Social Disequilibrium and the Risk of HIV Acquisition: A Multilevel Study in Rural KwaZulu-Natal Province, South Africa

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Background: Few population-based multilevel studies have quantified the risks that social context poses in rural communities with high HIV incidence across South Africa. We investigated the individual, social, and community challenges to HIV acquisition risk in areas with high and low incidence of HIV infection (hotspots/coldspots).

Methods: The cohort (N = 17,376) included all HIV-negative adults enrolled in a population-based HIV surveillance study from 2004 to 2015 in a rural South African community with large labor migrancy. Multilevel survival models were fitted to examine the social determinants (ie, neighborhood migration intensity), community traits (ie, HIV prevalence), and individual determinants of HIV acquisition risk in identified hotspots/coldspots.

Results: The HIV acquisition risk (adjusted hazard ratio [aHR] = 1.05, 95% confidence interval [CI]: 1.01 to 1.09) was greater in hotspots with higher neighborhood migration intensity among men. In women, higher neighborhood migration intensity (aHR = 1.02, 95% CI: 1.01 to 1.02) was associated with a greater HIV acquisition risk, irrespective of whether they lived in hotspot/coldspot communities. HIV acquisition risk was greater in communities with a higher prevalence of HIV in both men (aHR = 1.07, 95% CI: 1.03 to 1.12) and women (aHR = 1.03, 95% CI: 1.01 to 1.05), irrespective of hotspot/coldspot locations.

Conclusion: HIV acquisition risk was strongly influenced by gender (ie, young women), behavior (ie, sexual debut, contraception, circumcision), and social determinants. Certain challenges (ie, community disease prevalence) for HIV acquisition risk impacted both sexes, regardless of residence in hotspot/coldspot communities, whereas social determinants (ie, neighborhood migration intensity) were pronounced in hotspots among men. Future intervention scale-up requires addressing the social context that contributes to HIV acquisition risk in rural areas with high migration.

Key Words: HIV, geographical information systems, hotspot, rural South Africa, social disequilibrium, social disorganization

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INTRODUCTION

Decades of groundbreaking research have transformed the global response to the HIV epidemic. Preexposure prophylaxis, male circumcision, and early antiretroviral therapy[1–3] are a number of biomedical approaches that have proven effective in preventing the transmission of HIV at the individual level. However, the limited efficacy noted in the South African Treatment as Prevention (TasP) trial[4,5] because of poor linkage to care has underscored the potential challenges associated with the biomedical paradigm. Many of the challenges that impede linkage to care and limit the scale-up of community-based interventions across the sub-Saharan Africa are social in nature, and include migration patterns,[6] stigma/fear of disclosure related to HIV status and treatment,[7,8] and patient dissatisfaction with health care systems.[9] In addition, it is well understood that HIV risk is impacted by a range of social determinants at the community and neighborhood levels in which individuals reside.[10] The notion of community is central to traditional African life,[11] and HIV interventions at the population level are therefore unlikely to achieve their desired goals if the social context[12] that have resulted in South Africa having the largest HIV epidemic (≈6.4 million people[13]) in the world are not investigated.

A systematic review of the literature indicated a relationship between labor migration and HIV risk,[14] with circular migration patterns having contributed to the explosive spread

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of HIV in South Africa, particularly during the early phase of the epidemic.[15] There is little multilevel evidence about the impact of social and individual challenges (including the role of migration) in a typical rural South Africa setting that might explain the processes driving the high infection rates of HIV.

In an attempt to strengthen the evidence base for a comprehensive prevention strategy in a rural setting, our multilevel study analyzed various social and individual determinants of HIV acquisition risk. While acknowledging the entrenched high levels of poverty and socioeconomic inequality[16] that influence the HIV epidemic,[17–19] the underpinning of our investigation is based on social disorganization theory,[20,21] due in large part to the labor migration history of South Africa.[22] The theory posits that high population turnover and heterogeneity (ie, migration pattern, residential instability) undermine the ability of communities to achieve common values and solve common challenges.[23,24] Although some communities buffer social disorganization by enhancing neighborhood informal social controls that are based on participation in civic and social organizations,[25] others fail to adjust to the changing conditions, giving way to social disequilibrium, and various socially risky behaviors.[26] In this article, we draw on social disorganization theory to examine the impact of various social and individual challenges on HIV acquisition risk across rural communities with varying HIV infection rates in KwaZulu-Natal Province, South Africa.

METHODS

Study Area

The study area is the Africa Centre Demographic Surveillance Area that is situated in the southern part of the uMkhanyakude District in northern KwaZulu-Natal. It is approximately 440 km^2 in extent and consists of 94,000 individuals living across 11,000 households in scattered neighborhoods in a predominantly poor rural setting populated by isiZulu-speaking people. The Africa Centre's Demographic Information System (ACDIS) was launched in 2000, being the first extensive surveillance system designed to monitor the demographic, social, and health impacts of the rapid HIV epidemic in rural KwaZulu-Natal. Data from the ACDIS were used to identify the social and individual determinants of HIV risk acquisition. At the height of the epidemic in this study area between 2004 and 2010, the HIV incidence peaked at 4.1 per 100 person-years in men aged 29 years, and 6.6 per 100 person-years in women aged 24 years.[27]

Pertinent to the social context of this investigation is the significant role of nonresident household members, who account for one-third of all individuals observed in the surveillance area.[28] In the ACDIS, the nonresident household members are analogous to migrants who may move between the Africa Centre Demographic Surveillance Area and (at least) one other place outside the surveillance area. On return to the area, they often reside in areas proximate to the National Road, a major corridor of both population movement and commercial transportation. It links the port city of Durban in the south with South Africa's Mpumalanga Province, as well as Mozambique and Swaziland to the north. Equally important to the social context is the large variations in population densities (20–3000 people/km^2) in the area.

