Epidemiology poster session 4: Methodological aspects

P1-S4.01 HIV/STD COINFECTION IN ARIZONA, 2000–2008: IDENTIFYING OPPORTUNITIES FOR INTEGRATED SURVEILLANCE AND PARTNER SERVICES

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Background Persons with HIV who acquire STDs such as chlamydia, gonorrhoea, and syphilis likely represent high-risk sources of HIV and STD transmission. Some state and local STD and HIV programs do not allow data sharing that would identify these individuals due to concerns with data security and confidentiality.
Objective To identify the number of STD cases that were known to have HIV prior to the time of the STD diagnosis.
Methods A probabilistic matching method was used to merge the HIV and STD surveillance databases at the Arizona Department of Health Services (ADHS). Partial matches were reviewed by hand to avoid misclassification. The person and diagnosis events from the HIV-STD merge were limited to gonorrhoea (GC), chlamydia (CT), primary and secondary syphilis (PS) and early latent syphilis (EL) diagnosed during 2000–2008. Persons diagnosed with GC, CT, PS or EL diagnosis were considered to be co-infected with HIV if the HIV diagnosis date was more than 60 days before the STD diagnosis date.
Results During 2000–2008, 1494 reported STD cases occurred among persons with previously diagnosed HIV. These cases included 14% (271/1960) of the PS, 9% (173/2043) of the EL, 2% (725/39 779) of the gonorrhoea, and 0.2% (325/171 010) of the CT cases reported to ADHS. HIV coinfection among syphilis cases was highest among males ages 35–39 (PS 25%, EL 19%), 40–44 (PS 27%, EL 24%) and 45–49 (PS 22%, EL 34%). Among male GC cases the age group with the greatest percentage of HIV coinfection was 40–44 at 9%. HIV coinfection among females reported with syphilis was highest in the age group 25–29 for PS (4%, 3 cases) and 40–44 for EL (2.4%, 2 cases). Among syphilis cases, white males had the greatest percentage of HIV co-infection (PS 31%, EL 32%). Similarly among GC and CT cases, white males had the highest percentages of HIV coinfection at 7% and 1% respectively. HIV coinfection was less than 1% among women in all age groups with CT and GC. A dramatic increase in the overall percent of HIV coinfection for syphilis was seen during the study period ranging from 0.5% in 2000 to 24% in 2008 for PS and 2% to 21% during the same time interval for EL. A similar but smaller increase in the overall percent of HIV co-infection for gonorrhoea was seen during the study period ranging from 0.7% in 2000 to 2.6% in 2008.
Conclusion Retrospective data integration identified many coinfected HIV/STD cases. Timely integrated HIV and STD surveillance would allow rapid identification of these persons who could be reached for more intensive counselling and partner services. Public STD and HIV programs should address comorbidity using methods that facilitate public health intervention.

P1-S4.02 ETHNICITY BASED ON THE COUNTRY OF BIRTH IS BETTER TO IDENTIFY THE YOUNG POPULATION AT HIGH RISK FOR CHLAMYDIA INFECTION THAN SELF-DEFINED ETHNICITY

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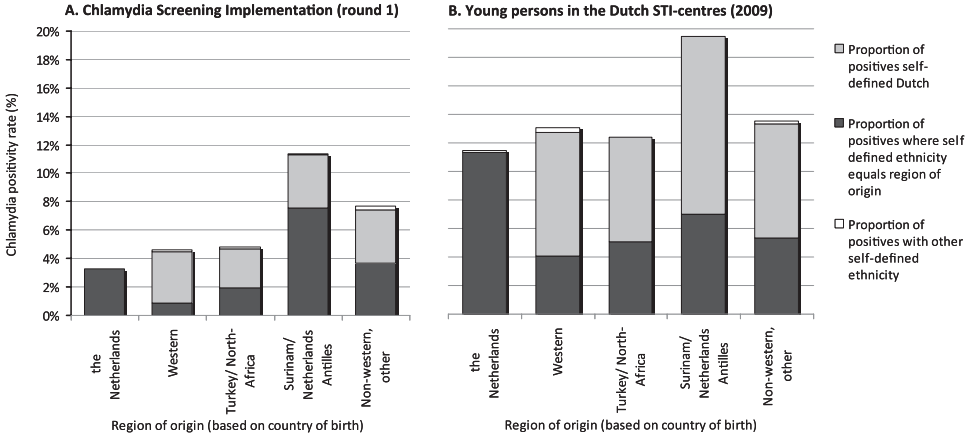
Background Chlamydia infections are frequently found in young persons and ethnic minorities. Ethnicity can be defined in different ways. In this study, ethnic disparities in *Chlamydia trachomatis* positivity in the Netherlands were assessed comparing two definitions of ethnicity. The study objective was to determine which definition is most useful to discriminate persons at risk for Chlamydia infection.
Methods Chlamydia positivity rates in persons aged 16–29 years, were investigated using data from the first round of the Chlamydia Screening Implementation (CSI, 2008–2009) and surveillance data from specialised at STI centres in the Netherlands (2009), comparing self-defined ethnicity and ethnicity based on the country of birth of a person and his parents (first and second generation immigrants). The relation between ethnicity and Chlamydia positivity rates were evaluated using logistic regression, adjusting for age, sex and SES, in both data sets.
Results Overall, the Chlamydia positivity rate was 13 % in the STI centres, and 5% in CSI. Being a young (first or second generation) immigrant was associated with Chlamydia positivity in both CSI (adjusted OR 2.3 [95% CI 2.0 to 2.6]) and the STI centres (adjusted OR 1.4 [95% CI 1.3 to 1.5]). Classifying the population by self-defined ethnicity resulted in a considerable group labelling themselves as Dutch (57% of the immigrants in CSI and 60% of those in the STI centres), especially second generation immigrants (72% in CSI and 80% in the STI centres). Self-defined non-Dutch ethnicity



