For Better or Worse, Till Death Do Us Part: Estimating the Marriage Contribution to the HIV Epidemic in Sub-Saharan Africa [*]

by
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ABSTRACT: In this paper we estimate the maximal effect that changes in individual-level sexual behavior alone can have on the present HIV pandemic. We simulate a series of estimates of HIV prevalence resulting from the drastic hypothetical scenario of all individuals alive today and in the future suddenly *absolutely* adhering to the stated goals of abstinence before marriage, and faithfulness within marriage. We start with initial populations that reflect ranges of HIV prevalence and differing marriage market patterns. We then move those populations forward in time assuming that no individuals falter in following prescribed sexual expectations (the A&B of the ABCs of AIDS prevention). The aim of this exercise is to determine whether, and estimate how substantially, individual sexual behavior change alone can alter the trajectory of the HIV pandemic.

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EXTENDED ABSTRACT

Introduction

What would happen to the trajectory of the present HIV pandemic, or the many local epidemics that make it up, if all people were to suddenly *universally* adopt the behavior prescriptions that underpin existing prevention strategies? Current scholarship does not provide an answer to that question, yet vast amounts of time and financial resources continue to be devoted to strategies targeting behavior change (PEPFAR 2007; USAID et al. 2003). The prevailing models for HIV-prevention strategies focus almost exclusively on individuals' behaviors, presuming that changes in individual behaviors are sufficient to curtail an individual's risk level.

One such model, The ABCs of HIV prevention – **a**bstinence, **b**e faithful and use a **c**ondom remain – remains the dominant prescription for protecting oneself from contracting the disease (Sinding 2005; Singh, Darroch and Bankole 2003). While the level of support for promoting the "C" in that model – condom use – varies considerably (Cohen 2004; Trinitapoli 2006),[1] support for promoting A&B – abstinence and being faithful – is virtually universal (adams 2007b; Cohen 2004; Trinitapoli 2006). Furthermore, many of the conditions wherein "C" is accepted refer to cases where A&B are not followed (adams 2007b; Trinitapoli 2007). Specifically, condom usage is rarely considered a relevant prescription for individuals who have faithfully followed the other components of the ABC message – e.g., sex involving spouses (Reniers 2006; (Ali, Cleland and Shah 2004). This focus however does not consider recent evidence that demonstrates having ever been married as one of the single strongest predictor of HIV status for women in sub-Saharan Africa (SSA) (Clark 2004; Reniers 2006; Trinitapoli 2007; (Auvert et al. 2001)). This recent evidence has lead many researchers to conclude that many women in SSA are contracting *within* marriage (Clark, Kohler and Poulin 2006; (Bongaarts 2007)). While common explanations resort to ascribing this effect to faithful women getting HIV from their unfaithful husbands, there is little evidence to demonstrate empirically whether this is the case.

In this paper we attempt to empirically estimate the potential success of dramatic reductions in individual-level risk behaviors. Namely, we generate a series of simulated epidemic curves to estimate the potential effect of a sudden *universal* adherence to A&B – abstinence before marriage, and faithfulness within marriage. To date, we are not aware of any research that has addressed the potential effect such a dramatic shift could generate. While we do not suggest that the assumptions in these models are realistically attainable, we seek to demonstrate the "best case scenario" of the effect that individual behavior models alone can have in the ongoing fight against the HIV pandemic.

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[1] In fact, promotion of condom use has been so contentious in some settings that the ABC's of AIDS prevention have come to be known as the "Anything but condoms" approach (Allen 2006).

Model Assumptions

Transmission dynamics of HIV are implicitly built on the longstanding equation which estimates the reproductive rate of the virus, represented by:

$$\mathbf{R_0 = ß\ c\ D} \qquad (1)$$

where **ß** represents the probability of transmission per contact, **c** represents the number of contacts per time period and **D** represents the duration of infectivity. Any population where $\mathbf{R_0}$ is greater than or equal to one will necessarily have a sustained epidemic. Prevention strategies are therefore targeted at limiting these parameters, for example with abstinence and fidelity particularly aimed at reducing **c**. Recent work has demonstrated however that these factors alone are not sufficient to accurately represent $\mathbf{R_0}$ (Aral and Roegner 2000; Morris 2004, 2007), and an equation more ready to handle sexually transmitted diseases is represented by:

$$\mathbf{R_0 = ß\ c\ p\ D} \qquad (1a)$$

where **ß** instead represents the probability of transmission per *act*, **c** represents the number of acts per partnership, **p** represents the number of partnerships per unit time, and **D** still represents the duration of infectivity (adams 2007a; Morris 2007). Morris (2007) further explains that this minor alteration forces several substantial changes in the underlying mechanisms suggested by the model. Incidentally, each of these changes would be directly influenced by the absolute adherence to A&B simulated in our models here. First, susceptibility is act-specific, not contact specific – which is substantially influenced by marriages in that exposure is typically elongated within marriages compared to other sexual partnerships. Second, small changes in numbers of partners can have an impact on epidemic potential that far outstrips the statistical significance of the number of partners (Moody et al. 2007), which can be directly tied to fidelity in marriage. And finally, partner sequencing matters (Kretzschmar and Morris 1996; Moody 2000; Morris and Kretzschmar 1995), which if we assume no concurrent partners (absolute fidelity), places the importance directly on partner *order*, not on number of partners.

Simulation Parameters

Rather than attempting to match estimates used in these simulations to any single population, we include a range of estimates of initial HIV prevalence and marital dynamics constrained by gender and age. First, we generate a series of populations (N = 1000) with existing marriages and the number of initial HIV positive individuals matched according to ranges reflected across the region. A range of hazard ratios each for marriage, death[2] and remarriage – constrained by age and gender – are then tied to each of these populations. We then step the population forward in 1-year increments for a total of 80 years, with marriages starting and people dying according to the gender- and age-specific hazard rates within the given parameter set. New individuals are introduced into the population at a constant rate representing newly marriageable individuals (also

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[2] The hazard rate for death is assigned separately for HIV positive and HIV negative individuals.

specified by age and gender). Throughout the simulations, the number of sexual contacts within a marriage (2 per week) and probability of infection per contact (ß = 0.001) are held constant across the entire population. We then present the HIV-epidemic curves generated by each parameter set – separately by initial HIV prevalence. These curves will represent how readily strict adherence to A&B could potentially alter present HIV prevalence trajectories, varying by level of initial HIV-prevalence and marriage-market dynamics.

Usefulness & Implications

From the series of parameter sets presented, researchers will be able to match population estimates for HIV prevalence and marriage hazards found in particular populations to estimate the potential impact that strict adherence to A&B prevention messages could have in their region of interest. To ease this process, we will highlight parameter sets that closely coincide with four existing empirical studies. The varying effects that result across the population sets will better inform decisions about where to direct prevention efforts – particularly highlighting those settings in which a continued focus on individual-behavior messages alone are likely to have the least impact.

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