

genital and oropharyngeal sites in early 2018, with the aim of exploring whether tongue kissing transmits gonorrhoea.

Methods Participants independently provided extremely detailed interview accounts of sexual activity with one another, to permit inter-participant verification. Testing for *N. gonorrhoeae* was by nucleic acid amplification testing (NAAT). Whole genome sequencing (WGS) was performed on available culture-positive samples to assess genomic relatedness between samples.

Results Sexual contact included tongue kissing for all participants, and many participants participated in oro-genital and genito-genital intercourse with one another. All sexual contact occurred during a 1-week period in Victoria, Australia. Two participants had samples available for WGS and these were highly related genomically, and these participants were separated in this network by two other participants. All seven participants had gonorrhoea, six participants had oropharyngeal gonorrhoea in the absence of genital gonorrhoea, and the other participant had only vaginal gonorrhoea. No men acquired urethral gonorrhoea.

Conclusion The fact that six of seven participants had oropharyngeal gonorrhoea in the absence of urogenital gonorrhoea supports the notion that tongue kissing is a common mode of gonorrhoea transmission. No men acquired urethral gonorrhoea from oro-penile sex, suggesting that transmission from oropharynx to urethra may be less likely than by tongue kissing. Our WGS results, when viewed in conjunction with the extremely-detailed sexual behaviour data, support the notion that gonorrhoea diagnoses in this network were likely the result of within-network transmission. Our findings highlight the need for more research to define the transmission routes for gonorrhoea in heterosexuals, to inform screening policies.

Disclosure No significant relationships.

P681

IMPORTATION OF CIPROFLOXACIN RESISTANT *NEISSERIA GONORRHOEAE* INTO THE UK: A PUBLIC HEALTH CHALLENGE

¹Martina Furegato*, ²Claire Broad, ²Laura Phillips, ¹Mark Harrison, ²Marcus Pond, ³Liqing Zhou, ⁴Ngeekeong Tan, ⁵Sandra Okala, ³Sebastian Fuller, ⁶S Tariq Sadiq, ¹Emma Harding-Esch. ¹St George's, University of London, Applied Diagnostic Research and Evaluation Unit, Institute for Infection and Immunity, London, UK; ²St George's University of London, Applied Diagnostic Research and Evaluation Unit, London, UK; ³St George's, University of London, Applied Diagnostic Research and Evaluation Unit (ADREU), London, UK; ⁴St George's University Hospitals NHS Foundation Trust, London, UK; ⁵Public Health England, HIV/STI Department, London, UK; ⁶St George's, University of London, Applied Diagnostic Research and Evaluation Unit (ADREU), Institute for Infection and Immunity, London, UK

10.1136/sextrans-2019-sti.747

Background Current UK guidelines for managing *Neisseria gonorrhoeae* (NG) infection include ciprofloxacin use if antimicrobial susceptibility is indicated, but this option would be less useful if ciprofloxacin resistant NG (CpR-NG) rates increased, for example to levels reported in some parts of Asia. CpR-NG rates in the Americas are lower than in the UK. We investigated whether having recent condomless sex in "high" CpR-NG (HCpR-NG) regions (sex abroad, but not in the Americas) was associated with being infected with CpR-NG.

Methods We conducted two cross-sectional surveys of UK Sexual Health Clinics (March 2015-March 2016; May 2017-June 2018). Patients aged ≥ 16 years with symptoms of an STI

provided samples: vulvovaginal swab (females); first void urine (men-who-have-sex-with-women (MSW) and men-who-have-sex-with-men (MSM)); pharyngeal and rectal swabs (MSM). Data were collected on travel-associated sexual behaviour, including condomless sex abroad (CSA) in the past three months with a new partner. Routine clinic NG results were obtained. Resistance-associated mutations in *gyrA* (fluoroquinolones) for NG were identified using Sanger sequencing. Patients reporting CSA in HCpR-NG regions were compared to no sex abroad using Pearson's chi-squared test and multi-variable logistic regression models.

