Purpose Little research addresses sexual pleasure in young men who have sex with men (YMSM). In this qualitative study, we developed a sexual health focused conceptual framework to explore relationships that emerged between condom use and sexual pleasure in sexual relationships among a sample of gay, bisexual, and transgender males.
Methods 30 YMSM (ages 18–24 years) were recruited (through advertisements on social networking sites, participant referrals, and flyers posted at local venues frequented by YMSM) to complete a 90-minute, semi-structured interview seeking to better understand partner-seeking behaviours of YMSM. Interviews were transcribed verbatim. Analysis used inductive open coding such that emergent concepts were connected across interviews and major themes identified.
Results Median age was 22 years old (M = 21.96; SD = 1.75). Most (N = 18, 60%) of participants self-identified as White, and gay (N = 22, 73%). Over 90% (N = 28) reported having had sex with someone met on a dating website in the past 3 months. Five (17%) participants reported being HIV-positive and 12 (40%) reported a prior history of a sexually transmitted infection. Emotional effects (such as connectedness with others) and physical effects (loss of sensation and erectile difficulties) mediated the relationship between pleasure and condom use during insertive penile-anal intercourse. Specific characteristics of sexual events (e.g., use of lubricant), relationship with the partner, and of the specific sex act (including sexual position) moderated the relationship, with pleasure and satisfaction greater during receptive anal sex without a condom with emotionally intimate or regular partners.
Conclusions Our findings suggest that relationship between sexual pleasure and condom use may be mediated by both emotional and sexual factors. Prevention work with YMSM need to acknowledge the centrality of pleasure in sexual health and focus on modifiable factors that may impact pleasure among YMSM.

YI.2 TEENS, THE INTERNET, AND STD RISK: FINDINGS AND LESSONS LEARNED FROM THE COMMUNICATION, HEALTH, AND TEENS (CH@T) STUDY

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Background Few studies have examined the association between sexual health risks and online sex seeking among teenagers. The purpose of this study was to assess the associations between meeting sex partners online and a range of sexual risk behaviours and outcomes among adolescents.
Methods Participants aged 13–19 years were recruited from a publicly funded teen clinic in Florida. After obtaining informed consent/assent, 273 participants completed an audio computer-assisted self-interview (ACASI) that included questions on demographics, sexual behaviour, STD history, and online sex-seeking behaviours and experiences. Participants also provided urine samples for chlamydia and gonorrhoea testing. Data were analysed using logistic regression to identify the association between having an online sex partner and sexual behaviours/outcomes.
Results After adjusting for significant bivariate correlates, teens reporting online sex partners were more likely to be male, be multiracial, have a history of same-sex sexual activity, report a higher number of vaginal sex partners, and report a lower age at first vaginal sex. However, teens with online sex partners were no more likely to have ever had an STD or a current biological STD.
Conclusion This study is one of the first to link biological STD results to online sex-seeking data in a youth population. While meeting a sex partner online was not associated with past or current STDs, it was associated with other sexual risk behaviours. Future research is needed to examine the complex nature of online sexual partnering among adolescents and to develop intervention approaches. In-depth qualitative interviews, currently being conducted with teens, are exploring the process and context of meeting partners online. These interview data will also be discussed in light of the ACASI and biological STD data findings.

YI.3 SEXUALLY TRANSMITTED INFECTIONS (STIS) VARY AMONG AFRICAN AMERICAN WOMEN WHO HAVE SEX WITH WOMEN BASED ON EXPOSURE TO MALE SEXUAL PARTNERS

