Published in final edited form as:

AIDS. 2016 August 24; 30(13): 2099–2105. doi:10.1097/QAD.0000000000001150.

Migration and HIV Infection in Malawi: A Population-Based Longitudinal Study

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Abstract

Objective—To evaluate the assumption that moving heightens HIV infection by examining the time-order between migration and HIV infection, and investigate differences in HIV infection by migration destination and permanence.

Methods—We employ four waves of longitudinal data (2004–2010) for 4,265 men and women from a household-based study in rural Malawi, and a follow-up of migrants (2013). Using these data, we examine HIV status prior to migration. Migrants are disaggregated by destination (rural, town, urban), and duration (return, permanent); all compared to individuals who consistently resided in the rural origin (“non-migrants”).

Results—HIV positive individuals have significantly greater odds of migration than those who are HIV negative (OR 2.75; 95% CI 1.89–4.01). Being HIV positive significantly increases the relative risk that respondent will be a rural-urban migrant (RRR 6.28; 95% CI 1.77–22.26), rural-town migrant (RRR 3.62; 95% CI 1.24–10.54), and a rural-rural migrant (RRR 4.09; 95% CI 1.68–9.97), instead of a non-migrant. Being HIV positive significantly increases the relative risk that a respondent will move and return to the village of origin (RRR 2.58; 95% CI 1.82–3.66), and become a permanent migrant (RRR 3.21; 95% CI 1.77–5.82) instead of not migrating.

Conclusion—HIV-positive status has a profound impact on mobility: HIV infection leads to significantly higher mobility through all forms of migration captured in our study. These findings emphasize that migration is more than just an independent risk factor for HIV infection: greater prevalence of HIV among migrants is partly due to selection of HIV positive individuals into migration.

Keywords

HIV infection; migration; Malawi; sub-Saharan Africa

Introduction

A strong association between HIV infection and migration is well-established. Across sub-Saharan Africa (SSA), China, and South East Asia, migrants have higher HIV prevalence or greater HIV risk behaviors than non-migrants [1–10]. Given this higher HIV prevalence, migrants are typically considered a high HIV risk group [1], and their mobility is often cited as one of the most important factors in the spread of HIV in sub-Saharan Africa and elsewhere [11–13]. This may indeed have been the case during the early days of the epidemic when mobile men, such as long-distance truck drivers, seem to be spreading HIV from low prevalence areas to high prevalence areas [14]. Once HIV became established throughout the general population, however, the direction of causality may have changed. Thus, it is important to examine more closely the pathways of transmission. This task, in turn, has higher data demands than did the earlier work, since migration is becoming more ubiquitous and HIV more diffusely spread in the general population [15–18].

Despite important shifts in the patterns of migration and the epidemiology of HIV, assumptions regarding the underlying mechanisms connecting migration and HIV have persisted. Many continue to argue that risky behavior increases after individuals are released from the relatively more rigid social norms in rural pre-migration settings [19–21]. Other persistent hypotheses stem from enduring assumptions regarding urban settings, a common migration destination; since HIV prevalence is typically higher in urban than in rural areas, migrants would be at greater risk of infection even if their behaviors remained the same [16,22]. A third persistent hypothesis is that migration may also facilitate the acquisition of new partners by the migrants themselves and by the partners they left behind, due to time spent apart [23–24].

The assumption that migration causes HIV infection implies that HIV infection occurs after migration [1,4], but this assumption has seldom been tested because the required longitudinal data with pre- and post-migration HIV status have seldom been available. Cross-sectional data are typically used to identify whether individuals who previously migrated are more likely to be HIV positive than those without a history of migration or mobility. These data, however, cannot tell us which event (migration or infection) preceded the other.

