Background Recent reports have described increasing trends of gonorrhoea among men who have sex with men (MSM) in the United Kingdom and women in Sweden. European Union (EU/EEA) surveillance data has also shown increasing rates of gonorrhoea since 2008. We analysed surveillance data to identify the contributions of key populations to this increase.

Methods Surveillance of gonorrhoea in the EU/EEA is co-ordinated by the European Centre for Disease Prevention and Control (ECDC). Data reported to ECDC in 2008 and 2011 were compared, focusing on countries with an increasing number of gonorrhoea cases, to analyse changes among key populations.

Results In 2011, 39 179 cases of gonorrhoea were reported from 28 EU/EEA countries. Of these countries, 21 reported a median increase in the number of reported cases of 31% (interquartile range: 22–79%). Among countries reporting increasing cases, 15–24 year olds accounted for 43% of reports in 2011; males accounted for 72%; MSM for 40%. Among MSM, the largest proportion of cases was reported among 25–34 year olds (42%).

Between 2008 and 2011, the number of reported cases increased by 37%. Increases were observed among all age-groups, particularly among 25–34 year olds (61%) and those aged 45+ (78%). Reported cases increased by 51% among males compared to 30% among females. Transmission among MSM increased by 124% since 2008 and, among MSM, the largest increase in reported cases was among those aged 45+ (192%) and 25–34 year olds (173%).

Conclusions Although reported cases of gonorrhoea increased among all age-groups and both genders between 2008 and 2011, the highest increase occurred among MSM above 25 years of age. Increasing trends may be due to increased awareness and testing, and improved reporting; increased transmission, however, is also likely. Prevention messages targeting these groups need to be reinforced.

USING MOLECULAR TYPING TO INVESTIGATE N. GONORRHOEAE STRAIN TURNOVER: A COMPARATIVE STUDY OF GISP ISOLATES COLLECTED FROM BALTIMORE AND SAN FRANCISCO

[1]K Espinosa, [1]J Gerrity, [2]M Pandori, [3]V Marsiglia, [4]J Hardick, [4]M Barnes, [1]D Hess, [4]**C Gaydos**. [1]Santa Clara University, Santa Clara, CA, United States; [2]San Francisco Department of Public Health Labs, San Francisco, CA, United States; [3]Baltimore City Health Department, Baltimore, MD, United States; [4]Johns Hopkins University, Baltimore, MD, United States

Background One internationally accepted method for the molecular epidemiologic typing of *Neisseria gonorrhoeae* is *Neisseria gonorrhoeae* Multi Antigen Sequence Typing (NG-MAST). NG-MAST utilises DNA sequencing of two variable regions of the *N. gonorrhoeae* genome to classify gonococcal isolates into strain types.

Method We assessed the genetic diversity of *N. gonorrhoeae* isolates in Baltimore (N = 277) spanning the years 2009–2011 compared to San Francisco (N = 539) from 2005–2011, using NG-MAST. All isolates in this project were obtained from the CDC Gonococcal Isolate Surveillance Project (GISP). San Francisco strains were mostly from MSM, while the Baltimore isolates were mostly from a heterosexual population.

Results NG-MAST results from isolates across that time period revealed a surprising degree of sequence type turnover within the Baltimore area. When compared to the data from San Francisco, the *N. gonorrhoeae* genetic diversity trends revealed minimal overlap in sequence families between the two metropolitan areas; SF8238, SF210, and SF 2992 were present in both populations. However, a pair-wise comparison of other strain families revealed two relatively distinct populations; the most prevalent strain families in San Francisco were SF437, SF23, SF3935, and SF1407, while those in Baltimore were SF8234, SF8240, SF865, and SF8262.

Conclusion These data may imply that the traditional understanding of a gonococcal transmission pattern from west to east cannot accurately depict the strain flow of *N. gonorrhoeae* isolates within these populations. Our data revealed a large amount of strain turnover in both metropolitan areas by year. This raises questions about the entry and transmission of *N. gonorrhoeae* within the U.S., and the implications of this turnover in regards to the evolution of this organism.

O.04 - Vaginal infections and PID

THE INFLUENCE OF HORMONAL CONTRACEPTION AND PREGNANCY ON THE VAGINAL MICROBIOME, SEXUALLY TRANSMITTED INFECTIONS, AND CYTOKINE RESPONSES IN A COHORT OF RWANDAN SEX WORKERS

[1,2]M C Verwijs, [1]**H Borgdorff**, [1]F W N M Wit, [3]F H Schuren, [4]R Lutter, [5]R Verhelst, [2]M J M Bonten, [6]J H H M van de Wijgert. [1]Amsterdam Institute for Global Health and Development (AIGHD), Amsterdam, The Netherlands; [2]Utrecht University Medical Center, Department of Medical Microbiology, Utrecht, The Netherlands; [3]TNO Microbiology & Systems Biology, Zeist, The Netherlands; [4]Department of Experimental Immunology, Academic Medical Center, Amsterdam, The Netherlands; [5]International Center for Reproductive Health (ICRH), Ghent University, Ghent, Belgium; [6]University of Liverpool, Institute of Infection and Global Health, Liverpool, UK

Background The effects of hormonal contraception and pregnancy on the vaginal microbiome (by molecular methods), acquisition and persistence of sexually transmitted infections (STIs), and genitourinary mucosal immunology are still largely unknown.

Methods HIV-negative, non-pregnant female sex workers (n = 397) in Kigali, Rwanda, were followed for two years. Demographic, behavioural, clinical, STI and pregnancy data were collected at regular intervals. The vaginal microbiome was cross-sectionally determined using a phylogenetic microarray (n = 174). Women with STIs were purposefully oversampled in this subsample. Inflammatory cytokines were measured in cervicovaginal fluid using Luminex and ELISA methodology (n = 343). Hormonal exposure was defined as use of hormonal contraception (oral or injectable) or a positive urine pregnancy test. Women in the exposure groups were compared to non-pregnant women who did not use hormonal contraception. Adjustments were made for demographic data and sexual risk taking.

Results At baseline, 12% of the women used hormonal injectables, and 6% oral contraceptives (OC); 7.7% was pregnant. OC use was associated with higher HPV prevalence (aOR 3.09; 95% CI 1.42–7.72), higher *Chlamydia trachomatis* incidence (aOR 7.13; 95% CI 1.40–36.30), and lower syphilis prevalence (0% vs 7.2% in controls) and incidence (0% vs 1.2%). Hormonal injectables were associated with higher HSV-2 prevalence (aOR 2.08; 95% CI 1.23–3.50). Pregnancy was weakly associated with higher *Trichomonas vaginalis* (aOR 1.67; 95% CI 0.97–2.88) and vaginal yeast (aOR 1.95; 95% CI 0.99–3.82) incidence. Six vaginal microbiome clusters were identified. No associations between hormonal exposure status and vaginal microbiome clusters were found; however, pregnant women had lower *Gardnerella vaginalis* levels. Pregnant women had higher IL-8 levels in cervicovaginal fluids than non-exposed women.

Conclusions Both hormonal contraception and pregnancy were associated with higher STI incidence. Overall, vaginal inflammation and microbiome composition were similar among groups, but pregnant women had lower *Gardnerella* and higher IL-8 levels.

HORMONAL CONTRACEPTION IS ASSOCIATED WITH A REDUCED RISK OF BACTERIAL VAGINOSIS: A SYSTEMATIC REVIEW AND META-ANALYSIS