

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.

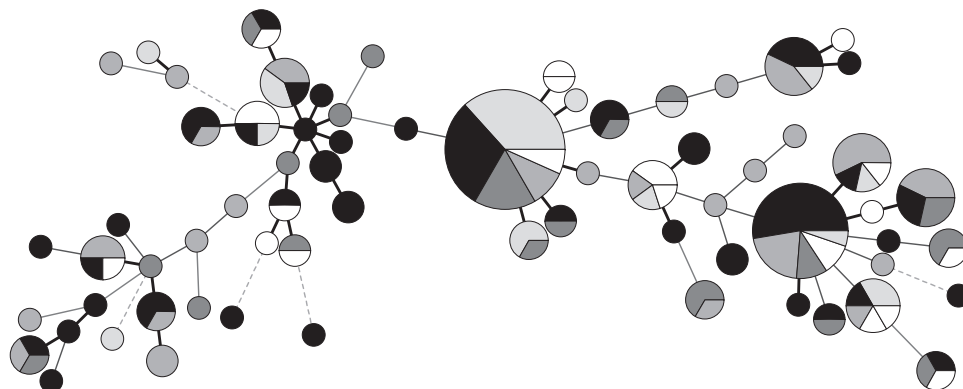
Conclusions The diversity among chlamydial types within the Surinamese population was shown to be high, as about half of the sequence types were unique. The distribution of sequence types over the population seemed not to be influenced by ethnical background. This could possibly be explained by the high 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.