An examination of these important questions of timing has also been hampered by limited measures of migration and mobility [16]. Migration differs by destination and origin (e.g. urban, rural), distance travelled, permanence, duration, and motivation, among other characteristics. Yet researchers have often had to rely upon simple binary measures of migrant/non-migrant status [4,10,19,25–26]. When destination is measured for migrants, the focus of migration research has typically been on rural-to-urban migration [3,12,27] even though in SSA rural-rural migration (often related to marriage or work) is more common [28]. This is important, as a major change in the epidemiology of HIV has been its spread to rural areas in SSA. While rural-to-urban migration may have been critical in early phases of the epidemic to sustain its spread, this is no longer the case [4], and rural-to-rural migration has become a critical pathway through which HIV spreads throughout rural populations. Given the limited knowledge about these types of migration flows, as well as the limitations

of common measures of migration types used in research on this topic, it is not surprising that leading scholars have called for examining migration patterns in greater detail [16].

To address several of these major shortcomings in the existing research that examines the links between migration and HIV infection, we use longitudinal panel data from Malawi to explore the causal pathway between HIV infection and migration. We also employ more detailed measures of migration than has typically been the case in earlier work. Contrary to the predominant assumption in the literature, we examine whether HIV positive individuals are more likely to migrate than those who are HIV negative. We then examine the relationship between HIV infection and migration using more detailed measures of migration; disaggregated by destination (rural-rural, rural-town, rural-urban) and permanence of stay (return/permanent migration).

Methods

Study Design and Data

Our longitudinal panel data enable us to overcome important limitations of previous efforts. We use data from two related sources: the Malawi Longitudinal Study of Families and Health (MLSFH), and the Migration and Health in Malawi (MHM) projects [29,30]. The MLSFH was designed as a couples' survey, targeting a population-based representative sample of approximately 1,500 ever-married women aged 15–49 and 1,000 of their husbands in three rural sites of Malawi, starting in 1998. The first follow-up, in 2001, sought to re-interview all respondents from the first wave, along with any new spouses. The MLSFH returned to re-interview all previous respondents and new spouses in 2004, 2006, 2008 and 2010. Over the course of the MLSFH, two additional samples were added: in 2004 a new sample of approximately 1,500 young adults (15–27) was added; the 2008 wave of the MLSFH interviewed approximately 800 parents of respondents. Comparisons of background characteristics between the MLSFH data and the rural sample of the Malawi DHS found relatively few substantive differences [31–32]. Other MLSFH sample characteristics and analyses of data quality have been previously published [29–33].

MLSFH initiated home-based HIV testing for all respondents in 2004, with follow-up testing in 2006 and 2008 [34]. Respondents were given the opportunity to find out their test results, and the vast majority elected to do so: 68%, 98% and 93% in waves 3–5, respectively, learned their HIV test results.

In all waves of MLSFH, the most common reason for non-interview was migration out of the sample area. The MHM project was designed to trace and re-interview MLSFH migrants [30]. From its initiation, the MHM attempted to trace respondents who had migrated out of the sample after the first survey wave in 1998. To do this, the study team returned to the migrant's previous MLSFH village of residence, where they asked family members or friends where the migrant was currently living. For the majority of migrants, the team collected detailed information on the migrant's current location. The team then traced the migrant to his or her new residence.

The data collected by the MHM permit us to identify migration stream and destination. Rural-rural migrants are those who definitively moved to another rural part of Malawi, at least 20km outside of an MLSFH sample area. Individuals moving to one of Malawi's three regional capitals (Mzuzu in the North, Lilongwe in the Central, Blantyre in the South), and the third largest city (and former capital), Zomba, were considered rural-urban migrants. Finally, rural-town migrants are those who moved to the capital of one of Malawi's 22 districts. The MHM also identified return migrants, who were reported to be permanent migrants in migration tracking but were found in their MLSFH village of previous residence by the MHM in 2013.

Ethical considerations

The data collection and research conducted by MLSFH and MHM was approved by the Institutional Review Boards (IRB) at the University of Pennsylvania, and Tulane School of Public Health and Tropical Medicine, respectively. Both studies were approved in Malawi by the College of Medicine Research Ethics Committee (COMREC) or the National Health Sciences Research Committee (NHSRC).

