Background Neisseria gonorrhoeae (NG) infections are not reportable in Germany. The GONORRHEA infections in Switzerland. The aim of this study was to examine molecular, clinical and social epidemiological aspects of gonorrhea infections in Switzerland.

Methods In 2015–2016, we studied routinely collected specimens from patients in three clinics predominantly attended by men who have sex with men (MSM) and female sex workers (FSW). Antibiotic susceptibility testing (AST) was performed using 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. Two patients (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 penAAXXIV 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 penAX in an NG-MAST 10537 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 gonorrhea, 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.

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