Labor Migration and the Spread of STD: Gonorrhea in Japanese-Occupied Micronesia, 1919 – 1945

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> *"If you wanted to spread a sexually transmitted disease, you'd take thousands of young men away from their families, isolate them in single-sex hostels, and give them easy access to alcohol and commercial sex. Then, to spread the disease around the country, you'd send them home every once in a while to their wives and girlfriends."*
> -Mark Lurie

1. Introduction

Migration and mobility have increased over the years with the ease and availability of transportation, the opening of countries' borders, and the recent rise of globalization. This movement has increased the spatial scale of disease and the rate of spread, which incited considerable population health problems. Most people associate *recent* movement of information, goods and people with globalization; however, this is by no means the first episode of globalization. When looking at health consequences from population mobility, much can be learned from past episodes of globalization, specifically colonization. Population movement was slower, much more deliberate, and much more selective. This simplified episode of globalization allows a clearer picture of how the movement of people is associated with population health. Many complicating factors seen today—speed of movement, complicated transmission routes, vaccinations, preventative health care—did not exist early in the 20th century. In fact, the circumstances on a Japanese-occupied island in Micronesia (1919 – 1945) allow for a very simple and clear study of population movement and disease; there was a severe gonorrhea epidemic, and besides male labor migration enforced[1] by the Japanese, there were no other means for many new disease cases to infiltrate the island[2].

With human movement becoming faster and more common, disease will continue to spread rapidly around the globe reaching people who, under alternative conditions, would not have been exposed to these diseases. Understanding the association between migration and disease and being able to predict the consequences is imperative.

Historically gonorrhea was a major health concern often resulting in female sterility, and today—even with effective treatment—the sexually transmitted disease has been on the rise in many parts of the

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[1] Some claim that native labor migration was not forced, but rather "encouraged". In fact, local chiefs were paid to produce a pre-set number of young men. Thus, some volunteered but some were forced to participate.

[2] In 1930, 241 Japanese were living on the island of Yap. According to the author's interviews, there was little to no sexual contact between Japanese men and Micronesian women. There is some evidence of comfort women (forced prostitution by the Japanese) in Micronesia, but there were no stations on Yap.

world (Barnes and Holmes 1984; Landry and Turnbull 1998). Before WWII, gonorrhea was a major epidemic in some Japanese-occupied territories. This paper uses data from Yap, a small island in Japanese-occupied Micronesia where more than 40% of women 8 years and older were suffering from gonorrhea in 1930 (South Seas Government 1920-1937). This epidemic had huge demographic consequences, contributing to severe depopulation (Cassels and Singer 2004). Additionally, native Micronesian males were forced to work at phosphate mines 500 km away from home by the Japanese. Women did not migrate, and due to the distance between islands and lack of quick transportation, very few people left the island for reasons other than work at the phosphate mines.

This paper looks at the effect of labor migration on gonorrhea transmission. Past work has shown that migration can sustain or increase prevalence rates by constantly contributing new infections to a population. The objective of this paper is to demonstrate the potential magnitude of that process, and identify characteristics of migration that significantly affect prevalence rates.

Migration and sexually transmitted disease (STD) have long been associated: evidence has shown that migrants not only suffer from STDs more than non-migrants, but they are also responsible for spreading disease. Recent research has pinpointed the underlying mechanisms behind the association between migration and disease: risky sexual behavior such as numerous sexual partners and sex with prostitutes, poor living and working conditions, and then disease transmission to their partners once home (Brockerhoff and Biddlecom 1999; Chirwa 1997; Hirsch, Higgins, Bentley, and Nathanson 2002; Hunt 1989; Lurie et al. 2003a; Poudel et al. 2003; Quinn 1994; UNAIDS 2001; Yang 2004; Zuma, Gouws, Williams, and Lurie 2003). However, due to the inherently complicated process of migration, measuring the effect of migration on disease prevalence at home is difficult. For instance, how prevalent would HIV/AIDS be in South Africa if there were no institutionalized labor migration? This population health question is in many ways unanswerable *today* due to the complexity of transmission and migration routes. Nonetheless, since migration is predicted to be such a strong determinant of disease prevalence, understanding the magnitude of the effect would be valuable. This paper analyzes a simple historical case where the effect of labor migration on STD prevalence can be practically modeled.

The objectives of this paper are 1) to model gonorrhea transmission and migration, using historical data from Yap, Micronesia in order to estimate how much labor migration increased gonorrhea prevalence at home, and 2) to identify characteristics of the migration process that play an important role in spreading disease. But first, this paper reviews literature showing the links between migration and infectious disease, and why the links exist. The focus then shifts to Japanese-occupied Micronesia, where a look at the historical situation suggests that labor migration was very important in forming the gonorrhea epidemic. The microsimulation model is described, incorporating features of past models of gonorrhea transmission but explicitly modeling the migration process, and then fitted with data from Yap. Results show that male migration is an important determinant of the initial rate of increase of gonorrhea prevalence, but over time when prevalence rates stabilize, migration contributed to only a 3% increase in female gonorrhea prevalence in Yap. The model also predicts that under alternative migration scenarios, male migration could indeed account for a much larger increase in overall gonorrhea prevalence rates. Important determinants include the sexual behavior of migrants while away, the percentage of male migrants in the population, and their behavior once home. Other significant determinants include female behavior and the rate of migrant turnover.