Analytic methods

We conduct our analysis in three steps. First we examine whether HIV positive individuals are more likely to migrate than those who are HIV negative. To do so, we use the longitudinal MLSFH data from 2004 (the year when HIV testing started for the MLSFH) through 2010. In this analysis we focus on two variables: (1) to establish the time-order between these measures, the dependent variable, migration, is measured from a future wave; (2) HIV infection is measured at a prior wave, i.e., before migration.

Using this approach, we pool the four most recent waves of MLSFH data (from 2004 to 2010), and run random effects logistic regressions in which the dependent variable is future migration (measured as migrant or non-migrant) and the independent variable of primary interest is HIV status before migration. Random effects regression is used to account for correlation in the residual due to multiple observations of the same individual over time. In our first regressions we control for age, sex and a time trend in migration (measured by MLSFH survey interval). We then add two additional variables: (1) previous migration experience, measured as having lived elsewhere for six months or more since the age of 15, and (2) an interaction term for HIV positive status and previous migration history. The second regression permits us to examine whether those who were HIV positive and previously moved are more likely to move again. Results are shown in odds ratios.

The next step is to identify the destination for HIV positive migrants. We use similar approach as above, in which HIV status is measured prior to migration. But instead of using the binary measure of migrant or non-migrant, we divide migration by stream: rural-rural, rural-town, and rural-urban migration (reference category is non-migrants). With this four-category dependent variable, we run random effects multinomial logistic regressions, using the same pooled MLSFH data from 2004–2010. As before, we also control for time trend, age, and sex.

Finally, we examine whether return migrants are also more likely to become HIV positive than those who remain in rural areas of origin. We again use the same lagged-variable regression approach, with HIV status measured before migration, and control for age, a quadratic age measure, sex, and a time trend. The dependent variable for these regressions is a three-category measure of non-migrant (reference category), permanent migrant, and return migrant. Results for the final two sets of regressions are shown in relative risk ratios.

Results

The most recent wave of MLSFH, in 2010, sought to interview 5,914 individuals, of whom 3,701 (62.5%) successfully completed the survey, and 1,096 (18.5%) had moved elsewhere by 2010. In previous MLSFH waves, 8.4% (464) moved by 2008 and 4.4% (217) by 2006. A total of 4,265 respondents have full HIV testing and survey information from at least one MLSFH wave since the start of HIV testing in 2004. HIV prevalence in the most recent wave of testing, 2008, was 9.8% (Table 1).

The 1,096 migrants by 2010 formed the initial target sample for the MHM. As shown in Table 1, the location was unknown for 77 migrants (7.0%), an additional 83 (7.6%) moved internationally, and 39 (3.6%) died. After omitting these, the final target sample was 897. Data collection took place in 2013; the study successfully found and interviewed 723 migrants (80.6%), of whom 94.1% (680) were tested for HIV; the final response rate is therefore 62.5% (680/1096). Nearly one-third (31.0%) were return migrants. Most moved to other rural areas (67.9%), 170 (23.5%) moved to towns, and 62 (8.6%) moved to one of Malawi's four largest cities. HIV prevalence among migrants was 14.3% in 2013. The total sample size used in our regression analysis is 4,265, which includes all MLSFH men and women who were interviewed and tested for HIV at least once between 2004 and 2008 by the MLSFH, among whom a total of 897 eventually moved (and had available traceable information) by 2010 and formed the final target sample for the MHM study (i.e., a total of 897 migrants and 3368 non-migrants by 2010).

