Abstracts

We described the reported samples by sex and age and characterised isolates tested in NRL by resistance patterns. We calculated proportions and medians, together with interquartile range (IQR), where appropriate.

Results Between April and December 2014 we received information on 651 isolates tested in 19 laboratories. Altogether, 90.3% of isolates were from men and 8.5% from women. Median age of tested men was 36 (IQR 29–49) and women 28 (IQR 22–41) years.

NRL received 502 isolates, 342 were vital and 253 were tested for AMR. From those 0 were resistant towards ceftriaxone, 1.6% towards cefixime, 11.1% towards azithromycin, 73.1% towards ciprofloxacin, and 30.4% towards penicillin. Further 37.9% and 50.6% isolates were intermediate susceptible to Azithromycin and to Penicillin. From 205 isolates tested for beta-lactamase, 25.9% were positive.

Conclusion In Germany isolates tested for NG-AMR were mostly from men. We assume that a substantial proportion of these isolates could be from men having sex with men. NG-AMR to ceftriaxone and cefixime remains low, while resistance and intermediate susceptibility to azithromycin, ciprofloxacin and penicillin is substantial. Monitoring of NG-AMR should be highly prioritised.

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PO5.12 ANALYSIS OF BACTERIAL FLORA OF THE URINE SPECIMENS FROM MALE PATIENTS WITH URETHRITIS BY THE CLONE LIBRARY METHOD BASED ON THE 16S rRNA GENE

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Introduction Chlamydia trachomatis, Mycoplasma genitalium or Trichomonas vaginalis are the pathogens for non-gonococcal urethritis, but pathogenicity of other microorganisms for the male urethral has not be confirmed. In this study, the bacterial flora of urine specimens from male patients with urethritis was analysed by the clone library method based on the 16S rRNA gene.

Methods The first voided urine specimens of male patients with urethritis were collected. The detection of Neisseria gonorrhoeae, C.trachomatis were examined by transcriptional mediated amplification (TMA) method and M. genitalium, Ureaplasma urealyticum, Ureaplasma parvum and Mycoplasma hominis were examined by real-time PCR method. The urine specimens were strained by Ethidium bromide and the number of bacterial cells were counted. DNA was extracted from the urine and amplification of the 16S rRNA gene via PCR (universal primers) and determination of the nucleotide sequences of 96 colonies were performed. The homology search was performed with a basic local alignment search tool (BLAST) using in-house software system and phylogenotypes of bacteria in each specimens were analysed.

Results Urine specimens were collected from 58 patients and the divided to 4 group; gonogoccal urethritis (n=9), chlamydial urethritis (n=12), non-chlamydial non gonococcal urethritis detecting with Ureaplasmas or Mycoplasmas (UM+NCGU, n=15) and non-chlamydial non gonococcal urethritis detecting without Ureaplasmas or Mycoplasmas (UM-NCGU, n=22). Cell numbers were higher in UM+NCGU than in UM-NCGU. Among specimens, 2427 clones in 38 bacterial flora could be analysed and 91 bacterial phylogenotypes were detected together with N.gonorrhoeae, C.trachomatis, Mycoplasmas or Ureaplasmas positive specimens among chlamydial urethritis or UM+NCGU groups. Gardnerella vaginalis was detected with Mycoplasma/Ureaplasma in Chlamydial urethritis or UM+NCGU.

Conclusion The clone library method by using 16S rRNA gene is the new technology for analysis the bacterial flora of urine with urethritis. The relationship between G. vaginalis and Ureaplasma/Mycoplasma was found by this analysis.

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