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The Model of Venereal Disease Transmission Among Male Homosexuals Considering Multiple Channels

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Abstract Background

Male homosexuals are at particularly high risk of venereal diseases (VDs) and some of these diseases are hard to be noticed without test. Herein, it is important to study the potential infection time of VDs for male homosexuals.

Methods

The sexual activities are divided into two types: one is the transmission during the private date between two homosexuals and another is the transmission during a homosexual's visit to the gay gathering spot. We use three different Poison distributions to manipulate the two types of sexual activities and the number of people contacted. Combining three Poison distributions, we propose a model to estimate the infection time of VDs for male homosexuals. This model is general in the sense that it is suitable for different types of VDs.

Results

The infection probability during an exposure period and the expected time of infection can be estimated according to the proposed model.

Keywords: Homosexual Males, Poisson Process, Transmission, Venereal Diseases,

Introduction

Venereal Diseases (VDs) are a class of contagious diseases (such as gonorrhea or syphilis) that are typically acquired in sexual intercourse by infecting viruses or bacteria [1-4]. In traditional theory, VDs include syphilis, gonorrhea, chancroid, venereal lymphogranuloma and inguinal granuloma etc., which are generally only transmitted through sexual contact [5]. In 1975, the World Health Organization put forward the concept of Sexually Transmitted Diseases (STDs) which are transmitted through sexual contact, indirect contact, etc. STD expands the scope of VD, where the pathogen includes some viruses such as CMV, HIV, HPV and HSV [6].

Generally, the infection of viruses or bacteria that lead to VDs may not display obvious symptoms in the initial stage, which is called incubation. Hence, VDs are easily to go unnoticed for a period of time [7-10]. If VDs are undetected, the infected people are under an undiscovered risk of having developed VDs, while the others are also under a risk of being transmitted venereal viruses or bacteria.

If someone's sexual history and current signs and symptoms suggest having a VD, medical tests can identify the cause and detect coinfections contracted. Basically, there are three kinds of test for VD: 1). Blood tests. Blood tests can confirm the diagnosis of HIV or later stages of syphilis; 2). Urine samples. Some VDs can be confirmed with a urine sample; 3). Fluid samples. If there are active genital sores, testing fluid and samples from the sores may be done to diagnose the type of infection. Laboratory tests of material from a genital sore or discharge are used to diagnose some VDs [11]. In these tests, some technologies are developed to detecting the pathogen, such as Polymerase Chain Reaction (PCR) which is a method to make many copies of a specific DNA segment [12]. Using PCR, copies of DNA sequences are exponentially amplified to generate thousands to millions of more copies of that particular DNA segment. PCR is now a common and often indispensable technique used in medical laboratory and clinical laboratory to detect the bacteria and viruses that are dominant in infectious diseases [13,14].

In 1984, the original model of STD transmission was proposed, suggesting that the critical element for the persistence of gonorrhea is the existence of a 'core group' with a high rate of change of sexual partners [15]. 'Sexual mixing' between members of the core group then maintains a subpopulation of individuals with a high STD prevalence within a larger community with much lower partner change rates and disease prevalence. A model proposed in 2009 also found that the epidemiology of gonorrhea is largely driven by subpopulations with higher than average concentrations of individuals with high sexual risk activity [16]. In addition to the change of sexual partners and high sexual risk activity, the structures of sexual networks are essential for understanding the dynamics of sexually transmitted infections. Standard epidemiological models largely disregard the complex patterns of intimate contacts. Social network analysis offers important insight into how to conceptualize and model social interaction and has the potential to greatly enhance the understanding of disease epidemics [17, 18].

Due to the sexual behavior of the male homosexuals [19], VDs may be more easily transmitted among male homosexuals. Say, homosexuals are more often into unprotected anal penetration

which may break the skin and facilitate the transmission of the viruses [20]. In addition, some of them may be involved in the group sex which happens frequently in gay gathering spots, such as parks, sauna, etc. Previous studies found that homosexual adolescent men are at particularly high risk for sexually transmitted diseases [21,22]. Though more and more homosexuals are regularly undergoing the test for VDs nowadays, some of them are still not willing to get tested for several reasons [23]. Some simply feel shy to get tested, some are simply afraid to see a bad result, some are concerned with the privacy, and some may not be able to find nearby testing spot. Though some VDs become quickly noticeable even without test, some may be latent for a long time, such as AIDS [24,25]. Thus, a homosexual who does not get tested frequently may get infected with certain VD and not know it for a long time. The later one is aware of the infection, the more difficult to cure the diseases and the more people are likely to be infected by him.

In order to facilitate the risk evaluation of male homosexuals, we propose a model to estimate the infection time of VDs male homosexuals during their exposure time in this study. Using this model, people can calculate their infection probability themselves by substituting suitable parameters and judge whether they need to have a test It should be noted that we only consider VDs in the traditional sense rather than STDs under the new definition because some of STDs may transmit through not only sexual contact (e.g. HIV). Since we want to focus the infection probability attributed to sexual activities, the infection discussed is limited to VDs in this study. The remaining of this paper is arranged as follows. Section 2 states the assumptions. Section 3 presents the model. Section 4 concludes.

