Thailand. We assessed whether baseline HPV prevalence was predicted by STIs which were newly detected and laboratory-confirmed within 2 years prior to enrolment. Prevalence ratios (PRs) with 95% CIs were estimated using generalised linear models.

Results Baseline prevalence of any HPV and high-risk (HR)-HPV were 19.9% and 8.7% respectively. Having genital chlamydia (CT) or gonorrhoea (NG) in the past 2 years was associated with increased risk of any HPV as well as HR-HPV infection after controlling for current and past sexual behaviours, age, contraceptive use and other concurrent STIs [adjusted PRs (aPRs) for any HPV: CT: 1.7 (95% CI 1.1 to 2.7), NG: 1.8 (95% CI 1.1 to 3.1); aPRs for HR-HPV: CT: 2.9 (95% CI 1.3 to 6.5); NG: 3.4 (95% CI 1.7 to 6.7)]. Association between CT and prevalent HR-HPV was statistically significant only among non-hormonal contraceptive users [aPR: 2.7 (95% CI 1.2 to 6.3)] but not among those using hormonal contraceptives in the past 2 years [aPR: combined oral contraceptive (COC) users: 1.1 (95% CI 0.5 to 2.4); users of depot medroxyprogesterone acetate (DMPA): 1.1 (95% CI 0.4 to 3.3)] (Abstract P1-S5.32 table 1). Association of NG with prevalent HR-HPV was observed among those who used COC [aPR: 6.2 (95% CI 2.2 to 17.7)] or DMPA [aPR: 3.5 (95% CI 1.1 to 10.9)] during the past 2 years but not among non-hormonal contraceptive users [aPR: 1.9 (95% CI 0.3 to 10.3)] (Abstract P1-S5.32 table 1). No significant association was found between other STIs and baseline prevalence of HR-HPV in this cohort.

Conclusions The differential impact of recent hormonal contraceptive use on the associations of CT and NG with HR-HPV prevalence suggests that the observed correlations may be attributed to biologic interactions between the pathologies of HPV and CT or NG, and not merely residual confounding by shared sexual risks.

Epidemiology poster session 5: Transmission dynamic: partners: concurrency

P1-S5.33 TIMING OF INCIDENT STI RELATIVE TO SEX PARTNER CHANGE IN YOUNG WOMEN

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M Ott, J Harezlak, S Ofner, J D Fortenberry. *School of Medicine, Indiana University, Indianapolis, USA*

Objectives Partner concurrency is associated with STI acquisition, even when partners are sequential (ie, serial monogamy). However, little is known about the timing of STI relative to partner change. This is due, in part, to lack of documentation of STI before and after partner change. Using prospective behavioural and STI screening data, we compared the proportion of an STI occurring before and after partner change within a 12-week period.

Methods As part of a larger study of risk and protective factors for STI in a mid-sized US city, young women provided weekly vaginal swabs and completed daily diaries of sexual behaviours for a 12-week period twice a year for up to 8 years. Vaginal swabs were tested for chlamydia (CT), gonorrhoea (NG) and trichomonas (TV) using amplified DNA-based tests. We limited analysis to the 12-week periods in which young women reported one sex partner change (ie, 2 sequential partners, no overlap). STIs with partner 1 were defined as those diagnosed before 1st sex with partner 2; STIs with partner 2 occurred after 1st sex with partner 2. Published data shows a higher odds of infection after a partner change (compared to

Abstract P1-S5.32 Table 1 Association between recent genital infections and prevalent detection of high-risk HPV (N=1046)

	Total study population a				Study population stratified by use of contraceptives in the past 2 years*					
	Detection of any HR-HPV				Detection of any HR-HPV					
					Non-hormonal contraceptive users (n=339)		COC users (n= 294)		DMPA users (n= 413)	
	N = 1046, N (col %)	HR-HPV+ n=91 (8.7%), n (row %)	PR (95% CI)	aPR‡ (95% CI)	PR (95% CI)	aPR§ (95% CI)	PR (95% CI)	aPR§ (95% CI)	PR (95% CI)	aPR§ (95% CI)
Detection of the following in the past 2 years†										
Genital chlamydia										
No	925 (88.4)	72 (7.8)	1	1	1	1	1	1	1	1
Yes	121 (11.6)	19 (15.7)	2.02 (1.26 to 3.22)	2.93 (1.33 to 6.47)	3.73 (1.69 to 8.26)	2.74 (1.18 to 6.34)	1.70 (0.84 to 3.47)	1.14 (0.54 to 2.39)	1.22 (0.44 to 3.35)	1.08 (0.35 to 3.28)
Genital gonorrhea										
No	1020 (97.5)	84 (8.2)	1	1	1	1	1	1	1	1
Yes	26 (2.5)	7 (26.9)	3.27 (1.68 to 6.36)	3.40 (1.73 to 6.65)	2.31 (0.37 to 14.46)	1.87 (0.34 to 10.29)	4.24 (1.79 to 10.03)	6.22 (2.18 to 17.73)	3.29 (1.13 to 9.60)	3.51 (1.13 to 10.93)
Bacterial vaginosis										
No	875 (83.7)	74 (8.5)	1	1	1	1	1	1	1	1
Yes	171 (16.4)	17 (9.9)	1.18 (0.71 to 1.94)	1.05 (0.63 to 1.75)	1.03 (0.40 to 2.66)	0.75 (0.31 to 1.82)	1.04 (0.46 to 2.36)	0.90 (0.40 to 2.03)	1.57 (0.66 to 3.68)	1.46 (0.57 to 3.70)
Positive for HSV-2 serology										
No	626 (59.9)	47 (7.5)	1	1	1	1	1	1	1	1
Yes	420 (40.2)	44 (10.5)	1.40 (0.94 to 2.07)	1.26 (0.83 to 1.91)	1.99 (0.90 to 4.38)	1.75 (0.78 to 3.90)	1.53 (0.84 to 2.80)	1.67 (0.89 to 3.15)	0.88 (0.41 to 1.88)	0.73 (0.30 to 1.79)

