¹

¹ Federal University of Technology, Owerri, Nigeria
² Rahi Medical Outreach, Portharcourt, Nigeria

Background: This preliminary study reports the first documented evidence of antimalarial drug resistance polymorphisms in South Eastern Nigeria.

Methods & Materials: Real Time PCR (RT-PCR) assay was used to type for *pfmdr1* genes whereas *pfdhfr*, *pfdhps* and *pfcrt* genes were typed with the Restriction Fragment Length Polymorphism of PCR(PCR-RTLP) from blood spots of two hundred under five children attending pediatric clinics in the Federal Medical Centre, Owerri, South Eastern Nigeria.

Results: Treatment with antimalarial drug in the last two days was reported by 10.3% of the children. Antimalaria drug resistance mutations were detected in all the samples with *pfdhfr* S108T(76%) and *pfdhps* A438G(72%) recording the highest prevalence. Mutation in the *pfcrt* gene however was only detected in 43% of the samples. Mixed polymorphisms were observed more in triple mutations of *pfdhps* (69%) and *pfdhfr* (64%) respectively while quintuple and sextuple mutations accounted for 20% and 32% respectively.

Conclusion: These results ascertain the prevalence of antimalarial drug resistance polymorphisms in South Eastern Nigeria with their changing patterns of occurrence. This may form a baseline for the continuous monitoring of drug resistance in South Eastern Nigeria to inform more effective and sustainable planning and implementation of evidence based antimalarial drug policies.

http://dx.doi.org/10.1016/j.ijid.2014.03.774

Type: Poster Presentation

Final Abstract Number: 45.035 Session: Parasitology and Parasitic Infections Date: Thursday, April 3, 2014 Time: 12:45-14:15 Room: Ballroom

Diagnosing female genital schistosomiasis



S.D. Holmen^{1,*}, M. Onsrud¹, B.J. Vennervald², F. Albregtsen³, M. Taylor⁴, J. Moodley⁵, L. van Lieshout⁶, P. Pillay⁷, K. Lillebø¹, E. Kleppa¹, E.F. Kjetland¹

¹ Oslo University Hospital, Oslo, Norway

- ² University of Copenhagen, Copenhagen, Denmark
- ³ University of Oslo, Oslo, Norway
- ⁴ University of KwaZulu-Natal, Durban, South Africa
- ⁵ Nelson R Mandela School of Medicine, University of

KwaZulu-Natal, Durban, South Africa

⁶ Leiden Univerity Medical Centre, Leiden,

Netherlands

⁷ Durban University of Technology, Durban, South Africa

Background: Almost 100 million women in Sub-Saharan Africa are thought to be at risk of female genital schistosomiasis. It is manifested by genital lesions, causes pain, discharge and possibly increased risk of HIV transmission. There is currently no gold standard for diagnosing FGS. Urine diagnostics (PCR/microscopy of urine, haematuria, CAA, and antibodies) are nonspecific and insensitive predictors of genital pathology. Biopsy of lesions with detection of ova by microscopy may confirm positive cases. However, FGS is largely co-endemic with HIV, rendering this approach unethical, as the iatrogenic lesion may increase the risk of HIV transmission. The characteristic yellow lesions may serve as a diagnosis when visualised by a trained expert who is using a colposcope. However, objective and simple diagnostic tools are needed.

Methods & Materials: Women from an endemic area were recruited for gynaecological examinations with colposcopy. Samples were collected for schistosomiasis PCR, urine microscopy and STI analyses. Computer colour analysis was applied on colposcopic data to identify yellow lesions. The state of the art diagnosis for *S. haematobium* diagnosis will be presented.

Results: We found a strong association between the output from the computer colour analysis and the expert FGS diagnosis (adjustedOR 6.51, 95% CI 2.56 - 16.56, p < 0.001). Likewise, the computer colour analysis was associated with urinary *Schistosoma haematobium* (OR 3.52, 95% CI 1.50- 8.27, p = 0.004). In the absence of a gold standard we applied latent class analysis (LCA). We used data from six variables: computer image analysis, clinical findings, microscopy of urine, PCRs in cervico-vaginal lavage and urine, and school prevalence. We found that computer colour analysis may yield a sensitivity of 80.5% and a specificity of 65.4% for the diagnosis of FGS.

Conclusion: A computerised tool for automated detection of lesions may be of help to the clinician, offering an objective assessment of lesions. This software could be used in simple electronic devices, in rural, endemic areas as a point of care diagnosis. Further research is needed on the texture and shape of the lesions to improve the performance and to explore how this could be merged with the imminent technology for cancer screening.

