

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 different 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 screening 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P1.48 ABSTRACT WITHDRAWN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 GONORRHOEA* 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.