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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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