The Africa Centre Demographic Information System

The ACDIS contains data from 2 data collection surveys, these being at individual and household levels. During the annual individual data collection cycle, trained enumerators capture demographic, health, and behavior data from eligible adults aged ≥15 years. The only eligibility criteria for the study are household membership within the surveillance area, which results in the ACDIS containing data of both residents and nonresidents, as long as they are identified as members of a household within the surveillance area. Individuals qualify as members of a household if they spend at least one night in residence in the 12 months before the annual survey.

The individual data collection cycle consists of annual HIV (dried blood spot) testing in addition to a serosurvey, as well as information on sexual behaviors. The eligibility criteria for confidential HIV testing and serosurvey is adult men (aged 15–54 years) and women (aged 15–49 years) in the surveillance area. HIV status is based on antibody testing with 2 parallel rapid tests using HIV-1/HIV-2 enzyme-linked immunosorbent assay (Vironostika HIV-1 Microelisa System; Biomérieux, Durham, NC and Wellcozyme HIV 1 + 2 GACELISA; Murex Diagnostics Benelux B.V., Breukelen, the Netherlands). The individual response rate for HIV testing has been approximately 80% over time.

During the biannual household data collection survey, questionnaires (including geographic location, memberships, birth, death, and migration information) are administered to a key informant. The average household size was 7.9 members (SD = 4.7), and the response rate of the survey was greater than 95%. The University of KwaZulu-Natal Biomedical Research Ethics Committee approved the implementation of the ACDIS. The detailed profiles of the ACDIS cohort are provided elsewhere in a published article.[29]

Study Measures

Outcome

Consistent with our previous studies,[27,30] the primary outcome of this current investigation was time to HIV acquisition at the individual level. The target sample population were adult individuals who had participated in HIV testing at least twice between 2004 and 2015, and who had been determined to be HIV negative in the initial test (hereafter labeled "ACDIS HIV cohort"). The HIV acquisition date was obtained, consistent with the previous investigation,[30] by randomly selecting a time point between the last HIV-negative and first HIV-positive test date. Individuals who remained HIV negative at their most recent test were right censored.

Neighborhood Migration Intensity

The main social determinant investigated in the study was migration intensity within the various neighborhoods.

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The measure was constructed by calculating the percentage of time the study participants spent outside the surveillance area, and subsequently aggregated at neighborhood level among individuals residing in that particular area. Because of the positive skewness of the data, a median aggregation method was used. Migration intensity reflects the extent of social disequilibrium, operationalized by the magnitude of migration movement into or out of the surveillance area[31] experienced within each neighborhood. There is considerable debate and variation in how individuals perceive neighborhood boundaries.[32] Our present study defined neighborhoods as a collection of multiple households that have recognizable boundaries.[28]

Neighborhood Civic Participation

The other social determinant was neighborhood civic participation. Essential to our current investigation are the social ties that may influence the relationship between the societal structures that maintain order, and prevent crime and risk behavior. Data on civic participation were obtained from household questionnaire. The key informed was asked whether any household member belonged to the following 19 social organizations: stokvel, burial societies, community garden groups, farmer's associations, sewing groups, sports groups, study groups, choir/music groups, youth groups, informal trader's associations, men's associations, women's associations, school committees, water committees, policing forums, tribal authorities, community health workers, or development committees. Similar measures (17 rather than 19 social organizations) have been used in other population-based investigation, namely the South African National Income Dynamics Study.[33] The neighborhood civic participation was subsequently aggregated at neighborhood level to construct neighborhood civic participation, by dividing the number of households with any members belonging to 1 of the 19 social organizations by the total number of households in a specific neighborhood. As the data were only available for the year 2000, assumptions had to be made that the nature of civic participation did not change over time.

Community HIV Prevalence

In addition to the above-mentioned social determinants, we also investigated the role of several community traits (ie, HIV prevalence and hotspots) that could influence the risk of HIV acquisition in the study area. We use the term community because clear geographic-bounded subdivision of land was lacking,[34] signifying larger unit compared with that of neighborhood in our study. As a major predictor of HIV incidence,[35] a geospatial grid-based technique using the geographic information system was used to construct a community-based HIV prevalence estimate for each study years. This estimate was computed by means of a moving 2-dimensional Gaussian kernel of 3 km search radius, a method consistent with our previous study.[36] The kernel moves systematically across the grid and measures the spatial variation in HIV prevalence across the surveillance area at the household level. The resulting HIV prevalence and geographic distribution of the total eligible population were used to calculate the number of HIV-negative individuals in the area surrounding each cell on the grid. The method is well suited to the scattered distribution of the population, as it does not impose any static geographical boundaries on the data. Instead, it uses the location of each neighborhood to derive a sensitive community-level measure that is both responsive to local variations and robust to the effects of random noise.

