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The Available Pool of Sex Partners and Risk for a Current Sexually Transmitted Infection

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Abstract

PURPOSE—STI transmission models propose that incident STIs are related to exposure to infected sex partners. The objective of this study was to determine whether the prevalence of STIs among the available pool of sex partners in a neighborhood, measured indirectly, is an independent determinant of a current incident STI.

METHODS—The target population comprised 58,299 English-speaking, sexually active 15–24 year olds in 486 census block groups (CBGs) in Baltimore, MD. A sample of 65 CBGs was selected using a stratified, systematic, probability-proportional-to-size strategy and 13,873 households were randomly selected. From 2004–2007, research assistants administered an audio-CASI survey and collected biologic samples for gonorrhea and chlamydia testing.

RESULTS—The final sample size included 575 participants from 63 CBGs. Additional data provided gonorrhea prevalence from 2004–2005 per 15–49 year olds per 100,000 per CBG. After adjusting for individual-level STI risk factors in a multilevel probability model, adolescents and young adults living in high (vs. low) prevalence STI areas were 4.73 times (95% confidence interval (CI): 3.65–6.15) more likely to have a current incident STI.

CONCLUSIONS—To inform prevention programs, future research should focus on identifying mechanisms through which context causes changes in local sexual networks and their STI prevalence.

Keywords

Sexually transmitted diseases; gonorrhea; residence Characteristics; adolescent; urban population; urban health

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INTRODUCTION

Sexually transmitted infection (STI) transmission and acquisition models propose and research shows that incident infections are due in part to demographic factors (age and gender) and sexual behaviors (condom nonuse and number of sex partners) (Figure 1) (1–5). The natural and likely assumption is that these demographic factors and sexual behaviors explain in part the persistence of STIs in geographic areas (6–9). That is, some geographic areas may have a higher incidence of infection because they have a greater percentage of residents who are demographically and/or behaviorally at higher risk for STIs. For example, a high STI area may contain a greater proportion of adolescent girls or a greater proportion of people who do not use condoms. This would suggest that neighborhood of residence is just a proxy for individual characteristics of the residents and not in of itself an independent risk factor.

STI transmission and acquisition models, however, also propose that incident STIs are related to exposure to infected sex partners (Figure 1). As such, it can be argued that another independent risk factor for STIs may be the prevalence of STIs among the available pool of sex partners in a neighborhood (3,9–12). For example, some geographic areas may have a higher incidence of infection because they have a greater proportion of infected sex partners within the local available sex partner pool. This hypothesis assumes that local sex networks are at least in part formed on the basis of propinquity, i.e. physical proximity between people (13,14), and that local sex networks may be comprised by residents and non-residents.

The objective of this study was to determine whether the prevalence of STIs in the available pool of sex partners in a neighborhood is an important determinant of incident STIs. Since the prevalence of infection in the available sex partner pool could not be measured directly, we used an indirect approach to assess the association between infection in neighborhood sex partner pools and individual-level risk for STIs. In Baltimore there are areas with historically higher and lower prevalence and presumably incidence of STIs. In this study, we selected a random sample of census block groups, our indicator of neighborhood, which varied in their historical prevalence of STI. We then recruited a random household sample of adolescents and young adults from each block group and tested whether the likelihood of a participant having a current incident STI was associated with the prevalence of STIs in their neighborhood. And then finally, we tested whether this association persisted after adjusting for individual-level STI risk factors of the participants in each CBG. To the extent that the association persists, we argue that geographic variation in the available pool of sex partners is associated with individual-level risk of an STI.

MATERIALS AND METHODS

Overview

The current study was conducted in Baltimore City, Maryland. Baltimore is a city in the Mid-Atlantic United States (U.S.) with a 2000 population of 651,154 people. Baltimore has a history of consistently high gonorrhea prevalence. In 2007, it ranked ninth in gonorrhea prevalence per 100,000 population among counties and independent cities in the U.S. (15).

Data for this study were collected from several sources. We obtained data from a household study which is detailed below. We also obtained public health surveillance data from the Baltimore City Health Department to measure gonorrhea prevalence among 15–49 year olds per 100,000 per CBG for the period 2004–2005.