Assumptions

1. Two types of transmission channels are considered. One is the transmission during the private date between two homosexuals. Another is the transmission during a homosexual's visit to the gay gathering spot.
2. The contact in the first kind of activity is one-to-one, that is, one person contacts with another. Consider a homosexual who are frequently involved into one-to-one date with some other homosexual and assume that the date with unprotected sex happens with frequency $\square_1$.
3. The contact in the second kind of activity is one-to-many, that is, one person contacts with more than one other persons at a time. Consider a homosexual who goes to gay gathering spot with frequency $\square_2$. During each visit, the person has unprotected sex with a random number of people and the number is assumed to follow Poison distribution with the parameter of $\square_1$.
4. For each unprotected sex with an infected person, the healthy one gets infected with a probability of p_I. Note that this probability depends on the role of the homosexual and should be assigned different values accordingly. Say, a homosexual who is anal penetrated by an infected partner without protection has a bigger probability to be transmitted than if he is penetrating the partner instead. Comparatively, for the homosexual who only participates in oral sex, the transmission probability is relatively lower no matter he gives or receives the oral sex.

5. The size of the studied population is N. Say, the population of concern may be a specific city. It is well known that the transmission happens more in cities with bigger population.
6. The number of infected people among the studied population is N_I.

Assumption 1 approximates the reality. Though some people also date with multiple people even during private date, it happens less often than one-to-one date. Actually, the typical means for a homosexual to find a sex partner nowadays is through the dating apps in smart phones, such as "blued", "aloha", etc. Besides the private dating, some homosexuals also go to gay gathering spots, such as the gay cruising areas which are typically some parks or woods, gay saunas, etc. The Poison process is usually used to describe the occurrence of a kind of event per unit time, and the parameters involved in assumptions 2-4 are specific to individual homosexual. To estimate the infection time for a different person, different values should be used. Such values can be estimated by the individual itself considering its activities. Assumptions 5 and 6 are established with the assumption that the population and its proportion of infected people are stable during the studying period.

Model

From assumptions 5 and 6, we know that there are N people in area and of them, the number of infected people is N_I. Then we can have the proportion of infected people as

$$R=\frac{N_I}{N} \qquad (1)$$

According to assumptions 1-3, we can obtain the distribution for the number of each kind of activity during time [0, t). Specifically, for the first kind of activity

$$p\,k\,t_{1\,1}(\quad|\,)=\frac{}{(t\square_1)_{k1}\,k_1!}e_{-t\square_1} \qquad (2)$$

where, k_1=0, 1, 2, 3….
Similarly, for the second kind of activity

$$p\,k\,t_2(\ _2|\ ) = \frac{}{}e^{-t\square_2}(t\square_2)^{k_2}\,k_2!$$

(3)

where, k_2=0, 1, 2, 3….

According to assumption 3, the distribution for the number of people that one has unprotected sex with during each gay gathering spot visiting is

$e^{-\square k_3}$

$$p\,k_3(\ )_3 = \frac{}{}\,k_3!$$ (4)

where, k_3=0, 1, 2, 3….

Then, the probability of infection for a healthy male homosexual during time [0, t) is

$$PI\,t(\ ) = -1\square\square_{+\square}\,p\,k\,t_{1\ 1}(|\ )(1-R\,p\square_{I\,k1}\square\square_{+\square}\,p\,k\,t_2(\ _2|\ )\square\square_{+\square}\,p\,k_3(\ _3)(1-R\,p\square_{I})_{k3}\square\square_{k2}$$

$$\square\square\square$$

$$)\ \square\ \square\square\ \square$$

$$\square_{\ 0}\qquad\qquad\square\ \square\square_{\ 0}\qquad\qquad\square_{\ 0}\qquad\qquad\square\ \square^{\square}$$

(5)

Finally, we can estimate the expected time of infection for a healthy homosexual male as

$$T = \square_0^{+\square}\,t\,PI\,t\,dt^{\square}\qquad(\ )\qquad(6)$$

Conclusion

In this study, we proposed a model to calculate the expected time of VDs infection for healthy male homosexual who have regular sexual activities. Both private sex date and sex at gay gathering spots are considered. The model is proposed under some assumptions with combined use of three Poison distributions. This study can be used by individual homosexual to calculate its probability of infection and its expected time of infection for different types of VDs. In addition, it can also be used by decision makers of public health care to better control the infection of venereal disease among male homosexuals with regular sexual activities. This model is just an initial model, and can be extended to incorporate more factors in the future. Say, male homosexuals sometimes also have sex with women or heterosexual men, and the interactions between homosexuals and heterosexuals can be modelled in the future. Some

homosexuals may also be infected through drug injection. Moreover, the dependency for infection of different VDs can be investigated in the future.

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