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Introduction Little is known about partner characteristics or rates of STIs among African American women who have sex with women (AAWSW).
Methods African American women aged ≥ 16 years attending a Health Department STD clinic were enrolled in this ongoing study if they reported sexual activity with a female partner during the preceding year. Participants completed a study questionnaire and were tested for curable (trichomoniasis, Chlamydia, gonorrhoea, and syphilis) and non-curable (HSV-2, HIV) STIs.
Results Of 128 participants reporting female partners during the preceding year, 52% (67/128) also reported sex with men during the same interval (WSWM). WSW and WSWM did not differ with regards to age, lifetime number of female partners, or number of female partners during the preceding year. WSWM reported increased numbers of lifetime male partners compared to WSW ($p = 0.01$). During the 30 days preceding enrollment, WSWM reported a median of 2 sexual partners (interquartile (IQR) range 0–4) while WSW reported a median of 1 sexual partner (IQR 0–2). WSWM were significantly more likely than WSW to report new or casual female partners within 30 days preceding enrollment (46% vs. 28%; $p = 0.03$) while WSW were more likely to report regular female partners (75% vs. 34%; $p = 0.01$). Additionally, 39% (26/67) of WSWM reported new or casual male partners within 30 days preceding enrollment. Although not statistically significant, diagnosis of all curable STIs (trichomoniasis, Chlamydia, gonorrhoea, and syphilis) was more common among WSWM than WSW (30% vs. 16%; $p = 0.07$). Similarly, seropositivity for HIV and HSV-2 was more than twice as common among WSWM as WSW.
Conclusions AAWSW in this study were at high risk for STIs. AAWSWM, as a subgroup, may demonstrate heightened STI rates compared to exclusive AAWSW, perhaps influenced by partnership characteristics. Sexual health services for AAWSW should take into account partner gender heterogeneity when screening for STIs.

YI.4 GONOCOCCAL GENOMICS SHOWS IMPACT OF RECOMBINATION ON OBSCURING PHYLOGENETIC SIGNAL AND DISSEMINATING RESISTANCE LOCI

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Background Recombination plays a significant role in the plasticity of the *Neisseria gonorrhoeae* genome by generating antigenic diversity and as a mechanism of spread of antibiotic resistance elements.

Extensive recombination in a population can also limit inferences about phylogenetic history. Here, we investigate the impact of recombination in the study of isolates with reduced susceptibility to cefixime (cef^{RS}; cefixime MICs ≥ 0.25 μg/ml) in the United States.
Methods We generated draught genome sequences for 242 gonococcal isolates collected by CDC's Gonococcal Isolate Surveillance Program (GISP). These isolates comprise all 141 cef^{RS} isolates from GISP in 2009–10 and 141 susceptible isolates matched by location, collection date, and sexual orientation of the infected individual. We predicted recombinant regions and generated a maximum likelihood phylogenetic tree from core SNPs. We performed *in silico* MLST and NG-MAST typing, and compared phylogenies of antibiotic resistance loci to whole genome-based phylogenies.
Results Per site *r/m* ratios (relative likelihood that a polymorphism was introduced through recombination rather than mutation) of recent branches in the phylogenetic tree are higher and fraction of homoplasic sites much lower than for the overall tree, suggesting that extensive recombination reduces confidence in the phylogeny's deep branches. Comparison with *in silico* MLST and NG-MAST reveals that traditional typing-based phylogenetic inferences, even for recent events, are confounded by recombination. Of the 21 penA alleles in this dataset, mosaic PBP2 pattern XXXIV was the most common (present in 116/121 cef^{RS} isolates). We find several recombination events introducing this allele into distinct lineages, and an event within the *dcw* gene cluster, which includes the penA allele, associated with reversion from cef^{RS} to cefixime susceptibility.
Conclusions Genomic methods reveal the impact of recombination on phylogenetic history, spread of resistance elements, and genome evolution, and offer a superior approach to traditional typing schemes in understanding population structure and dynamics.

