Study Design and Measurement Methods of Sexual Networks in Ghana

PAA 2013 Extended Abstract

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1 Introduction

The prevalence of HIV-1 infection in Ghana is estimated by UNAIDS to be 2.1% in 2011 [1]. Neighboring West African countries are similarly affected, much below the rates seen in eastern and southern African countries [2]. Ghana, like many other lower prevalence countries, has experienced disparities within the larger population: prevalence is nearly 10% in some urban areas and as high as 25% among commercial sex workers [1].

Understanding the impact of these disparities on the larger trajectory of the regional epidemic is challenging because population-level transmission occurs within a feedback loop, in which an individual's current infection risk is non-linearly dependent on the rate of infection of those in her sexual network. Like any infectious disease, HIV may propagate through a population as a result of small changes in contact network configurations [3]. One example is sexual partner concurrency, which occurs when a sex act with one partner occurs between two acts with another partner [4]. HIV transmission in particular is influenced by these network-level factors because of the low per-exposure transmission rate of the virus and the long asymptomatic period of infection.

Migration and travel have also been foci of ongoing research on HIV in Africa [5], although the findings on their etiologic impact have been mixed [6, 7]. No meta-analyses on this relationship have been published, partially because of the difficulty in aggregating exposure measurements. There is no consensus about how to measure either migration or travel [8]; there are many different patterns of both across regions and cultures. With limited exceptions [9], most studies on migration and HIV are cross-sectional that do not distinguish recent versus long-standing HIV infections, limiting any claims about causality because of the unknown temporal precedence of exposure to outcome.

Mathematical modeling can help disentangle the complex relationship between migration, concurrency, and HIV infection by simulating epidemic dynamics under a variety of counterfactual conditions [10]. Our research is motivated by the question of whether migration and travel indirectly drive HIV infection through concurrency, since migrants may have more opportunities for concurrent partnerships that bridge geographically separate sub-epidemics [11]. This will

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require stochastic network-based models in which HIV propagates through dynamically forming and dissolving sexual partnerships, the probability of which could be partially determined through geographic proximity [12].

Here we demonstrate our innovative approaches to survey sampling, network-based behavioral measurement, and assessment of selection bias within a complex urban environment for the study of the role of mobility in sexual network configurations and their role in larger HIV transmission dynamics. This work is based on our recently completed study of sexually active adults in Agbogbloshie, a slum in Accra, Ghana that is a hub for migrants from across the country and region [13]. Its residents have been long-thought to be at high risk for HIV infection from network-based risks like concurrency, but ours was the first biomarker study of HIV in this population. Conducting rigorous research in this environment was challenging, and we conclude with recommendations for future research on these issues in similar settings.

2 Sampling Design

Our sampling strategy benefited from the previous work of Codjoe et al. on the *Edulink* study of Agbogbloshie residents in 2010, during which the entirety of the area was systematically censused. All housing structures, unique households (distinct familial units) within each structure, and household members were enumerated. Housing structures were physically marked and the surnames of each household head were recorded.

We used this census in a two-stage sampling design for primary 'index' subjects. First households then individuals within households were randomly selected. With a target sample size of $n = 475$ for index subjects, a total number of households in the census of $n = 1158$, and an expected study completion rate of 68%, we drew a simple random sample of 60% of households (then randomly selected one household member). Given differences in household size, we used a weighting scheme for differential inclusion probabilities by household: the probability for selecting any household was proportional to the size of that household. This sampling scheme requires a weighted estimator for statistical analysis. If π_i is the inclusion probability for individual household members, then the Horvitz-Thompson estimator [14] for a population mean is:

$$\hat{\mu} = \frac{1}{N} \sum_{i=1}^{\nu} \omega_i y_i$$

where N is the total population size, ν is the number of sampled units, and ω_i is the inverse of the inclusion probability (that is, π_i^{-1}).

In our study, π_i was estimated based on the enumerated household size in 2010. However, the estimated π_i may be incorrect because: 1) the household size may have changed in two years; and 2) π_i is based on the total enumerated household size from the census whereas ν and N correspond to the target population of *our* study, which includes only sexually active household members between the ages of 18 and 49 years. Therefore, there will be a systematic bias in any

$\hat{\mu}$, and the size of that bias is a function of the difference between our estimated and the true π_i:

$$\delta_\pi = \hat{\pi} - \pi$$

We therefore collected information on the true π for selected households successfully approached in our study. This will be used in our statistical weighting scheme to update ω_i based on the assumption that misspecification of π was non-differential with regard to selection (i.e., $\delta\pi$ will be independent of study sampling). The implications of the bias in the estimation of the population characteristics will be discussed further.