Communities With High and Low HIV Acquisition Risk

Hotspot communities, signifying spatial clusters of excess incidence of HIV infection, were identified using the Kulldorff spatial scan statistic in a previous analysis.[37] Briefly HIV incidence was summed for all individuals ≥15 years of age in each homestead and mapped to an accuracy of <2 m. The Kulldorff elliptical spatial scan statistic (survival model) was then applied to formally identify clusters of new infections at the microgeographical level ($P < 0.05$) using the SaTScan software (version 9.1). Areas intersecting the high-risk clusters were classified as exposure to hotspot, as well as coldspot communities (or nonhotspots), where no risk clusters were identified.

Analyses

The analysis consisted of 2 components: descriptive statistics of the individual baseline characteristics and statistical multivariate modeling analyses. Descriptive statistics were used to summarize the baseline (initial) individual characteristics of the study that consisted of demographic background, socioeconomic status, migration history, and the health and sexual behavior profiles of men and women separately. The main analysis involved using multilevel survival models to estimate the time to HIV acquisition, and is presented with respect to both social-level (nonindividual) and individual-level determinants, and a combination of the 2 [Note: community HIV prevalence and hotspots are noted as social (nonindividual) determinants in the subsequent sections for ease of presentation].

The analysis was stratified by gender, as health data in the ACDIS contain specific questions that pertain to male (ie, circumcision, history of fatherhood) and female participants (ie, history of pregnancy, contraception use). Eight separate 2-level random-intercept models were sequentially fitted for both men (models 1a–1h) and women (models 2a–2h). Models 1a/2a fitted a null model without any explanatory variables. Models 1b–1e/2b–2e considered the effect of social variables one at a time without individual determinants on HIV acquisition. Models 1f/2f examined the effect of all individual determinants of HIV acquisition, but without social determinants. Models 1g/2g considered all explanatory variables at social and individual levels, but without the interaction terms that assessed the varying effect of the social determinants between hotspots and coldspots. Last, models 1h/2h (full model), which address the main research question of our study, considered all explanatory variables at social and individual levels, including the interaction terms, to establish whether the effect of the social determinants on HIV acquisition risk varies between hotspot and coldspot

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communities. Models 1g–1h/2g–2h were adjusted for individual-level predictors from models 1e/2e. Akaike Information Criterion (AIC)[38] was used to assess model fit, where the lower values signify a better fit. The likelihood ratio (LR) test was used to compare the goodness of fit of the 2 (nested) models. Variance and the intraclass correlation coefficient (ICC), which explains the proportion of total variance at social and individual level, were computed for each model, with STATA 14 being used for the model analysis.

RESULTS

Baseline Individual Characteristics

The baseline characteristics of the male (n = 7582; 46.63%) and female study participants (n = 9794; 53.37%) are presented in Table 1. Nearly half of men (n = 4044; 53.34%) and women (n = 5220; 53.30%) entered the cohort before 2007. Most men (n = 4459; 58.81%) and women (n = 4906; 50.09%) were below the age of 20 years. Approximately a third of men (n = 2927; 38.60%) and women (n = 3727; 38.05%) reported residing outside the surveillance area at some stage. Nearly half the women reported contraception use (n = 3127; 52.54%), and a sixth of the men indicated being circumcised (n = 793; 15.53%). Approximately a third of the women had a history of sex activity before the age of 17 (n = 2183; 33.39%), while being the case for more than half of the men (n = 2095; 50.90%). Of the male participants, 14.66% (n = 418) reported having more than one sexual concurrent relationships at a time, this being considerably less for the women (n = 27; 0.61%). For individual baseline link to hotspots (ie, residing in hotspot communities), 2 clusters across the surveillance area indicating significant spatial clustering for excess incidence of HIV infection were identified, based on the SaTScan analysis. Two locations with individuals at high-risk of new infection, overlapping spatial clusters (RR = 1.44 and 1.90) with 641 cases (67.97% of all cases) were identified in a periurban community near the national highway, based on the Kulldorff statistic ($P < 0.01$), and are indicated in Figure 1. Nearly a quarter of men (n = 1968; 26.28%) and women (n = 2324; 23.91%) resided in a "hotspot" community.

