ARTICLE IN PRESS

Epidemics xxx (xxxx) xxx–xxx

Contents lists available at ScienceDirect

Epidemics

journal homepage: www.elsevier.com/locate/epidemics

Dynamics and control of infections on social networks of population types

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ARTICLE INFO

Keywords:
Case reproduction number
R0
Social networks
Viet Nam
Epidemic control
Type reproduction number

ABSTRACT

Random mixing in host populations has been a convenient simplifying assumption in the study of epidemics, but neglects important differences in contact rates within and between population groups. For HIV/AIDS, the assumption of random mixing is inappropriate for epidemics that are concentrated in groups of people at high risk, including female sex workers (FSW) and their male clients (MCF), injecting drug users (IDU) and men who have sex with men (MSM). To find out who transmits infection to whom and how that affects the spread and containment of infection remains a major empirical challenge in the epidemiology of HIV/AIDS. Here we develop a technique, based on the routine sampling of infection in linked population groups (a social network of population types), which shows how an HIV/AIDS epidemic in Can Tho Province of Vietnam began in FSW, was propagated mainly by IDU, and ultimately generated most cases among the female partners of MCF (FPM). Calculation of the case reproduction numbers within and between groups, and for the whole network, provides insights into control that cannot be deduced simply from observations on the prevalence of infection. Specifically, the *per capita* rate of HIV transmission was highest from FSW to MCF, and most HIV infections occurred in FPM, but the number of infections in the whole network is best reduced by interrupting transmission to and from IDU. This analysis can be used to guide HIV/AIDS interventions using needle and syringe exchange, condom distribution and antiretroviral therapy. The method requires only routine data and could be applied to infections in other populations.

1. Introduction

Epidemiological theory assumes that infections are transmitted through random contacts between infected and uninfected people. The reality is usually different, and simple assumptions can give misleading results. One example is the spread of HIV/AIDS in 'concentrated epidemics', where populations contain small groups of people at high risk and large groups of people at low risk. Various approaches have been developed to analyse and interpret transmission on social networks of population types in which individuals may belong to several different types. In the case under consideration here these types consist of men who have sex with men, MSM, intravenous drug users, IDUs, female sex workers, FSWs, male-clients of FSW, MCF, female partners of MCF that we shall refer to as low risk women, LRW. If a person has only one risk factor, then that determines their population type. If people have more than one risk factor this defines a separate type and the ones of interest here are MSM who are also IDUs, and FSW who are also IDUs giving a total of seven types. It is clear that the population size of the different types, the transmission rate between people of a given type, and the transmission rates between people of different types will vary greatly. Given the differential equations for a model such as this, the calculation of the overall reproduction number, R_0, is straightforward (Diekmann et al., 1991; Diekmann et al., 1990; Diekmann et al., 2010; Heesterbeek, 2002; Roberts and Heesterbeek, 2007). If overall transmission of a pathogen can be reduced by a factor of $1/R_0$ then elimination is guaranteed but when the size of groups, the prevalence of the pathogen within each group, their interactions and their risks of infection vary by orders of magnitude, R_0, averaged over the whole network, may not be the most useful guide to controlling the epidemic. To address this issue Heesterbeek and others (Heesterbeek et al., 2015; Heesterbeek and Roberts, 2007; Roberts and Heesterbeek, 2003, 2007, 2012; Shuai et al., 2013) have introduced the Type Reproduction Number T_0. By analogy with R_0, T_0 is the number of secondary cases that arise when one individual of a given population type is introduced into a fully susceptible population of all types. In the case under consideration here, introducing infected one infected FSW will lead to infections in many clients but introducing one infected LRW will lead to no further infections since we assume that they are an epidemiological dead end (Kato et al., 2013). While one would need to calculate T_0 for each of the seven Population Types in the Can Tho network, this provides more nuanced

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https://doi.org/10.1016/j.epidem.2017.10.002
Received 13 October 2017; Accepted 18 October 2017

Please cite this article as: Williams, B.G., Epidemics (2017), http://dx.doi.org/10.1016/j.epidem.2017.10.002

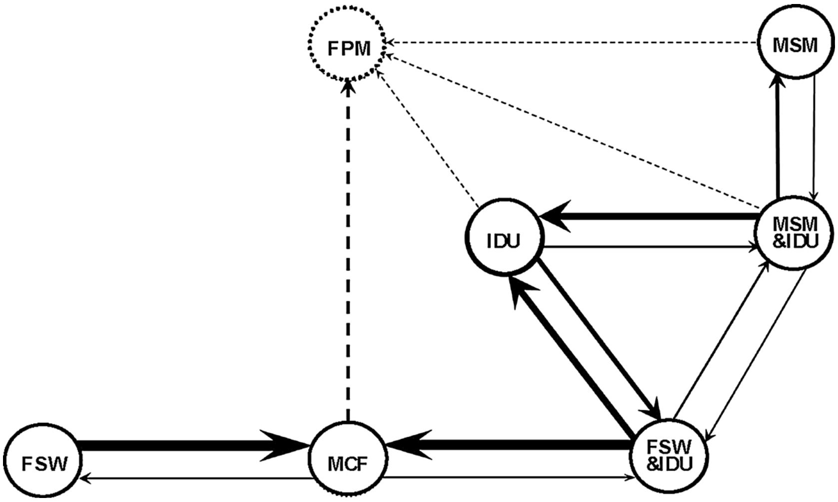

Fig. 1. The network model for HIV in Can Tho Province, Viet Nam. IDU: Injection drug users; MSM: Men who have sex with men; FSW: Female sex workers; MCF: Male clients of FSWs; FPM: Female partners of MCF and other women at low risk.