2. Migration and sexually transmitted disease

Attempting to slow or stop infectious disease from travelers to local populations has been a public health concern for hundreds of years (Deaton 2004; MacPherson and Gushulak 2001). Local populations have been decimated by introduced disease to which local populations have no protection. These diseases affected local populations in two ways; some diseases increased morality rates while others lowered fertility rates. Pacific island populations experienced devastating depopulation from introduced disease such as tuberculosis, influenza, venereal diseases and cholera in the 1800's from sustained contact with Westerners. Gonorrhea was one of many diseases introduced to Micronesia during this time (Hezel 1983) that contributed to depopulation. But even today with extremely easy and effective treatment, gonorrhea is still a major disease burden in Micronesia and throughout the world (Barnes and Holmes 1984).

Migrants commonly suffer from infectious disease, specifically STDs, more than non-migrants (Gras, Weide, Langendam, Coutinho, and van den Hoek 1999; Lurie et al. 2003b; Poudel et al. 2003; UNAIDS 2001; Zuma et al. 2003). Indeed the act of migration increases risk of STD infection (Chirwa 1997). Studies in Africa (Chirwa 1997; Hunt 1989; Lurie et al. 2003b), India (Poudel et al. 2003), South America (Hirsch et al. 2002) and Europe (Gras et al. 1999) have documented this fact. More than 10% of migrant workers in India were infected with HIV compared to only 2.5% of non-migrants, for example (Poudel et al. 2003).

Recent literature has explored the complexities of population mobility and disease, especially labor migration and reasons why migrants suffer disproportionately from STDs. This research has shown that migrants suffer more than non-migrants because of their risky sexual behavior such as concurrent partners and sex with prostitutes, exposure to a new social environment and lack of social controls, and potentially because they are pre-selected for characteristic conducive to higher risk of infection (Brockerhoff and Biddlecom 1999).

This is not a new phenomenon. Migrants have a history of suffering from STDs long before the HIV/AIDS epidemic. For instance in Africa, where economic development was largely based on migrant labor, the migrant labor system changed the social environment. It caused a breakdown in family and sexual patterns and an explosion in STDs occurred (Hunt 1989). A common pattern of migration-induced societal changes is seen in many parts of the world today, contributing to risky migrant behavior and STD spread.

Migrant men exhibit risky sexual behavior that is conducive to STD infection, both while gone and after returning home (Poudel et al. 2003). They have a higher rate of sexual partner change (Chirwa 1997; Gras et al. 1999; Hunt 1989; Poudel et al. 2003), a higher rate of concurrent partnerships (Brockerhoff and Biddlecom 1999), more sex with prostitutes, and more common pre- or extra-marital sex (Poudel et al. 2003).

While away from home, migrants are exposed to a new social environment. Men often migrate to crowded urban places where they feel anonymous, or to underdeveloped regions haphazardly organized around gold mines, for example, where living conditions are poor and unhealthy. In South African mining towns, the migrant labor system created a market for prostitution (Quinn 1994). Women would turn to prostitution to make money since they lacked alternate earning opportunities. Male migrants, separated from their wives and living in an almost exclusively masculine environment, often had difficulty forming healthy relationships with women. The unequal sex ratio and peer pressure also encouraged prostitution.

Enclaves of labor migrants usually consist of great numbers of male workers living together in insecure and depressing conditions, lacking benefits of family life and other customary supports (Doyal and Pennell 1981). These men often feel anonymous and free from familial roles or social norms guided by family (UNAIDS 2001). The lack of village or social controls, plus the contextual effects of the new environment (young men, uneven sex ratio) and access to prostitution lead to STD epidemics (Hunt 1989).

Some evidence points towards a lingering effect, or a difference between migrants and non-migrants regarding sexual behavior even after they return home. This could be migrant selectivity, i.e.

men who migrate exhibited different characteristics from the start, or because individual attributes changed due to the process of migration. In Malawi, one study suggested that newly returned migrants would have money and were attractive to women. Thus, they would have multiple sex partners, both as a symbol of economic and social success, but also as a form of entertainment (Chirwa 1997).

Lastly, an understudied determinant of the relationship between male migration and disease transmission has been female sexual behavior while their migrant partners are away (Lurie *et al.*, 2003). This recent study of HIV/AIDS in African couples has shown the women are likely to become infected outside of their primary relationship; the woman was the infected partner in 1/3 of the HIV/AIDS discordant couples in their study. They also found that women with absent partners are more likely to have additional sexual partners than women whose partners are present. These results suggest that risky female sexual behavior while men are gone is also important to consider.

The link between migration and STD has been documented, yet far fewer studies have examined the impact of migrants' return home (Lurie 1997). STDs are often carried home by returning migrants, infecting women who lacked previous exposure. Circular migration, through a constant input of new infections to a pool, can sustain or increase prevalence rates at home (Chirwa 1997; Doyal and Pennell 1981; Hunt 1989; Lurie et al. 2003a; Lurie 1997; Poudel et al. 2003; van Onselen 1976).