HIV positive individuals selected into migration

Our first set of results show that HIV positive individuals are significantly more likely to migrate than those who are HIV negative. As shown in Table 2, model 1, HIV positive individuals had 2.75 times greater odds of migrating by the next MLSFH wave than those who were HIV negative (OR 2.75; 95% CI 1.89–4.01). The relationship between HIV positive status and migration persists even after controlling for previous migration history: results for model 2 show that, although those who migrated before have greater odds of moving again, individuals who moved before and are HIV positive are not significantly more likely to migrate. We also find a non-linear relationship between age and future migration, in which the likelihood of migration first decreases for young and then increases at older ages.

Migration of HIV positive by destination

Table 3 shows results for multinomial random effects regression, in which the dependent variable is categorized by migration destination (rural, town, urban). Our results compare these migration destinations with the non-migrants. Results show strong associations

between HIV positive status and all migration destinations; those who are HIV positive are more likely to move to another rural area, a town, and a city (compared to not moving). The relative risk ratio (RRR) that an HIV positive individual will be a rural-rural migrant rather than a non-migrant is more than 4 times greater than it is for an HIV negative respondent (RRR 4.09; 95% CI 1.68–9.97). Similarly, being HIV positive significantly increases the relative risk that respondent will be a rural-town migrant (RRR 3.62; 95% CI 1.24–10.54) and a rural-urban migrant (RRR 6.28; 95% CI 1.77–22.26) instead of non-migrant. Regressions comparing HIV infection across migration destination did not show statistically significant differences (results not shown). Taken together, therefore the results in Table 3 indicate that a HIV-positive status raises the odds of migrating to *all* the different destinations---rural areas, towns and cities---rather than increasing only the odds of one specific migration flow (such as rural-to-urban). We also find the same convex non-linear relationship between age and all three migration destinations. As indicated by the measures of MLSFH wave, the likelihood of migration increases over time for all destinations.

Migration of HIV positive by permanent or return migration

An examination of migration by permanence shows that HIV positive individuals are more likely to be both return migrants and permanent migrants than non-migrants. Table 4 shows results of multinomial random effects regressions, in which the RRR that an HIV positive individual will be a permanent migrant rather than a non-migrant is more than two times greater than it is for a HIV negative respondent (RRR 2.58; 95% CI 1.67–3.37); being HIV positive significantly increases the relative risk that a respondent will move and return to the MLSFH village of origin instead of not moving (RRR 3.21; 95% CI 1.59–5.18). Similar to the above finding, therefore, Table 4 suggests that a HIV-positive status increases the odds of *both* permanent and temporary migration, rather than merely one type of migration. For other measures in these regressions, we again find the same convex non-linear relationship between age and all three migration destinations. The likelihood of return migration increases over time (RRR 1.71, 95% CI 1.50–1.95). We also find differences in migration permanence by gender, in which women are less likely to be both return and permanent migrants than men.

Discussion

We find that migration is not simply an independent risk factor for HIV: there are significant differences in HIV status between non-migrants and migrants *prior to* migration. HIV positive individuals are more likely to leave their village than those who are HIV negative. We also find distinct patterns by destination and permanence: HIV positive individuals are more likely to move to both rural areas and cities than they are to stay in rural areas of origin, and the HIV positive are more likely to move permanently and cyclically than to consistently reside at their rural homes. Hence, geographic mobility and migration per se, rather than one specific type of migration flow (e.g., rural-to-urban or permanent migration) are elevated subsequent to becoming infected with HIV in our rural Malawi study population, suggesting that migration from rural areas contributes both to the rural-to-rural spread of HIV and the higher HIV prevalence that is found in peri-urban and urban areas.

The goal of this study is not to refute the possibility that migration can cause HIV infection, as this may have been the predominant pattern early in the epidemic and may continue to be important in some settings. Instead, we seek to demonstrate the importance of a longitudinal approach to studying the relationship between HIV infection and migration, and the value of distinguishing between different types of migrants. With cross-sectional post-migration data only, one might mistakenly conclude that the differences in HIV infection between migrants and non-migrants were primarily due to migration instead of differences that existed prior to migration. Our results based upon our longitudinal data support the assertion that higher HIV prevalence among migrants is driven at least in part by their HIV status prior to migration. Therefore, higher HIV prevalence among migrants is likely explained by two pathways: greater likelihood of HIV positive individuals to migrate, and the greater likelihood of individuals who move to become HIV infected. Past literature has primarily focused on the latter group, under the assumption that individuals typically become HIV positive after migration, rather than before.

