9.02% of the population. A total of 31 (88.57%) specimens harbouring HPV DNA were genotypes using multiplex PCR versus 11.43%, which were not genotyped using HPV 16,18, 31, 33, 35, 45 and 51 by multiplex PCR. HPV genotyping gave 63 differents HPV with 28.57% who had a single infection while 71.43% have a multiple infection. HPV genotypes prevalence were the followed: HPV 16 (28.57%), HPV 18 (23.80%), HPV35 (19.04%), HPV 45 (19.04%), HPV 51 (3.17%) and HPV 33 (1.58%). By using PCR as gold standard VIA sensibility was 16.12% and the specificity 95.45%.

Conclusion HPV circulate in Cote d'Ivoire in women attending for cervical cancer screnning by visual inspection with acetic acid or lugol. Visual inspection with acetic acid or lugol seem to have a good specificity. HPV Genotypes 16 and 18 included in the vaccine available seem to be the most prevalent.

P1.48 ABSTRACT WITHDRAWN

P1.49 THE MUTATIONS ON GENES RELATED TO MACROLIDE OR FLUOROQUINOLONE RESISTANCE ON *M. GENITALIUM* IN JAPAN

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Introduction The condition of antimicrobial resistance in *Mycoplasma genitalium* has been becoming serious in the world. The macrolide-resistance is closely related to mutation on region of 23S rRNA gene. The fluoroquinolone-resistance is probably related to mutation on gyrase or Topoisomerase IV genes such gyrA or parC, like as other fluoroquinolone-resistant bacteria. In our study, we analysed the mutations related to antimicrobial resistance among *M. genitalium* genes which collected in Japan and compared with mutations of M6489, the multidrug-resistant strain.

Methods The *M. genitalium* genomes were collected from the urine specimens of Japanese males with urethritis during the period between 2005 and 2016. In addition, the genomes of M. genitalium strain which can grow in the culture media, included M6489, the multidrug-resistant strain were used. The region V of 23S rRNA and quinolone-resistance determining region (QRDR) on gyrA and parC genes were sequenced and the mutations related to macrolide- or quinolone-resistance were analysed.

Results The *M genitalium* genomes from 157 Japanese males and 10 *M. genitalium* strains were analysed. Among the genomes from Japanese males, mutations related to macrolide-resistance such as A2058G or A2059G were detected in 4.4% (4/90) genomes at 2005–2009 and in 40.3% (27/67) at 2010–2016. Two types of mutations on the gyrA gene with amino-acid change and 11 types of mutations on the parC gene with amino-acid change were found. These mutations were detected in 26.6% (24/90) at 2005–2009% and 53.7% (36/67) at 2010–2016. Most frequent mutations were Pro69→Ser in 18 genomes and Ser80→Ile in 16 genomes. M6489 had A2059G on 23S rRNA and Asp87→Asn on gyrA and Ser80→Ile on parC gene. If these mutations on M6489 were related to fluoroquinolone-resistance, the fluoroquinolone-resistant *M. genitalium* increased 3.4% (3/87) to 16.4% (11/67).

Conclusion The mutations related to macrolide-resistance and fluoroquinolone-resistance genes increased in Japan.

P1.50 ABSTRACT WITHDRAWN

P1.51 ANTIMICROBIAL RESISTANCE (AMR) AND NG-MAST PROFILE OF *NEISSERIA GONORRHOEAE* ISOLATES COLLECTED FROM STD PATIENTS FROM ACROSS INDIA

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Introduction *Neisseria gonorrhoeae* multiantigen sequence typing (NG-MAST) is a highly discriminatory technique for assessing the genetic diversity of *N. gonorrhoeae* (NG) and has also been put forward as a tool for predicting specific antimicrobial resistance (AMR) phenotypes. In light of the above, the present study was undertaken to investigate the molecular epidemiology of NG in India and to examine if it can be used as a means for predicting AMR.

Methods A total of 204 consecutive NG isolates collected between April 2010 - October 2013 were investigated. Antimicrobial susceptibility testing was done using disc diffusion method and E test and the results interpreted using the breakpoint criteria of CDS technique. NG-MAST was performed as described previously. WHO *N. gonorrhoeae* reference strains F, G, K-P were used as controls. Association between NG-MAST sequence type (ST) and antimicrobial susceptibility was probed using χ^2 and fisher's exact tests.

Results Rates of resistance to classical antibiotics were high. Decreased susceptibility (DS) to ceftriaxone (MIC 0.032–0.25 μg/ml) was seen in 7.3% while azithromycin resistance (MIC $\geq$1 μg/ml) in 2.5% isolates. A total of 202 NG isolates were assigned into 108 different STs while 2 were not typable, The high genetic diversity arose from the allelic combination of 80 *por* and 44 *tbpB* alleles and the overall mean genetic distance was 85.5 (SE 4.6) nucleotide differences. Out of 108 STs, 84 (77.8%) were novel. The majority of STs (75.9%, 82 of 108) were represented by singletons, whereas the remaining STs included between 2 and 38 isolates. The most common STs were ST6058 (n=38, 18.8%), ST2990 (n=6, 2.9%), ST6069, ST9775, ST9783, ST9875 (n=5, 2.5% each). There was a significant association between ST6058 and resistance to penicillin (p=0.00) and tetracycline (p=0.00) and ST6069 and ST 6083 and DS to ceftriaxone (p=0.00 and p=0.01 respectively).

Conclusion The present study highlights a heterogeneous gonococcal population in India. Our data, although on a limited number of NG isolates, testify to an association between genotype and AMR phenotype.