The role of worldwide dissemination of HIV/AIDS from migrants is well known. Some work has documented this on a smaller scale, linking countries with recent (and historically) high rates of migration with significant HIV infection, such as Rwanda and Burundi (Pison, Le Guenno, Lagarde, Enel, and Seck 1993; Quinn 1994). For STDs other than HIV, some work has identified labor migration as the primary factor in disease spread. In Zambia, urethral stricture—a long-term result of gonorrhea—was spatially mapped, and results showed that the highest area of concentration was in the copper belt, the primary labor concentration area. The second highest area of prevalence was in the northeast, a labor reserve area for the mines (Hunt 1989), suggesting that the migrant labor system accounted for differences in STD prevalence. Gonorrhea prevalence in eastern Africa also resembles patterns of labor migration (Bennett 1962; Verhagen and Gemert 1972). To explicitly show the relationship on an individual level is however quite difficult due to exogenous factors. One study attempted to explicitly measure the association between migration and HIV infection among migrant men and their rural partners, but did not find that being a partner of a migrant was a significant risk factor for HIV infection among women (Lurie et al. 2003a).

Migration has been shown to be a major structural factor in the spread of sexually transmitted disease. Nonetheless, this important literature is lacking quantitative answers of “how much (faster) can labor migration increase STD prevalence in women at home?” To begin to answer this question, I first present a historical example that suggests that labor migration contributed to a severe gonorrhea epidemic, and then demonstrate how migration can increase gonorrhea prevalence. Next is a description of Yap during the Japanese occupation, followed by the microsimulation model of migration and gonorrhea transmission.

3. Gonorrhea and Labor Migration on Yap

The Japanese first came to Micronesia in 1914 and were officially mandated the islands in 1919 by the League of Nations. They were not the first foreigners to rule Micronesia, but they were by far the most influential. Sustained contact with missionaries, traders and whalers began in the early 1600’s. Spain was the first foreign power to colonize the islands in 1886, and then the Germans ruled Micronesia from 1899 until WWI when the Japanese arrived. Unlike the other two colonial powers, the Japanese had plans to convert Micronesia into an economic asset. Eventually more than 70,000 Japanese lived on the islands, outnumbering the native population. They also succeeded in building a thriving economy based on four main exports: sugar, copra, dried fish, and phosphate. This paper focuses on native labor migration to phosphate mines, and a gonorrhea epidemic that we argue was associated with that migration.

During the Japanese occupation, Yap (one of the islands in Micronesia) was gaining international attention because the native population was drastically decreasing. In 1924, the population was 7,523. Five years later, it had decreased by more than 13% reaching 6,545 in 1929, and still falling. The League of Nations ordered Japan to investigate the cause of the population decline; thus an in-depth study of native health on Yap began in 1929, led by Dr. Fujii, the Japanese director of the Yap hospital. He carefully examined almost all of the inhabitants on the main island of Yap from 1929 to 1930. Dr. Fujii concluded that the decrease in population was due to a high death rate caused mostly by tuberculosis, and a low birth rate resulting from gonorrhea. In fact, gonorrhea infections on Yap had reached endemic proportions.

Dr. Fujii examined 2,354 of the 3,884 natives living on Yap for gonorrhea. His results were shocking. He found 312, or 25% of males suffering from gonorrhea, and 472, or 43% of women with gonorrhea (South Seas Government 1920-1937). Figure 1 depicts the percentage of natives suffering from gonorrhea by age. No patients under eight years old were examined. Young women had the highest gonorrhea prevalence, reaching 63% of women aged 16-20 and 51% of women aged 20-25 (South Seas Government 1920-1937). The prevalence of gonorrhea in men peaked later than women, in the age-group 31-35 years (39%).

- Insert Figure 1 about Here -

At the same time of this episode of severe depopulation and the gonorrhea epidemic, the Japanese were recruiting a large portion of young men from Yap to work at the phosphate mines in Angaur (Palau), an island 500 km away. This process started during the German occupation around 1909 and continued through the Japanese occupation up until 1945. Every six months a new cohort of young men replaced the previous group of workers (Decker 1940). Officially labor was optional, but in fact the Japanese government ordered strict quotas from native chiefs; they were required to supply a set number of workers. In 1922, 283 men from Yap—nearly 4% of the total Yapese population—were working at the mines (South Seas Government 1920-1937). Considering that no women or elderly men left for the mines, 283 men accounted for a considerable proportion of working-age men.

Once arriving at the mines, migrant laborers were required to work six days a week. All of the men slept on bunk beds in single-sex dormitories with other migrants from Yap. Working and living conditions were poor, according to respondents in interviews conducted by the author in Yap and Angaur (Palau) in 2004, although the migrants did find some time to relax. Some men made their own alcohol, or occasionally stole supplies from the Japanese, and organized traditional dances. There was a Japanese prostitution house with Japanese women on the island at this time, but responses from interviews by the author varied as to whether migrant men visited these women. They were not officially allowed to visit, but some of them might have snuck in. No matter whether the migrants visited the prostitutes, the laborers mingled with native Angauran women at the phosphate mines. As many respondents mentioned, they were free to date and be sexually uninhibited with these women. The sex ratio of men to women was high, about 3 to 1. It increased to 5 to 1 if we consider only Micronesian women and men aged 15 to 45 on the island, for the only women on island were Japanese wives, children and native Angauran women in addition to the large numbers of young male migrants.