Study Design and Sampling Strategy

The household study was conducted from April 2004 to April 2007. The target population included English-speaking, sexually-active persons between the ages of 15 and 24 years who

resided in 486 CBGs. We estimate that the target population comprised approximately 58,299 persons living in the 486 CBGs in 2005.

The sampling selection for the study was conducted in two stages. In the first stage, among the 710 CBGs in Baltimore City 75% or 533 CBGs were selected consisting of CBGs with greater than the 25th percentile in gonorrhea prevalence. This subsample was selected for two reasons: 1) to increase the likelihood of identifying infected individuals, and 2) to focus on distinguishing factors associated with a current STI among higher risk areas rather than focusing on comparisons between very low and very high risk areas. Gonorrhea prevalence was generated from public health surveillance data among 15–49 year olds per 100,000 per CBG from 2004–2005. We subsequently restricted CBGs to those with 35 or more estimated eligible households (486 or 91%). Estimates of eligible households were generated using Census 2000 information (16). The CBGs were then placed into primary strata by deciles of gonorrhea prevalence, and ordered by the percent of households below the Federal poverty line and by geography. A final sample of 65 block groups was selected using a stratified, systematic probability proportional to size sampling strategy, where size was defined by the estimated number of eligible households (Figure 2).

In the second sampling stage, we obtained address lists from three different vendors for the 65 selected block groups to create a household sampling frame. A total of 27,194 addresses associated with the 65 selected block groups served as the second-stage sampling frame. We then used non-linear optimization to allocate a sample of 13,873 households to the three lists in a way that reduced screening costs while controlling for design effects (17). Our target enrollment for each block group was 10 participants based on Optimal Design power and sample size calculations (18).

Data Collection

All sampled households received a lead letter describing the study approximately two weeks before the households were contacted for enumeration. Enumeration, to determine whether the household had at least one age-eligible individual, was conducted by telephone for those households with available numbers (approximately 33% overall) or in-person by trained research assistants. Screening was conducted to determine eligibility. In selected households with more than one age-eligible person, one was randomly selected for screening. Parental/guardian informed consent and adolescent informed assent was conducted with individuals less than 18 years of age and informed consent was conducted for individuals 18 years or older. If eligible and willing to participate, consenting individuals were enrolled and research assistants administered an audio computer-assisted self-interview (audio-CASI) in a private setting. The audio-CASI survey captured information on demographics as well as sexual risk-related information including individual- and partner-related sexual histories and risk behaviors. For example, we asked each individual whether they had ever been infected with gonorrhea, chlamydia and other specific STIs. We also asked number of sex partners in their life and in the past 90 days and whether they had ever had sex with an HIV-infected individual or an injection drug user. For each sex partner named in the last 90 days we the same if not similarly specific questions.

Biologic samples including urine samples for males and self-administered vaginal swabs for females were collected for nucleic acid amplification testing (NAAT) specifically polymerase chain reaction assay (Amplicor® CT/NG Test, Roche) for gonorrhea and chlamydia. Self-administered vaginal swabs for females and urine samples for males have been shown in previous research to be feasible and acceptable methods for collecting biologic samples for STI testing and to have high sensitivity and specificity with NAAT (19–22). Participants received \$25 to \$45 remuneration for participation in the study dependent on their year of entry.

The study protocol was approved by the Western Institutional Review Board for Johns Hopkins University.

Measures

The main outcome of interest at the individual-level was current diagnosis with chlamydia and/or gonorrhea and is referred to as a current incident STI.

The main variable of interest at the neighborhood level was gonorrhea prevalence among 15–49 year olds per 100,000 per CBG from 2004–2005 coded as a continuous variable and as a dichotomous variable (above or below/equal to the median split). Gonorrhea cases identified by this study from 2004–2005 and reported to the city health department ($n=3$) were excluded from the gonorrhea prevalence calculation for the respective CBG. Gonorrhea prevalence was selected as the indicator of STI prevalence because of the standard reporting procedures for gonorrhea and the relatively large number of cases reported in any one year, thus providing stable estimates of disease prevalence. We chose not to use reported cases of chlamydia in our indicator of STI prevalence because of the ascertainment bias associated with chlamydia surveillance.