TABLE 1. Baseline Individual Characteristics of ACDIS Cohort by Gender

	Male (n = 7582), n (%)	Female (n = 9794), n (%)
Age category, yrs		
15–19	4459 (58.81)	4906 (50.09)
20–39	2336 (30.81)	3490 (35.63)
40+	787 (10.38)	1398 (14.27)
Migration history outside surveillance area		
No	4655 (61.4)	6067 (61.95)
Yes	2927 (38.60)	3727 (38.05)
Marital history		
Never married	7127 (94.01)	8439 (86.18)
Married	454 (5.99)	1353 (13.82)
Residing in a hotspot area		
No	5520 (73.72)	7394 (76.09)
Yes	1968 (26.28)	2324 (23.91)
Quintile household income		
Bottom 20%	1229 (16.21)	1567 (16.00)
Lower 20%	1633 (21.54)	2208 (22.54)
Middle 20%	1672 (22.06)	2202 (22.48)
Higher 20%	1611 (21.25)	2064 (21.07)
Top 20%	1436 (18.94)	1753 (17.90)
Presence of concurrent relationships		
No	2434 (85.34)	4401 (99.39)
Yes (more than 1 at a time)	418 (14.66)	27 (0.61)
Sexual debut		
Before age of 17	2095 (50.9)	2183 (33.39)
On or after age of 17	2021 (49.1)	4355 (66.61)
History of tuberculosis exposure		
No	5005 (97.79)	6751 (98.97)
Yes	113 (2.21)	70 (1.03)
Circumcision		
No	4312 (84.47)	
Yes	793 (15.53)	
Fathered a child in the past		
No	5895 (77.79)	
Yes	1683 (22.21)	
Contraception use		
No		2825 (47.46)
Yes		3127 (52.54)
Pregnancy		
Never		4929 (50.34)
History of pregnancy		4863 (49.66)

HIV testing is limited to adult men (aged 15–54 years) and women (aged 15–49 years).

Total sample size based on 17,376 study participants (from years 2004 to 2014). Nearly half (53.3%) entered the study before 2007.

Multilevel Analytical Models to Estimate the Time to HIV Acquisition Risk

The results are presented with respect to social-level (models a–e) and individual-level (model f) determinants, and a combination of the 2 (models g and h).

Social-Level Determinants (Models a–e)

The results of the multilevel analyses relating to social determinants are provided in Table 2 (men; models 1a–1e) and Table 3 (women: models 2a–2e). The results of the null model, containing only the response variable, are indicated in models 1a and 2a in Tables 2 and 3, respectively. The ICC from models 1a and 2a indicate that approximately 7% and 13% of the variation in HIV acquisition risk among men and women can be attributed to differences between neighborhoods, respectively.

The results from models 1b and 2b, which incorporated only the main social explanatory variable, indicated that a higher neighborhood migration intensity (ie, higher proportion of migration experienced in neighborhoods) was

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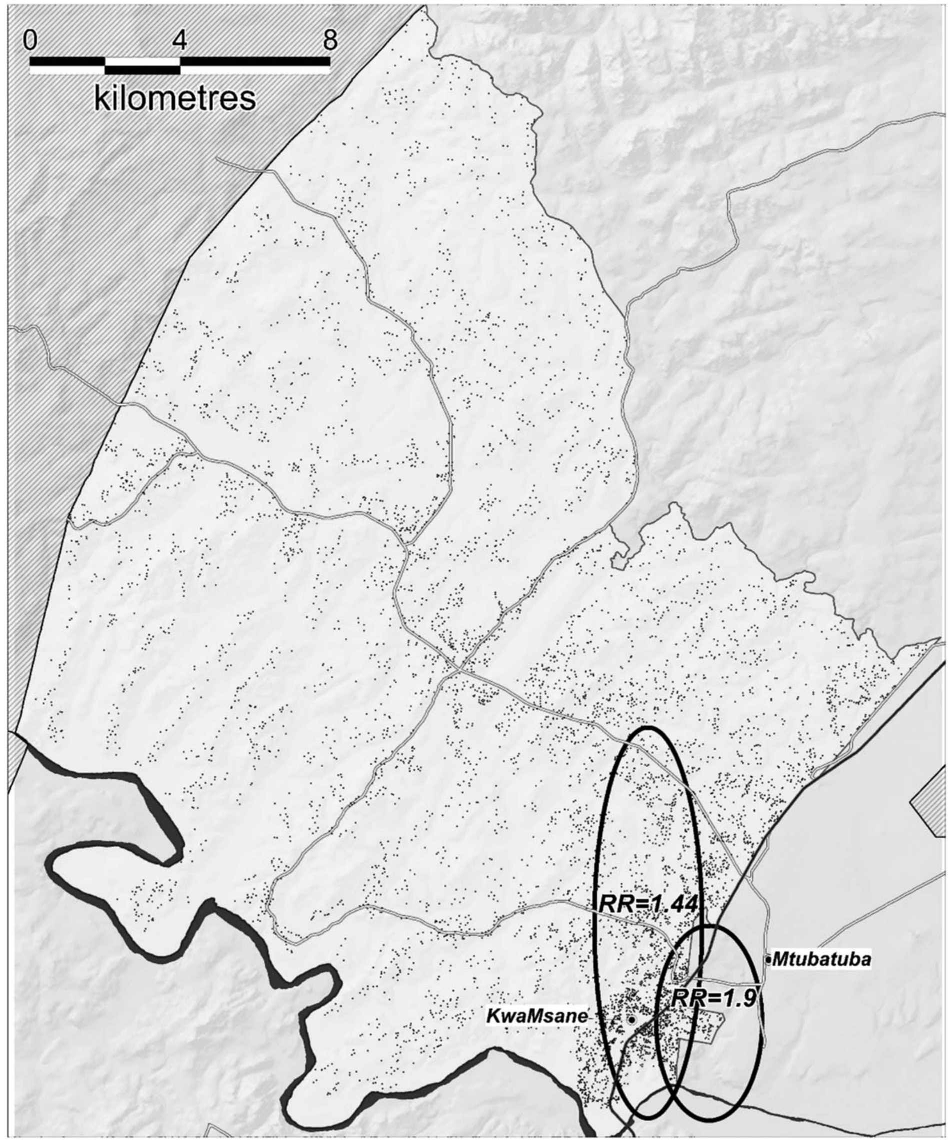

