

P636

HIGH DIVERSITY OF *NEISSERIA GONORRHOAE* IN GERMANY REVEALED BY MOLECULAR TYPING USING NG-MAST (2014–17)

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Background *Neisseria gonorrhoeae* (NG) infections are not reportable in Germany. The Gonococcal Resistance Network (GORENET) is a laboratory network to monitor antimicrobial resistance (AMR) in Germany, linking data from sequence typing to epidemiological data. We described prevalence of gonococcal sequence types in Germany and associations to AMR to improve future treatment and prevention strategies.

Methods NG isolates collected between April 2014 and December 2017 were tested by E-test and sequence typed by NG multiantigen sequence typing (NG-MAST). For sequence typing, DNA was extracted and internal fragments of *porB* and *tpbB* were amplified by polymerase chain reaction. Fragments were sequenced by Sanger sequencing and evaluated using a global database (www.ng-mast.net). Genogroups were assigned to sequence types which shared one allele and exhibited ≥99% homogeneity in the other allele.

Results 1220 isolates were sequence typed (106 in 2014, 96 in 2015, 525 in 2016, and 495 in 2017). In total, we detected 422 different sequence types that grouped into 17 genogroups. Among the most prevalent genogroups were G2400 (6.8%), G1407 (6.8%), G5441 (6.2%), G25 (5.6%), G2992 (5.5%) and G10557 (5.3%). The multi-resistant G1407 and G2400 were most prevalent in 2014 (12.4% and 10.5%, respectively) and declined to 6.1% and 7.3% in 2017. Two new genogroups, G11461 (3.6%) and G17420 (2.1%), emerged showing high prevalence in 2017 and no association to extended-spectrum cephalosporin resistance. Furthermore, a novel genogroup-association with cefixime resistance and reduced cephalosporin susceptibility was identified.

Conclusion From 2014 to 2017 prevalence of G1407 declined and two novel extended-spectrum cephalosporin sensitive clones G11461 and G17420 seem to have replaced the multidrug resistance clone G1407. To verify these results, continuous testing with an increased number of isolates should be performed.

Disclosure No significant relationships.

P637

NEISSERIA GONORRHOAE GENOMIC DIVERSITY IN HIGH RISK GROUPS IN SWITZERLAND

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Background *Neisseria gonorrhoeae* cases are increasing in Europe, with decreasing susceptibility to first line antibiotics.

Whole genome sequencing (WGS) provides detailed information about gonococcal molecular epidemiology and prediction of antimicrobial resistance (AMR), especially if linked to epidemiological data. The aim of this study was to examine molecular, clinical and social epidemiological aspects of gonorrhoea infections in Switzerland.

Methods In 2015–2016, we cultured urethral, cervical, vaginal, rectal, and pharyngeal specimens from patients in three clinics predominantly attended by men who have sex with men (MSM) and female sex workers (FSW). MSM also completed a sexual behaviour questionnaire. Minimal inhibitory concentrations (MIC) were assessed by Etest, interpreted using EUCAST breakpoints except azithromycin (≥2 mg/L); WGS used an Illumina Miseq.

Results We sequenced 140 isolates from 116 participants, MSM (107, 92%, mean age 35.8 years) and FSW (6, 5%, mean age 25.3 years). Amongst MSM, 48/105 respondents (45.7%) reported recent sex abroad. Three patients (two MSM and one FSW) carried different strains at different body sites. The isolates show large genomic diversity, with 69 NG-MAST types and 37 MLST sequence types, largely embedded within characterised European Union clusters. NG-MAST 1407 was identified in n=4 isolates from two patients (FSW, not travel-associated and MSM, sex elsewhere in Europe). Mosaic *penA*XXXXIV was seen in these isolates, and also in an NG-MAST 13488 from an MSM, which was also not travel associated. One isolate (heterosexual male, not travel-associated) with elevated cefixime MIC (0.19 µg/ml) carried a mosaic *penA* in an NG-MAST 10557 background. Ciprofloxacin resistance was seen in these six isolates, and overall in 59/140 (42%), all containing GyrA mutations S91F and D95A/G/N.

Conclusion Switzerland has a high diversity of circulating gonorrhoea, generally related to European clusters. Multidrug resistant isolates were not identified in this study, but NG-MAST 1407 and *penA* mosaics, associated with elevated cephalosporin MICs, are circulating.

Disclosure No significant relationships.

P638

SURVEILLANCE OF GONOCOCCAL INFECTION TREATMENT FAILURES 2015–2018 IN QUÉBEC, CANADA

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Background Incident cases of gonococcal infection are increasing. Antibiotic resistance may compromise the effectiveness of treatment. In 2017, the proportion of azithromycin-resistant strains reached 31% in Quebec and a first strain non-susceptible to ceftriaxone and cefixime was detected.

Methods Since November 2014, public health departments are invited to report possible cases of treatment failures. Clinical and epidemiological information is collected using a standardized form for each report of gonococcal infection occurring <42 days after a previous episode in the same person. Antimicrobial susceptibility testing (AST) is conducted at the