There are no existing data showing gonorrhea prevalence on Angaur. However, Micronesians living on Angaur visited the hospital on average three times a year, and 30% of natives were treated for infectious disease—which includes gonorrhea—during these visits (South Seas Government 1920-1937) which suggests that gonorrhea prevalence was high.

The circumstances in Japanese-occupied Micronesia and high turnover of labor migrants from the phosphate mines suggest that migration was partially responsible for the gonorrhea epidemic on Yap. Recent work has shown that a small core-group of individuals, especially migrants, often account for the majority of disease spread (Korenromp, vanVliet, Bakker, deVlas, and Habbema 2000; Kretzschmar and Morris 1996; Lurie et al. 2003a; Lurie et al. 2003b; Morris and Kretzschmar 1995; Morris and Kretzschmar 2000; Yang 2004). The core-hypothesis suggests that relatively small populations of highly sexually active infected men and women are directly or indirectly responsible for all cases. One study found that 15% of a infected population—or less than 0.1% of the total population—accounted for nearly 30% of know gonorrhea cases (cited in (Barnes and Holmes 1984; Garnett and Anderson 1993). These core transmitters, who could be migrants, may be responsible for maintaining the level of the disease, while migrants continue to introduce disease constantly from the outside. The following microsimulation model will test this hypothesis.

4. Model of population mobility and gonorrhea transmission

Introduction & past models of mobility and epidemics

The model presented in this paper simulates the sexual activity of a population over time and the associated spread of gonorrhea. The objective of the model is to introduce population mobility of males and demonstrate how male migration affects gonorrhea prevalence over time.

Human mobility plays an important role in the spreading of disease. Many empirical papers have documented this fact (Chirwa 1997; Hunt 1989; Lurie et al. 2003a; Poudel et al. 2003; UNAIDS 2001; Zuma et al. 2003). Only a few papers have included human mobility in their epidemic models (Arino and van den Driessche 2003; Sattenspiel and Dietz 1995). These models use sets of differential equations to model the general mobility process between discreet regions. These equations can specify the rate of movement ranging from complete isolation—where no one travels—to constant travel. These models define where people are going, the per capita rate of their leaving, and per capita return rates, thus defining duration of stay. The mobility rates then influence the rate of contact between individuals, and probability of disease transmission, in epidemic models.

One major advantage of these models, as with the present simulation model, is that they allow for simultaneous consideration of both population mobility (behavior) and epidemic processes, enabling study of interactions between the two processes. The additional advantage of the present simulation model is that it can model complex *individual* dynamics in a transparent way. With this model we can recreate any historical situation, and experiment with different sets of assumptions about the mobility process to see how the epidemic process is affected, or which variables are the most potent determinants of the epidemic. For instance, we can experiment with the proportion of residents migrating, their behavior while away, and the prevalence of disease in the return-migrant population to see how these changes affect disease prevalence in the home population. This simulation model, unlike the previously mentioned models, can also disclose the amount of random variability inherent in the process (Wachter, Hammel, and Laslett 1978).

Gonorrhea—the real world

Neisseria gonorrhea, the bacteria responsible for gonococcal infection, grows on mucous membranes and cannot live outside the human body for long. The disease is transmitted by sexual exposure; the probability of transmission from an infected male to a susceptible female during a single exposure is .5 to .7, while it is much lower from an infected female to a susceptible male, ranging from .2 to .3 (Hethcote and Yorke 1984) (Barnes and Holmes 1984) to 0.6 (Garnett and Anderson 1993; Swinton, Garnett, Brunham, and Anderson 1992).

Gonorrhea infection does not confer protective immunity in the future, and individuals who acquire gonorrhea become infectious within a few days. Many women remain asymptomatic, which is quite dangerous since without treatment about 12% of cases will induce infertility: 20% of women with gonococcal infection will suffer from pelvic inflammatory disease (PID), and 60% of women with PID will become infertile (Anderson 1994; Swinton et al. 1992). Today, gonorrhea can be cured with a single dose of antibiotics.

Without treatment, the duration of a gonorrhea infection is debatable. A pre-antibiotic era study cited in Hethcote and Yorke (1984) followed the infections of 73 female inmates of the New York House of Detention in 1942 (Mahoney *et al*., 1942). Each woman was tested two or three times a week, for three to four months. Three patterns were observed: 46% of the women remained positive, 42% became and remained negative, and 12% reverted to negative but then had one or two positive findings. All the women were initially symptomatic, and most were prostitutes. This finding leads to two questions: does duration of infection depend on the number of previous infections (here we assume a prostitute would have more infections, on average, than other women), and without treatment does an infection with symptoms last longer or shorter than an asymptomatic infection? Additionally, when does the infectivity stop?

Past models of gonorrhea transmission have used drastically different estimates of duration. Estimates range from 6 months (Swinton et al. 1992) for all people, to 3 – 12 months for asymptomatic women, 3 – 6 months for asymptomatic men, 3 – 45 days for symptomatic women, and 2 – 30 days for symptomatic men (Hethcote and Yorke 1984), to 71 days and 48 days for asymptomatic women and men, and 16 and 7 days for symptomatic women and men (Kramer and Reynolds 1981).