YI.5 SEXUAL RISK FACTORS AMONGST WOMEN WHO HAVE SEX WITH MEN AND WOMEN: THE WOMEN IN INDIANA SEXUAL HEALTH AND EXPERIENCE STUDY (WISHES)

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Background Previous research suggests that women who have sex with women and men (WSWM) may be at a higher risk for STI than women with exclusively male (WSM) or female (WSW) partners. In contrast to previous research which has compared WSWM to WSW/WSM, the present study explored risk factors which may be unique to WSWM.
Methods Local women aged 18 or older who reported genital contact with a male and female partner within the past year were invited to participate in the study. Upon completion of an internet-based baseline survey about their sexual and STI history, participants were invited to participate in an in-person interview. During the meeting, participants engaged in a semi-structured interview followed by completion of a sexual event history calendar (SEHC). Participants were then asked to self-collect oral, vaginal and anal samples to screen for Chlamydia, Gonorrhea and Trichomoniasis.
Results Eighty participants with a mean age of 26.74 (SD = 7.97) completed the survey. The majority of the participants reported genital contact at an earlier age with a male partner (M = 16.02, SD = 3.31) than with a female partner (M = 18.93, N = 5.13).The most common type of genital contact was external genital rubbing with a male (97.5%, N = 78) and/or female (93.5%, N = 74) partner. Most participants reported a wide variety of sexual behaviours. Over half of the participants (57.5%, N = 44) reported engaging in a threesome/orgy within the past year. Data on the sequence of sexual acts was captured using the SEHC. Most participants self-collected a sample for STI screening. Approximately 30% (N = 25) of the participants reported an STI diagnosis within their lifetime and close to 10% of the participants tested positive for Chlamydia.
Discussion The study was successful in recruiting a sizable number of participants with a range of sexual experiences. The majority of participants opted to participate in all phases of the study.

Oral sessions

0.01 - Microbial virulence and host response

001.1 ASSOCIATION OF GENETIC VARIANTS WITH *CHLAMYDIA TRACHOMATIS* REINFECTION

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Background Up to 20% of *Chlamydia trachomatis* (CT)-infected patients are reinfected within months after treatment, suggesting some fail to develop protective immunity. Genetic determinants influencing CT reinfection risk have not been fully elucidated. Our primary research objective is to identify genetic determinants of CT reinfection. Based on previously reported associations of HLA class II alleles with CT complications, our initial investigations focus on HLA class II genes.
Methods In an ongoing prospective natural history study, CT-infected subjects are enrolled, treated with azithromycin 1 g single dose, and return for a 6-month follow-up visit for repeat CT testing using the Gen-Probe APTIMA Combo 2 assay (Gen-Probe, Inc., San Diego, CA). HLA class II alleles are resolved by a combination of PCR-based techniques. Genomic DNA is stored for further genotyping.
Results A total of 199 African American subjects have been studied to date: 90% women and median age 23. CT reinfection at follow-up was noted in 18%. Subjects with *HLA-DQB1*05* more often had reinfection (20 [26%] vs. 16 [13%], P = 0.018), which remained significant after controlling for age and gender (OR 2.6, 95% CI 1.2–5.6, P = 0.012). Other *HLA-DQB1* alleles were not significantly associated with reinfection (P ≥ 0.1).
Conclusion *HLA-DQB1*05* was associated with CT reinfection, suggesting it could influence protective immunity. More comprehensive genotyping from larger prospectively studied cohorts should help confirm or refine this observation. Analysis of additional HLA class II genes and genes beyond the human MHC is in progress.

001.2 INNATE IMMUNITY MODULATION BY TRICHOMONAS VAGINALIS GALECTIN-BINDING GLYCOLIPID DOMAINS

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Background *Trichomonas vaginalis* is a protozoan extracellular parasite causing long-lasting and recurrent vaginitis with a wide range of symptoms and increased risk of HIV and other viral STIs. The protozoan virulence factors that subvert the mucosal immune response are poorly understood. Here we investigate the role of the ceramide-phosphatidyl-inositol glycolipid core (CPI-GC) of the protozoan lipophosphoglycan (LPG), which is the major glycoconjugate on the trichomonad surface (2–3 million copies/parasite). We have previously determined that CPI-GC lacks mannose but