health laboratories, modify surveillance systems for enhanced data collection and rapid communication of AST results, and initiate partner services and investigations among patients with GC demonstrating reduced susceptibility (RS) to ceftriaxone, cefixime or azithromycin.

Outcomes/Impact SURRG grantees incorporated robust genital, pharyngeal, and rectal gonococcal culture collection from all genders at participating clinics. During 2018–2019, grantees performed AST on >10,700 isolates with a five-day median turnaround time from specimen collection to reporting AST results to providers. Fifty-nine percent of patients with RS GC returned for a test-of-cure; no resistance-related treatment failures were detected. Among 4,511 isolates, we found $\geq 95\%$ concordance (within one doubling dilution) between AST performed locally using Etest® compared to agar dilution (reference method) for ceftriaxone, cefixime and azithromycin. We conducted investigations among cases and partners, identifying >100 new GC cases. Finally, we merged epidemiologic and partner data with isolate genomic data to further explore sexual networks with GC transmission and identify opportunities for local interventions.

Innovation and Significance SURRG successfully built clinic, laboratory, and epidemiological capacity for local ARGC rapid detection and response. Notable outcomes/innovations include establishing best practices for collecting and transporting gonococcal culture specimens, implementing Etest® in local jurisdictions, and measuring the value of containing ARGC spread through partner services. Lessons learned and project-informed identification of additional ARGC control needs at the local and national level are being used to inform CDC's ongoing ARGC control efforts.

008.5

IMPACT OF INCREASED ASYMPTOMATIC TESTING FOR GONORRHOEA AMONG MSM ON PREP ON THE TRANSMISSION AND DEVELOPMENT OF ANTIMICROBIAL RESISTANCE

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Background In many countries, men who have sex with men (MSM) using pre-exposure prophylaxis (PrEP) are routinely three-monthly tested and treated for *Neisseria gonorrhoeae* (gonorrhoea), which might increase antimicrobial resistance (AMR). However, there is uncertainty about how AMR emerges. We investigated the impact of frequent testing and treating on gonorrhoea prevalence and AMR assuming different ways of AMR emergence.

Methods We developed a compartmental model, which included three sexual activity classes that differed in unprotected sex partner numbers and testing uptake. AMR to ceftriaxone was incorporated as stepwise increases in minimum inhibitory concentrations and eventual resistance (MIC drift) in three separate ways: direct selection pressure through ceftriaxone treatment; indirect selection pressure through antimicrobials treatment for other reasons; or imported infection. Each model was calibrated to the ceftriaxone MIC curve from the Dutch Gonococcal Resistance to Antimicrobials Surveillance program (2015–2019). We estimated the impact of three-monthly testing of high-risk MSM on overall and AMR prevalence in 2030.

Results Overall gonorrhoea model prevalence was 3.4% (95% uncertainty interval 3.2%–3.5%), and 14.3% (11.7%–18.0%) in high-risk MSM. Three-monthly testing resulted in 66%–93% reductions in overall prevalence for all three ways in which AMR development was modelled. AMR prevalence was low in 2030 for all three mechanisms, but increased fastest with direct selection compared to indirect or imported. With direct selection, AMR prevalence was 1.7 (1.3–2.0) times higher than with indirect selection and 8.2 (2.7–16.1) times higher than through imported infection. When high-risk MSM increased numbers of unprotected sex partners, three-monthly testing reduced overall prevalence less and AMR prevalence increased, especially with direct selection.

Conclusion With frequent testing of MSM, direct selection pressure through treatment leads to more gonococcal resistance than indirect selection or imported infection. This study highlights the need to increase our understanding of mechanisms of AMR emergence in *N. gonorrhoeae*.

008.6

ASSESSING WITHIN-HOST GENETIC VARIATION IN NEISSERIA GONORRHOEAE AT DIFFERENT ANATOMICAL LOCATIONS AND OVER TIME

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Background Recent trials focus on novel antibiotic treatment options for *Neisseria gonorrhoeae* (Ng), since resistance against currently used cephalosporins is emerging. To assess antibiotic potential, patients with mixed infections or those who are reinfected after treatment should be identified. Comparing levels of within-host genetic variation in Ng isolates at different anatomical locations and over time could identify those patients and could inform thresholds for similarity.

Methods Isolates from the New AntiBiotic treatment Options for uncomplicated GONorrhoea (NABOGO) trial were used in this study. Whole-genome sequences were obtained from paired isolates from 86 patients with multiple isolates from different anatomical locations (n pairs=59) or from different time points (n pairs=48). All isolates were typed according to the typing schemes: NG-Multi-Antigen Sequence Typing (NG-MAST), NG-Sequence Typing for Antimicrobial Resistance (NG-STAR), Multi-Locus Sequence Typing (MLST) and core genome MLST (cgMLST).

Results Identical NG-MAST/NG-STAR/MLST profiles were identified within 93/107 (87%) isolate pairs. Different strains were found in 8/59 (14%) paired isolates from different anatomical locations, according to completely different NG-MAST/NG-STAR/MLST profiles. Five other isolate pairs from multiple anatomical locations differed in NG-MAST but were similar in NG-STAR/MLST. One case of reinfection was identified (1/48, 2%) according to

a completely different NG-MAST/NG-STAR/MLST profile in an isolate pair from different time points. One other isolate pair from multiple time points differed only in NG-MAST, suggesting a potential case of reinfection. However, the level of similarity between typed cgMLST alleles was still >99% within the 5 isolate pairs with varying NG-MAST, which was only 4–87% within isolate pairs with completely different NG-MAST/NG-STAR/MLST profiles.

