Polygyny and HIV transmission in SSA: explanations for the benign concurrency effect

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Abstract

In a previous study, we identified a negative ecological correlation between the prevalence of polygyny and HIV at both the national and sub-national level (Reniers & Watkins, 2010 in AIDS), and therefore dubbed polygyny a case of *benign partnership concurrency*. In this contribution we restate the relationship between polygyny and HIV using a multilevel analysis. At the individual level, we find that polygyny positively correlates with HIV status, particularly for junior wives of polygynous men. At the aggregate level, however, the correlation is negative, suggesting that polygyny inhibits the propagation of the virus. We those results in mind, we investigate four mechanisms that contribute to the contrasting individual and aggregate-level correlations. These relate to (1) the *sexual network structure* characteristic of polygyny, (2) the disproportionate *selection* of HIV positive women into polygynous unions, (3) a reduction in the frequency of intercourse in conjugal dyads of polygynous unions *(coital dilution),* (4) and the restricted access to sexual partners for younger men in populations where polygynous men presumably monopolize the women. We find evidence for several of these mechanisms, and together they support the proposition that polygynous marriage systems contain or slow down the spread of HIV. We relate these results to recent discussions of partnership concurrency as one of the major factors explaining the differential spread of HIV.

Extended abstract

Sexual partnership concurrency has become a popular behavioral explanation for the elevated HIV seroprevalence levels in some sub-Saharan African countries (Epstein 2007; Halperin and Epstein 2004; Hudson 1993; Morris and Kretzschmar 1997; Watts and May 1992). Despite the merits of the work around partnership concurrency (e.g., it underscored the importance of sexual networks in the spread of HIV in addition to individual attributes and behavior), one of the weaknesses of the concurrency hypothesis is lack of strong empirical support (Lurie and Rosenthal 2010; Sawers and Stillwaggon forthcoming). The latter stems in large part from the methodological challenges in measuring partnership concurrency and modeling its effects (Morris 2010).

A detailed empirical study of the relationship between polygyny –a particular and institutionalized form of partnership concurrency– and HIV status thus offers a perspective on a research question that has otherwise been quite elusive. In these analyses, we will treat polygyny as an individual-level risk factor, but also invoke polygyny as a cultural system with indirect implications for the spread of an STI, HIV in particular. In that sense, our approach echoes that of social scientists who have studied the relationship between polygyny and fertility (e.g., Ezeh 1997; Pebley and Mbugua 1989; Pison 1986). The analogy with the fertility literature does not stop there. HIV and fertility share several proximate determinants (e.g., coital frequency), and we will refer to some of those for developing hypotheses about its relationship with HIV.

As a first step in the empirical analysis, we use twenty surveys with individually-linked HIV serostatus data to restate the negative ecological association between polygyny and HIV presented in Reniers and Watkins (2010) using a multilevel model. We confirm the results from the earlier study, but also identify a positive individual-level correlation for junior wives of polygynous men. The association between HIV and polygyny status is negligible for men and first wives of polygynous men. Coincidentally, a similar discrepancy between the individual and ecological-level relationship (albeit reversed) also exists for polygyny and fertility.

The multilevel analysis is followed by an investigation into the mechanisms that could account for what we conveniently dubbed a case of *benign concurrency*. These mechanisms relate to (1) the *sexual network structure* characteristic of polygyny, the (2) *selection* of HIV positive women into polygynous unions, (3) a reduction in the frequency of intercourse in conjugal dyads of polygynous unions *(coital dilution),* and (4) the restricted access to partners for younger men in populations where polygynous men possibly monopolize the women in their community (*monopolizing polygynists*). Below, we explain the rationale for each of these mechanisms in greater detail.

Sexual network structure. The sexual network structure produced by polygyny is one of gender asymmetric partnership concurrency because men can have concurrent partners whereas women are –in principle– monogamous. Compared to gender symmetric concurrency it limits the size of the temporally connected network components to the number of wives of the polygynous men in the population[1] (Reniers and Watkins 2010; Santhakumaran et al. 2010). The latter is important because large network components are known to be most conducive to the spread of an STI (Bearman, Moody and Stovel 2004; Morris and Kretzschmar 1997). This is the idealized form of polygyny, however, and it is important to realize that the protective effect of the sexual network structure will start to disintegrate as soon as women in polygynous unions have affairs on the side. In that a scenario, the women with multiple partners act as bridges between otherwise disjoint network components of monogamous and polygynous men.

