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=253), chlamydial urethritis (n=252), or no infection (n=257) 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.

Background Gonorrhea infection is increasing and becoming harder to treat. In England, incidence among men who have sex with men (MSM) has increased eight-fold since 2008, reaching ≥21,000 cases in 2017. This epidemic, coupled with the growing threat of potentially untreatable antibiotic-resistant infection, has renewed interest in a gonococcal vaccine. Previous vaccine development attempts have failed; however, observational evidence suggesting the MenZB meningococcal B vaccine is partially protective against gonorrhea, with 31% effectiveness but uncertain duration, indicates it may be possible to develop a suitable vaccine.

Methods We fitted a stochastic transmission-dynamic model, incorporating asymptomatic and symptomatic infection and heterogeneous sexual behaviour, to gonorrhea incidence in MSM in England over 2008–17 using particle Markov Chain Monte Carlo methods. Bayesian forecasting, considering realistic vaccination strategies under different scenarios of antibiotic resistance, determined how vaccine effectiveness and duration of protection affect population-level impact, and examined feasibility of achieving WHO’s target of reducing gonorrhea incidence by 90% between 2016 and 2030.

Results Even a partially-effective vaccine could have a substantial impact if protection lasts long enough. In a worst-case scenario of untreatable gonorrhoea, vaccinating all MSM attending sexual health clinics with a 58% effective vaccine protecting for ≥12 years (with boosters if required), or a 66% effective vaccine lasting ≥6 years, reduces expected incidence below the WHO target. A vaccine conferring 30% protection for 2–4 years reduces expected incidence in 2030 by 34% if gonorrhoea becomes untreatable, but if ≥80% of gonorrhoea cases are treatable then incidence is reduced by 95%.

Conclusion Our statistically rigorous assessment shows that even a partially-effective vaccine, delivered through a practical targeting strategy, could have a substantial benefit in reducing gonorrhoea incidence in the context of an epidemic with rising antibiotic resistance. Our model can help design trials to measure vaccine effectiveness and duration of protection and assess cost-effectiveness of vaccination strategies.

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.

**P632 REGIONAL DIFFERENCES IN GONORRHOEA ANTIMICROBIAL RESISTANCE PATTERNS IN THE NETHERLANDS**

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**Background** The Gonococcal Resistance to Antibiotics Surveillance (GRAS) programme was established in the Netherlands to monitor gonorrhoea resistance patterns. Until now, GRAS data were only analysed and presented on a national level. This study aims to gain insight into regional differences and the representativeness of GRAS.

**Methods** 18 STI clinics participate in GRAS and monitor resistance to azithromycin, ciprofloxacin, cefotaxime and ceftriaxone by performing culture and susceptibility testing with Etest for gonorrhoea patients. To describe differences in antimicrobial resistance levels between STI clinic regions, data from 2013–2017 was used. Antimicrobial resistance was defined based on EUCAST breakpoints. For azithromycin and ciprofloxacin, variables associated with resistance in univariate analyses were added to a multilevel logistic regression model containing a random intercept for region. We calculated the proportional change in variance (PCV) to assess to what extend regional variance in antibiotic resistance was explained by these variables. We included patient characteristics (e.g. sex, age, ethnicity, anatomical location of infection) and laboratory characteristics (sample method and selective culture medium).

**Results** In 2013–2017, almost 9,000 susceptibility tests were performed. Resistance to azithromycin was 11.6% (varying between regions from 2.0%–41.5%), ciprofloxacin 29.4% (12.8%–61.1%), cefotaxime 2.0% (0.0%–4.2%) and ceftriaxone 0.0%. The PCV after adding patient characteristics to the model was 73.8% for ciprofloxacin, but for azithromycin –17.8%. For laboratory characteristics, these were 32.8% and 36.6%. Adding both patient and laboratory characteristics explained 78.6% of regional variance for ciprofloxacin, and 15.5% for azithromycin.

**Conclusion** Regional variations in antimicrobial resistance are reported, and need to be taken into account when interpreting national surveillance data. Further research is needed to determine the cause of these regional differences, including an evaluation of regional laboratory practices. Especially for azithromycin, as regional variance could not be explained by population characteristics.

**Disclosure** No significant relationships.