Abstract P1-S4.02 Figure 1 Chlamydia positivity rate by region of origin, by self-defined ethnicity, in young persons in the Chlamydia Screening Implementation (CSI) and the Dutch STI centres.

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.

P1-S4.03 USING ORGANISM LOAD OF *CHLAMYDIA TRACHOMATIS* AND *NEISSERIA GONORRHOEAE* IN CLINICAL SPECIMENS AS AN EPIDEMIOLOGIC TOOL

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Background The Abbott Realtime m2000 system (m2000) is a qualitative real-time PCR assay for the detection of CT and NG that has the capability to provide a relative measure of target DNA. Results from the m2000 were used to determine CT and NG organism load by comparing the delta cycle (DC) value of each specimen to a set of lab developed standards containing known concentrations of each organism.

Methods Vaginal swabs and male urine specimens were evaluated. Six standards of each organism were prepared by inoculating collection tubes with lab strains in concentrations ranging from 0 to 4×105 organisms. The log10 organism load for each positive specimen was determined by comparing the DC value to the calibration curve. Self-reported symptoms were available for each patient.

Results A total of 99 vaginal and 284 urine specimens were available for analysis. There was no statistical difference in DC value of mean organism load by gender. Neither was there a difference based on the presence or absence of symptoms in people infected with CT. For NG, there was a significant difference in mean DC value and organism load by gender ($p<0.001$ for both DC and organism load) with men having higher loads. In NG positive men the mean DC was 15.2 [95% CI 14.7 to 15.8] and 11.4 [95% CI 9.0 to 13.7] for men with and without symptoms ($p=0.003$). This translated in mean log10 organism loads of 6.5 [95% CI 6.3 to 6.6] and 5.4 [95% CI 4.7 to 6.1] for men with and without symptoms ($p=0.005$). In NG positive women there was no difference in organism load based on presence or absence of symptoms ($p=0.220$).

Conclusions Advantages to using this methodology include being able to quantify organism load from specimens obtained for routine diagnostic testing, using standardised test reagents that can be purchased commercially, and using an automated platform. Even in those settings that do not have the capacity for calibration, the DC values may provide useful relative loads. This exploratory study demonstrated the feasibility of using this method to obtain relative quantitation measures. Application of this tool to epidemiologic questions using larger data sets may prove useful.

P1-S4.04 BIASES IN THE DESIGN OF STUDIES ASSESSING THE ROLE OF SEXUALLY TRANSMITTED INFECTIONS AS HIV RISK FACTORS

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Background For over 20 yearss sexually transmitted infections (STIs) have been studied as risk factors for HIV infection. We show how the design of studies in this field has inherent biases due to inappropriate confounder definition, coinfection, and heterogeneity in exposure to HIV. We use herpes simplex virus 2 (HSV2) to illustrate these biases and show that use of a serodiscordant couple design can remove them. Such findings are timely given the interest in using HPV vaccination for HIV prevention based on similar data.

Methods We developed an individual based model (IBM) using published data from an existing STI IBM (STDSIM). This model permits simulation of multiple cohort studies to show the direction and magnitude of these biases. The model is written in Matlab. Analyses were performed using Cox regression in SAS.

Results We identified four causes of bias. (1) While confounding by sexual behaviour is widely appreciated it is less well understood that perfect measurement of sexual behaviour will not permit adequate control of confounding as data on the frequency of HIV exposure is

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

	Null Median HR (Lowest HR, Highest HR)	Different transmissibility Median HR (Lowest HR, Highest HR)	Coinfection increases hiv infectiousness Median HR (Lowest HR, Highest HR)	Susceptibility Median HR (Lowest HR, Highest HR)
Expected	1	1	1	10
Standard Design	1.32 (0.84, 2.26)	1.58 (0.64, 1.44)	1.26 (1.01, 1.56)	4.38 (3.28, 5.65)
Serodiscordant Couples	1.03 (0.84, 1.44)	1.07 (0.70, 2.11)	1.03 (0.72, 1.25)	10.33 (9.65, 12.77)

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.