We also demonstrate the leverage that more detailed information on migrant destination and permanence can provide in studies of migrant health. Not only are HIV positive individuals more likely to move to urban areas, they are also more likely to move to other rural areas. Moreover, they are more likely to return to the village in which they were first interviewed. The analysis of HIV infection and migration destination also suggests that greater HIV prevalence among migrants in cities may not be due to changes in risk behavior or exposure, since many are HIV positive before moving. These patterns of mobility are likely to be important for informing adherence to ART.

It is beyond the scope of this research to identify why HIV positive individuals are more likely to migrate. Previous studies suggest that the higher HIV prevalence among migrants before moving is due to HIV positive individuals who disproportionately move after marital dissolution [18,28]. Since migration and marriage are closely linked in Malawi [35], this relationship may not hold in settings with different patterns. The link between marriage, HIV infection and migration is supported by the information on reason for migration from the MHM study, in which marriage-related reasons made up a substantial percentage: 38.5% of all migrants moved to start a new marriage or as a result of marital dissolution (24.8% of men and 48.5% of women) (see [34] for a full tabulation and more details). It is also possible that the greater rural-urban migration among HIV positive could be motivated by better access to antiretroviral treatment (ARTs) in urban areas [18]. ART access may also explain the greater HIV prevalence among return migrants, who go into the city for treatment and later return: with successful treatment, they remain in the numerator. In addition to better ART access, HIV positive individuals could seek anonymity in urban areas, and freedom from scrutiny about HIV positive status that characterizes rural Malawi [36]. However, our findings clearly show that it is not only such rural-to-urban migration that is elevated among HIV-positive individuals; it is also rural-to-rural and rural-to-town migration, indicating that better health infrastructure and the anonymity of urban areas are not the only aspects driving the migration decisions of HIV-positive individuals.

Despite our more robust measures of migration, some potentially-important aspects of the migration process are not included here. We cannot fully capture migration streams, since

our population does not include migrants originating in urban areas. We also acknowledge that other features of migration not included here may be importantly related to the relationship with HIV infection (duration at destination, distance travelled, reason for migration); these should be the topic of future research.

Our results have important implications for HIV/AIDS research and prevention programs in sub-Saharan Africa. Recent modeling studies have shown that the epidemic can continue to be fueled by circular migration if migrants engage in high risk behavior at both origin and destination [22] and when HIV positive individuals marry someone who is HIV negative [37]; thus, change in marriage and sexual behavior after migration may affect the future course of the epidemic in SSA. While some have called for targeting migrants in HIV-prevention campaigns, our results suggest that it may be too late to prevent HIV infection if many migrants are already HIV positive. Instead of identifying migrants as a population at greater risk of becoming HIV positive, programs may instead seek to inform migrants of locations to access HIV antiretroviral therapy and other resources to support their HIV positive status. In addition, our results suggest that, although migrants to urban areas have been the predominant focus of the literature, it is not only rural-to-urban migrants who have higher HIV prevalence, but rural migrants to other destinations as well.

Acknowledgments

The authors thank Invest in Knowledge Initiative, which collected data for the MHM and MLSFH, as well as two reviewers, whose helpful comments improved this research. This research was funded by National Institute of Child Health and Development (NICHD) [MHM grant #R21HD071471-01], [MLSFH grants# R03 HD05 8976, R21 HD050652, R01 HD044228, R01 HD053781, R24 HD-044964]. All authors contributed to the study design and data collection. PA developed the research question, conducted the statistical analysis, and wrote the first draft of the paper. All authors provided comments and edits on the manuscript at each stage.