FIGURE 1. The study area with high-risk, overlapping elliptical clusters (Relative Risk = 1.44 and 1.9; ($P \leq 0.011$)) identified by the Kulldorff statistic in peri-urban communities near the National Road (Tanser et al 2011).[37] The National Road continues along the eastern boundary of the surveillance area towards Mozambique. All homesteads (black dots) are superimposed.

significantly associated with a far greater likelihood of HIV acquisition among women (hazard ratio [HR] = 1.005, 95% confidence interval [CI], >1.00 to 1.01), but not men. The result of model 1c–1e and 2c–2e, which incorporated neighborhood civic participation, community HIV prevalence, and linkages to hotspots separately, indicated that residing in areas with excess incidence of HIV infection had a higher likelihood of HIV acquisition among both men (HR = 1.47, 95% CI: 1.22 to 1.76) and women (HR = 1.39, 95% CI: 1.24 to 1.56), but with significant effect being detected regarding civic participation. The community HIV prevalence was positively associated with a higher likelihood of HIV acquisition among men (HR = 1.03, 95% CI: 1.02 to 1.05) and women (HR = 1.03, 95% CI: 1.02 to 1.03).

Individual-Level Determinants (Model f)

Adjusted multilevel analytical models (models 1f and 2f), incorporating only individual-level explanatory variables (model 1f) indicated that that a history of circumcision (adjusted HR [aHR] = 0.18, 95% CI: 0.07 to 0.46), and fatherhood (aHR = 0.60, 95% CI: 0.41 to 0.88) was associated with a lower likelihood of HIV acquisition among men. The results from model 2f indicated that older age (aHR = 0.21, 95% CI: 0.12 to 0.37), history of marriage (aHR = 0.23, 95% CI: 0.15 to 0.37), pregnancy (aHR = 0.56, 95% CI: 0.42 to 0.75), use of contraception (aHR = 0.77, 95% CI: 0.61 to 0.99), and sexual debut only after the age of 17 (aHR = 0.59, 95% CI: 0.49 to 0.72) was associated with a significantly lower likelihood of HIV acquisition among women.

Combining Social- and Individual-Level Determinants (Model g and h)

The adjusted multilevel analytical models (models 1g and 2g) incorporated all the social and individual-level determinants (but without interaction terms). The results from

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TABLE 2. Hazard Ratio Based on Multilevel Mixed-Effects Survival Models for Male ACDIS Cohort

	Category of Interest	Model 1a (Null) HR	SE	95% CI	Model 1b HR	SE	95% CI	Model 1c HR	SE	95% CI	Model 1d HR	SE	95% CI
Social determinants													
Neighborhood migration intensity, %					1.00	<0.01	1.00 to 1.01						
Neighborhood civic participation, %								1.00	<0.01	1.00 to 1.00			
Community HIV prevalence, %											1.03	0.01	1.02 to 1.05
Exposure to coldspot community	Hotspot community												
Interaction term 1	Hotspot × migration intensity, %												
Interaction term 2	Hotspot × civic participation, %												
Interaction term 3	Hotspot × community HIV, %												
Individual determinants													
Age category: [15–19 yr]	20–39												
	40+												
Ever married: [No]	Yes												
Migration %													
Fathered a child: [No]	Yes												
Number of concurrent relationships: [0–2]	3 or more												
Circumcision: [No]	Yes												
Sexual debut: [Before 17 yr]	On/after 17												
Tuberculosis history: [No]	Yes												
Household income: [bottom 20%]	Lower 20%												
	Middle 20%												
	Higher 20%												
	Top 20%												
Model													
Variance component, σ2 (SE)		0.42 (0.20)			0.41 (0.20)			0.45 (0.20)			0.35 (0.19)		
Intraclass correlation for community		12.63%			12.54%			13.54%			10.75%		
AIC		3995.63			3996.49			3432.11			3967.49		

	Model 1e HR	SE	95% CI	Model 1f HR*	aHR	SE	95% CI	Model 1g aHR	SE	95% CI	Model 1h (Full/Ideal Model) aHR	SE	95% CI
Social determinants													
Neighborhood migration intensity, %								0.99	0.01	0.97 to 1.01	0.98	0.01	0.95 to 1.00
Neighborhood civic participation, %								1.00	<0.01	1.00 to 1.01	1.00	<0.01	1.00 to 1.01
Community HIV prevalence, %								1.07	0.02	1.03 to 1.12	1.06	0.03	1.01 to 1.11
Exposure to coldspot community	1.47	0.14	1.22 to 1.76					0.69	0.21	0.38 to 1.24	0.15	0.27	<0.01 to 5.16
Interaction term 1											1.05	0.02	1.01 to 1.09
Interaction term 2											0.99	<0.01	0.98 to 1.00
Interaction term 3											1.05	0.05	0.95 to 1.17
Individual determinants													
Age category: [15–19 yr]				1.50	1.46	0.41	0.83 to 2.54	1.08	0.33	0.60 to 1.97	1.09	0.33	0.60 to 1.98
				0.57	0.57	0.33	0.18 to 1.77	0.25	0.18	0.06 to 1.04	0.24	0.18	0.06 to 1.00
Ever married: [No]				0.39	0.39	0.30	0.09 to 1.77	0.56	0.45	0.12 to 2.70	0.57	0.45	0.12 to 2.70
Migration %				1.00	1.00	0.01	0.99 to 1.01	1.01	0.01	0.99 to 1.02	1.01	0.01	0.99 to 1.02
Fathered a child: [No]				0.84	0.60	0.12	0.41 to 0.88	0.72	0.15	0.47 to 1.09	0.71	0.15	0.47 to 1.09
Number of concurrent relationships: [0–2]				1.01	1.09	0.33	0.60 to 1.97	0.89	0.31	0.45 to 1.77	0.91	0.32	0.46 to 1.80
Circumcision: [No]				0.32	0.18	0.09	0.07 to 0.46	0.20	0.09	0.08 to 0.51	0.18	0.09	0.07 to 0.46

