

no change) with the ORs ranging from 2.0 to over 4.0. We used a non-equivalency test to identify the odds for not detecting differences in STI acquired with partner 1 vs partner 2. If there is a difference between rates for partner 1 and partner 2, it will not be higher than the upper bound of the CI.

Results Ninety-two women provided 111 12-week periods with one partner change. Mean age was 17.8 years; 94% were African American. Rates of STI were high for both Partner 1 and Partner 2 (see Abstract P1-S5.33 table 1). For CT, TV, and any STI, the upper bound of the 95% CI was lower previously reported rates. We have 95% confidence that the OR for infection with partner 2 vs partner one is not greater than 1.83 for CT, 1.47 for TV, and 1.68 for any STI. In contrast, the true OR for GC may fall within or higher than previously reported. We have 95% confidence that the OR for GC infection with partner 2 vs partner 1 is between 0 and 9.7.

Abstract P1-S5.33 Table 1

	Partner 1 n (%)	Partner 2 n (%)	95% CI for OR*
CT	11 (9.9%)	10 (9.0%)	0 to 1.83
GC	3 (2.7%)	9 (8.1%)	0 to 9.70
TV	8 (7.2%)	5 (4.5%)	0 to 1.47
Any STI	21 (18.9%)	19 (17.1%)	0 to 1.68

* One-sided OR.

Conclusion Many young women already have an STI when a partner change occurs. These data suggest that the relationship contexts of partner change—in addition to the risk characteristics of a new partner—are also relevant to the epidemiology of STI in a specific common form of partner concurrency (ie, serial monogamy).

P1-S5.34 **DIFFUSE DISTRIBUTION AND EXTENSIVE DISASSORTATIVE MIXING OF *CHLAMYDIA TRACHOMATIS* GENOTYPES BETWEEN ETHNIC GROUPS IN PARAMARIBO, SURINAME**

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Background Suriname is a multicultural society with many ethnic groups, such as Creoles and Maroons (descendants from the African diaspora due to slave trade), Indian, Javanese and Chinese (descendants from labour immigrants), Caucasian (descendants from Dutch immigrants during colonisation) and indigenous Amerindian people. The prevalence of *Chlamydia trachomatis* (CT) in Suriname is high (between 10 and 23% among respectively low-

risk birth control and high-risk STI clinic visitors). We aim to study the influence of sexual mixing on the transmission of CT in Paramaribo, Suriname.

Methods Samples were collected at a birth control clinic and an STI clinic in Paramaribo. Detailed questionnaires were given to visitors, concerning ethnic background, both self considered as well as that of their parents. The samples were tested with NAAT for CT. Positive samples were typed using multilocus sequence typing (MLST). Minimum spanning trees were generated and clusters were combined with the epidemiological data.

Results We retrieved full MLST profiles for 181 of 233 samples. Eighteen ompA variants from nine different genovars were found, which were split up into 68 MLST sequence types. Although the predominant genovars were E (32.6%), F (18.8%) and D (18.8%), a remarkably large proportion was genovar I (14.4%). The sequence types of most genovars clustered together, but possible recombination events were seen for genovar B, D, E and J. The minimum spanning tree showed two large clusters for genovar E and F (30 and 19 samples each) and 28 smaller clusters (2 to 7 samples). More than half of the sequence types (38/68) consisted of singletons. When ethnicity was superimposed on the minimum spanning tree, it was diffusely distributed over all clusters (Abstract P1-S5.34 figure 1). Almost all participants (175/181) had sex partners in Suriname. Disassortative sexual mixing with other ethnic groups (having a partner from a different ethnic background) was reported by 56.0% (98/175) of the participants.

