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.

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

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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

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

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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.

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

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Background We conducted a systematic review and meta-analysis of published data to examine the association between hormonal contraception (HC) and bacterial vaginosis (BV).
Methods Three databases (Medline, Web of Science and Embase) were searched until the end of January 2013 and duplicate references removed. Inclusion criteria were (1) > 20 BV cases; (2) data available to derive the association between HC and BV; (3) > 10% of participants used HC; (4) accepted BV diagnostic method. Data extracted included: type of HC, BV diagnostic method, and BV outcome (prevalent, incident, recurrent). Meta-analyses were conducted to calculate overall and pooled odds/risk ratios (OR/RR), stratified by HC-type and BV outcome. This systematic review is registered with PROSPERO (CRD42013003699).
Results Of 1710 unique references identified, 328 were assessed for eligibility and 48 studies met inclusion criteria. Overall, 36 reported BV-prevalence, 12 BV-incidence and 3 BV-recurrence. Twenty three studies reported data for combined-HC, 9 for progesterone-only HC and 23 did not specify HC-type. Diagnostic methods included: Nugent's (n = 31), Amsel's (n = 15), Spiegel's (n = 1) and Ison-Hay (n = 1). Pooled BV prevalence was 30.7% (95% CI: 26.7–34.7%) and ranged from 4.7%–66.7%, with > 99% of the observed variance of prevalent BV explained by heterogeneity (I^2 = 99.6%). The pooled effect of any HC-use on the composite-BV outcome (prevalent/incident/recurrent) was OR = 0.67 (95% CI: 0.62–0.71). When stratified by BV outcome, any HC-use was associated with decreased risk of prevalent (OR = 0.63; 0.58–0.68), incident (RR = 0.78; 0.68–0.87) and recurrent (RR = 0.61; 0.49–0.73) BV. When prevalent BV was stratified by HC-type, combined-HC (OR = 0.68; 0.62–0.74), unspecified HC-type (OR = 0.60; 0.53–0.67), and progesterone-only methods (OR = 0.67; 0.46–0.88) were all associated with decreased risk of prevalent BV.
Conclusion HC-use is associated with a significant and consistent decreased risk of all BV outcomes, with a greater reduction in risk for prevalent than incident BV. Surprisingly, both combined and progesterone-only contraceptive methods were associated with reduced risk of prevalent BV.

004.3 CORRELATES OF INCIDENT *TRICHOMONAS VAGINALIS* INFECTIONS AMONG AFRICAN-AMERICAN ADOLESCENT FEMALES

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Background *Trichomonas vaginalis* is associated with adverse reproductive health outcomes, including HIV. Despite marked racial disparities, few studies have reported factors related to incident *T. vaginalis* infection exclusively among young African-American women. The objective was to identify correlates of incident *T. vaginalis* infections among African-American adolescent females.
Methods Data were collected via audio computer self-interviews at baseline and every 6 months for 18 months from 701 African-American females (14–20 years) enrolled in an HIV prevention trial. Vaginal swabs were self-collected at each assessment and assayed for *T. vaginalis*, *Chlamydia trachomatis* and *Neisseria gonorrhoeae* using DNA amplification. Generalized estimating equations assessed associations between incident *T. vaginalis* infection, defined as a positive test result subsequent to a negative result or documented treatment, and sociodemographic characteristics, partner-level factors, HIV/STI-associated behaviours and STIs. Factors significant at p < 0.1 in bivariate analyses were entered into a multivariable model, adjusting for age and trial condition. The final model was obtained using backward selection procedures.
Results Of 606 (86.4%) participants who completed ≥ 1 follow-up assessment, an incident *T. vaginalis* infection was detected among 20.0% (n = 121). Trial condition was not independently associated with incident infection (p = 0.21). Significant correlates included: receipt of an increasing number of forms of government assistance (AOR: 1.20, 95% CI: 1.01, 1.42), cigarette smoking (AOR: 1.70, 95% CI: 1.08, 2.67), smoking marijuana an increasing number of days in the past 3 months (AOR: 1.02, 95% CI: 1.00, 1.04), concurrent *C. trachomatis* (AOR: 2.28, 95% CI: 1.43, 3.66) and *N. gonorrhoeae* (AOR: 5.99, 95% CI: 3.10, 11.57) infection and testing positive for *T. vaginalis* at the previous assessment (AOR: 4.56, 95% CI: 2.99, 6.96).
Conclusions Incident *T. vaginalis* infections were common. Strategies to reduce infection rates among this population may include improving partner notification and treatment services and addressing the role of substance use on sexual risk.

004.4 SEROPREVALENCE OF HERPES SIMPLEX VIRUS TYPES 1 AND 2 UNITED STATES, 1999–2010

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Background Herpes simplex virus types 1 and 2 (HSV-1 and HSV-2) are common infections with serious sequelae. HSV-1 is an increasingly important cause of genital herpes in industrialised countries, potentially due to less acquisition of HSV-1 during childhood or to changes in sexual behaviour.
Methods Using nationally representative data from the National Health and Nutrition Examination Surveys (NHANES), we examined change in seroprevalence of HSV-1 and HSV-2 among 14–49 year olds in the United States. We compared seroprevalence in 1999–2004 with 2005–2010, and examined seroprevalence among 14–19 and 20–29 year-olds stratified by socio-demographic characteristics and sexual behaviours. We also reviewed HSV-1 and HSV-2 seroprevalence from 1976–1980 to 2005–2010.
Results In 2005–2010, the seroprevalence of HSV-1 was 53.9%, and the seroprevalence of HSV-2 was 15.7%. From 1999–2004 to 2005–2010, HSV-1 seroprevalence declined by nearly 7% (P < 0.01), but HSV-2 seroprevalence did not change significantly. The largest decline in HSV-1 seroprevalence from 1999–2004 to 2005–2010 was observed among 14–19 year olds, among whom seroprevalence declined by nearly 23%, from 39.0% to 30.1% (P < 0.01). In this age group, HSV-1 seroprevalence declined among young men and women, non-Hispanic blacks and whites, and those living above and below the federal poverty level. Overall, HSV-1 seroprevalence declined more than 10% from 60.1% in 1976–1980 to 53.9% in 2005–2010 (P < 0.01). Among 14–19 year olds, HSV-1 seroprevalence declined more than 29%, from 42.6% to 30.1% (P < 0.01). Overall, HSV-2 seroprevalence increased slightly from 13.4% in 1976–1980 to 15.7% in 2005–2010 (P = 0.02).
Conclusions An increasing number of adolescents lack HSV-1 antibodies at sexual debut and are susceptible to genital HSV-1 infection. In the absence of declines in HSV-2 infections, the prevalence of genital herpes may increase.