Background Recent research suggests that Neisseria meningitidis (Nm) OMV serogroup B vaccination protects against gonorrhea (caused by Neisseria gonorrhoeae, Ng). Since 2015, we have monitored a large cluster of urethritis cases caused by a uropathogenic, non-groupable Nm clade (US NmNG urethritis clade). The US NmNG urethritis clade encodes for MenB-4C vaccine antigens (FHbp, NhbA, NadA), but whether natural infection reduces subsequent risk of urethral gonorrhea is unknown.

Methods We constructed a dataset combining surveillance and medical record data from men diagnosed with US NmNG clade urethritis (n=128) in a local STD clinic. We used time-to-event analyses of clinic visits between 1/2015 and 4/2018 to examine prospective urethral gonorrhea risk. As gonorrhea is a common event in STD patients, we compared subsequent gonorrhea acquisition for men with US NmNG clade urethritis at baseline to men with Ng urethritis (n=255), chlamydial urethritis (n=123), and no infection (n=275) at baseline.

Results Participants were primarily Black (65%) and heterosexual (82%), with a median age of 28 years. At baseline, 13% had prior gonorrhea history. Only one participant had prior MenB vaccination. Half (49%) of men returned for STD screening at least once during the follow-up period. Men with US NmNG clade urethritis at baseline had similar gonorrhea risk as men with Ng at baseline (HR: 1.03, 95% CI: 0.60–1.76). Results were not meaningfully different when assessing extragenital gonococcal infections, or after adjustment for time since baseline, age, race, sexual orientation, prior gonorrhea infection, and sexual behavior (number of partners, condom use, and oral sex). In contrast, those with US NmNG clade urethritis had increased gonorrhea incidence compared to men with chlamydial urethritis (HR: 2.02, 95% CI: 1.11–3.69) and men with no infection at baseline (HR: 3.84, 95% CI: 1.87–7.91).

Conclusion Natural infection with US NmNG urethritis clade does not appear to protect men against subsequent acquisition of gonorrhea.

Disclosure No significant relationships.
agar dilution as described by the Clinical Laboratory Standards Institute. Molecular genotyping was determined using N. gonorrhoeae multi-antigen sequence typing (NG-MAST).

**Results** In 2016–2017, NML received 8,300 N. gonorrhoeae isolates; 668 of the isolates were associated with multiple infection sites from a total of 307 cases. Of the 307 cases, 92.8% (n=285) had isolates with similar AMR profiles and the same NG-MAST ST. Twenty-two cases (7.2%) with isolates originating from multiple infection sites were found to have different AMR profiles and different STs. Of the 134 cases with throat and rectal isolates, 3.7% (5/134) had isolates with different STs. Of the 144 cases with both urogenital and rectal isolates, 6.3% (9/144) of isolates had different STs. Of the 132 cases with both urogenital and throat isolates, 9.9% (13/132) had different STs. Three cases had all three infections sites (throat, rectal and urogenital), each with different AMR profiles and different ST types.

**Conclusion** The majority of gonococcal cases with isolates from multiple infection sites have the same AMR profile and ST indicating a single infection. Approximately 7% of gonococcal cases with multiple infection site isolates were found to have very different AMR profiles and sequences types which may have implications in test-of-cure strategies, treatment failure investigations and surveillance programs.

**Disclosure** No significant relationships.

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**P633 LOW GONORRHOEA ANTIMICROBIAL RESISTANCE AND CULTURE POSITIVITY RATES IN GENERAL PRACTICE: A PILOT STUDY**

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**Background** In the Netherlands, the gonorrhoea resistance to antimicrobials surveillance (GRAS) programme is carried out at STI clinics, which provide care for high-risk populations. However, half of gonorrhoea infections are diagnosed in general practice (GP). We performed a pilot study to explore expanding GRAS to the GP population using laboratory-based surveillance. Additionally, antimicrobial resistance patterns of GP and STI clinic patients were compared.

**Methods** Three laboratories from different regions were included, which all perform gonorrhoea diagnostics for GPs and STI clinics and used eSwab for patient sampling. Additional culturing for all GP patients with gonorrhoea took place from February to July 2018. After positive PCR-NAAT test, residual eSwab material was used for culture. In positive cultures, susceptibility testing was performed for azithromycin, ciprofloxacin, cefotaxime and ceftriaxone using Etest.

**Results** During the study period, 484 samples were put in culture. 16.5% of cultures were positive (n=80). Antimicrobial resistance levels were low, with 2.6% resistance to azithromycin, 21.5% to ciprofloxacin and 0.0% to cefotaxime and ceftriaxone. Resistance levels in STI clinic GRAS data (first half of 2018) were 19.2% for azithromycin, 31.5% for ciprofloxacin, 1.9% for cefotaxime and 0.0% for ceftriaxone.

**Conclusion** Culture positivity rates for GP patients were low, probably due to long transportation times and awaiting PCR test results. Positivity rates might be improved by making changes in sampling and/or transportation methods, but that would require involvement of GPs and patients instead of keeping the surveillance lab-based. Resistance levels appeared to be much lower at the GP than at STI clinics, indicating that resistance might emerge first in more high-risk populations that visit the STI clinics. It is important to consider all potentially relevant patient populations when establishing a surveillance programme. Based on the findings from this study the current GRAS programme will not be extended to the GP population.