PAA 2025. Due 9/29.

Submit to: 1212 Flash: Methodological Innovations in Migration Research

603 Migration and Consequences within, between and from Low- and Middle-Income Countries. Claudia Masferrer El Colegio de México

IUSSP 2025 Due 9/15.

Submit to: 41. APPLYING NEW DATA AND METHODS TO INTERNATIONAL MIGRATION IN LOW- AND MIDDLE-INCOME COUNTRIES.

Organiser: Victoria Prieto Rosas, Universidad de la República, Uruguay

KEYWORDS for IUSSP submission. International migration, networks, survey research, Africa

Innovations in multi-sited approaches to sampling international migrants: A feasibility and evaluation study

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Short Abstract

Multi-sited, longitudinal sampling designs of international migration that cross international boundaries to link migrants at origin and destination (or vice versa) and follow migrants over time have aided our understanding of migration processes. But they have also highlighted considerable challenges of establishing linked origin-destination samples for achieving representation of origin and destination communities, accounting for the selection of who migrates through appropriate comparisons across groups, recruiting meaningful samples of sufficient size and following movers and stayers over time. Here we evaluate an innovative multi-sited, multi-method sampling design of migration from Ghana to the US, which aims to refine previous multi-sited approaches. Our design establishes origin-destination linked samples of households using conventional as well as innovative network sampling designs that capitalize on peer referral to achieve coverage and representation of the Ghanaian immigrant population in the US, includes migrants linked by ties to origin as well as those without ties to origin but linked by a network of ties in the US. We assess the feasibility of obtaining cross-border referrals and evaluate the sampling strategy to achieve population representation through multiple tests grounded in data collected among four distinct samples of origin and destination households successively recruited in Ghana and the US.

Long Abstract

Introduction

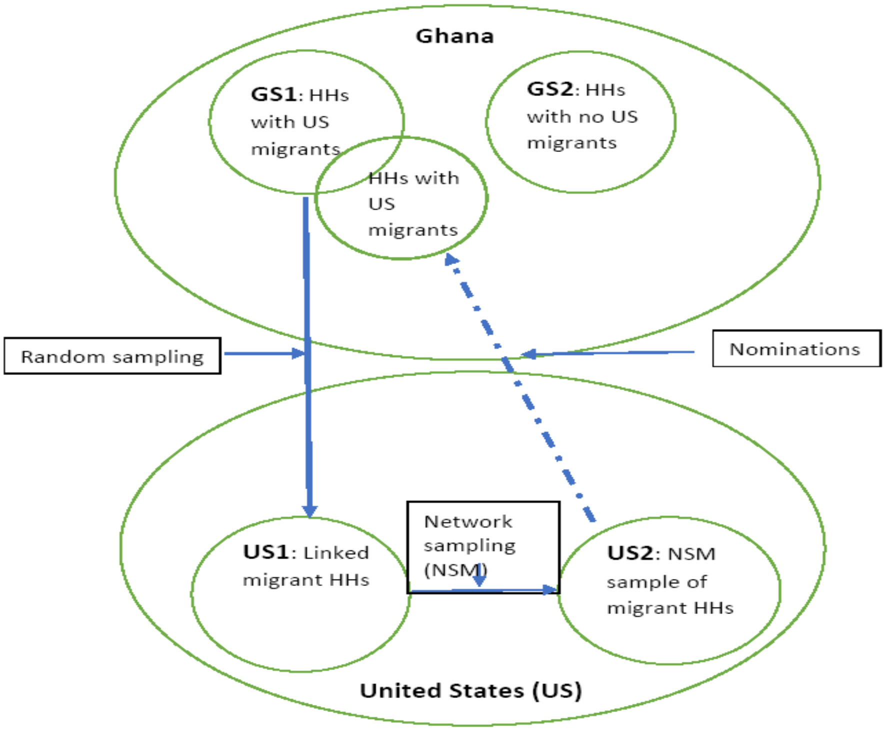
Multi-sited, longitudinal sampling designs of international migration that cross international boundaries to link migrants at origin and destination (or vice versa) and follow migrants over time can facilitate the understanding of migration processes such as the decision to migrate or the long term dynamics of social and economic incorporation, immigrant acculturation or health (Beauchemin 2014). Several large community-based demographic studies of international migration—such as the Mexican Migration Project (MMP) (Fussel and Massey 2004; Massey et al. 1987), the Latin America Migration Project (LAMP) (Donato et al. 2010) and the Migration between Africa and Europe (MAFE) (Beauchemin 2015; 2018)—have contributed substantially to the recruitment of origin samples linked to destination communities. Another major migration survey, the Mexican Family Life Survey (MxFLS), has demonstrated the benefit of following migrants across borders over time for measuring migrant selectivity (Genoni et al. 2017). But these studies have also highlighted considerable challenges of establishing linked origin-destination samples for achieving representation of origin and destination communities, accounting for the selection of who migrates through appropriate comparisons across groups, recruiting meaningful samples of sufficient size and following movers and stayers over time. For example, samples of migrants that rely solely on referrals from household (HH) members in origin countries yield samples that over-represent migrants with strong ties to kin in origin and miss HHs with weak ties or migrants whose entire HHs moved (Donato et al. 2010). Also, previous studies often did not integrate randomized protocols for recruiting migrant samples in destination (MMP, LAMP, MAFE), reducing their population representation potential. When they did, the size of the US sample was small due to the rarity of the migration event (MxFLS). Previous studies also focused on migration from LAC to the US (MMP, MxFLS, LAMP) or from SSA to Europe (MAFE) with different selection processes than to the US, given different legal regimes and immigration policies. Innovative approaches that build on and refine prior methods for studying migration to the US are needed (Massey and Centeno 2000; Donato et al. 2010; Beauchemin 2014, Billsborrow 2016). This is important because migration is of substantial public health and sociological interest due to its strong relation to the new dynamics of population diversity, issues of health disparities and the heterogeneity of immigrants' incorporation pathways, and the importance of social connections at origin and destination in shaping these pathways.