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TABLE 2. (*Continued*) Hazard Ratio Based on Multilevel Mixed-Effects Survival Models for Male ACDIS Cohort

	Model 1e			Model 1f				Model 1g			Model 1h (Full/Ideal Model)		
	HR	SE	95% CI	HR*	aHR	SE	95% CI	aHR	SE	95% CI	aHR	SE	95% CI
Sexual debut: [Before 17 yr]				1.02	1.15	0.22	0.80 to 1.67	1.18	0.25	0.79 to 1.78	1.23	0.26	0.82 to 1.85
Tuberculosis history: [No]				0.89	0.92	0.49	0.33 to 2.59	0.98	0.54	0.33 to 2.86	1.01	0.55	0.34 to 2.95
Household income: [bottom 20%]				0.80	0.83	0.26	0.44 to 1.54	0.88	0.32	0.43 to 1.78	0.82	0.30	0.41 to 1.66
				1.07	1.26	0.36	0.72 to 2.21	1.10	0.37	0.57 to 2.11	1.03	0.34	0.54 to 1.98
				0.93	1.00	0.30	0.56 to 1.79	0.98	0.33	0.51 to 1.88	0.95	0.32	0.50 to 1.84
				0.83	0.70	0.23	0.37 to 1.32	0.70	0.25	0.35 to 1.42	0.68	0.24	0.33 to 1.38
Model													
Variance component, σ2 (SE)	0.37 (0.19)			0.22 (0.61)				0.47 (0.71)			0.39 (0.78)		
Intraclass correlation for community	11.37%			6.74%				14.17%			11.99%		
AIC	3981.41			879.35				745.98			742.96		

Reference category in bracket.
Variance, ICC, and AIC for model 1f column are for the aHR model.
*iHR for model 1f based on bivariate analyses. Older age, being married, and history of circumcision and fatherhood were significantly associated with lower risk of HIV acquisition.

model 1g and 2g indicated that community HIV prevalence was associated with a greater likelihood of HIV acquisition in men (aHR = 1.07, 95% CI: 1.03 to 1.12) and women (aHR = 1.03, 95% CI: 1.02 to 1.05), whereas neighborhood migration intensity (ie, proportion of migration experienced in neighborhoods) was only significantly related to the outcome among women (aHR = 1.01, 95% CI: 1.01 to 1.02). In terms of social-level covariates pertaining to women (model 2g), those who were significant in model 2f remained significant. For men (model 1g), a history of circumcision was the only covariate that remained significant (aHR = 0.20, 95% CI: 0.08 to 0.51) from model 1f.

The full models (models 1h and 2h) incorporated social and individual-level determinants variables, including the 3 interaction terms, to establish if the effect of social determinates on HIV acquisition risk varied by linkage to a hotspot site. The analysis of the interaction terms from model 1h indicated that increased neighborhood migration intensity (aHR = 1.05, 95% CI: 1.01 to 1.09) in the hotspot communities had a higher likelihood of HIV acquisition in men. Similar to these findings (model 1g), a history of circumcision (aHR = 0.16, 95% CI: 0.07 to 0.41) was the only individual-level explanatory variables found to be a significant predictor of HIV acquisition. The ICC of the full model indicated that approximately 12% of the variation in HIV acquisition among men can be attributed to differences between neighborhoods, with the AIC being the lowest in model 1g. The LR test indicated that adding interaction terms (to model 1g) resulted in significant improvements in the model fit (LR $\chi^2 = 9.0$, df = 3, $P = 0.03$).

The analysis of the (full) model 2h in Table 3 indicated that neither of the 3 interaction terms was significant in the samples of women. The covariates mentioned as being significant from the previous model (model 2g) remained mostly relevant: neighborhood migration intensity (aHR = 1.02, 95% CI: 1.01 to 1.03), community HIV prevalence (aHR = 1.04, 95% CI: 1.01 to 1.06), older age (aHR = 0.22, 95% CI: 0.12 to 0.42), history of marriage (aHR = 0.15, 95% CI: 0.08 to 0.28), history of pregnancy (aHR = 0.62, 95% CI: 0.44 to 0.87), use of contraception (aHR = 0.69, 95% CI: 0.52 to 0.93), and sexual debut only after the age of 17 (aHR = 0.58, 95% CI: 0.46 to 0.73) regarding significantly lower likelihood of HIV acquisition among women. The ICC of the full model indicated that approximately 12% of the variation in HIV acquisition risk among women could be attributed to differences between neighborhoods. The AIC was lowest in model 2g (full model without interaction terms) and not in model 2h, and the LR test indicated that adding the 2 interaction terms (to model 2g) did not result in significant improvements in the model fit (LR $\chi^2 = 5.51$, df = 3, $P = 0.14$).

