quadrivalent HPV vaccination (qHPVvax) randomised controlled trial in MSM aged 16–26 years, qHPVvax significantly reduced the risk of anal warts, persistent anal HPV infection and anal precancerous lesions. An RCT of qHPVvax among HIV-positive individuals aged over 26 years was stopped early due to futility, largely due to lack of statistical power. Current evidence suggests little benefit of vaccination for established HPV infections. Nonetheless, qHPVvax has been shown to be safe and highly immunogenic among older HIV-positive MSM. Findings from cohort studies suggest potential benefits of vaccination beyond 26 years of age. Among HIV-negative MSM (median age 35), HPV16 seroincidence did not decline until after 35 years of age. A cohort of HIV-negative and HIV-positive MSM (median age 49) found anal HPV16 was only detected in one-third of men at baseline, and acquisition of new 9vHPVvax types occurred at a rate of almost 20 per 100 person-years. A similar-aged cohort of HIV-positive MSM suggested potential protection of almost 30% of participants against acquisition of new hrHPV types contained in the 9vHPVvax.

Conclusion Despite a lack of evidence of HPV vaccine efficacy in older/HIV-positive MSM, some existing data theoretically support a role of vaccination. Further studies are required to confirm whether any benefit exists.

Disclosure No significant relationships.

S14 – SEXUAL NETWORKS AND STI TRANSMISSION: FROM MODELLING TO PRACTICE

Tuesday, July 16, 2019 4:15 PM – 5:45 PM

S14.1 SEXUAL CONTACT NETWORKS, STI TRANSMISSION AND THE EFFECTIVENESS OF INTERVENTIONS: INSIGHTS FROM MATHEMATICAL MODELLING

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Sexual contact networks are a key determinant for the spread of sexually transmitted infections (STIs). The impact of different sexual contact structures on the effectiveness of interventions is not always well understood. Mathematical modelling provides an excellent tool to study the interrelationship between sexual contact networks, STI transmission and intervention effectiveness. We use deterministic, population-based as well as stochastic, individual-based transmission models to study the effects of control interventions against *Chlamydia trachomatis* and *Neisseria gonorrhoeae*. We illustrate that an accurate description of heterosexual contact networks is critical to evaluate the effectiveness of screening and partner notification strategies against chlamydia. We further analyse antibiotic resistance surveillance data to estimate the rates at which antibiotic-resistant *N. gonorrhoeae* spread in heterosexual men (HetM) and men who have sex with men (MSM). Interestingly, we can show that antibiotic-resistant *N. gonorrhoeae* spread faster with more treatment, not more sexual partners. The effectiveness of control interventions for an STI strongly depend on the life history of the disease and the underlying sexual contact structure.

Disclosure No significant relationships.

S14.2 USE OF WHOLE GENOME SEQUENCING TO EXPLORE TRANSMISSION BETWEEN SEXUAL NETWORKS IN AN STI OUTBREAK

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10.1136/sextrans-2019-sti.66

Whole genome sequencing (WGS) is increasingly being used to describe the molecular epidemiology of *Neisseria gonorrhoeae* at a population level, mainly as part of national surveillance programmes or research studies. Recently, Public Health England has used WGS as part of outbreak investigations to understand the spread of resistant *N. gonorrhoeae*, and inform public health interventions in real-time. The benefits and difficulties of this approach will be explored.

Disclosure No significant relationships.

S14.3 MAXIMIZING THE ACCEPTABILITY, FEASIBILITY AND VALIDITY OF SEXUAL NETWORK STUDIES: LESSONS FROM THE FIELD

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Network studies are an increasingly important source of evidence explaining the movement of sexually transmitted infections (STIs) through at-risk populations. This design type complements traditional epidemiological measures by incorporating spatial and temporal data about people's social and sexual connections to evaluate the spread of STIs. This applied presentation describes the speaker's experience initiating a multi-site sexual network study of syphilis transmission among men who have sex with men (MSM) in an LGBTQ-friendly Midwestern US city. She discusses challenges and field-tested solutions specific to chain-referral network studies across multiple domains, including: 1. ethical review, which required extensive education of IRB members and changes to local IRB policy prior to approval; 2. feasibility and acceptability, which required community engagement and sensitization to assuage participant concerns about confidentiality in the use of peer referrals and with the enumeration of sexual partners using modified identifiers; and, 3. data capture, including management challenges inherent to tracking sexual partners and behaviors over time, in the context of changing relationships (e.g., evolution and devolution of relationships from anonymous to casual to primary to dissolved to reinitiated), changing disease exposure, and use of a smartphone app to capture inter-visit behavioral risk data. She describes strategies used prior to and after study initiation to develop, maintain and enhance relationships with the target community, and future

plans for continued engagement around dissemination of results. Accurate measurement of sensitive or stigmatized behavior presents a challenge to the validity of nearly all STI research. Maximizing the acceptability, feasibility and validity of network studies will lead to more accurate estimates of the drivers of STI transmission and will provide more valid insights about the opportunities for interventions to prevent and control STI outbreaks.
Disclosure No significant relationships.