In this paper we evaluate an innovative multi-sited, multi-method sampling design implemented in Ghana and the US on a pilot basis, in preparation for a larger multi-sited, longitudinal data collection study which will aim to examine the countervailing forces promoting and undermining African immigrant health over time. Our design aims to refine previous multi-sited approaches to recruit binational samples of migrants.

Methods

The sampling design, described in Figure 1, links Ghana's sending areas of international migrants to destinations in the US. Ghana is the third largest sending country of African migrants to the US, where immigration from the African continent is growing rapidly (Capps, McCabe and Fix, 2012; Anderson 2015; Elo et al. 2015; Tamir and Anderson 2022). The design consists of two samples of HHs in Ghana's greater Accra region, one of Ghana's two top sending regions of international migrants to the US: HHs with migrants to the US (Ghana Sample 1 – GS1) and HHs without migrants to the US (GS2), where migrants are defined as former household members in the US for six months or more. These two samples were drawn with conventional probability sampling using the Ghanaian 2021 Census sampling frame of HHs. The third sample (US Sample 1 – US1) consists of Ghanaian migrants living in the US linked by kin ties to their origin HHs in Ghana via nominations and referrals (i.e. provision of contact information) provided by GS1 respondents. The fourth sample (US2) is a sample of migrant HHs who live in the US, seeded with a random sub-sample of US1 respondents and recruited with Network Sampling with Memory (Mouw and Verdery 2012; Merli et al. 2022). NSM is an innovative sampling approach that allows migrant recruitment through their networks through multiple waves of respondents. This sampling method incorporates a probability sampling framework and a peer-referral process which increases participation. It was shown to achieve adequate representation of rare immigrant populations (Merli et al. 2022; Attané and Merli 2024; Merli et al. 2024). US2 respondents are also asked to nominate and provide information on their origin HHs in Ghana, sufficient to enable the spatial placement of their origin HHs, some of which may overlap with GS1 HHs.

Figure 1: Sampling Design



Recruitment and in-person interviews with GS1 and GS2 HHs were completed in Ghana in June 2024, yielding a total of 96 GS1 HHs (with migrants in the US) and 292 GS2 HHs (without migrants in the US) with an overall household response rate of 79.6%. The low number of migrant households compared with non-migrant households was due to a disproportionately higher refusal rates among migrant households. In addition, household survey interviews revealed that some households that were originally listed as having migrants to the US had in fact migrants to countries other than the US. These households were re-classified as GS2 HHs. GS1 and GS2 HH respondents (usually the household head or their spouse) were administered a household roster questionnaire which included questions on the past migration experience to the US or elsewhere of each current household member. GS1 HH were administered a US kin roster questionnaire which solicited nominations and referrals (i.e. provision of contact information) to kin of HH heads and their spouses who are currently living in the US. US kin referred by GS1 households make up the US1 sample.