Results Overall, 71/1055 (6.7%) reported CSA in HCpR-NG regions. Of these, 12/71 (16.9%) compared to 85/984 (8.6%) not reporting CSA had NG ($p=0.02$). Among-NG positive patients, fluoroquinolone resistant mutations were found in 9/12 (75.0%) patients reporting CSA in HCpR-NG regions, compared to 35/85 (41.2%) who did not report CSA ($p=0.03$). After adjustment for other risk factors, the association between fluoroquinolone resistant NG and CSA in HCpR-NG regions remained significant (aOR:2.33[95% CI:1.03–5.24]).

Conclusion Having recent condomless sex with a new partner in regions of high ciprofloxacin resistance was associated with being NG-positive in the UK and having ciprofloxacin resistant NG. Importation of resistance may undermine attempts to recycle older antibiotics in the management of NG infection.

Disclosure No significant relationships.

P682

EFFICACY OF SECURIDACA LONGIPENDUCLULATA FRESEN (POLYGALACEAE) AGAINST STANDARD ISOLATES OF *NEISSERIA GONORRHOEAE*

Meshack Omolo*. University of Nairobi, Obstetrics and Gynaecology, Nairobi, Kenya

10.1136/sextrans-2019-sti.748

Background A study was carried out to determine the in vitro antibacterial activity of ethanol extract of root and bark of *Securidaca longipenduclulata* against standard isolates of *Neisseria gonorrhoeae*.

Methods The plant materials were collected early in the morning and dried at room temperature, followed by ethanol extraction using a rotary pump. Antibacterial activity assay was done against two bacterial isolates, viz. US standard isolate NO. 0296 and WHO standard isolate K using the agar diffusion method with dimethyl sulphoxide as a negative control and ceftriaxone antibiotic as a positive control. Antimicrobial activity was determined by measuring the zone of inhibition around each well. The minimum inhibitory concentration of the extract was determined using different concentrations of the extract and plated on the GC media. For each extract six replicate trials were conducted against each organism. The protocol of Odebiyi and Herbune (1978) was followed to determine the presence of phytochemical compounds.

Results The results obtained showed that both the root and bark extracts of *Securidaca longipendulata* have antibacterial activity against the two bacterial strains with a zone of inhibition of ≥ 10 mm in both root and bark and a bactericidal activity at 10^{-2} thus 0.01 $\mu\text{g/ml}$ of 10% crude extract in tube dilution. The antibiotic susceptibility tests on the common antibiotics in comparison with the extract showed that the root and bark extract have a higher susceptibility than

tetracycline, penicillin and ciprofloxacin. The extracts showed presence of saponins, steroids, glycosides, flavonoids, terpenes, alkanoids, phenolics and tannins.

Conclusion The demonstrated antibacterial activity of *Securidaca longipedunculata* against *Neisseria gonorrhoeae* provides a scientific basis for the traditional use in treating venereal diseases in Kenya. This investigation and further studies will pave way for use of this plant in antibacterial drug development for alleviating human suffering and open u reseach in discovery of new antimicrobial a gents.

Disclosure No significant relationships.

P683 RACIAL AND ETHNIC DISPARITIES RELATED TO *NEISSERIA GONORRHOEAE* AMONG U.S. MILITARY ACTIVE DUTY SERVICE MEMBERS

¹June Early*, ¹Sandra Waggoner, ²Eric Garges. ¹The Henry M. Jackson Foundation for the Advancement of Military Medicine, Inc., Bethesda, USA; ²Uniformed Services University of the Health Sciences, Department of Preventive Medicine and Biostatistics, Bethesda, USA

10.1136/sextrans-2019-sti.749

Background *Neisseria gonorrhoeae* is the second most common reportable infection in the United States, which if undiagnosed and untreated, can lead to severe long-term sequelae. Active duty U.S. Military service members are risk-taking young adults; however, military service offers some inherent control for social determinants often associated with increased risk of sexually-transmitted infections. Even in the absence of disparities in income and education, increased burden of disease among racial and ethnicity minorities may still exist. Herein, we describe the association between race/ethnicity and gonorrhea among active duty service members.