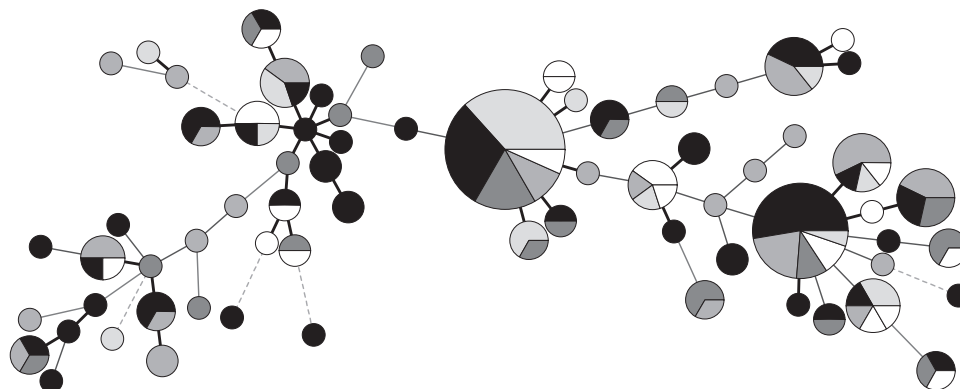
Conclusions The diversity among chlamydial types within the Surinamese population was shown to be high, as about half of the sequence types were unique. The distribution of sequence types over the population seemed not to be influenced by ethnical background. This could possibly be explained by the high degree of disassortative mixing. This is in contrast to previous studies on HIV transmission in Suriname where clustering within ethnic groups was found and disassortative mixing was lacking.

P1-S5.35 **MULTIPLE CONCURRENT SEXUAL PARTNERSHIPS AMONG ADOLESCENTS IN TANZANIA AND SOUTH AFRICA: A COMPARISON BETWEEN AREAS WITH CONTRASTING LEVEL OF HIV MAGNITUDE**

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Background Modelling and empirical evidence suggest that population differences in the practice of concurrent sexual partnership



Abstract P1-S5.34 Figure 1 Ethnical background superimposed on the minimum spanning tree generated from the MLST data of 181 chlamydial infections from Paramaribo, Suriname. Depicted are the predominant ethnic groups for *Chlamydia* infections: Creoles are given in black, people from mixed race in grey, Maroons in dark grey and Javanese people are given in light grey. Indian, Amerindian and Caucasian people are given in white.

could be the most important explanation of the observed heterogeneity in HIV epidemic in sub-Saharan Africa. Biomedical and some behavioural evidence have not sufficiently explained the variation. This study aimed at comparing the rate of concurrent sexual partnerships among adolescents in Arusha, Tanzania and Polokwane, South Africa, two areas with contrasting level of HIV magnitude.

Methods A baseline cross-sectional study involving junior secondary school adolescents in Arusha, Tanzania and Polokwane South Africa was conducted in 2010 as part of the school-based Health Intervention project (LASH). Adolescents from 12 randomly selected schools from each country were interviewed regarding their socio-demographic characteristics, sexual behaviours and substance use. Data were entered and analysed using SPSS statistical package.

Results A total of 2408 adolescents from Arusha and 1649 from Polokwane participated in the study. Adolescent interviewed in Arusha were significantly older than their Polokwane counterpart (Mean age (SD) 19.3(0.5) and 15.5(0.7), respectively, $p < 0.001$). The overall prevalence's of reported multiple concurrent sexual partnerships were 9.2% in Arusha and 25.2% in Polokwane (OR, 3.7, 95% CI 3.0 to 4.7. Both males and Females adolescents from Polokwane were significantly more likely to report concurrent sexual partnerships than those from Arusha ($p < 0.001$). Moreover, adolescents from Polokwane reported practice of other HIV risk behaviours as compared to those in Arusha ($p < 0.001$). History of sexual experience (vaginal, oral, anal), ever use of condom and substance use were independent predictors of multiple concurrent sexual partnerships in both sites.

Conclusions High practice of multiple concurrent sexual partnerships among adolescent living in high HIV prevalent area as compared to those in low prevalence area indicate that concurrent partnership could be the most important explanation of the observed heterogenic HIV transmission in sub-Saharan Africa. Being sexually active and substance use predict practice of concurrent sexual partnerships among adolescents. Delaying sexual debut and addressing substance use among adolescents may have a significant impact on HIV epidemic.

P1-S5.36 CONCURRENCY AMONG WOMEN <25 YEARS OF AGE SCREENED IN FAMILY PLANNING AND REPRODUCTIVE HEALTH CLINICS IN US PUBLIC HEALTH SERVICE REGION X, JANUARY 2009–JUNE 2010

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Background To better understand the dynamics of STIs and HIV, researchers are increasingly examining the determinants and consequences of sexual networks. In January 2009, the Infertility Prevention Project (IPP) in US Public Health Service Region X-one of 10 regional projects funded by the Centers for Disease Control and Prevention (CDC)-began collecting a new network sexual risk behaviour for IPP chlamydia (CT) tests. The Region X IPP decided to collect sex partner (SP) concurrency based on the literature, research conducted in California, CDC input and regional interest.