We are currently preparing to contact and interview US1 sample members, who will be administered a household roster and migration history questionnaires using WhatsApp video call interviews, a messaging and video calling app popular among African immigrants in the US and Europe. Interviews with US1 members will be followed by the recruitment of US2 members using NSM techniques (Merli et al. 2022). In NSM, sample recruitment usually starts with the identification of a limited number of initial respondents, or seeds. Seeds and subsequent waves of respondents are asked to nominate their social contacts who are target population members (referred to as alters) by providing nominations (e.g. minimally identifying information such as first name and last four digits of a cellphone number though any sufficiently detailed information will do) and referrals (i.e. provision of contact information). This information allows the reconstruction of the underlying social network of nodes (i.e. individuals in a network connected by links) who make up the target population by combining all nominated individuals into a single network and identifying those nominated by more than one respondent. Specifically, we will randomly select 10 US1 respondents to seed the US2 NSM sample of 200 Ghana-born immigrants, recruited through multiple waves of nominations and referrals. In addition to a household questionnaire and a migration history, seeds and successive waves of respondents selected for participation in the US2 sample will also be administered a social-network-roster questionnaire for their non-co-resident Ghana-born friends and relatives living in the US. The collection of a network roster is one of the steps required by NSM to reconstruct and sample the network, but it also includes information on attributes of nominated Ghanaian social contacts in the US and of the social ties between respondents and their nominated social contacts, such as frequency and domain of the social tie.

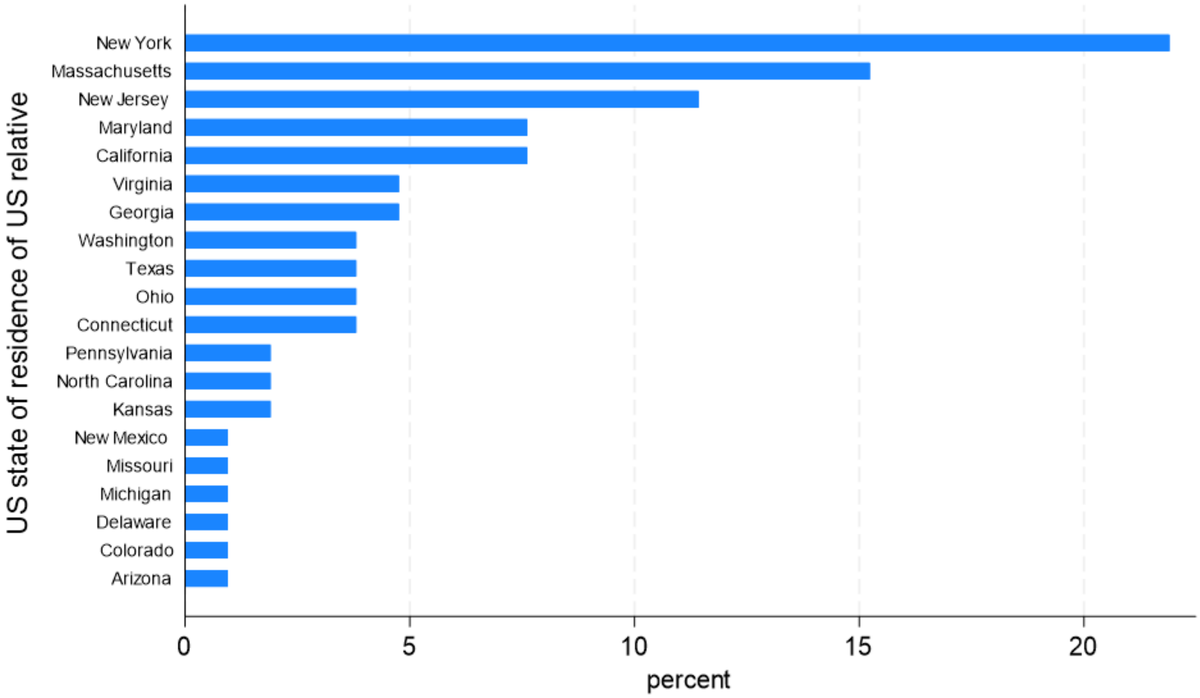
The combined population represented in GS1, US1, and US2 will consist of individuals who are members of a binational network connecting the greater-Accra sending community in Ghana to various destinations in the US. Because the target populations in origin and destination represent small fractions of the overall populations in Ghana and in the US, the screening necessary to recruit samples of Ghanaian migrants with conventional probability sampling would be very costly, particularly in the US. Thus, one advantage of the NSM link tracing sampling design is efficiency and cost-effectiveness. A second advantage is that the combined sample of Ghanaians in the US (US1 and US2) includes individuals linked by kin ties to their origin HHs in Ghana, as well as immigrants without ties to origin HHs but who are linked by a network of non-kin and kin ties in the US. The latter are exactly the type of ties that are missed by multi-sited studies which start at origin and rely on cross-border ties to recruit samples of migrants at destination (e.g. MMP and its successors). Our combined US1-US2 sample is thus heterogeneous with respect to presence or absence of ties with origin and new ties at destination, which should allow researchers to evaluate the roles of kin, non-kin, local and cross-border ties for immigrant outcomes.