[1] Morris and Kretzschmar (1997) model the spread of HIV in a sexual network with gender symmetric concurrency but acknowledge the gender asymmetry produced by polygyny. In a later paper (2000), they relax the assumption of gender symmetry with the expected dampening effect on component size and epidemic potential. See Reniers and Watkins (2010) for an illustration of a simulated sexual network with gender symmetric and gender asymmetric concurrency.

One of the reasons to expect a higher prevalence of extra-marital partnerships in populations with polygyny is that the institution of polygyny itself seems to endorse the belief that men require more than one woman for sexual satisfaction[2] (Caldwell et al. 1993). For men, non-marital partnerships can also be part of the quest for an additional spouse. With respect to women, observers have pointed out that extra-marital liaisons of (junior) wives of patriarchs are tolerated as long as the couple acts with the necessary discretion. It is also understood that the husband retains the paternity rights to the children that might ensue (Delius and Glaser 2004). A similar argument is made by Caldwell et al. (1991) for the Yoruba in Nigeria. The empirical evidence for an elevated prevalence of extra-marital affairs in polygynous unions to date is far from overwhelming, but it does indeed point in that direction. A few studies have found that men (sometimes also women) in polygynous unions have more extra-marital affairs than their counterparts in monogamous marriages (Carael, Ali and Cleland 2001; Mitsunaga et al. 2005; Reniers and Tfaily 2008). One Nigerian study could not detect a clear pattern for either men or women (Isiugo-Abanihe 1994), and a study in Tanzania suggests that non-marital partnerships are less common in polygynous men, but more frequent among women in polygynous unions (Nnko et al. 2004). Bearing in mind that the trustworthiness of self reports of non-marital sexual partners may not be very good, we evaluate whether these are more commonly reported by men and –particularly– women in polygynous unions.

Adverse selection. The maintenance of polygynous marriage systems via the rapid remarriage and disproportionate recruitment of divorcees and widows as junior wives into polygynous unions has been described well before the advent of the large scale HIV epidemic (Goldman and Pebley 1989; Lesthaeghe, Kaufmann and Meekers 1989). Timæus and Reynar (1998) present an analysis of more recent data. This is particularly relevant in a context of high HIV prevalence because these women could bring HIV into the household. In a study in rural Malawi, we found that women in their second or third marriage are disproportionately recruited into polygynous unions, and higher marriage order, in turn, is a good predictor of HIV positive status (Reniers and Tfaily 2008). A comparable selection effect has been identified in the fertility literature. Levels of female subfecundity or infecundity are often higher in women with polygynous husbands because presumed infecundity is the rationale for divorce and divorcees are more likely to end up in a polygynous union. Alternatively, the infecundity of one of the spouses may motivate the husband to add a wife to his household (Pebley and Mbugua 1989; Timæus and Reynar 1998).

Coital dilution. The hypothesis about a reduction in the coital frequency in polygynous unions is also derived from the literature on polygyny and fertility. Compared to a monogamous husband, a polygynous man divides his time between two or more women, and that is likely to reduce the frequency of sexual intercourse with each of his wives. This is claimed to have implications for fertility, but the evidence is mixed (Barrett 1971; Garenne and van de Walle 1989; Josephson 2002; Musham 1956; Pebley and Mbugua 1989). In HIV research, the attention has traditionally been on the number of partners as opposed to the number of sex acts, but the latter may have more immediate repercussions for the transmission of HIV (Blower and Boe 1993). As a first step in the

[2] See Delius and Glaser (2004) for a critique.

evaluation of a coital dilution effect, we compare the reported frequency of sexual intercourse by monogamous and polygynous women.