Individual-level demographic information and a well-established, relatively complete list of individual-level behavioral STI risk factors were utilized to adjust the regression models for the most proximal individual-level factors associated with a current incident STI and to determine the independent association of gonorrhea prevalence as a marker for STI infected sex partner pools. We chose our individual level factors based on STI transmission and acquisition models. In these models, the most proximal risk factors for acquisition are efficiency of transmission, sexual behaviors, and probability that a sexual contact is infected, i.e., prevalence of STIs in sex available partner pools. Since the purpose of this study was to examine the effect of prevalence in STIs in available sex partner pools, we chose to control for those demographic factors associated with efficiency of transmission - age (continuous), gender (male, female) - and sexual behaviors - condom use (yes, no) and number of recent sexual contacts (partners in the past three months (0,1, 2, 3 and greater than or equal to four sex partners). All other known risk factors for STIs are only markers for these proximal risk factors.

Statistical Analyses

Statistical analyses included the calculation of statistical analysis weights, and weighted and unweighted summary statistics. We also conducted exploratory analyses culminating in the generation of a series of multilevel probability models. Multilevel models represent the most appropriate method of analysis as the data form a nested data structure; i.e., the participants (level one) are nested within the census block groups (level two). Multilevel analysis accounts for the non-independence of observations within groups, uses empiric Bayes adjustments for the group means and allows for statistical testing of the between and within group variances on the outcome, current incident STI. All analyses were conducted using Stata, version 9.0 (Stata Corporation, College Station, TX).

Statistical analysis weights enable design-consistent estimation of population parameters by adjusting for disproportionate characteristics between sample members and the target population. In this study weights were generated to reflect the unequal probabilities of selection of an individual and a CBG and to adjust for potential biases attributable to differential response and coverage between sample members and the target population. In multilevel analysis, the sampling weights need to be constructed differently than the sampling weights for single-level or population-average models. A common approach and the one utilized in our analyses is a method of computation devised by Pfefferman et al. (1998) for multilevel data (23,24).

To calculate weighted and unweighted response rates for both the interview and the collection of a biologic specimen, we used the operational definitions and formulas for in-person household surveys described by the American Association of Public Opinion Research (25). Specifically we used the formulation RR3 which uses the known eligibility rate to pro-rate eligibility among cases with unknown eligibility. We used the RR3 formulation because there were no partial interviews and because most of the addresses with unknown eligibility were occupied housing units and at least some were likely to have eligible persons.

Exploratory analysis was conducted and summary statistics were generated for the individual-level variables and census block group-level variables. A series of multilevel probability models were generated to determine if and the extent to which the prevalence of gonorrhea, as a marker for infected sex partner pools, at the census block group-level was significantly associated with a current incident STI after adjusting for the most relevant individual-level demographic and behavioral STI risk factors including age, gender, condom use at last sex and number of sex partners in the last 90 days. In all models two requirements were used for statistical significance including a confidence interval that did not include 1.0 and $p < .05$.

First, an unconditional multilevel model was used to assess the extent of variation in current incident STIs between the communities. Then individual-level variables were added to this model to determine the extent to which the individual-level variables were significantly associated with a current incident STI. Subsequently, models were generated to assess the independent relationship between gonorrhea prevalence at the CBG level and current incident STI. Finally, all individual-level and CBG gonorrhea prevalence were entered into a multilevel model to assess the independent relationship of gonorrhea prevalence after adjusting for the individual-level factors. For ease of interpretation, we conducted all models which included gonorrhea prevalence in two ways -- one, with gonorrhea prevalence as a continuous variable and two, with gonorrhea prevalence as a dichotomous variable. We also conducted all analyses using weighted and unweighted data.

RESULTS

Study Population

Of the 27,194 addresses in the second stage sampling frame, 50% (13,699) were fielded and of these, 74% (10,173) households were successfully screened. During the screening, two of the 65 CBGs were found to be comprised exclusively of retirement communities and thus were excluded. Among households enumerated, 12% (1,270) had at least one English-speaking person between the ages of 15 and 24. One age-eligible person was randomly selected for screening from each household. Among these households, screenings for sexual activity were attempted in 77% (981) of the age-eligible households with a completion rate of 70% (682) yielding a response rate to the interview among those selected of 68%. This yielded an overall interview response rate of 51% (599) and overall interview with a biologic specimen response rate was 50% (589) (25). Of the 589, an additional 2% (14) were excluded from this analysis. Two percent (12) were missing surveys due to technical issues and <1% (2) had missing STI tests. The final sample size at the individual-level was 575. The number of individuals within a CBG ranged from 1 to 23 (mean 11.48, SD 5.04).