In addition to index subjects, we also sampled married and cohabiting sexual partners of index subjects who were willing to refer them. These data will allow for such comparisons as knowledge of a spouse's secondary (concurrent) partners. This subset of linked data will also be used to investigate the mobility patterns at the level of the partnership dyad, to go beyond individual-level exposure variables (e.g., the index's HIV status is associated with the partner's concurrency).

3 Measurement Methods

Our survey tool included measures on demographics, HIV testing history, lifetime and past-year migration and travel history, and lifetime and past-year sexual behavior. Detailed past-year mobility and past-year sexual behavior with the last three sexual partners was mainly collected on an event history calendar, extending the general approach developed by Luke et al. [15] to include mobility events in time (days within months) and space (specific city and neighborhood destinations).

Below is a diagram of two survey questions, on the duration and type of sexual relationship, that were asked. The example shows that the relationship started last August and continues to the present (right arrow), and that the type of relationship changed over the course of the year from causal (4) to dating (3) to engaged (2) to married (1).

		2011					2012						
		Aug	Sep	Oct	Nov	Dec	Jan	Feb	Mar	Apr	May	Jun	Jul
D12	Duration	———————————————→											
D16	Type of Rel.	4 ———⊣			3 ———⊣				2 ———⊣			1 ——→	

The main strength of the calendar was its visual format, with its interactive and non-linear method of response completion. Lack of standardization in how questions were answered was a main limitation, and the visual format was lost on study subjects who were illiterate. We also used a *Travel Spells* module, in which subjects were asked about their three most recent trips in a standardized format. Interviewers were then asked to probe subjects for additional qualitative information to help further inform future measurement design. Data from this module will be compared with the calendar data to investigate which measurement methods excel in accuracy and efficiency. We will present the results of the comparative performance of these methods.

4 Selection Bias

A concern with our household-based study design is the biased estimation of mobility, since potential subjects who are traveling are not able to participate. The estimated prevalence of migration in our study may be underestimated since sample selection is conditional on non-current mobility during the data collection period. Of the total selected subjects, 3.9% could not be interviewed because of their long-term travel, according to other household members. An additional 14.1% could not be located at all, and some proportion of them may be traveling. Some have remedied these problems by sampling subjects at the destination point of their travel; for example, recruiting labor migrants at their occupational destinations [16]. We will explore analytic adjustments to the prevalence estimate of mobility with our secondary recruitment data.

In addition, causal inferences to be made between mobility and such outcome measures as HIV infection may also be subject to selection biases. If the probability of selection is associated with both exposure and the outcome of interest, the selection process acts as 'conditioning' on that latent mutually dependent variable and inducing a relationship [17]. At least two methods have been developed to conceptualize selection bias and account for it in statistical analyses. Heckman's two-stage probit regression modeling methods have been used in econometrics and other social sciences [18], while Hernan and Robins have defined a graphical approach to adjustment through inverse probability weighting in the epidemiological literature [19]. We will compare those two methods for understanding and adjusting for selection biases related to mobility in our study data.

5 Conclusions

A goal of our study is to generate unbiased estimates of relevant population parameters (including variances) that will be used in the network-based modeling of HIV transmission dynamics in West Africa and similar regions. At the end of our data collection, we recruited 589 subjects, of whom 106 were partners in linked cohabitating or marital dyads. Of the 694 households selected for primary index subjects, we recruited 481 (69.3%). The reasons for non-recruitment were ineligibility of all household members due to age or lack of sexual activity (6.6%), refusal of participation (1.9%), long-term travel (3.9%), lack of success locating the subject (14.1%), and other reasons including the demolition of the sampled housing structure (4.2%). The response rate for HIV testing (survey participants could decline testing) was 91.0%. Of those who tested, 3.7% (unweighted) were positive for HIV-1 (no HIV-2 infections were detected).

In our field work, we conducted a scientifically rigorous study in a dense, urban slum environment. Complex data on sexual networks and mobility were obtained, and ours was the first biomarker study of HIV in this population. This study design was dependent on prior research to enumerate the larger population that we sampled. Our field work provides insight into the methods for statistical weighting of study data, measurement methods for mobility and sexual partnerships, and considerations about selection biases for causal inference from household-based surveys on mobility. In our future transmission modeling, we will account for these uncertainties with appropriate sensitivity analyses.

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