Monopolizing polygynists. Another aspect of polygyny with possible consequences for the spread of HIV relates to the access to sexual partners among younger men. Polygynous men usually have wives that are considerably younger than themselves, and they may squeeze the youngsters out of the market for sexual partners. Restricted access to sexual partners implies less exposure to HIV. The speculation around the plausibility of this mechanism is rooted in observations by anthropologists (e.g., Goody 1973), and cartoonists (Figure 1). Interestingly, it is also a concurrency compensating factor that is built into the simulation work of Morris and Kretzschmar (2000). To set up a comparison with serial monogamy, the number of partnerships in the simulated population is held constant, and an increase in concurrency thus produces more isolated nodes in the sexual network. When gender asymmetric concurrency is modeled, it is the men in particular who end up as isolates. As two manifestations of access to sexual partners, we assess how the age at sexual debut and young men's reported coital frequency varies with the prevalence of polygyny in a population.

Figure 1 about here

2. Data and methods

We use data from twenty African Demographic and Health Surveys (DHS) and HIV/AIDS Indicator Surveys (AIS) with individually linked survey and HIV serostatus data. In alphabetical order, these are Burkina Faso (2003), Cameroon (2004), Democratic Republic of Congo (2007), Ethiopia (2005), Ghana (2003), Guinea (2005), Ivory Coast (2005), Kenya (2003), Lesotho (2004), Liberia (2007) Malawi (2004), Niger (2006), Rwanda (2005), Senegal (2005), Sierra Leone (2008), Swaziland (2006-2007), Tanzania (2003), Zambia (2007) and Zimbabwe (2005/6).

The DHS and AIS use a two-stage randomized cluster sample design. Survey clusters are the smallest area units, comparable to enumeration areas in a national census. A cluster contains about 100 households, and there are on average 379 (standard deviation = 80) clusters per survey in the surveys used here. In the second sampling stage, a predetermined number of households are selected from each cluster. In each household, all women aged 15-49 are eligible for an interview. The age ranges are a little broader for men (usually 15-54 or 15-59), but the number of households selected for male interviews are often substantially lower. Between 20 and 40 women are typically interviewed per survey cluster (Macro International 1996). DHS and AIS data, survey instruments, and other documentation can be retrieved from the Measure DHS website (http://www.measuredhs.com). An important disadvantage of the DHS and AIS for this analysis is the lack of detail on marriage and partnerships (e.g., no full marriage histories) and, sometimes, the lack of standardized questions (e.g., the wording of the question about current marital status has changed slightly over time). Marriage durations for higher-order marriages, and the outcome of previous marriages is only reported in a few surveys. The wife's rank in a polygynous household is missing in a few surveys as well. The DHS and AIS are nonetheless important resources for studying concurrency because they constitute the largest collection of comparable datasets from African countries with partnership information linked to HIV serostatus. In our analysis we combine consensual and formal unions, and our measure of polygyny is based on a question about the number of (co-)wives. We refer to a study by Timæus and Reynar (Timæus and Reynar 1998) for a discussion of the correspondence between husbands and wives in survey responses to these questions.

Because of the cross-sectional nature of the data we are restricted to using a contemporaneous measure of polygyny (and most of the other covariates) whereas our primary outcome of interest–HIV prevalence–is the result of cumulated exposure over the 10-years prior to the survey. Important temporal changes in the prevalence of polygyny driven by HIV prevalence itself cannot be excluded and strong causal claims are thus difficult to justify using this dataset[3]. A limitation of the DHS that is relevant for individual-level analyses is that the data do not permit us to identify men and women who have ever been in a polygynous union, but were not so at the time of the interview.

The empirical analyses start with a multilevel analysis wherein we evaluate the association between polygyny and HIV at the individual and ecological or survey-cluster level. We present the results for a pooled sample of all countries, and for three groups countries stratified by HIV prevalence (i.e., low (<2%), medium (2-10%), and high (>10%)). The multilevel model is followed by an inquiry into the mechanisms that can reconcile the findings from the individual-level and ecological-level analyses. These test the selection and coital dilution hypotheses, evaluate permeability of the protective the sexual network structure in populations that practice polygyny and compare the access to sexual partners among younger men in populations with varying levels of polygyny. We present the individual-level analyses in terms of survey cluster fixed-effects models with a minimal set of other covariates. For the ecological analyses, we use logit regression models. The analyses of the hypothesized mechanisms are carried out and presented for all countries separately. Survey weights (if appropriate also HIV seroprevalence survey weights) are used for computing aggregate level indices of the prevalence of polygyny, HIV, etc. No other form o weighting is used in the regression analyses.

