Abstracts

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.

P1.49 THE MUTATIONS ON GENES RELATED TO ANTIMICROBIAL RESISTANCE (AMR) AND NG-MAST

The mutations related to macrolide-resistance and fluoroquinolone-resistance 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P1.50 ABSTRACT WITHDRAWN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

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 x^2 and fisher’s exact tests.

Results

Rates of resistance to classical antibiotics were high. Decreased susceptibility (DS) to ceftriaxone (MIC 0.032–0.23 μg/ml) was seen in 7.3% while azithromycin resistance (MIC ≥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 hupB 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, ST7977, ST7983, 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.