DISCUSSION

Based on the social disorganization theory, the study provided clear evidence that the likelihood of HIV acquisition is influenced by gender, behavior, and social context. For men, the likelihood of being HIV positive was significantly greater in hotspot communities that had higher neighborhood migration intensity. For women, higher neighborhood migration intensity led to a significantly greater risk of HIV acquisition irrespective of whether they lived in hotspot/coldspot communities. Social determinants, such as community HIV prevalence, were also identified as a significant risk predictor of disease acquisition in both sexes, irrespective of residing in hotspot/coldspot communities. These results, in summary, demonstrate that certain community traits (ie, community disease prevalence) for HIV acquisition were robustly evident in men and women, hotspot/coldspots alike. The effect of other determinants (ie, neighborhood migration intensity) were more pronounced and localized in hotspot communities over and above individual mobility levels, particularly among men, attesting to the complexity in social and geographic context of the disease.

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TABLE 3. Hazard Ratio Based on Multilevel Mixed-Effects Survival Models for Female ACDIS Cohort

		Model 2a (Null)			Model 2b			Model 2c			Model 2d		
	Category of Interest	HR	SE	95% CI	HR	SE	95% CI	HR	SE	95% CI	aHR	SE	95% CI
Social determinants													
Neighborhood migration intensity, %					1.01	<0.01	>1.00 to 1.01						
Neighborhood civic participation, %								<1.00	<0.01	0.99 to 1.00			
Community HIV prevalence											1.03	<0.01	1.02 to 1.03
Exposure to nonhotspot community	Hotspot community												
Interaction term 1	Hotspot × migration intensity, %												
Interaction term 2	Hotspot × civic participation, %												
Interaction term 3	Hotspot × community HIV, %												
Individual determinants													
Age category: [15–19 yrs]	20–39												
	40+												
Migration %													
Ever married: [No]	Yes												
Ever pregnant: [No]	Yes												
Number of concurrent relationship: [0 or 1]	2 or more												
Contraception: [No]	Yes												
Sexual debut: [Before 17 yrs]	On/after 17 yrs												
TB history: [No]	Yes												
Household income: [bottom 20%]	Lower 20%												
	Middle 20%												
	Higher 20%												
	Top 20%												
Model													
Variance component, σ2 (SE)		0.25 (0.08)			0.24 (0.08)			0.30 (0.09)			0.21 (0.08)		
Intraclass correlation for community		7.46%			7.34%			9.13%			6.39%		
AIC		10,418.39			10,416.29			8402.96			10,361.36		

	Model 2e			Model 2f				Model 2g (Ideal Model)			Model 2h (Full Model)		
	HR	SE	95% CI	HR*	aHR	SE	95% CI	aHR	SE	95% CI	aHR	SE	95% CI
Social determinants													
Neighborhood migration intensity, %								1.01	0.01	1.00 to 1.02	1.02	0.01	1.00 to 1.03
Neighborhood civic participation, %								1.00	<0.01	0.99 to 1.00	1.00	<0.01	1.00 to 1.00
Community HIV prevalence								1.03	0.01	1.01 to 1.05	1.04	0.01	1.01 to 1.06
Exposure to nonhotspot community	1.39	0.08	1.24 to 1.56					1.01	0.17	0.72 to 1.42	3.28	3.65	0.37 to 29.12
Interaction term 1											0.98	0.01	0.96 to 1.01
Interaction term 2											1.00	<0.01	1.00 to 1.01
Interaction term 3											0.96	0.03	0.90 to 1.03
Individual determinants													
Age category: [15–19 yrs]				0.89	0.85	0.11	0.66 to 1.10	0.81	0.13	0.60 to 1.10	0.81	0.12	0.60 to 1.09
				0.14	0.21	0.06	0.12 to 0.37	0.22	0.07	0.12 to 0.42	0.22	0.07	0.12 to 0.42

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TABLE 3. (*Continued*) Hazard Ratio Based on Multilevel Mixed-Effects Survival Models for Female ACDIS Cohort

