

However, when considering only those with documented PNC (n=226/101/183): 94%/95%/94% received syphilis screening, 88%/88%/89% initiated treatment, 87%/85%/87% met treatment adequacy, and CSPR were 84%/81%/84% (p=0.84).

Conclusion Compared to NMU, PMU and NI were associated with a decreased CSPR. When considering only those with documented PNC, significant differences between groups were not observed, suggesting PNC entry may be a key intervention for CS prevention.

Disclosure No significant relationships.

019 – MODELS, NETWORKS AND TRANSMISSION DYNAMICS: NEW INSIGHTS FOR PROGRAMS

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1:45 PM – 3:15 PM

019.1 MODEL-BASED STUDY DESIGN FOR ESTIMATION OF ROUTE-SPECIFIC GONORRHEAL TRANSMISSION PROBABILITIES

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Background Gonorrheal infection occurs at multiple anatomical sites as a result of different types of sex. Assuming anal sex, oral sex, rimming, and kissing transmit infection leads to seven possible routes of transmission. Recent models of gonorrheal infection have shown that the route-specific transmission probabilities cannot be directly estimated from currently available data. Here, we have illustrated how theoretical models can be used to inform epidemiological study designs aimed at estimating these transmission probabilities. This methodology that we call ‘model-based study design’ informs 1) necessary sample sizes, 2) which variables need to be measured, and 3) how sensitive resulting estimates are to the analytical model misspecification.

Methods We simulated cohorts of high risk MSM over 2 years, where every three months, each man completes a sexual behavior questionnaire and has gonorrheal testing at all sites. Cohorts were simulated under many of conditions, such as measuring different variables, different levels of under and over reporting of sex acts, and different patterns of sexual behavior in the population. The simulated data were analyzed in a Bayesian framework where prior knowledge of the joint prevalence of single-site and multi-site gonorrheal infection was integrated into the analysis using the Stan programming language. Outcomes included coverage of true transmission probabilities, bias, and uncertainty in route-specific transmission probabilities.

Results Under ideal conditions, we have shown that route-specific gonorrheal transmission probabilities can be estimated from study designs similar to ongoing CDC projects.

However, we also found that failure to measure heterogeneity in sexual behavior, a high preponderance of very high-risk behavior, and systemic under-reporting of certain sex acts (but not random recall bias) significantly limit the power of cohort studies regardless of the design.

Conclusion Model-based study design provides a general method for the design, analysis, and evaluation of studies for complex parameters that cannot be estimated directly from available data.

Disclosure No significant relationships.

019.2 BRIDGING OF NEISSERIA GONORRHOEA ACROSS DIVERSE SEXUAL NETWORKS IN THE HIV PREP ERA

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Background Despite ‘best effort’ public health measures, the incidence of gonorrhoea is increasing in many countries. Recently, whole genome sequencing (WGS) has been used to investigate transmission of *Neisseria gonorrhoeae*, including antimicrobial-resistant (AMR) lineages, but to date, most studies have not combined genomic data with detailed patient-level information on sexual behaviour to define the extent of transmission across population subgroups (‘bridging’).

Methods We performed an observational study and undertook WGS and bioinformatic analysis on all cultured clinical isolates of *N. gonorrhoeae* in the state of Victoria, Australia, from January to December 2017. Antimicrobial susceptibility testing was performed on all isolates, and detailed epidemiological data was obtained, including data on sexual orientation, HIV status, use of HIV pre-exposure prophylaxis (PrEP), sex work, and overseas travel. Epidemiological associations were made with dominant genetic clusters of *N. gonorrhoeae*.

Results A total of 2,186 isolates were sequenced from 2,055 patients, 86.3% of whom were male. We identified eleven dominant genetic clusters, containing thirty or more patients, with the largest cluster comprising 181 patients. There was extensive bridging of clusters between men who have sex with men (MSM) and heterosexuals, with bisexual males identified in seven of the major clusters. Eight major clusters contained HIV-positive and HIV-negative patients (including individuals receiving PrEP). We also identified transmission of a novel azithromycin-resistant clone, associated with a mosaic *mtr* locus.

Conclusion To our knowledge, our study is the first to combine WGS with comprehensive individual-level behavioural risk data, providing verification for transmission of multiple gonococcal lineages within and across distinct sexual networks. Application of these methods in real-time will allow gonorrhoea transmission and antimicrobial resistance to be tracked, with ‘hotspots’ identified for interventions aimed at improving gonorrhoea control.

Disclosure No significant relationships.