Preliminary studies

Respondents in GS1 HH heads nominated 144 kin in the US, of whom 135 were related to the household heads and the rest to their spouses. HH respondents provided state-of-residence information for 73% of their nominated kin and contact information for 60% of them (n=86).

State of residence of US kin is shown in Figure 2. 54% of US kin of GS1 migrant HH in the greater Accra region reside, in ranking order, in New York, Massachusetts, New Jersey, California, Maryland, Virginia, and Georgia. For comparison, these states host 62% of all Ghanaian born immigrants estimated from the 2022 5-year American Community Survey (ACS) sample (Ruggles et al. 2024).

Figure 2. Top US states of destinations of kin of Ghanaian migrant households with known destinations (N=105)



Although the interviews of US1 sample members and the NSM recruitment and interviews of US2 sample members are forthcoming, we are confident they will be completed by early 2025 and that the analyses needed to test our hypotheses will be completed by the PAA meetings in April 2025. Members of our team have successfully conducted numerous field-tests of NSM among Chinese immigrants in Tanzania, the US and France (Merli et al. 2016; Merli et al. 2022; Attané and Merli 2024), reaching the conclusion that the peer-referral element of NSM can achieve sufficiently large numbers of nominations and referrals and high response rates to recruit samples that accurately describe populations of interest when compared with conventional population representative probability samples or census enumerations (e.g. the ACS in the US and the French census). Although the implementation of NSM to recruit US2 sample will be facilitated by the team's previous experience with implementing the NSM sampling infrastructure, the evaluation of NSM to achieve representativeness of the Ghanaian immigrant population in the US remains one of the empirical questions to be addressed in this paper.

Proposed analyses and expected findings

Evaluate feasibility of obtaining cross-border nominations and referrals

(H1) GS1 respondents with more schooling and more frequent contacts with US kin will be more likely to nominate and provide contact information to US kin. Higher socioeconomic (SES) HHs are more likely to have more kin who have migrated in the US, to maintain frequent contacts with them and to know their kin's contact information. To test this hypothesis, we will estimate logit regressions for referral (provision of contact information) of US1 members as a function of GS1 characteristics and their frequency of contacts with nominated kin. If the estimates are consistent with this hypothesis, this will point to one selective dimension of the origin ties of origin-nominated samples.

Evaluate sampling strategy

(H2) Migrants from higher SES HHs and with more frequent contacts with origin HHs are more likely to participate in US1 once referred, as they have more to lose if contact with their origin HHs diminishes. To test this hypothesis, we will estimate logit regressions for participation in US1 among nominees for US1 as a function of GS1 HH characteristics. If the estimates are consistent with this hypothesis, this will point to another selective dimension of origin-nominated samples.

(H3) US1 respondents with more schooling and more frequent communication with origin HH will be more likely to participate in successful interviews once referred and provide referrals to their non-kin and kin alters.

(H4) US2 respondents with more frequent communication with their referrers will be more likely to participate in successful interviews once referred because referrers will have shared their positive participation experience with respondents. To test this hypothesis, we will estimate logit regression for participation in US2 as a function of the frequency of communication between the referrer-respondent dyads.

(H5) US2 respondents will have fewer and weaker ties to origin, to be in the US for longer, and to be older than US1 respondents. If the estimates are consistent with our hypothesis, this will point to yet another selective dimension of origin-nominated samples.

(H6) US2 migrants have comparable sociodemographic characteristics as Ghanaians in the ACS. If NSM leads to the recruitment of a representative sample, there should be limited or no significant differences between US2 and Ghanaians in the 5-year 2017-2022 ACS IPUMS sample, which includes 6,972 Ghana-born respondents. After applying appropriate weights to generate ACS and NSM sample characteristics such as gender, SES, years in the US and location in the US, we will use t-ratios to test differences between them.

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