information concerning the optimal strategy for controlling the epidemic. This concept has been further refined by introducing the Target Reproduction Number in which control is targeted at particular interactions between types (Shuai et al., 2013). In Can Tho, for example, male circumcision would reduce transmission from FSW to MCF but not from MCF to FSW. The analysis presented here is essentially an application of the Type Reproduction Number. We consider a situation in which members of a given Type are rendered uninfectious by providing them with anti-retroviral therapy (ART). Given that ART will be rolled-out over time one wishes to determine which Types should be given priority and in what order so as to have the greatest impact on the overall value of R_0. Each time a person is started on ART the number of people of that Type is reduced by 1.

Here we show that, when investigating the control of such epidemics, routinely collected data are a rich source of information. Using surveillance data to characterize the transmission network for HIV/AIDS in Vietnam we find that the best way to minimize infections in the whole population is first by targeting high-risk injection drug users, then men who have sex with men, and finally female sex workers.

Generalized epidemics of HIV/AIDS, such as those prevailing in Eastern and Southern Africa, are driven mainly by heterosexual transmission in the population at large (Gouws and Cuchi, 2012; Williams et al., 2015). Concentrated epidemics, on the other hand, are focused on networked groups of people who acquire and transmit virus by a mix of sexual transmission (between men and women and among men) and by non-medical needle injection of contaminated blood. Investigations of the structure of these networks have usually been carried out with social surveys (Helleringer et al., 2009; Lurie et al., 2003) or by identifying transmission links with genetic markers (Brenner and Wainberg, 2013; Grabowski et al., 2014; Leventhal et al., 2012; Stadler et al., 2012) in order to track the spread of infection through populations and models have been developed to take various levels of network structure into account (Sattenspiel and Simon, 1988). However, the accurate reconstruction of transmission pathways by these methods is labour intensive both in the field and in the laboratory. In this paper we consider an alternative method of constructing an epidemic network based on the routine sampling, through time, of infection in linked population groups. We have used the method to gain insights into the way an epidemic of HIV/AIDS unfolded in Vietnam, and to investigate how the spread of infection can most effectively be reversed.

The control of HIV in concentrated epidemics demands different interventions for different risk groups. In Thailand, the ‘100% Condom Programme’ for female sex workers, combined with other interventions, significantly reduced HIV transmission (Park et al., 2010). For injecting drug users a meta-analyses suggests that access to clean needles and syringes could reduce HIV transmission by 66% (Aspinall et al., 2014) while another meta-analysis suggests the opiate substitution therapy could reduce transmission by 54% (MacArthur et al., 2012). In generalized epidemic settings early treatment has been found to reduce transmission by 96% (Cohen et al., 2011; Cohen et al., 2012). While both the impact and the cost of different combinations of interventions vary, we are concerned in this paper with the population impact that can be achieved for a given reduction in the individual risk of transmission however it is brought about.

2. Methods and data

This analysis focuses on the spread of an HIV/AIDS epidemic in Can Tho province, Vietnam, as described by data collected as part of the annual National Sentinel Surveillance system (1994–2010) and from Integrated Biological and Behavioural Surveillance surveys in 2006 and 2009. The data used in this analysis, details of the model, choice of parameters and the fitting process are discussed in detail in a previous study (Kato et al., 2013).

In 2010, the prevalence of HIV was highest among injection drug users (IDU: 48%), then men who have sex with men (MSM: 9.5%), followed by female sex workers (FSW: 5.8%), male clients of FSW (MCF: 1.1%) and finally female partners of men in each group (FPM: 0.5%). While the prevalence of infection is lowest in FPM, this group carries the largest number of infections, making up 49% of all infected people, because they are by far the largest group among those at risk of infection.

We use a previously constructed network including transmission within groups and all probable links between pairs of groups (Fig. 1) (Kato et al., 2013). Injecting drug users (IDU), men who have sex with men (MSM), and female sex workers (FSW) and their male clients (MCF), each have potentially self-sustaining epidemics. They are connected through MSM and FSW who are also IDU. The female partners of men who visit sex workers (FPM) and of other men are assumed to be an epidemiological dead end, and do not infect anyone else (Kato et al., 2013). In Fig. 1, the weight of the arrows indicates the expected extent of transmission. For example, each FSW may infect many MCFs but each MCF is likely to infect relatively few FSWs.

The differential equations for the network in Fig. 1, are given in the Appendix. The initial prevalence (in 1980) and the transmission parameters were varied to obtain the maximum likelihood fit to the trend data assuming binomial errors (Kato et al., 2013). This gives the estimated size and prevalence in each group and sub-group in 2011 (Table 1) and the fitted trends shown in (Fig. 2).

In order to provide a quantitative guide to controlling the epidemic we analyse the elements of the next-generation matrix (NGM) which give the case reproduction numbers (Diekmann et al., 2010) within and