Methods This study was conducted among symptomatic and high risk patients enrolled at military infectious disease clinics from 2012 to 2017. Outcome variables were based on nucleic acid amplification test results extracted from medical records. The magnitude of association was assessed using adjusted odds ratios and 95% confidence intervals.

Results Data from 488 active duty participants were analyzed. The crude prevalence of gonorrhea and chlamydia among this clinic population was 17% and 25%, respectively. After adjusting for sex and age, non-Hispanic black service members had 3.5 times greater odds ($p=0.000$) and Hispanic service members had 2.9 times greater odds ($p=0.009$) of gonorrhea compared to non-Hispanic white service members. This phenomenon was not observed when comparing odds of chlamydia among blacks or Hispanics to whites.

Conclusion Despite similarities in income and education, black and Hispanic service members still bear a disproportionate burden of gonorrhea illness. Service members of color may have unique risk factors that predispose them to gonorrhea. Findings suggest that interventions aimed at reducing gonorrhea should be targeted towards persons of color to ensure disparities in disease burden are effectively addressed. Future studies should examine sexual behaviors among black and

Hispanic service members that may be contributing to increased odds of gonorrhea within the military population.

Disclosure No significant relationships.

P684 GONORRHEA SEQUENCE TYPES IN NON-CULTURED SPECIMENS FROM A PROVINCIALLY REPRESENTATIVE SAMPLE IN BRITISH COLUMBIA CANADA, 2018

¹Amalia Plotogea*, ²Irene Martin, ³Linda Hoang, ³Ana Paccagnella, ³Robert Azana, ⁴Troy Grennan, ⁴Jason Wong. ¹Public Health Agency of Canada, Canadian Field Epidemiology Program, Ottawa, Canada; ²Public Health Agency of Canada, National Microbiology Lab, Winnipeg, Canada; ³BC Centre for Disease Control Public Health Laboratory, Vancouver, Canada; ⁴British Columbia Centre for Disease Control, Clinical Prevention Services, Vancouver, Canada

10.1136/sextrans-2019-sti.750

Background In British Columbia (BC), Canada, enhanced gonorrhea surveillance to monitor sequence types (STs) is based on cultures which are typically performed on symptomatic individuals, at extra-genital sites, and at clinics in the Greater Vancouver Area (GVA), leaving certain subpopulations under-represented. We sought to describe *Neisseria gonorrhoeae* multi-antigen sequence types (NG-MASTs) in a provincially representative sample using remnant nucleic acid amplification tests (NAATs).

Methods A sample of gonorrhea positive NAATs diagnosed at the BC Centre for Disease Control Public Health Laboratory from March 1 to September 31, 2018 were sent to the National Microbiology Laboratory for sequence typing using the NG-MAST method. Samples were selected to be representative of the distribution of gonorrhea in BC by sex and geography. NG-MAST was linked to case information from the provincial sexually transmitted infections surveillance database. Associations were tested using Chi-square or Fisher's exact test.

Results There were 261 NAAT-positive gonorrhea specimens selected: 129 (49%) from urine, 71 (27%) from rectal, 35 (13%) from vaginal, 19 from cervical (7.3%) and 7 (2.7%) from urethral sites. Males represented 60% of the sample (156/261) and 21% (55/261) were from outside GVA. Mean age was higher in males than females (33 vs 28 years, $p<0.01$). Co-infection with chlamydia was more common among females than males (16% vs 5%, $p<0.01$). To date, results were available for 186 (71%) of the sample. The most common NG-MASTs were ST-7638 (11/186, 5.9%), ST-4207 (10/186, 5.4%), ST-12302 (9/186, 4.8%), ST-15246 (9/186, 4.8%) and ST-5985 (9/186, 4.8%). ST-12302 and ST-5985 were more common outside GVA ($p<0.01$ and $p=0.03$, respectively).

Conclusion We were able to use remnant NAAT specimens from a provincially representative sample to identify STs not routinely found using culture-based surveillance (e.g. ST7638, ST-4207). Moreover, some STs were more common outside GVA supporting the need for molecular methods to improve representativeness for gonorrhea surveillance.

Disclosure No significant relationships.