Characteristics of the Study Population

The weighted and unweighted statistics were quantitatively and qualitatively similar so we present only the weighted results. The summary statistics were as follows: the average age of participants was 19 years (standard deviation (SD) 0.15), 63% of the study population was female, 88% was Black and 45% reported that their mother had a high school education or General Equivalency Diploma (GED) (Table 1). Thirty-nine percent reported no condom use

at last sex and 27% had greater than one partner in the past 90 days. Six percent of participants were diagnosed with a current chlamydia and/or gonorrhea infection. At the neighborhood-level, the average overall gonorrhea prevalence per CBG was 1,488.8 (standard error (SE) 82.4) per 15–49 year olds per 100,000 population.

Multilevel Probability Models

The mean current incident STI was 6.43 with a standard deviation of 0.25 and a range of prevalence from 0.00 to 50.00. The unconditional multilevel model showed variation in current incident STIs between CBGs (SD 1.16).

Next we generated a multilevel model to confirm the expected association between individual-level factors and individual-level current incident infection accounting for the clustering of participants within CBGs (Table 2, model 1). As expected, younger age, female gender, higher numbers of sex partners in the past 90 days and condom nonuse were all associated with increased likelihood of a current incident STI (although only age was significantly associated).

Next in multilevel models, we ascertained the relationship between the gonorrhea prevalence (in two separate models as continuous (*results not shown*) and dichotomous) and current incident STI (Table 2, model 2). In both models, increased gonorrhea prevalence at the CBG level was significantly associated with an increased likelihood of an individual-level current incident STI. Specifically, individuals in high gonorrhea prevalence areas compared to individuals in low prevalence areas were 26 times more likely to be diagnosed with a current STI (weighted odds ratio (OR) 26.43, 95% confidence interval (CI): 12.44–56.13).

In the final multilevel models, all individual-level factors and gonorrhea prevalence (measured in two ways) were entered into the models (Table 2, model 3). The link between the likelihood of a current incident STI and gonorrhea prevalence decreased but remained highly significant after controlling for the most relevant individual-level STI risk factors (weighted OR 4.73, 95% CI: 3.65–6.15). In this final model, gonorrhea prevalence helped to explain an additional 12 percent of the level two variance associated with a current incident STI.

DISCUSSION

The current study finds that the gonorrhea prevalence in areas is independently associated with a current incident bacterial STI after controlling for individual-level STI demographic and behavioral risk factors. To the extent that our measure of gonorrhea prevalence after controlling for individual STI risk factors represents the infected pools of available sex partners, we argue that geographic variation in STI infection in the available pool of sex partners is associated with individual-level risk of an STI. The findings fill a critical gap in a growing body of research recognizing the limitations of research where individual-level STI risk factors alone explain increased risk for STIs (5,29,30).

This study provides further quantitative evidence of the neighborhood nature of disease. The findings are similar, for example, to a community-based network study of ethnographically representative adolescents by Rothenberg, et al. (31). This study found that chlamydia and gonorrhea infected individuals were more likely to be connected to higher STI prevalence sexual and social networks than individuals not infected.

Since this study sought only to provide the first explicit test of whether and the extent to which the local sex partner pools mattered for this outcome, we did not attempt to identify cross-level processes clarifying the association between individual risk for an STI and the STI prevalence of areas. There has been, however, some promising work in this area already. Fichtenburg, et al. (2009), using non-egocentric data among a household sample of African American

adolescents in San Francisco, showed that the maintenance of hyperendemic areas may be highly dependent on sexual network structures and connections (32). In future work, we intend to add to this growing literature on the association between historically high STI areas and increased risks for STIs.

This study also has a number of limitations. Although this is a household study conducted in a high prevalence setting with a complex probability sampling strategy designed to be representative at the CBG- and individual-levels, it captures just one city at one point in time. Only future work can confirm whether results generalize to other cities and periods. In addition, the gonorrhea prevalence was assigned to each participant based on their primary residential address. Information about the location of residence of the sex partner/s was not included. Our work thus overlooks potential contributions of multiple contextual memberships for those whose partners reside in different CBGs. Whether that additional information attenuates the current contextual impact observed here, or instead captures another independent impact of context, awaits future work. Multiple membership classification models prove to be helpful (33). Finally, the current work is cross-sectional and thus the question of whether changing hyperendemic area status affects changes in individual diagnosis awaits future work.

