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 multitignen 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%), GI407 (6.8%), G5441 (6.2%), G25 (5.6%), G2992 (5.5%) and G10557 (5.3%). The multi-resistant GI407 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 GI407 declined and two novel extended-spectrum cephalosporin resistant clones G11461 and G17420 seem to have replaced the multidrug resistance clone GI407. To verify these results, continuous testing with an increased number of isolates should be performed.

Disclosure No significant relationships.