P658

## DID MINIMUM INHIBITORY CONCENTRATIONS IN *N. GONORRHOEAE* ISOLATES CHANGE IN GERMANY SINCE 2014?

<sup>1</sup>Thalea Tamminga\*, <sup>2</sup>Susanne Buder, <sup>3</sup>Sandra Dudareva, <sup>4</sup>Gabriele Zuelsdorf, <sup>5</sup>Sebastian Banhart, <sup>5</sup>Tanja Pilz, <sup>4</sup>Kerstin Dehmel, <sup>2</sup>Eva Guhl, <sup>2</sup>Ingeborg Graeber, <sup>2</sup>Peter Kohl, <sup>6</sup>Viviane Bremer, <sup>7</sup>Dagmar Heuer, <sup>3</sup>Klaus Jansen. <sup>1</sup>Robert-Koch-Institute, Unit 34: HIV/AIDS, STI and Blood-borne Infections, Berlin, Germany; <sup>2</sup>German Conciliar Laboratory for Gonococci, Department of Dermatology and Venerology, Vivantes Hospital, Berlin, Germany; <sup>3</sup>Robert Koch Institute, Infectious Disease Epidemiology, Berlin, Germany; <sup>4</sup>Robert Koch Institute, Unit for HIV/AIDS, STI and Blood-borne Infections, Berlin, Germany; <sup>5</sup>Robert Koch Institute, Unit for Sexually Transmitted Bacterial Infections, Berlin, Germany; <sup>6</sup>Robert Koch Institute, Berlin, Germany; <sup>7</sup>Robert Koch Institute, Sexually Transmitted Bacterial Pathogens, Berlin, Germany

10.1136/sextrans-2019-sti.726

Background German national guidelines recommend ceftriaxone combined with azithromycin for *Neisseria gonorrhoeae* (NG) treatment since 2014. The Gonococcal-Resistance-Network (GORENET) monitors gonococcal antimicrobial resistance (AMR) in Germany. The aim is to assess whether national guidelines are still effective in Germany and which factors affect higher minimum inhibitory concentrations (MICs).

Methods GORENET laboratories sent NG isolates to the conciliar laboratory for centralized retesting of AMR using E-test. We included infection year, sex, age, infection site and clinical service type in the analysis. Geometric means were calculated for MICs for infection year. The effects of infection year, sex, age, infection site and clinical service type on MICs for ceftriaxone, cefixime, and azithromycin were investigated by multiple linear regression.

Results

Overall, 278 (2014), 303 (2015), 438 (2016) and 409 (2017) isolates were analysed. Of these, 90% of isolates came from men. Median age was 33 years (IQR: 25-44). Cumulative geometric means of MICs 2014-2017 were 0.006 µg/ml for ceftriaxone, 0.022 µg/ml for cefixime, and 0.185 µg/ml for azithromycin. In adjusted analysis, MICs decreased for ceftriaxone, cefixime and azithromycin by 0.74 (CI-95% 0.70-0.79), 0.89 (CI-95% 0.87-0.92) and 0.79 (CI-95% 0.75-0.83) per year, respectively. For ceftriaxone, isolates from urology (1.40; 95%-CI 1.15-1.69) and other service types (1.39; 95%-CI 1.10-1.77) compared to internal medicine, and from women (1.58; 95%-CI 1.14-2.18) were associated with increased MICs. Regarding cefixime isolates collected from urology (1.14; 95%-CI 1.02-1.28) compared to internal medicine, and from women (1.41; 95%-CI 1.18-1.69) were associated with increased MICs. For azithromycin, isolates from urology (0.82; 95%-CI 0.70-0.97) compared to internal medicine, and from women (0.77; 95%-CI 0.59-1.00) were associated with decreased MICs.

Conclusion Treatment options as recommended by German national guidelines are still applicable. The lower MICs after 2014 may be due to the change of national treatment guidelines in 2014. Differences in MICs regarding service types and sex need to be further investigated.

Disclosure No significant relationships.

P659

## IMPROVED TYPEABILITY USING CULTURE-FREE GENOTYPING OF *NEISSERIA GONORRHOEAE* COMPARED TO ROUTINE CULTURE-DERIVED SURVEILLANCE

<sup>1</sup>Michiel Slaats, <sup>2</sup>Brian Van Der Veer\*, <sup>1</sup>Petra Wolffs, <sup>3</sup>Christian Hoebe, <sup>4</sup>Nicole Dukers-Muijrers, <sup>1</sup>Lieke Van Alphen. <sup>1</sup>Maastricht University Medical Center (MUMC), Medical Microbiology, Care and Public Health Research Institute (CAPHRI), Maastricht, Netherlands; <sup>2</sup>Maastricht University Medical Centre, Medical Microbiology, Maastricht, Netherlands; <sup>3</sup>Public Health Service South Limburg, Maastricht University Medical Center (MUMC), Sexual Health, Infectious Diseases and Environmental Health, Medical Microbiology, Care and Public Health Research Institute (CAPHRI), Heerlen, Netherlands; <sup>4</sup>Public Health Service South Limburg, Sexual Health, Infectious Diseases and Environmental Health, Heerlen, Netherlands

10.1136/sextrans-2019-sti.727

Background Surveillance of *Neisseria gonorrhoeae* (NG) is important to monitor NG transmission and dissemination of resistant strains. A widely used surveillance method is NG multi-antigen sequence typing (NG-MAST) which relies on genotyping of cultured strains while culture frequently fails. Recently, we developed a culture-free genotyping method with a higher typing rate compared to culture-based methods. As typing rate is lower in the routine culture-based NG-MAST, some sequence types (ST) might be missed in surveillance. Therefore the aim of this study was to compare genotyping results of culture-positive and culture-negative NG.

Methods All positive nucleic acid amplification test (NAAT) screening samples of which a routine culture was performed were retrospectively collected from January 2017 till August 2018. In total, 179 samples were collected (100 male urine, 22 vaginal swab, 57 anorectal swab). DNA was isolated and culture-free NG-MAST was applied. A phylogenetic tree was constructed of Sanger sequence data using multiple alignment and unweighted pair group method with arithmic mean.

Results Of 179 samples, 143 (79.9%) were successfully genotyped with culture-free NG-MAST, 24/179 failed and 12/179 showed possible mixed strain infections. Culture was successful in 113/179 samples of which 92/113 NAAT samples were successfully genotyped with culture-free NG-MAST and 8/113 showed possible mixed strain infections. Results showed six genogroups (n≥5 samples), which all included both culture-positive and negative NG. However, culture-free NG-MAST successfully genotyped 51/66 culture-negative samples revealing six additional ST (n=7 samples).

Conclusion With both the culture-free and routine culture based method, the same genogroups were identified. This would mean that major trends could be identified with both methods. However, some ST were missed using routine surveillance. Therefore, the culture-free NG-MAST method could be used to genotype culture-negative or uncultured samples to aid in early detection of outbreaks and resistant genotypes.

Disclosure No significant relationships.