Gonorrhea is passed from an infected person to a susceptible person through sexual contact; thus the probability that a person is infected depends greatly on individual behavior. Someone who exhibits risky sexual behavior, i.e. someone with many partners, someone who visits prostitutes, or someone with concurrent partners, has a high risk of being infected. Furthermore, past work on gonorrhea transmission has shown that a relatively small population of highly sexually active infected men and women are directly or indirectly responsible for all cases of gonorrhea. These groups are called "core" groups; in the following model core men and women switch partners more often and have more sex acts on a given day than non-core men and women. They are also more likely to choose a partner in the same sexual activity group. For example, a core woman has a higher change of infection than a non-core woman because she 1) has more sexual partners on average than a non-core woman, and 2) she chooses core males as partners more often.

Core men can maintain the level of disease in a population, while migrant men can introduce new diseases to the population. Many studies have shown that core transmitters are extremely significant in transmitting and maintaining high levels of gonorrhea in a population (Barnes and Holmes 1984; Brooks, Darrow, and Day 1978; Potterat et al. 1985; Rothenberg 1983; Yorke, Hethcote, and Nold 1978). Additionally, past sociological work on migration and the behavior of migrants has shown that migrants exhibit risky sexual behavior have a higher risk of infection than non-migrants. These two groups—core men and migrants—are not necessarily mutually exclusive categories, and can work in combination to initiate or exacerbate a gonorrhea epidemic. This model attempts to replicate the process of sexual activity and gonorrhea transmission, while "experimenting" with different migration scenarios in order to make tenable inferences about the relationship between male migration and gonorrhea transmission.

Details of the model

In this simulation model each person is represented by a numbered set of characteristics; at the outset of the model some characteristics are assigned and stay constant, such as sexual activity group and the number of sexual partners per month. Other characteristics vary during model runs, such as infection status and the characteristics of an individual's sexual partner. These changes are driven by stochastic events, which are determined by Monte-Carlo sampling from probability distributions.

Cohorts of men and women are modeled separately every day. To keep the model simple, specific individuals in a couple are not followed; rather, men and women choose a partner from a specific category, such as a core man/woman, non-core man/woman, or a return migrant, and the risk of infection from a partner in that category is constant on any given day. For example, let a woman choose a core man as a partner; the probability that a core man is infected on day y is the proportion of infected core men on the previous day, y-1.

On day one, each woman is considered as she steps through a set of risks: recovery, sexual partner change, and infection. After the last woman is through, gonorrhea prevalence for each sexual activity group is recorded: core women and non-core women. Now, the men are modeled on day one, also stepping through the same set of risks, but using the newly calculated characteristics of gonorrhea prevalence in females to calculate risk of male infection. The chance that a male becomes infected is directly associated with the chance that his partner—either a core or non-core female—is infected. After the men have finished day one, their characteristics are recorded and used for modeling sexual activity and risk of gonorrhea infection for the female population on day two. This cycle repeats for the duration of the model run.

Factors affecting gonorrhea transmission can be described in six modules (Van der Ploeg et al. 1998): demography, sexual behavior, transmission, natural history, health care, and interventions. See Table 1 for a list of parameters and point estimates used in the model, and a list of sources for those estimates. Age structure and parameters defining the migration process are described in the demography module. The sexual behavior module describes relationships that are responsible for transmitting gonorrhea, which depend on factors such as their umber of sexual partners per month, average number of sex acts per day while in a relationship, and the waiting time between relationships. The transmission module specifies transmission probabilities, and other relevant epidemiological factors of gonorrhea transmission are defined in the natural history module. The present model does not incorporate either the health care or the interventions module since we are modeling gonorrhea transmission at a time when treatment for gonorrhea was not yet available, but these modules could easily be incorporated later.

- Insert Table 1 about Here -

Modeling return migration

Migrants are known to acquire new infections while they are gone and then carry them home; this translates to higher gonorrhea prevalence in newly-returned migrants compared with gonorrhea prevalence in the non-migrant population in the model. In the present model, if a man is currently a migrant—the chance of a man being a migrant will be specified in each model run—his sexual behavior is different than if he were at home. While away, migrant men do not stay in long relationships. Rather, they engage in sexual acts with prostitutes once a week. Prostitutes are assumed to have a 75% chance of gonorrhea infection at any given time (Anderson 1994), which leads to high gonorrhea prevalence in migrants as well.

Gonorrhea prevalence in return migrants depends on the following factors, some of which are time-sensitive: how many infections were acquired while away, the assumed duration of gonorrhea, how often a group of migrants return home, and their sexual behavior once home. See Figure 2 for an illustrative explanation of how migration is conceptualized in the model.

- Insert Figure 2 about Here -

Figure 2 depicts the probability that a woman's partner is infected if she chooses a return migrant as her new partner during the course of a year. For instance, if she chooses a return migrant with core characteristics as a partner on day 140, her partner's chance of infection is 0.33. The assumptions in figure 2 are as follows: 1) 50% of return migrants are infected when they return home. 2) A gonorrhea infection in males lasts 30 days. 3) A cohort of migrants returns home three times a year, or migrant turnover is every 120 days. On days 0, 120, and 240 one out of every two migrants is infected with gonorrhea. However, not all of the men who acquired infections while away acquired them on the day before they returned home; we assume that the acquired infections were uniformly spaced over the previous 30 days. Therefore 1/30th recover one day after returning home, and 100% of the migrants have recovered from infections acquired while away after 30 days at home.

