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

Sebastian Banhart, Tanja Pilz, Thalea Tamminga, Sandra Dudareva, Eva Guli, Ingeborg Graber, Volunare Bremer, Peter Kohl, Susanne Buder, Klaus Jansen, Dagmar Heuer, Robert Koch Institute, Unit for Sexually Transmitted Bacterial Infections, Berlin, Germany; Robert-Koch-Institute, Unit 34: HIV/AIDS, STI and Blood-borne Infections, Berlin, Germany; Robert Koch Institute, Infectious Disease Epidemiology, Berlin, Germany; German Conciliar Laboratory for Gonococci; Department of Dermatology and Venerology, Vivantes Hospital, Berlin, Germany; Robert Koch Institute, Berlin, Germany; Robert Koch Institute, Sexually Transmitted Bacterial Pathogens, Berlin, Germany

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 tbpB 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 G10537 (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.

No significant relationships.