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MLSFH and MHM Study Characteristics, 2004–2013

Table 1

	MLSFH Survey Wave				MHM Study	
	2004	2006	2008	2010	2010	2013
Target sample size	4415	4950	5492	5914	897	897
Interviewed	3261	3431	3895	3701	723	723
Migrated since previous wave	----	217	247	632	----	----
Migrants eligible for MHM study	----	162	199	536	----	----
With complete survey and HIV testing information	2877	2869	3182	3694	680	680
Mean age (SD)	33.7 (14.1)	35.1 (13.6)	41.1 (17.0)	42.2 (16.8)	39.3 (14.7)	39.3 (14.7)
Percentage female	54.6%	54.9%	58.5%	58.8%	67.2%	67.2%
Percentage HIV positive	6.2%	8.5%	9.8%	----	14.3%	14.3%
Return migrant	----	----	----	----	31.0%	31.0%
Rural-rural migrant	----	----	----	----	67.9%	67.9%
Rural-town migrant	----	----	----	----	23.5%	23.5%
Rural-urban migrant	----	----	----	----	8.6%	8.6%

Abbreviations: Malawi Longitudinal Study of Families and Health (MLSFH), Migration and Health in Malawi Project (MHM). Notes: MLSFH respondents migrating by 2004 were not included in the study since they had not previously been tested for HIV. MLSFH did not test respondents for HIV in 2010. Eligible migrants include those migrating within Malawi, still living, and with information about their current location. The initial target sample size for MHM study was 1,096 migrants, of whom the location was unknown for 77 (7.0%), 83 (7.6%) moved internationally, and 39 (3.6%) died. The final target sample is therefore 897; 723 were interviewed (80.6%), and 680 (75.8%) were interviewed and tested for HIV. Absolute numbers of HIV positive are 177 (2004), 245 (2006), 311 (2008) and 97 (2013).

Table 2

Odds Ratios for Analysis of Selection of HIV Positive into Migration, MLSFH 2004–2010 (n=4265)

	Model 1			Model 2		
	Unadjusted Odds Ratios	95% CI	Adjusted Odds Ratios	95% CI	Adjusted Odds Ratios	95% CI
HIV positive	2.36	(1.61–3.45)	2.75	(1.89–4.01)	2.71	(1.62–4.54)
Age	0.96	(0.95–0.97)	0.89	(0.86–0.91)	0.88	(0.85–0.91)
Age ²	1.00	(1.00–1.00)	1.00	(1.00–1.00)	1.00	(1.00–1.00)
MLSFH survey wave	0.03	(0.98–1.08)	1.06	(1.00–1.13)	1.06	(1.00–1.13)
Female	0.92	(0.77–1.11)	1.02	(0.83–1.25)	1.05	(0.85–1.30)
Previous migration	1.26	(1.06–1.50)	----	----	1.46	(1.19–1.80)
Inter: previous migration*HIV positive	----	----	----	----	0.94	(0.46–1.90)

Abbreviations: Malawi Longitudinal Study of Families and Health (MLSFH). Notes: Tests for the relationship between age and migration revealed that a non-linear relationship was the most accurate representation; random effects logistic regressions were used for the multivariate analysis shown here; model 2 includes measures of previous migration and an interaction between previous migration and HIV status, the purpose of which is to determine whether HIV positive individuals may have become infected in previous migration episodes. The total sample size used in regression analysis is 4265, which includes all MLSFH men and women who were interviewed and tested for HIV at least once between 2004 and 2008 by the MLSFH, among whom a total of 897 eventually moved by 2010 and formed the final target sample for the MHM study (i.e., a total of 897 migrants and 3368 non-migrants by 2010).