In the regression models, we define the prevalence of polygyny as the average of the percentage of married men and the percentage of married women in polygynous unions. We average male and female-centered definitions of polygyny because it smoothes some of the measurement error and random variation, and because it accounts for two aspects of polygyny, namely the *incidence* (the proportion of men with more than one wife), and the *intensity* of polygyny (the average number of wives per polygynyst) (Van de Walle 1968). Analyses with direct measures of the incidence and intensity themselves point in the same direction.

Preliminary results

[3] A previous assessment revealed no strong correlation between national-level HIV prevalence and the annual rate of change in the prevalence of polygyny (Reniers and Watkins 2010). Ideally, one would need to repeat such an analysis at the survey cluster-level, but that is unfortunately not possible.

The first step in an empirical analysis of the relationship between polygyny and HIV is to evaluate the association at different levels of aggregation. In Figure 2, we present the results from a multilevel logit model with three levels (individual, survey cluster and country) and HIV positive status as the outcome. The set of coefficient estimates at the top are odds ratios for a pooled analysis of all countries followed by estimates for groups of countries stratified by HIV prevalence. As statistical controls we use individual age, and a dummy for the urban character of the survey cluster.

From the estimates in the panel on the left, we can learn that that living in a survey cluster with higher prevalence of polygyny is negatively correlated with HIV status of both males and females. The coefficient estimates for the pooled analysis are much larger than estimates in the stratified analysis, and that is in large part due to important between-country variation in the prevalence of polygyny and HIV (Reniers and Watkins 2010). Adding country fixed-effects reduces the coefficient estimates, but they remain significant (not shown). Turning to the individual-level association between union type and HIV status in the panel on the right, we identify three suggestive results: first, there is no relationship between polygyny status and HIV status for men. The odds ratio does, however, approach statistical significance in high HIV prevalence settings. Second, first wives are no more likely to be HIV positive than wives of monogamous men, and third, higher-order or junior wives of polygynous men are more often HIV positive than spouses of monogamous men. Worth noting also is that the correlation between polygyny status and HIV status for all women combined is positive (not shown). Disregarding the wife's rank, in other words, may lead to important errors of interpretation.

Figure 2 about here

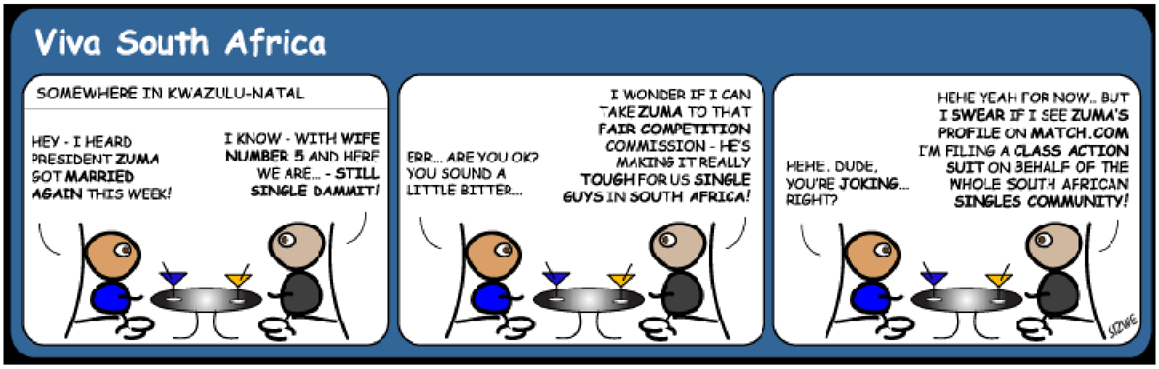
In sum, the relationship between polygyny and HIV is more complex than many would have anticipated. The negative ecological correlations confirm the *benign* association between polygyny and HIV that we postulated in an earlier paper (Reniers and Watkins 2010), and is in conflict with predictions of the concurrency hypothesis. This is probably the most captivating finding in Figure 1 because it suggests that some aspects of polygyny or other features of populations that practice polygyny inhibit the spread of HIV. In the remainder of the paper we explore some of the mechanisms that could account for that.

