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 (cefRS; cefixime MICs ≥ 0.25 µg/ml) in the United States. **Methods** We generated draft genome sequences for 242 gonococcal isolates collected by CDC’s Gonococcal Isolate Surveillance Program (GISP). These isolates comprise all 141 cefRS 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 FBP2 pattern XXXIV was the most common (present in 116/121 cefRS isolates). We find several recombination events introducing this allele into distinct lineages, and an event within the dcar gene cluster, which includes the penA allele, associated with reversion from cefRS 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.

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

**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 = 5.13) than with a female partner (M = 18.93, N = 5.18). The most common type of genital contact was external genital rubbing with a male (97.8%, N = 78) and/or female (95.5%, 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.
contains polyglactosamine repeats representing potential ligands for animal lectins called galectins, implicated in HIV pathogenesis.

**Methods** CPI-GC was isolated from *T. vaginalis* LPG by mild acid hydrolysis and C18-SepPak separation. Binding to galectin-1 and -3 (Gal-1 and –3) was determined by Biolayer Interferometry. Inflammation-related proteins and Gal-1 and 3 were measured by a multiplex immunoassay in supernatants from human cervical and vaginal epithelial cells infected with *T. vaginalis* or exposed to CPI-GC from different clinical isolates.

**Results** CPI-GC activated NF-kB and upregulated cFos, COX-2, IL-8, MIP-3α, IL-6, IL-1β and VEGF in a MEK1/2 dependent manner. In addition, IL-6, ICAM-1 and VEGF upregulation was mediated by p38 while IL-8 and MIP-3α were ERK 1/2 mediated. CPI-GC from different clinical isolates varied in their ability to bind Gal-1 and Gal-3, which were constitutively expressed by vaginal and cervical epithelial cells and released at higher levels in the extracellular space during exposure to live trichomonads and CPI-GC. CPI-GC from all isolates invariably reduced levels of the natural microbicidal SLPI. Mutant trichomonads that failed to bind Gal-1 and Gal-3 showed higher proinflammatory activity suggesting a role for the CPI-GC–galectin binding in suppressing innate immune responses.

**Conclusion** Interventions targeting CPI-GC or restoring the balance of natural immune defenses represent a promising strategy for preventing adverse outcomes from *T. vaginalis* infection.

---

**001.3 REGULATORY T CELLS IN PERIPHERAL BLOOD AND CEREBROSPINAL FLUID OF SYPHILIS PATIENTS WITH AND WITHOUT NEUROLOGICAL INVOLVEMENT: A COMPREHENSIVE AND COMPARATIVE STUDY**


LI K, C Wang, H Lu, X Gu, Z Guan, P Zhou. Shanghai Skin Disease Hospital, Shanghai, China

**Background** Syphilis, a sexually transmitted disease caused by spirochetal bacterium Treponema pallidum, can progress to affect central nervous system, causing neurosyphilis. While many neurosyphilis patients may be asymptomatic, some patients can develop severe neurological and psychiatric symptoms. Accumulating evidence suggest that skin lesions and clinical symptoms of early syphilis patients result from host immune and inflammatory responses. However, very little is known about the immune components in neurosyphilis.

**Methodology/Principal Findings** In the present study, we perform a comprehensive and comparative analysis of regulatory T cells (Tregs) between 102 neurosyphilis patients and 431 syphilis patients without neurological involvement. We found secondary and serofast patients had increased Treg percentage, suppressive function and TGF-β levels in peripheral blood compared to healthy donors and serum Rapid Plasma Reagin (RPR) titers were positively correlated with Treg numbers in these patients. Neurosyphilis patients had higher Treg frequency in peripheral blood than those of syphilis patients without neurological involvement. Importantly, CD4+ T cells were increased and predominated in cerebrospinal fluid (CSF) of both asymptomatic and symptomatic neurosyphilis patients. Interestingly, a significant decrease in CSF CD4+ CD25 high Treg percentage was observed in symptomatic neurosyphilis patients compared to those of asymptomatic neurosyphilis patients, which may be associated with low CSF TGF-β levels.

**Conclusions** Our findings suggest that neurological progression in syphilis patients may be associated with an enhanced systemic Treg response and an increased local CD4+ T cell infiltration. A decrease in Treg frequency in CSF of symptomatic neurosyphilis patients indicates that immune-mediate tissue damage might be involved in the development of neurological symptoms.