Conclusion Isolates with completely different NG-MAST/NG-STAR/MLST profiles can be considered as different strains, according to the low similarity in cgMLST alleles. Isolates with variable NG-MAST still had high similarity in cgMLST alleles, suggesting that NG-MAST might be too variable for identifying mixed- and re-infections.

Gonorrhoea epidemiology and antimicrobial resistance

009.1 TRENDS AND REGIONAL DIFFERENCES OF NEISSERIA GONORRHOEAE ANTIMICROBIAL RESISTANCE IN THE NETHERLANDS, 2013–2019

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Gonococcal antimicrobial resistance is emerging worldwide, and is monitored in the Netherlands in 18 out of 24 Sexual Health Centres (SHC) that perform culture and susceptibility testing for patients with gonorrhoea. This study describes trends, determinants and regional differences in azithromycin resistance and ceftriaxone decreased susceptibility in 2013–2019.

Data on person characteristics, STI diagnoses and MIC values (Minimum Inhibitory Concentration, measured by E-test) for gonorrhoea were reported by participating SHC. We describe azithromycin resistance (AZI-R, MIC >1 mg/L) and ceftriaxone decreased susceptibility (CEF-DS, MIC >0.032 mg/L) over time and per SHC. We use multilevel logistic regression analysis to describe determinants of AZI-R/CEF-DS among MSM and heterosexuals, correcting for SHC region. A separate multilevel model was made to quantify the effect of population differences on the regional variance of AZI-R and CEF-DS.

A total of 13,000 isolates were included from 2013–2019. AZI-R significantly increased from 2.8% (95% Confidence Interval 2.1–3.9%) to 9.3% (8.2–10.5%). CEF-DS significantly decreased from 7.0% (5.7–8.5%) to 2.9% (2.3–3.6%). Overall, regional differences were seen between SHC: AZI-R varied from 0.0% to 16.9%, CEF-DS from 0.0% to 7.0%. Regional variance could not be explained by population characteristics. Regression analyses found pharyngeal strain origin and year of consultation significantly associated with AZI-R and CEF-DS among MSM and heterosexuals. Among heterosexuals also a high number of partners was associated with AZI-R and CEF-DS.

No resistance or decreasing susceptibility was found for ceftriaxone, the first line gonorrhoea treatment in the Netherlands. However, azithromycin resistance is increasing, similar to trends worldwide. Differing levels of resistance/decreased susceptibility per SHC could not be explained by differences in population characteristics. This indicates the need for nationwide surveillance and reporting of results on a regional level. The association of pharyngeal strain origin with resistance/decreased susceptibility underlines the importance of including extragenital infections in gonococcal antimicrobial resistance surveillance.

009.2 LACK OF ASSOCIATION BETWEEN AZITHROMYCIN-RESISTANT NEISSERIA GONORRHOEAE INFECTION AND PRIOR EXPOSURE TO AZITHROMYCIN AMONG PERSONS ATTENDING A SEXUAL HEALTH CLINIC

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Background There is conflicting evidence on whether azithromycin (AZM) exposure is associated with subsequent AZM-resistance in persons with *Neisseria gonorrhoeae* (NG) infection.

Methods We included all patients from the Public Health-Seattle & King County Sexual Health Clinic (SHC) with culture-positive NG at ≥1 anatomic site whose isolates were tested for AZM resistance 2011–2019. We examined association of 1) any prescription of AZM from the SHC in ≤3, 6, and 12 months prior to NG diagnosis with AZM resistance (minimum inhibitory concentration [MIC] ≥2.0 µg/ml) using logistic regression and 2) the number of AZM prescriptions of either 1 or 2g in ≤3, 6, and 12 months and AZM MIC using linear regression. Both analyses controlled for race, age, HIV status, sex assigned at birth, gender of sex partner(s), anatomic site of infection, year/season of NG diagnosis, number of sexual partners in ≤12 months, and number of clinic visits in ≤3, 6, and 12 months.

Results Among 1,845 unique patients with 2,400 incident NG infections, 145 (6%) were resistant to AZM. In logistic regression, diagnosis with resistant NG was not associated with receipt of any AZM in ≤12 months (adjusted Odds Ratio [aOR] 0.69, 95% CI 0.43–1.12), ≤6 months (aOR 0.66, 95% CI 0.36–1.12) or ≤3 months (aOR 3.10, 95% CI 0.61–15.69). AZM MIC was not associated with the number of AZM prescriptions in ≤12 months (adjusted coefficient 0.06, 95% CI -0.07–0.18), ≤6 months (0.16, 95% -0.10–0.41) or ≤3 months (2.47, 95% CI -1.79, 6.7).

Conclusion Although our exposure variable is limited to receipt of AZM at a single clinic, we found no significant association between AZM exposure in ≤3, 6, or 12 months and subsequent AZM resistance among MSM with recurrent NG. These data suggest that individual-level AZM use for STI does not explain most cases of AZM resistant NG among MSM.