At the individual level it is not entirely clear how concurrency could be influencing these associations either. We will argue that the elevated prevalence of junior wives is produced by the selection of HIV positive women into polygynous unions. A pattern that is perhaps more suggestive of a concurrency effect are the increasing odds ratios for first wives of polygynous husbands as we move from low to high HIV prevalence strata because they may be exposed to the HIV virus present in junior wives through their husband. This is merely a speculation, because we are not well equipped to tease out individual-level concurrency effects with cross-sectional and ego-centered data.

[In the remainder of this paper, we will (1) explore the empirical evidence for the four hypothesized mechanisms that could explain both the positive individual-level correlation and the negative ecological correlation, and (2) present the results from the multilevel

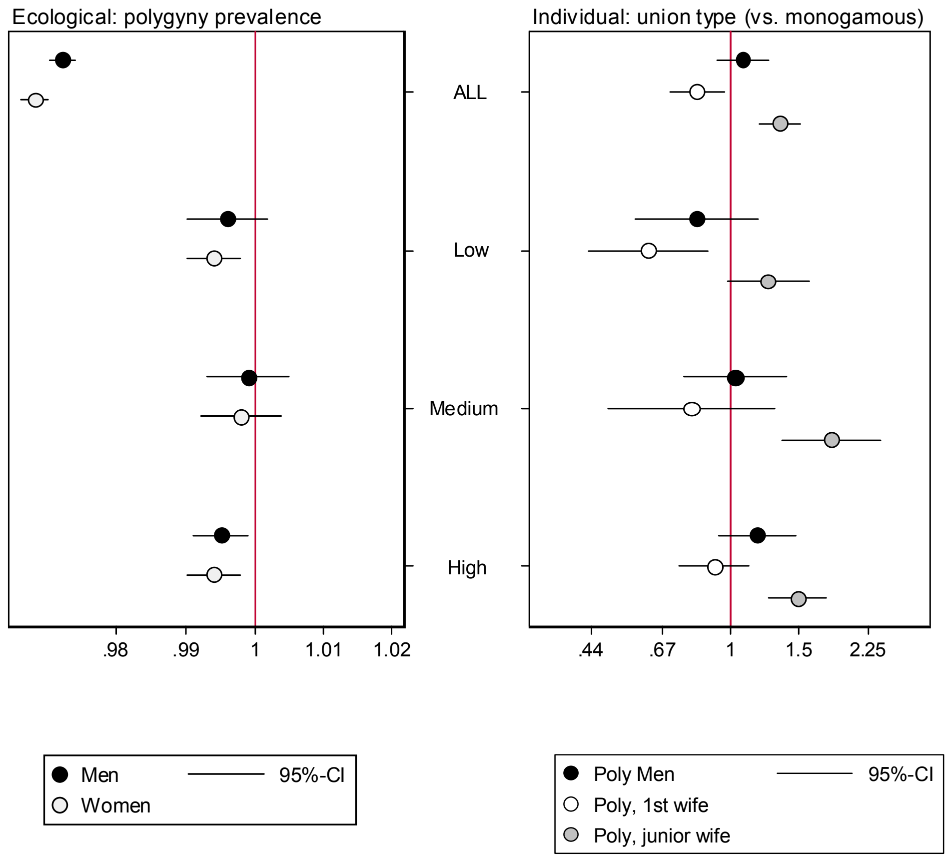
analysis with controls for other factors that are known to be correlated with the risk of HIV transmission (e.g., male circumcision, the presence of STIs, extra-marital partners and so forth). These analyses have yet to be finalized]

Figure 1: Are polygynists monopolizing the women in their community?



Source: wonkie.com

Figure 2: Predictors of individual-level HIV status, hierarchical logit model (odd ratios)



Notes: estimates adjusted for individual age and the urban/rural character of the survey cluster. The HIV prevalence strata are defined as low or <2%, medium or 2-10%, and high or >10%.

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