

the progress to neurosyphilis. Moreover, high expression of CSF CXCL13 mediated B cells migration both *in vitro* and *in vivo*. More importantly, there was a positive correlation between the CSF B cells, immunoglobulin indices, and CSF CXCL13 levels. Interestingly, ectopic germinal centres (EGCs), the important structures for the maintenance of humoral immunity, were observed in the intracranial syphilitic gumma. **Conclusion** CXCL13/CXCR5 mediated the aggregation of B cells, which directed the aberrant humoral immune responses via the formation of EGCs. Our observations suggest a molecular mechanism of neurological damage in neurosyphilis.

LB1.71 VAGINAL MICROBIOTA CONTROLS EPITHELIAL CELL PROLIFERATION AND SUSCEPTIBILITY TO *C. TRACHOMATIS* INFECTION

Steven Smith, Jacques Ravel. *University of Maryland, Baltimore, USA*

10.1136/sextrans-2017-053264.176

Introduction Dysbiotic states of the vaginal microbiota, including bacterial vaginosis (BV), are characterised by a paucity of *Lactobacillus* spp., the presence of an array of anaerobes, a pH >4.5, and are associated with increased susceptibility to STIs. The mechanisms by which vaginal microbiota protect or increase the risk to STIs remain unknown. By characterising the *in vivo* host miRNA response to different types of vaginal microbiota, we gained insight into functions that play a role in epithelial homeostasis. Understanding the molecular mechanisms driving vaginal dysbiosis may help develop strategies reduce the risk of STIs.

Methods Leveraging prospectively collected daily vaginal swab samples, miRNA-seq profiling was used to gain insight into host regulatory mechanisms controlled by vaginal microbial communities. Random Forest miRNA feature ranking was used to identify miRNAs expressed in response to different types of vaginal microbiota. *In vitro*, VK2 epithelial cells were exposed to vaginal bacteria culture supernatants, and miRNA expression was measured by qPCR, while cyclin D1 was measured by Western blot. Cell proliferation was quantified using scratch and EdU assays. Cell proliferation's effect on *C. trachomatis* infection was performed on cervical A2EN epithelial cells.

Results We leveraged daily collected vaginal samples in conjunction with a machine learning approach to discover eight miRNAs differently controlled by vaginal microbiota. Of these, expression of miR-193b, known to regulate host cell proliferation, was increased by *Lactobacillus* spp.-dominated microbiota. Recently, *in vitro*, VK2 cells exposed to *Lactobacillus*-conditioned supernatants exhibited reduced proliferation, high miRNA-193b expression and decreased abundance of cyclin D1. Importantly, epithelial cell proliferation was required for efficient *C. trachomatis* infection.

Conclusion These findings contribute to the vaginal microbiota's role in cellular homeostasis and susceptibility to STIs, which may lead to improved preventive strategies by modulating vaginal microbiota composition.

LB1.72 PREVALENCE OF HUMAN PAPILLOMA VIRUS INFECTION AND DETECTION OF HPV TYPES IN HIV- POSITIVE MALE PATIENTS FOLLOWED BY ANAL CYTOLOGICAL ABNORMALITIES IN EASTERN INDIA

Abhilasha; Jaya Chakravarty, Shyam Sundar, Madhukar Rai. *Banaras Hindu University, India*

10.1136/sextrans-2017-053264.177

Introduction India has a third large population of people living with Human Immunodeficiency Virus (HIV) in the world. Incidence of Human papilloma virus (HPV) infection anal cancer is high among People Living with HIV/AIDS (PLHIV). However, there are very few studies among HIV positive men in India. Thus this cross-sectional study was performed to assess the prevalence and risk factors of anal HPV infection and anal HPV types in HIV positive males attending the Anti-retroviral therapy (ART) centre.

Method We screened HIV positive men with Anal Papanicolaou smear cytology and HPV testing. HPV DNA was detected by Consensus Polymerase Chain Reaction (PCR) using dissimilar E6 consensus and MY09/11 consensus primers followed by sequencing for confirmation the type of HPV.

Results 126 HIV-positive men were included in the study. Mean age was 35.37±8.2 years. Median CD4+T cell counts were 253/μL. Mean weight and mean Haemoglobin was 49.53 ±8.45 Kg and 11.2±1.73 g/dl respectively. 74 patients were treatment naive and 52 were on Anti-Retroviral Therapy (ART) 48 (38%) gave positive for history of anal intercourse with other men although 91% were married. Anal cytology was done in 95 patients, out of which 61 (64.2%) had cytological abnormalities, of which 28 (29.4%) cases had LSIL, 33 (34.7%), had ASCUS. In multivariate analysis, an only risk factor for cytological abnormality was a history of anal intercourse Odds Ratio (OR) 0.122 (95% 0.036–0.410). HPV DNA was detected in 25.21% patients. The most prevalent HPV type in the study group was HPV-16 (10%) followed by HPV-18,31,35,17,66,72,52,68 and 107 (15.21%) genotypes were detected in anal pap samples.

Conclusion In our study, the prevalence of HPV infection was 25.21% and anal cytological abnormality was 64.2%, which is high. Anal Pap smear screening should be done especially in HIV positive males with the history of bisexuality. HPV DNA screening by using consensus PCR method followed by sequencing more beneficial and cost-effective for HPV genotyping HIV infected men on antiretroviral therapy.

Clinical Science

P2.01 ASSESSING THE IMPACT OF INDIVIDUALISED TREATMENT: AN INDIVIDUAL-BASED MATHEMATICAL MODELLING STUDY OF ANTIMICROBIAL RESISTANT *NEISSERIA GONORRHOEAE* TRANSMISSION, DIAGNOSIS AND TREATMENT IN MEN WHO HAVE SEX WITH MEN

¹Adam Zienkiewicz, ¹Martin Homer, ¹Hannah Christensen, ¹Darryl Hill, ²Neil Woodford, ²Helen Fifer, ²Gwenda Hughes, ¹Katherine Turner. ¹*University of Bristol, UK*; ²*Public Health UK*

10.1136/sextrans-2017-053264.178

Introduction Antimicrobial resistant (AMR) gonorrhoea is a global public health threat. In London, diagnoses in men who have sex with men (MSM) have more than quadrupled from