A model for the coupled disease dynamics of HIV and HSV-2 with mixing among and between genders

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ABSTRACT

Evidence indicates that those with genital herpes (HSV-2) infections have greater risks of infection by HIV; and, once co-infected, are more likely to transmit HIV. To better understand the interactions between HIV and HSV-2, we construct a mathematical model that describes the joint dynamics. A new feature of this model is the inclusion of both heterosexual and homosexual interactions. We derive and interpret the basic and invasion reproduction numbers for HIV and HSV-2 using the approach of next-generation matrices. We then perform scenario analyses and conduct a sensitivity analysis to investigate the impact of the model parameters on the reproduction numbers and disease prevalences. We conclude that homosexual transmission drastically changes the disease prevalences; hence, it is important to account for this interaction as models that ignore homosexuality may greatly underestimate the disease burden.

1. Introduction

Human immunodeficiency virus (HIV) and herpes simplex virus type-2 (HSV-2) are sexually transmitted diseases that affect thousands of individuals in the United States. HIV is a virus that targets cells of the immune system, with about 50,000 new cases in the United States every year and roughly 16% unaware of their infection[1]. The Centers for Disease Control and Prevention (CDC) report that about one in six Americans have HSV-2; however, many infected individuals may be unaware of their infections due to a lack of symptoms[2]. Individuals with HSV-2 experience a lifelong infection, alternating between periods of acute HSV-2 in which they are infectious and periods of latent HSV-2 in which the virus remains dormant. While both diseases have treatments available to reduce viral shedding or to prevent reactivation, currently neither is curable.

Further, HSV-2 may facilitate the spread of HIV[1,2]. Evidence suggests that HSV-2 infection increases the risk of acquiring HIV. This is mainly due to the lesions that are caused by HSV-2 infection and facilitate infection by other STDs, making infected individuals 2–5 times more likely to contract HIV[1–4]. Co-infection also allows for an enhanced transmission of HIV as co-infected individuals have a higher concentration of HIV in their genital fluids than individuals with HIV only[1,3,4]. Moreover, between 40 and 80% of individuals diagnosed with HIV are co-infected with HSV-2, with a large portion of these individuals from among the homosexual male population[5–7].

Many mathematical models discuss HIV or HSV-2 alone[8–12], and a few discuss the relationship between HIV and HSV-2 [5,6,13,14]. For instance, Blower and Ma [6] coupled an HIV compartmental model with an HSV-2 model to investigate the effects of HSV-2 prevalence on the number of new cases of HIV; Abu-Raddad et al. [5] consider a homosexual male population and suggest that HSV-2 prevalence, if near an endemic level, may predict the spread of HIV; and Foss et al. [13] developed a dynamic model to estimate the HIV infections directly due to HSV-2 in a heterosexual population. Most disease models incorporate either the heterosexual population alone [11,13,14] or the homosexual population alone [5,6,9]. However, with the growing number of same-sex couples in the United States and other countries, which may be due to the growing acceptance of homosexuality, it is important to consider these types of interactions [15]. In Malunguza et al. [12], an HIV model is presented that separates the male population into heterosexual and homosexual, with the possibility of interaction to create a bisexual class. The female population is considered to be completely heterosexual and the model only considers HIV transmission. Including the possibility of homosexual relations was beneficial in that Malunguza et al. were able to consider various treatment scenarios corresponding to the different types of interactions. To our knowledge, a model that incorporates heterosexual and homosexual encounters among both male and female populations and includes the role of co-infection has not yet been considered.

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