P1.52 RESISTANCE, CLONALITY AND CLINICAL ASPECTS ASSOCIATED WITH *STAPHYLOCOCCUS AUREUS* SAMPLES ISOLATED FROM COLONISATION SITES OF PAEDIATRIC AND ADOLESCENT PATIENTS INFECTED BY HUMAN IMMUNODEFICIENCY VIRUS

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Introduction HIV- infected patients are in a high-risk group to develop *Staphylococcus aureus* infections. From 6% to 20% of these individuals have presented colonisation by methicillin resistant isolates (methicillin resistant *S. aureus* "MRSA"). In addition, *S. aureus* isolates may carry genes encoding the Panton Valentine leukocidin (PVL), responsible for lysing leukocytes. This study aimed to detect and characterise *S. aureus* isolates from nares, oropharynx and saliva from paediatric and adolescent patients infected with HIV enrolled in a public paediatric outpatient clinic, between 2014 and 2015.

Methods The *S. aureus* identification was conducted after cultivation of specimens on mannitol salt agar, using conventional tests. The determination of antimicrobial susceptibility was performed by disk diffusion test, while the minimum inhibitory concentration (MIC) by the E-test was evaluated for mupirocin. PCR was used to detect the PVL genes and to determine the SCC*mec* types, while the PFGE technique was used for analysis of clonality.

Results Among 100 patients included in the study, 68 (68%) presented *S. aureus* colonisation, and 15 (22%) of them were colonised by MRSA isolates. Colonisation by MRSA isolates was detected in the nares (17,6%), saliva (10,2%) and oropharynx (8,8%) of the patients. Among the 107 s. *aureus* isolates, the highest percentage of resistance was 26.1% for erythromycin, followed by cefoxitin (23.4%), gentamicin (4.7%) and teicoplanin (3.7%). All MRSA isolates carried the SCC*mec* IV and the PVL genes were found in 26 isolates of 20 (29.4%) patients. The isolates were included in 11 genotype profiles.

Conclusion The study confirms the high frequency of colonisation by *S. aureus* in paediatric and adolescent patients with HIV. Besides the high rate of colonisation in nostril over than a third of the patients presented colonisation in the oropharynx and/or saliva, important aspects to be considered in the control and prevention of infections caused by *S. aureus* isolates in HIV-positive individuals.

P1.53 MICRORNA EXPRESSION INDUCED BY VAGINAL MICROBIOTA CONTROLS CELL PROLIFERATION

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Introduction Bacterial Vaginosis (BV) is a condition of the human vagina characterised in part by a paucity of *Lactobacillus* spp. and the presence of a wide array of strict and facultative anaerobes such as *Gardnerella vaginalis* and *Atopobium vaginae*. BV is associated with the acquisition of sexually transmitted infections such as HIV and *Chlamydia trachomatis*. Host microRNAs (miRNAs) are an uncharacterized factor that may control host cellular responses to *Lactobacillus* and BV-associated bacterial communities. Understanding the molecular mechanisms that drive or are induced by BV-associated vaginal microbiota may help identify targets and develop strategies to restore a healthy vaginal state, which would concurrently reduce the risk of STI acquisition. We hypothesised that specific miRNAs are associated with *Lactobacillus*-dominated and BV-associated Community State Types (CST) by affecting specific host functions.

Methods Leveraging prospectively collected daily vaginal swab samples, the types and abundance of human miRNAs were used to gain insight into host regulatory mechanisms that potentially associate with vaginal microbial community composition shifts using miRNAseq. Random Forest miRNA feature ranking was used to identify miRNAs correlated with types of vaginal microbiota. Additional *in vitro* cell culture experiments were performed to demonstrate the relationship between miRNA expression, vaginal bacterial culture supernatants and epithelial cell proliferation using qPCR and Western blots.

Results miRNASeq was performed on 100 samples from 16 unique subjects in 3 longitudinal microbiota profile groups. One of the most significant miRNAs associated with BV was miR-193b. *In vitro,* its expression correlated with decreased cell proliferation in cells exposed to *Lactobacillus* spp. culture media relative to *G. vaginalis* culture supernatants.

Conclusion miR-193b over expression is associated with reduced cell proliferation in non-BV samples. Control of cell proliferation could contribute to reducing the risk of STI in *Lactobacillus* dominated vaginal microbiota.

P1.54 DEVELOPMENT AND EVALUATION OF IN- HOUSE MULTIPLEX REAL-TIME PCR FOR DETECTION OF *NEISSERIA GONORRHOEAE, CHLAMYDIA TRACHOMATIS* AND *MYCOPLASMA GENITALIUM* INFECTION IN INFERTILITY PATIENTS

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Introduction: *C.trachomatis, N.gonorrhoeae* and *M.genitalium* are important cause of infertility but detection is usually by PCR which has to be performed indvidually for each pathogen.The aim of this study was to develop In house multiplex Real time PCR assay for simultaneous detection of all these pathogens in single run and will also help in detecting co infecion if present thus saving cost and time in cases of infertility.

Methods The Taqman probe based multiplex qPCR for detection of *C.trachomatis*, *N.gonorrhoeae* and *M.genitalium* was developed using different primers and probes. Analytical sensitivity of multiplex qPCR was determined using pGEMT Easy vector cloned with target genes. The detection limit for each organism was determined using 10 fold dilutions of targets. The multiplex qPCR was evaluated in 248 clinical samples i.e 98 infertile (endometrial biopsy and endocervical swabs) and 150 healthy controls (endocervical swabs). The sensitivity, specificity, positive and negative predictive value (PPV and NPV) of multiplex qPCR was calculated.