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.

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

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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.

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EFFICACY OF SECURIDACA LONGIPENDUCLULATA FRESN (POLYGALACEAE) AGAINST STANDARD ISOLATES OF *NEISSERIA GONORRHOEA*

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Background A study was carried out to determine the in vitro antibacterial activity of ethanol extract of root and bark of *Securidaca longipendulata* 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 μ 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