Methods CT positivity (CT+) was calculated by demographics, sexual risk behaviours, SP concurrency and clinical findings for 94,433 tests among women <25 years of age screened in Region X IPP family planning and reproductive health (FP/RH) clinics from January 2009 to June 2010. Univariate and multivariate analyses were conducted.

Results Of the 94 433 tests, 62% were age 20–24, and 72% were non-Hispanic white. 14% of clients reported their SPs definitely, 41% reported “possibly” and 38% reported it was “unlikely” their SPs had concurrent SPs in the last 12 months. CT+ ranged from 7.6% among clients reporting their SPs “definitely” had concurrent SPs to 5.2% among those reporting it was “unlikely.” Clients reporting their SPs “definitely” or “possibly” had concurrent SPs were more

likely to report other sexual risk behaviours and have clinical findings on examination. Significant ($p < 0.001$) factors for CT+ included SP concurrency (definitely: AOR=1.20; possibly: AOR=1.25); age (15–19 years: AOR=1.34); race/ethnicity (Black: AOR=1.55; American Indian/Alaska Native: OR=1.60; Native Hawaiian/Other Pacific Islander: AOR=1.92); CT infection in the last 12 months (AOR=2.06); new SP (AOR=1.43), multiple SPs (AOR=1.48), symptomatic SP (AOR=4.07) in past 60 days; clinical findings (cervicitis or PID diagnoses; AOR=2.22).

Conclusions It is feasible to collect SP concurrency with female clients in the context of a clinic visit. SP concurrency was a significant predictor of CT+ beyond other risk factors. Results for clients who reported their SPs “possibly” had concurrent SPs may reflect clients being less knowledgeable about their SPs’ sexual behaviours. Findings confirm the importance of assessing network characteristics such as SP concurrency, the need to incorporate SP concurrency in risk reduction counselling, and the potential to use this measure in empirically based screening decisions.

P1-S5.37 EVOLUTION OF SEXUAL NETWORKS OVER TIME IN MANITOBA, CANADA

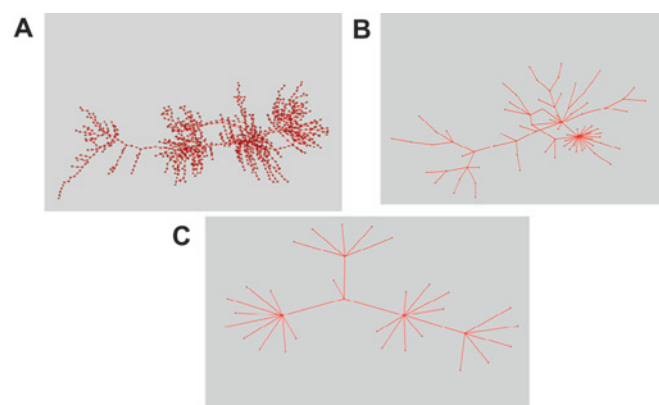
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Background Recent increases in bacterial STI in Canada and the resurgence of syphilis require further investigations into the transmission of STI. Specifically, adaptation of sexual networks and sexually transmitted pathogens to prevention efforts such as screening and partner notification have been proposed as a major factor in persistence of STI. We investigate the size and morphology of sexual networks generated by routinely collected contact tracing data for gonorrhoea, chlamydia and syphilis for the whole province of Manitoba, at three time points; 1990–1992; 1997–1998, and last, from 2002 to 2003.

Methods We compared the sizes of the components in which cases and contacts were connected by sexual intercourse at the three time points, and cross matched chart numbers of the cases from 1990–1992 with those from 1997–1998 in order to identify which individuals were active within specific networks 8–10 years later. We reviewed the changes in the networks along with the rates over time in order to assess the epidemic phases of the pathogen and their possible effects on the networks.

Results From 1990 to 1992, 20 223 cases were available for analysis; from a 6-month period in 1997–1998, 4544 cases and contacts were



Abstract P1-S5.37 Figure 1 Evolution of sexual networks over time in Manitoba, Canada A) Pruned largest component, $n=2,166$, 1990–1992, B) Largest component $n=82$, 1997–1998 and C) largest component $n=33$, 2003–2004.