This assumption does not mean that return migrants are eventually free from infection; our model allows return migrants to continue to acquire new infections from women at home. Over time gonorrhea prevalence in the return migrant population resembles gonorrhea prevalence of the overall population, which is characterized by two sexual activity groups. A return migrant will become either a "core male" or a "non-core male". Men in the core sexual activity group have more sexual partners, change partners more frequently, and have more sex acts on a given day than non-core men, thus have a higher gonorrhea prevalence rate than non-core men. The default assumption is that 20% of return migrants fall into the core male population; in fact, 20% of the non-migrating population is assumed to be in the core sexual activity group. Some research has suggested that migrant characteristics may change during the process of migration, and that return migrants display risky sexual behavior even after returning home. In the model, the proportion of return migrants defined as core therefore varies from 20% to 100%.

When a woman chooses a male partner, she has three options: whether he is a core male, a non-core male, or a return migrant. Her choice will affect her chance of acquiring gonorrhea, since the gonorrhea prevalence in each male category is different. Newly returned migrants have the highest gonorrhea prevalence, followed by core males, and then non-core males.

Model structure—overview

To attempt to make the inner-workings of this model as transparent as possible, we first review the broad structure of the model, then the daily algorithm of the model, and then one women's history over the course of a year as an example as we explicitly address each assumption.

At the beginning of the model, specific parameters for the model run are specified, such as parameters that define the migration process and initial characteristics of each individual. Individual characteristics include age, sexual activity group, and number of sexual partners per month. Then, activity is simulated for each individual one day at a time.

Each day an individual moves through the following three broad steps. 1) Recovery: The individual's infection status is recorded, and if she is infected, she has a chance of recovery on that day. 2) Sexual relationships: Is she currently in a relationship? If so, with whom? Relationships are at risk of dissolving. If the relationship dissolves, she is assigned a waiting period until she can begin a new relationship. 3) Risk of infection: If she is currently in a relationship that does not dissolve, then she is at risk of infection. Her risk of infection is determined by the probability that her partner is infected, the probability of transmission from an infected partner to a susceptible partner per sex act, and the number of sex acts in the day. This activity is repeated for each woman and man in the model for each day in the model run.

Let us now step through the daily structure of the model in more detail while referencing one hypothetical individual's history. Figure 3 depicts the timeline of one individual's relationships and infections status over one year (female #146).

- Insert Figure 3 about Here -

Model structure—initiating characteristics

In this specific model run, the percentage of males is as follows: 30% migrants, 14% core males, and 56% non-core males. As always, 20% of women are in the core sexual activity group and 80% are non-core. Migrant turnover occurs every 120 days; 50% of return migrants exhibit core characteristics.

The age structures of men and women in the model resemble the actual age structure of the Yap population in 1930 (data not shown). Men and women do not age in this model and there is no explicit fertility or mortality. Rather, we assume a stable population where an age group has the same proportion of the population over time. When the model begins, the woman being used as an example is assigned characteristics. She is 15 years old, in the non-core sexual activity group, with an average of one current partner per month.

Model structure (daily steps)—recovery

The first step in the daily simulation structure is to look at infection and recovery. Is the individual infected? If so, then her daily chance of recovery is equal to 1 / d, where d is the average infectious period. This risk of recovery is independent of how long the person has been infected, and she becomes susceptible to infection again once recovered. As discussed earlier, duration of infection without treatment is tricky to measure. In the present model, the average infectious period for females is set at 60 days, which is similar to that used in the Kramer and Reynolds simulation model of gonorrhea (1981), and is 30 days for males. The daily chance of recovery is 1/60 for females, thus actual length of infection varies. Woman #146 had two infections over the course of the year. The first one lasted 36 days, the second 26 days[3].

Model structure (daily steps)—sexual relationships

The next step in the daily cycle concerns relationships status. Choosing a partner—both initially and with each subsequent partner change—is an extensive process. Individual #146's first partner is a newly returned migrant with non-core characteristics, 15 years of age, and with a 0.11 chance of infection.

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[3] Durations of infection vary quite a bit. For instance, individual #195 had an infection that lasted 75 days that year.

Her age came into account when considering who her partner was. All individuals in the model are aged 15 – 45, with the proportion at each age determined by the age structure of Yap in 1930. At the beginning of the model and with each change in partners, a person chooses the age of his or her partner according to an age-preference matrix (see Table 2) (Korenromp et al. 2000). Females prefer somewhat older partners, on average about five years, and males prefer younger partners. Recall that woman #146 is 15 years old. Even though women choose older men on average, all of her relationships are with fellow 15 year olds.

- Insert Table 2 about Here -

Partner choice is also dependent on core group status. 20% of men and woman are categorized as "core" in this model. This assumption has two implications. First, both core men and women have a higher probability of gonorrhea infection than non-core men and women, respectively. Second, core individuals are more likely to partner with other core individuals; thus core women are more likely to become infected than non-core women, for example. The probability that a core woman will choose a core man, and visa-versa, depends on a mixing matrix.