S14.4 THE ROLE OF SEXUAL NETWORKS IN THE GLOBAL SPREAD OF ANTIMICROBIAL-RESISTANCE ENTERIC INFECTIONS

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10.1136/sextrans-2019-sti.68

In high-income countries, enteric pathogens have typically affected returning travellers or children, or spread from contaminated point sources. However, sexually transmitted enteric infections (STEI) are now well documented, particularly among men who have sex with men (MSM). The phenomenon was recognised in patients with HIV/AIDS in the early 1970's as arising from direct/indirect ingestion of faecal matter via sexual contact. Bacteria (*Shigella spp.*, *Salmonella spp.*, *Campylobacter spp.*, *Escherichia coli*), viruses (Hepatitis A), and protozoa (*Giardia spp.*, *Cryptosporidium spp.*, *Entamoeba histolytica)* have all been implicated. Following a nadir during the 90's and early-2000's, new epidemics of enteric pathogens affecting MSM have been reported internationally. Facilitated by global travel, these have familiar characteristics (oral-anal behaviours and HIV-associations), but also important new features (associations with 'chemsex', social media use, PrEP, syndemic STIs, and transmission in the absence of HIV). For some STEIs, notably Shigellosis, a worrying new feature is resistance to multiple antimicrobial classes found in most isolates from MSM. This may be collateral to frequent antibiotic exposure acting as a selection pressure among the sexual networks affected. Understanding of these sexual networks has been informed by a wide range of approaches, from qualitative patient interviews, through scrutiny of national surveillance trends (male-to-female ratios, gender excess, geographical distributions) and electronic data linkage, to population-level pathogen phylogenomics. These are challenging infections to study, not least due to being sometimes asymptomatic, as well as patient and clinician unawareness about sexual transmission leading to missed or mis-diagnoses, the hidden nature of the affected population, and stigma. Moreover, many questions remain about the prevalence, transmission, duration of infection, clinical implications, drivers of antimicrobial resistance, and effective public health and clinical interventions. Embracing transdisciplinary approaches to understand the sexual networks affected and the behavioural and pathogen-associated drivers seems essential if we are to move from observation to control.
Disclosure No significant relationships.

S15 – NEW APPROACHES TO STI DIAGNOSIS AND PREVENTION

Wednesday, July 17, 2019
10:45 AM – 12:15 PM

S15.1 FOUR *TREPONEMA PALLIDUM* PROTEINS DETECTED IN URINE FROM SYPHILIS-INFECTED INDIVIDUALS USING MASS SPECTROMETRY

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Background The direct detection of *Treponema pallidum* peptides in bodily fluids could facilitate the early diagnosis of initial-, repeat-, congenital- and neuro-syphilis.
Methods To this end, we prospectively recruited 54 individuals with a new diagnosis of syphilis and 6 controls. Their urine specimens were pooled according to disease stage and assessed using complementary mass spectrometry techniques (MALDI-TOF-TOFMS/MS, LC/ESI-IM-Q-TOF/HDMS^{E}) to uncover potential syphilis biomarkers.
Results In total, 26 unique peptides were uncovered corresponding to four unique *T. pallidum* proteins (Tp0486, Tp0742, Tp0804 and Tp0369) that have no, or minimal, genetic sequence similarity to other known proteins, including prokaryotes and human proteins.
Conclusion This is the first study reporting direct detection of *T. pallidum* proteins in human biofluid samples using MS-based proteomics methods. These could be promising diagnostic test targets.
Disclosure No significant relationships.

S15.2 CRISPR DIAGNOSTICS: EXPANDING THE NUCLEIC ACID DETECTION TOOLBOX BY HARNESSING MICROBIAL DIVERSITY

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10.1136/sextrans-2019-sti.70

Versatile, rapid, and portable sensing of nucleic acids is vital for applications in human health. The RNA-targeting CRISPR-associated enzyme Cas13 has recently been adapted for such purpose. This detection platform, termed SHERLOCK (Specific High Sensitivity Enzymatic Reporter UnLOCKing), can discriminate between inputs that differ by a single nucleotide at very low concentrations and can be lyophilized for portable deployment. However, this technology has several limitations, including the lack of quantitation and reliance on fluorescent detection equipment for readout. Here, we extend the SHERLOCK technology to address these limitations and further develop the utility of this platform. Many applications require detection of more than one target molecule in a single reaction, and we therefore sought to create a multiplex platform that relies on unique cleavage preferences of Cas enzymes. To identify possible candidate enzymes compatible with multiplexing, we biochemically characterized three members of the