

Conclusions Young adults reported that being tested for chlamydia had a positive impact on their willingness to engage with future testing, and a smaller impact on subsequent sexual behaviour. The use of online surveys is warranted as the results were comparable to those of nationally representative population based surveys. Addressing young adults' underlying attitudes towards testing and perceptions of risk could increase their willingness to test for chlamydia.

016.2 STRAIN TYPING TO RESOLVE REPEATED CHLAMYDIA TRACHOMATIS INFECTIONS IN YOUNG HETEROSEXUAL DUTCH POPULATIONS

doi:10.1136/sextrans-2013-051184.0174

H M Götz, ²R J M Bom, ¹M Wolfers, ²J S A Fennema, ³I V F van den Broek, ²A G C L Speksnijder, ²S M Bruisten. ¹Division of Infectious Diseases control-GGD, Rotterdam Rijnmond, The Netherlands; ²Public health service GGD Amsterdam, Amsterdam, The Netherlands; ³Epidemiology & Surveillance unit, CIB-RIVM, Bilthoven, The Netherlands

Repeated infections of *Chlamydia trachomatis* (CT) occur frequently in young adults. These may be new infections, or persistent infections due to treatment failure or unresolved infections in sex partners. We compared CT multilocus sequence typing (CT-MLST) to *ompA* genotyping in discriminating new from persistent Chlamydia infections. Samples from young heterosexual persons were selected from Dutch screening implementation studies in Amsterdam and Rotterdam, the Netherlands, between 2009 and 2011. Paired CT positive samples at baseline (T0) and after 6 months (T1) were genotyped with 6 MLST loci which included: *ompA*, *CT046*, *CT058*, *CT144*, *CT172* and *CT682*. The uniqueness of Chlamydia strains was assessed by adding samples from 256 heterosexuals in Amsterdam.

For 27 out of 34 persons with repeated infections, full MLST types were obtained for paired samples. In 17 of these 27 persons a multilocus (n = 13) or single locus variant (n = 4) was found, indicating new CT infections at T1. For 5 MLST discordant participants, the *ompA* genovar was identical. The 10 persons with concordant typing results were categorised as treatment failure (5 persons) or unresolved infections (5 persons). A minimum spanning tree, generated from all cases and 256 reference samples showed large and small clusters and singletons. Surprisingly, the persons with concordant samples had CT strains that were either unique (singleton) or found in small clusters. The median time between T0 and T1 did not differ between the persons with concordant and discordant samples. The number of sex partners before T0 however, was higher for the discordant group. High resolution sequence typing was superior compared to *ompA* typing in discriminating new from persisting Chlamydia infections. Many persons (37%) showed exactly the same Chlamydia strain after 6 months indicating possible treatment failure.

016.3 CONTROLLING CHLAMYDIA: POPULATION MODELING TO ASSESS PROMISING INTERVENTIONS

doi:10.1136/sextrans-2013-051184.0175

J W Glasser, ¹K Owusu-Edusei, ²S N Glick, ¹S O Aral, ¹T L Gift. ¹Centers for Disease Control and Prevention, Atlanta, GA, United States; ²George Washington University, Washington, DC, United States

Background Chlamydia is an important public health problem associated with neonatal sequelae, pelvic inflammatory disease, infertility, and ectopic pregnancy.

Methods Using a population model with 2 genders and ages 15–44 years in 5-year groups, but only heterosexual contacts, we evaluated the impact of actual and hypothetical interventions on chlamydia in the U.S. Parameters were obtained from the literature or estimated from the National Health and Social Life Survey and Seattle Sex Survey. The model was calibrated by adjusting gender-specific probabilities of infection on contact. We calculated the basic reproduction

number (R_0), defined as the average number of secondary infections per infectious person in a wholly-susceptible population without interventions. We also calculated the age- and gender-specific equilibrium prevalence and contributions to R_0 . And we assessed the impact of interventions by comparing reproduction numbers with and without them. To assess the feasibility of opportunistic screening, we analysed Market Scan, a commercial health insurance database, to determine the proportion of people seeking medical care.

Results Treating symptomatic men and women who seek care and screening 38% of women aged 15–24 years during annual examinations more than halve the reproduction number. The equilibrium age- and gender-specific prevalence of infection match those observed in the National Health and Nutrition Examination Survey. Men cause more secondary infections than women (contributing twice as much to R_0 in some age groups), and people aged 25–29 years cause as many as those aged 20–24. Analysis of the Market Scan database indicates that insured men seek care often enough for screening to have substantial impact. Screening women reduces the reproduction number by 3%; screening a similar proportion of young men would reduce it another 4%.

Conclusions Our modelling suggests that screening men as well as women and extending the upper age to 29 years may affect chlamydia transmission or sequelae.

016.4 HUMAN PAPILLOMAVIRUS IN VERY YOUNG MEN WHO HAVE SEX WITH MEN AND THE POTENTIAL BENEFIT FROM VACCINATION

doi:10.1136/sextrans-2013-051184.0176

H Zou, ²A Morrow, ³S Tabrizi, ⁴A Grulich, ³S Garland, ⁵J Hocking, ^{1,2,6}C Bradshaw, ^{4,7}G Prestage, ^{1,2}C Fairley, ^{1,2}M Chen. ¹School of Population Health, University of Melbourne, Carlton, Australia; ²Melbourne Sexual Health Centre, Alfred Health, Carlton, Australia; ³Department of Obstetrics and Gynaecology, University of Melbourne, Parkville, Australia; ⁴Kirby Institute, University of New South Wales, Sydney, Australia; ⁵Centre for Women's Health, Gender and Society, University of Melbourne, Carlton, Australia; ⁶Department of Social and Preventive Medicine, Monash University, Clayton, Australia; ⁷Australian Research Centre in Sex, Health and Society, Melbourne, Australia

Background Homosexually active men are at increased risk for human papillomavirus (HPV) infection and HPV associated anal cancer. Prophylactic HPV vaccines have maximum efficacy in people who have not already been infected with HPV. This study aims to determine the prevalence of HPV among teenage MSM.

Methods Same sex attracted males aged 16 to 20 were recruited in Melbourne via clinics, universities, community events, media, social networking and peer recruitment. At baseline, 3, 6, and 12 months anal and penile swabs and an oral rinse were obtained to test for 37 HPV genotypes.

Results 200 men were recruited. At baseline 39% had at least one type of HPV DNA detected from at least one site. High risk (HR), low risk (LR) and quadrivalent vaccine (QV) preventable types were detected in 31% (95% CI: 25–37%), 30% (95% CI: 24–37%) and 23% (95% CI: 17–29%) of men respectively. Multiple types of any, HR, LR and QV preventable HPV were detected in 27%, 13%, 11% and 8% of men respectively. The site specific prevalence of any HPV detected from the oral cavity, penis and anus were 2%, 9% and 31% respectively: the prevalence of QV preventable types at these 3 sites was 0.5%, 4% and 20% respectively. Anal HPV was absent in 27 of 30 men who reported never receiving anal sex. Additional results of serology for HPV 6/11/16 and 18 will also be presented.

Conclusion In this study, the first to focus on early HPV acquisition among teenage MSM, HPV was common but in the minority. HPV vaccination prior to the onset of sexual activity is ideal; however, short of universal vaccination of school aged males, selected vaccination of teenage same sex attracted young men could still prevent many infections.