	Model 2e			Model 2f				Model 2g (Ideal Model)			Model 2h (Full Model)		
	HR	SE	95% CI	HR*	aHR	SE	95% CI	aHR	SE	95% CI	aHR	SE	95% CI
Migration %				1.00	1.00	<0.01	1.00 to 1.01	1.00	0.01	0.99 to 1.01	1.00	0.01	0.99 to 1.01
Ever married: [No]				0.21	0.23	0.05	0.15 to 0.37	0.14	0.05	0.07 to 0.28	0.15	0.05	0.08 to 0.28
Ever pregnant: [No]				0.43	0.56	0.08	0.42 to 0.75	0.62	0.11	0.44 to 0.86	0.62	0.11	0.44 to 0.87
Number of concurrent relationship: [0 or 1]				0.94	0.67	0.29	0.29 to 1.54	0.64	0.31	0.25 to 1.64	0.66	0.32	0.25 to 1.69
Contraception: [No]				0.71	0.77	0.10	0.61 to 0.99	0.70	0.10	0.53 to 0.94	0.69	0.1	0.52 to 0.93
Sexual debut: [Before 17 yrs]				0.67	0.59	0.06	0.49 to 0.72	0.57	0.07	0.45 to 0.73	0.58	0.07	0.46 to 0.73
TB history: [No]				0.55	0.76	0.26	0.39 to 1.51	0.90	0.36	0.41 to 1.95	0.91	0.36	0.42 to 1.98
Household income: [bottom 20%]				0.99	0.89	0.14	0.66 to 1.20	0.96	0.18	0.67 to 1.39	0.98	0.18	0.68 to 1.41
				0.99	0.98	0.15	0.73 to 1.31	1.15	0.21	0.81 to 1.64	1.18	0.21	0.82 to 1.68
				0.90	0.98	0.15	0.73 to 1.32	1.07	0.20	0.74 to 1.53	1.06	0.2	0.74 to 1.53
				0.75	0.73	0.13	0.52 to 1.04	0.73	0.16	0.48 to 1.11	0.73	0.16	0.48 to 1.12
Model													
Variance component, σ2 (SE)	0.22 (0.08)			0.26 (0.25)				0.36 (0.31)			0.40 (0.32)		
Intraclass correlation for community	6.63%			7.99%				10.93%			12.09%		
AIC	10,388.97			2972.56				2221.26			2221.74		

Reference category in bracket.
Variance, ICC, and AIC for model 2f column are for the aHR model.
*HR for model 1f based on bivariate analyses. Older age, being married, history of pregnancy and contraception, TB history, and highest household income [compared to the lowest group] were significantly associated with lower risk of HIV acquisition.

Our findings are consistent with others who have found neighborhood characteristics to be attributable to HIV risk behavior,[39–42] including a large study of 26 sub-Saharan Africa countries[43] and the United States,[44,45] the research also being guided by social disorganization theory. We hypothesized that social disequilibrium (because of migration patterns) and HIV acquisition risk are linked, given the historical context of South Africa. Migration patterns and residential instability fostered anomie and weakened community standards that are considered important for regulating risk behaviors. Migration in South Africa was historically led by young men seeking employment opportunities. Men were required to live in single-sex hostels that lacked basic services. Most remained in the areas to which they emigrated, leading to conjugal infidelity, parental absenteeism, the erosion of the traditional way of life, and ultimately broken family ties.[46,47] The notion that migration helped fuel the spread of HIV is well established. There is good evidence to demonstrate that migrancy, and the movement/migration patterns of workers contributed to the early phase of the HIV epidemic in South Africa.[15,48–52] Although our study did not include hostels and informal settlements, it points to social disequilibrium challenges associated with migration intensity in certain neighborhoods. Little has changed regarding the living arrangements of migrant workers since the advent of democracy,[53] which may help to explain the lasting ramifications of neighborhood migration on HIV acquisition particularly among men in hotspot communities.

There were several limitations to our study, the first being an assumption that certain social-level determinants did not change over time. Although community HIV prevalence was treated as time covarying in the analysis, other predictors, which include hotspot areas, and neighborhood migration intensity were not considered time variant (partially because of the lack of statistically significant variations over time). We also acknowledge that the civic participation measure is relatively weak in our study. Assumption had to be made that the nature of neighborhood civic participation did not change during the course of the study as the data were available only for the year 2000. Furthermore, information on civic participation was obtained from a key informant at a household level and could not be linked to specific individual. As with any other self-reported data, recall bias is possible, particularly for households with large number of members. Second, our response rate for the questions relating to sexual behavior questions was not as high as expected (eg, response related to concurrent sexual relationship at baseline was less than half), possibly because of the sensitivity of the topic and survey wording, which prevented treating those variable as time-varying covariates in the regression model. We therefore used lifetime history of sexual behavior. Third, the inclusion criteria for the incident cohort study required the target sample population to have HIV testing at least twice between 2004 and 2015, and to be HIV negative in the initial test. It is possible that individuals with extensive migration history are less likely to participate in HIV testing, thus excluding them from our cohort and influencing the generalizability of our findings. Notwithstanding these limitations, the strength of our study includes the use of a large population data set on HIV incidence cohorts that was designed to examine the roles of social context in rural areas. Future studies exploring the mechanism that explain the connection between social contexts (ie, stigma), linkage to care, and HIV acquisition risk are warranted.

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Recognizing the importance of individual-based biomedical approaches in the fight against HIV, disequilibrium arising from dynamics of social structure and other challenges (ie, migration intensity and community HIV prevalence) has a marked effect on HIV risk in this typical rural sub-Saharan African setting. Although there are a number of documented interventions implemented at neighborhood level,[10] targeting residences in areas with high concentration of migrants may hold promise, as demonstrated by randomized trials on the effectiveness of housing project-based HIV prevention efforts.[54,55] As described in our previous reports,[36,56] we reaffirm our support for a scale-up of current intervention, particularly on a "place-based" approach,[57] that targets socially vulnerable communities and neighborhoods to reverse the tide of the rural HIV epidemic in South Africa.

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