The following covariates were *not* found to be statistically significantly associated with the outcomes (P>0.05) and *did not* significantly influence the effect size of the primary association of interest (<10%), and hence were not included in the final models: parity, smoking status, as well as other parameters assessed for sexual behavior, including age of sexual debut, having new partner in the past year, number of sex partners in the past year, frequency of sex in last 6 months.

HR-HPV: High-risk HPV, defined as HPV types 16, 18, 31, 33, 35, 39, 45, 51, 52, 56, 58, 59, 66 (IARC 2007).

* Subjects were *formerly* enrolled in a 2-year study addressing the effects of hormonal contraceptive use on HIV acquisition (HC-HIV). These subjects were required to adhere to the self-selected contraceptive method for at least 1 year of follow-up in that study (Morrison*et al. AIDS*. 2010;**24**:1778–81). These subjects were reconsented at the end of that study for inclusion in the current study.

† Genital infections were detected in pelvic exams and confirmed by laboratory assays.

‡ Estimates adjusted for age at baseline of the current study, number of lifetime partners, partners having sex with others in last 6 months, male partner using condom in last 6 months, other concurrent genital infections, types of contraceptive use in the past 2 years.

§ Estimates adjusted for age at enrollment of the current study, number of lifetime partners, partners having sex with others in last 6 months, male partner using condom in last 6 months, other concurrent genital infections.

COC, combined oral contraceptives; DMPA, depot medroxyprogesterone acetate; HSV-2, Herpes simplex virus 2; PR, Prevalence ratio.

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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[1]R Bom, [1]J van der Helm, [2]L Sabajo, [1]H de Vries, [3]A Grunberg, [1]S Bruisten. *[1]Public Health Service of Amsterdam, Amsterdam, Netherlands; [2]Ministry of Health, Paramaribo, Suriname; [3]Lobi Foundation, Paramaribo, Suriname*

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 ethnical 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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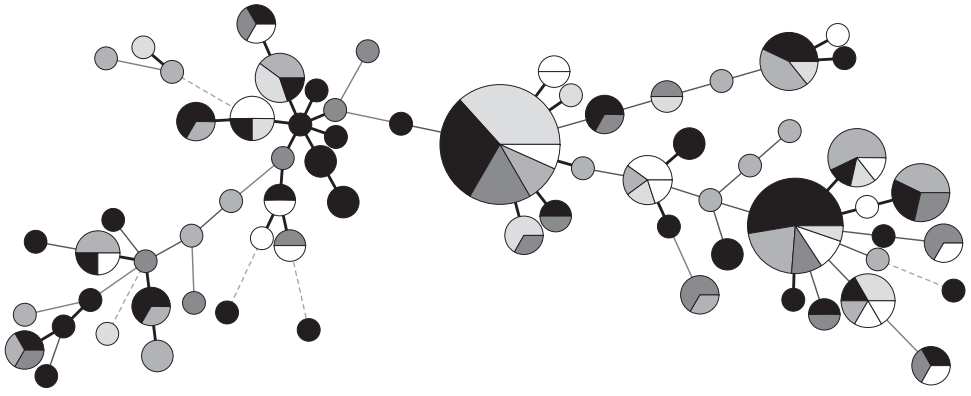
[1]E Mmbaga, [2]A Helleve, [1]G Leyna, [3]M Masatu, [4]H Onya, [2]K I Klepp. *[1]Muhimbili University of Health Sciences, DAR ES SALAAM, Tanzania, United Rep. of; [2]University of Oslo, Norway; [3]Center for Educational Development Arusha, United Republic of Tanzania; [4]University of Limpopo, South Africa*

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.