Table 3

Relative Risk Ratios (RRR) for Analysis of Selection of HIV Positive into Migration by Migration Destination, MLSFH 2004–2010 (n=4265)

Reference group: non-migrants	Unadjusted relative risk ratios		Adjusted relative risk ratios	
	RRR	95% CI	RRR	95% CI
Rural-rural migrants				
HIV positive	2.41	(1.50–3.89)	4.09	(1.68–9.97)
Age	0.98	(0.98–0.99)	0.85	(0.79–0.91)
Age ²	1.00	(1.00–1.00)	1.00	(1.00–1.00)
MLSFH survey wave	1.84	(1.64–2.08)	2.21	(1.81–2.70)
Female	0.84	(0.66–1.06)	0.65	(0.43–1.00)
Rural-town migrants				
HIV positive	2.03	(0.98–4.20)	3.62	(1.24–10.54)
Age	0.97	(0.96–0.98)	0.83	(0.77–0.91)
Age ²	1.00	(1.00–1.00)	1.00	(1.00–1.00)
MLSFH survey wave	1.56	(1.36–1.79)	1.80	(1.44–2.24)
Female	0.92	(0.66–1.29)	0.64	(0.38–1.08)
Rural-urban migrants				
HIV positive	2.48	(0.93–6.62)	6.28	(1.77–22.26)
Age	0.93	(0.91–0.95)	0.75	(0.66–0.86)
Age ²	1.00	(1.00–1.00)	1.00	(1.00–1.00)
MLSFH survey wave	1.54	(1.30–1.83)	1.94	(1.48–2.54)
Female	1.25	(0.77–2.04)	1.07	(0.52–2.21)

Abbreviations: Malawi Longitudinal Study of Families and Health (MLSFH). Notes: Tests for the relationship between age and migration revealed that a non-linear relationship was the most accurate representation; random effects multinomial logistic regressions were used for the multivariate analysis shown here. The total sample size used in regression analysis is 4265, which includes all MLSFH men and women who were interviewed and tested for HIV at least once between 2004 and 2008 by the MLSFH, among whom a total of 897 eventually moved by 2010 and formed the final target sample for the MHM study (i.e., a total of 897 migrants and 3368 non-migrants by 2010).

Table 4

Relative Risk Ratios (RRR) for Selection of HIV Positive into Migration by Return or Permanent Migration, MLSFH 2004–2010 (n=4265)

Reference group: non-migrants	Unadjusted relative risk ratios		Adjusted relative risk ratios	
	RRR	95% CI	RRR	95% CI
Permanent migration				
HIV positive	2.21	(1.58–3.09)	2.58	(1.82–3.66)
Age	0.97	(0.96–0.97)	0.90	(0.88–0.93)
Age ²	0.99	(0.99–0.99)	1.00	(1.00–1.00)
MLSFH survey wave	1.04	(0.99–1.09)	1.06	(1.00–1.12)
Female	0.83	(0.71–0.97)	0.80	(0.66–0.97)
Return migration				
HIV positive	2.94	(1.67–5.15)	3.21	(1.77–5.82)
Age	0.99	(0.98–1.00)	0.91	(0.86–0.95)
Age ²	1.00	(0.99–1.00)	1.00	(0.99–1.00)
MLSFH survey wave	1.59	(1.43–1.76)	1.71	(1.50–1.95)
Female	0.64	(0.47–0.85)	0.53	(0.37–0.76)

Abbreviations: Malawi Longitudinal Study of Families and Health (MLSFH). Notes: Tests for the relationship between age and migration revealed that a non-linear relationship was the most accurate representation; random effects multinomial logistic regressions were used for the multivariate analysis shown here. The total sample size used in regression analysis is 4265, which includes all MLSFH men and women who were interviewed and tested for HIV at least once between 2004 and 2008 by the MLSFH, among whom a total of 897 eventually moved by 2010 and formed the final target sample for the MHM study (i.e., a total of 897 migrants and 3368 non-migrants by 2010).