In this model, mixing may range from assortative (like with like) to proportionate (or random) where sexual partners are assumed to be chosen in relation to their sexual activity and the proportional representation of their activity class in the total population. The parameter *e* is a measure of the degree of assortativeness; when $e = 0$ mixing is assortative and when $e = 1$ it is proportionate. The parameter allows for an entire set of mixing probabilities to be included in the model. Only two sexual activity classes are defined in this simple model, core and non-core, which make the mixing matrix fairly simple. For example the probability that a core woman chooses a core man for her new sexual partner is:

$$e * \frac{N_1 * c_1}{N_1 * c_1 + N_2 * c_2} - (1 - e),$$

where N_1 is the percent of core women, N_2 is the percent of non-core women, c_1 is the average number of partners per month for core women and c_2 is the average number of partners per month for non-core women. In the present model run, the mixing parameter is set at 0.6, which implies that a core individual will choose another core individual 61% of the time.

Individuals in the simulation are allowed to have only one partner at a time; however, some have up to six partners a month. Figure 4A shows the average number of partners per month for core and non-core women, and 4B for core and non-core men. The number of partners per month determines the length of relationships.

- Insert Figures 4A and 4B about Here -

Individuals are not allowed to have concurrent relationships in this model, but some have multiple partners in a month. For men and women who have two or more partners per month, the daily probability of switching partners is q/30, where q is the number of sexual partners. People with two or more sexual partners in a month do not wait between relationships; new relationships begin when the current relationship ends.

Individual #146 has one partner per month on average. However, this is not modeled as a 1/30 daily probability of switching partners. In order to allow for some lengthy relationships, we interpret "one partner per month" as one partner *or less* per month, and set the duration of a relationship to about 5 months on average. For a non-core individual with one partner per month—like individual #146—20% of relationships randomly dissolve every 30 days (Kramer and Reynolds 1981). On average, individuals in the model with this specification have two to three different sexual partners in a given year. For people in the core sexual activity group, the risk of a relationship dissolving is 20% every 15 days. This high rate is appropriate for modeling the sexually promiscuous environment that was acceptable on Yap during the Japanese occupation. Once a relationship dissolves, an individual is assigned a waiting period until he/she is allowed to start a new relationship. The length of the waiting time between relationships is randomly drawn from an exponential distribution with a 30 day mean. He/she may wait simply a few days until initiating a new relationship, or he/she may have to wait 44 days like individual #146 does after her first relationship dissolves.

In the present model, women react to their partner's migrating in one of two ways. They either immediately change partners, and start a relationship with a man presently at home, or they remain abstinent while their partners are away then continue with the same partner when he returns home. In both situations, relationships have a risk of dissolving whether or not the current partner is present. The working assumption is that women switch partners if their partner migrates. Although partner change most likely is not immediate, the time lag in partner change would not significantly change the outcome of the model. The assumption that women change partners may not be appropriate for all situations, but partner sharing and extra-marital sex while male partners are absent has been documented (Lurie et al. 2003b) and was often the case in Yap during the Japanese occupation (author's interviews).

Model structure (daily steps)—risk of infection

The last major step in the daily simulation cycle pertains to gonorrhea infection. Risk of infection is a function of the number of sex acts in a day, the probability of transmission from an infected partner to a susceptible partner per sex act, and the probability that the partner is infected.

- Insert Figures 5A and 5B about Here -

Gonorrhea prevalence varies by age. In women, gonorrhea prevalence was the highest for young women, as shown in figure 5B. Figure 5A depicts how gonorrhea prevalence is higher for a 30 year old man than for a 45 year old man. For example, if overall male gonorrhea prevalence is 0.25, then a male in the 20 – 25 year age group would have a 0.28 chance of infection: 0.28 = 0.25*(1 + 0.13). These data come from the distribution of age-specific gonorrhea cases seen in males on the island of Yap, Micronesia in 1930, depicted in figure 1 (South Seas Government 1920-1937).

Past work has estimated the probability of transmission from infected men to susceptible women to fall between 0.5 and 0.8 per contact (Barnes and Holmes 1984; Hethcote and Yorke 1984; Swinton et al. 1992; Yorke et al. 1978). The present model uses 0.5 as the point estimate for the probability of gonorrhea transmission per exposure from an infected male to a susceptible female. This estimate was used in a previous microsimulation model of gonorrhea transmission (Kramer and Reynolds 1981). The probability of transmission from an infected female to a susceptible male falls between 0.2 and 0.3—we use 0.2 for the present model.

The final factor in risk of infection is the number of sex acts per day. For each sex act, risk of infection equals the product of the probability of transmission and the probability that the partner is infected. This is the probability of transmission for each single exposure. The number of sex acts in a given day depends on the sexual activity group of the individual. For a core individual, the number of sex acts per day is drawn from a Poisson distribution with mean = 0.314 (Kramer and Reynolds 1981). This translates to a little more than two sex acts per week on average. For a non-core individual, the number of sex acts is drawn from the same distribution, but with a mean of 0.15, which translates to about one sex a week. Lastly, the model assumes that an individual does not engage in sex while the woman is menstruating, for seven days out of every month.

