showed similar associations with testing positive in CSI (OR 2.4 [95% CI 2.1 to 2.7]) and the STI centres (OR 1.2 [95% CI 1.0 to 1.3]), but the model basing ethnicity on country of birth of a person and his parents had a better fit (higher likelihood). Self-defined ethnicity may allow for more personal input, this however also makes it a dynamic variable: in the second round of CSI, 15% of the immigrants identified themselves by a different ethnicity than in the first round see Abstract P1-S4.02 Figure 1.

Conclusions Both self-defined ethnicity and ethnicity based on the country of birth of a person and his parents, can be used to detect young persons at a higher risk of Chlamydia infection. However the definition of ethnicity based on the country of birth explains variation in the Chlamydia data better and is objective and constant, whereas self-defined ethnicity would disregard a large part of the young population at higher risk for Chlamydia infection.

Abstract P1-S4.04 Table 1 Comparison of standard study design and serodiscordant couples study design for estimating the per-sex act risk of HIV infection among HSV2 infected individuals compared to HSV2 uninfected individuals

<table>
<thead>
<tr>
<th>Scenario</th>
<th>Null Median HR (Lowest HR, Highest HR)</th>
<th>Different Transmissibility Median HR (Lowest HR, Highest HR)</th>
<th>Coinfection Increases HIV Infectiousness Median HR (Lowest HR, Highest HR)</th>
<th>Susceptibility Median HR (Lowest HR, Highest HR)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Expected</td>
<td>1</td>
<td>1</td>
<td>1</td>
<td>10</td>
</tr>
<tr>
<td>Standard Design</td>
<td>1.32 (0.84, 2.26)</td>
<td>1.58 (0.64, 1.44)</td>
<td>1.26 (1.01, 1.56)</td>
<td>4.38 (3.28, 5.65)</td>
</tr>
<tr>
<td>Serodiscordant Couples</td>
<td>1.03 (0.84, 1.44)</td>
<td>1.07 (0.70, 2.11)</td>
<td>1.03 (0.72, 1.25)</td>
<td>10.33 (9.65, 12.77)</td>
</tr>
</tbody>
</table>

20 simulations were performed for each bias scenario. Simulations were started in 1930. Cohort studies were conducted from 1992-95, which is the period during which the data used to parameterise the model were collected in rural Tanzania. The data from each run was analysed using Cox proportional hazards regression in two ways, both of which enrolled sexually active index subjects who were HIV negative and who could be HSV2 positive or negative:

1) Standard design — data on exposure to infection was not incorporated into the analysis.
2) Serodiscordant couples design — only those individuals who had an HIV infected partner were included and only for the length of time they were in the partnership.

All analyses adjusted for age in 5-year intervals, gender, and the baseline number of lifetime partners. Results presented are the median, lowest, and highest point estimates for the HR calculated from these runs. HIV and HSV2 per-sex act transmission probabilities were both equal to 0.02 unless otherwise stated.

Null: No interaction between HSV2 and HIV.
Different Transmissibility: No interaction between HSV2 and HIV. HSV2 per-sex act transmission probability = 0.03.
Coinfection Increases HIV Infectiousness: Coinfected individuals have twice the HIV per-sex act transmission probability than individuals infected with HIV alone (ie, 0.04 vs 0.02 respectively).
Susceptibility: The HIV per-sex act transmission probability to an HSV2 infected individual is 10 times higher than to an HSV2 uninfected individual (ie, 0.2 vs 0.02 respectively).

Note: Susceptibility is not affected in the first three scenarios. Also, parameter values have been changed from disease specific values to permit each bias to be presented separately. Concurrent partnerships are not permitted. Full sensitivity analysis results which relax these restrictions are not shown.
missing. We show that this bias can result in upward confounding. 2) As HSV2 is more infectious than HIV we expect HSV2 to be acquired from coinfected partners first followed by HIV. 3) As coinfection increases HIV viral load HSV2 infection may act as a proxy for a partner’s elevated infectiousness with HIV. Both of these mechanisms result in upward bias, the magnitude of which depends on the prevalence of coinfection. 4) Between subject heterogeneity in the risk of disease has been shown to attenuate estimates for any risk factor. We show that this bias can result in significant attenuation of the HR and that it depends on the prevalence of HIV among subjects’ partners and their sexual behaviour. We show that if HIV serodiscordant couples are enrolled all four biases can be removed see Abstract P1-S4.04 Table 1.

Conclusions The standard design is affected by at least four biases that preclude causative interpretations of all such HSV2-HIV studies performed to date. Use of a serodiscordant couple study design can remove these biases. It is impossible to correct previous results as the biases are not all in the same direction and their magnitudes depend on the unknown prevalence and transmissibility of both HSV2 and HIV among partners. These findings are expected to generalise to other STI-HIV risk factor studies and can help inform the decision to test HPV vaccination as an HIV prevention measure.

P1-S4.06 WHAT IMPACT DOES MISSING QUEBEC DATA HAVE ON NATIONAL HIV SURVEILLANCE DATA?

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Objective To quantify the difference in the exposure category breakdowns of national HIV surveillance figures if exposure data from the Institut national de Santé Publique du Québec (INS PQ) were included in national datasets.

Background National HIV/AIDS surveillance is coordinated by the Public Health Agency of Canada’s (PHAC) Surveillance and Risk Assessment Division’s (SRAD). HIV is reportable in all provinces and territories, although the degree of epidemiologic information collected and submitted varies. Québec’s case reports to PHAC come from their laboratory-based surveillance system, which contains positive test reports, by age and sex. All Quebec cases are classified in SRAD’s dataset as Not Reported, which contributes to the large proportion of cases at the national level with no known exposure category.

Methods Quebec’s provincial HIV surveillance system “Programme de surveillance de l’infection par le VIH au Québec” collects further epidemiological information, including exposure category and risk factor information, although recorded separately from the HIV laboratory test results file. This provincial system’s exposure category data was added to existing national surveillance data, and the exposure category breakdowns recalculated, in order to assess change in the proportion of unknown/not reported cases and to quantify the resulting difference in exposure category breakdowns at the national level.

Results With inclusion of Quebec data for 2009, there is a 50% decrease (from 45.5% to 23.1%) in the proportion of national HIV cases with unknown exposure category. There are also differences in the overall national exposure category breakdowns. For 2009, proportional increases were observed in the men who have sex with men (MSM) and heterosexual-endemic categories (5.4% and 2.8% respectively), while proportional decreases were observed in the exposure categories of injection drug use (−4.1%), heterosexual-risk (−2.0%), and no-identified-risk heterosexual (−2.2%).