Our findings provide compelling evidence that the force of infectivity of local neighborhood sex networks shape individual-level risks for STIs. The link shown helps fill critical gaps in research on how we may better understand the determinants of STIs and health disparities in STIs. The findings suggest that prevention programs designed solely to address individual-level factors may not be sufficient to decrease risk for STIs. We intend to dedicate future work to the investigation of whether these findings are indeed causal-in-nature and to the identification of mechanisms through which changes in the local sexual networks and their prevalence in STIs shape individual-level changes in STI incidence. With such information future prevention programs can be designed which consider both sexual networks as well as individual factors related to STI risk.

Abbreviations

AOR	adjusted odds ratio
audio-CASI	audio computer-assisted self-interview
CBG	census block group
CI	confidence interval
GED	General Equivalency Diploma
OR	odds ratio
SD	standard deviation
SE	standard error
STI	sexually transmitted infection
U.S.	United States

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FIGURE 1.

Hypothesized pathways through which historically high prevalence sexually transmitted infection (STI) areas relate to current incident STIs and ultimately currently high prevalence STI areas.

FIGURE 2.
Selected, Eligible and All Census Block Groups (CBGs) at the Stage One Sampling, Baltimore, Maryland, 2004–2006.

TABLE 1

Characteristics of a Household Sample of 15–24 Year Olds From Selected Neighborhoods, Baltimore, Maryland, 2004 – 2007 ^{*}, [†]

	Overall	
Individual-level characteristics (n=575)		
Demographics	Mean	SE
Age	19.1	0.2
Sex	N	%
Male	222	37.4
Female	353	62.6
Race/Ethnicity		
Black	498	87.8
White	46	7.7
Other	21	4.5
Maternal education		
Less than a high school degree/GED	106	19.5
High school degree/GED	255	45.0
Greater than a high school degree/GED	200	35.5
Sexual behaviors		
Condom use last sex, no	226	38.5
Number of sex partners in the past 90 days		
0–1	415	72.3
2–3	120	21.3
≥ 4	40	6.4
Current incident STI (chlamydia and/or gonorrhea)	37	6.4
Neighborhood-level characteristic (n=63)	Mean	SE
Gonorrhea prevalence among 15–49 year olds per 100,000 per CBG	1488.8	82.4

SE, standard error.

^{*} For some variables, the percentage was based on a smaller number of participants because of missing data.

[†] Unweighted counts and weighted means/percentages presented.

The Association Between Gonorrhea Prevalence (high versus low prevalence areas) and Current Incident Bacterial STI (Chlamydia and/or Gonorrhea Infection) Among a Household Sample of 15–24 Year Olds, Baltimore, Maryland, 2004 – 2007 ^{*,†}

TABLE 2

Individual-level characteristics (n=575)		Model 1 AOR	95% CI	Model 2 OR	95% CI	Model 3 AOR	95% CI
Age		0.85	0.73–0.99 [‡]			0.83	0.69–1.00
Sex	male	Referent				Referent	
	female	2.10	0.55–8.06			2.18	0.58–8.19
No. of sex partners in the past 90 days (categories including 0, 1, 2, 3 and greater than or equal to four sex partners)		1.59	0.88–2.87			1.62	0.93–2.83
Condom use last sex	yes	Referent				Referent	
	no	0.97	0.30–3.12			1.05	0.33–3.32
Neighborhood-level characteristic (n=63)							
Gonorrhea prevalence among 15–49 year olds per 100,000 per CBG				26.43 [‡]	12.44–56.13	4.73 [‡]	3.65–6.15
median split							

Model 1, individual-level (level one) variables and outcome; Model 2, CBG level (level two) variable and outcome; Model 3, individual-level and CBG level variables and outcome; OR, odds ratio; AOR, adjusted odds ratio; CI, confidence interval

^{*}The models are multilevel probability models.

[†]Data represent weighted results.

[‡]P < 0.05.