Individual #146 began a new relationship on day 4, but never acquired an infection from him. On day 165, individual #146 began another relationship, but had no sex act that day or the following. On day 167 she had one sex act with her partner and became infected with gonorrhea.

In the present model men, after recovering from an infection, avoid becoming reinfected by the same partner since they are more likely to be able to tell when they are infected and who infected them. Women—often unaware of an infection—are at risk of becoming infected on multiple occasions from their partner.

Overall prevalence is the proportion of individuals infected at any given day. The smallest time period considered in this model is one day, and the model assumes a month to have 30 days, thus a year is 360 days. Activity is simulated for each woman, and then for each man in the model, one at a time one day at a time for 20 years.

5. Results

Migration can sustain or increase prevalence rates through a constant input of new infections to a population. The goal of this exercise was to get a sense of the magnitude of the effect and which characteristics of migration contribute the most to the process of transmitting disease.

The results presented below show the relationship between migration and gonorrhea prevalence from models fitted with historical Micronesian data and without any form of gonorrhea treatment. Therefore, prevalence rates are quite high. In the following results, we see gonorrhea prevalence rates for women between 30% and 60%. Overall gonorrhea prevalence for women aged 8 – 45, as seen in figure 1, was near 43% in 1930 on the island of Yap, Micronesia. Therefore, the first goal was to re-create this situation with reasonable parameters and estimate how much lower prevalence would have been without labor migration.

Figure 6A and 6B shows gonorrhea prevalence rates over 20 years under three migration scenarios: no migration, likely migration (as seen on Yap in 1930), and extreme migration. An assumption of "likely migration" in these models implies that 30% of the male population migrates at any given time[4] with turnover every 120 days, and 50% of return migrants exhibit core-sexual activity group

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[4] The ages of the male population in the model ranges from 15 to 45 years. In 1922 (the earliest available data) 4% of the entire Yap population worked at the phosphate mines. Assuming 50% of the population is male and 40% of the male population is between the ages of 15 and 45, 20% of the male population aged 15 to 45 migrated to the

qualities once home. Assumptions of "extreme migration" means that 50% of the male population migrates with turnover every 30 days, and all return migrants exhibit core-sexual activity group qualities. Migrant men exhibit risky sexual behavior in all the model runs unless otherwise specified: they engage in sexual encounters with prostitutes once a week while away. Lastly, female migrant partners also engage in risky sexual behavior while their partners are away. Unless otherwise specified, women are at risk of infection from outside their primary relationship while their partners are away.

- Insert Figures 6A and 6B about Here -

Female gonorrhea prevalence is depicted in figure 6A. Overall female gonorrhea prevalence is the weighted average of gonorrhea prevalence from 20% core women and 80% non-core women. This figure shows two important results. First, prevalence rates under the likely-migration scenario are not very different than the no-migration scenario; but secondly, migration does play a significant role in the rate of increase of gonorrhea prevalence rates over time. Gonorrhea prevalence rates seem to eventually stabilize due to a combination of set parameters (disease duration, number of sexual partners, transmission probabilities) and a constant input of new infections by migrants over time. Average prevalence over the last five years is 0.40 under the no-migration scenario, increases to 0.43 under likely-migration assumptions, and jumps to 0.54 under extreme-migration assumptions. This shows that migration, assuming a likely scenario, contributes to only a 3% increase in female gonorrhea prevalence. Migration potentially can contribute to a significant increase in gonorrhea prevalence rates if we assume that more men migrate, the rate of migrant turnover is much quicker, and return-migrant behavior is drastically altered.

Although migration seems to not contribute to a drastic increase in female gonorrhea prevalence once the rates stabilize, it does alter the initial rate of increase of gonorrhea prevalence. For the first four years of the simulation female prevalence rates are increasing, but under likely- and extreme-migration assumptions the rate of increase is much faster. For example on day 360, female gonorrhea prevalence is 0.16 under the no-migration scenario, 0.36 under likely-migration assumptions, and 0.49 under extreme-migration assumptions. These translate to a daily rate of increase of 0.045%, 0.100%, and 0.145% respectively. Male migration seems to accelerate the introduction of gonorrhea and onset of a gonorrhea epidemic when no treatment is available.

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mines. We estimate that the likely proportion is 30% however, because the Germans employed many more Yapese at the mines than the Japanese (from 1906 until the end of WWI).

Figure 6B shows gonorrhea prevalence rates for male non-migrants; this category includes return migrants but excludes current migrants, therefore capturing the increased gonorrhea prevalence of newly returned migrants. This is why male gonorrhea prevalence seems to be much more variable over time than female gonorrhea prevalence. The same two results are seen with male prevalence rates. First, there is not a large difference between the no- and likely-migration scenarios. The average male prevalence from year 15 to 20 is 0.19 for the no-migration scenario and 0.21 for the likely migration scenario. Assuming an extreme migration scenario, male prevalence rates jump to 0.30. Therefore, migration can play an important role in increasing gonorrhea prevalence in males also, but most likely, migration as it was in Yap in 1930 only contributed to a 2% point increase in male non-migrant gonorrhea prevalence.

Second, according to the model, male migration contributed to a steep rate of increase in male prevalence rates over the first 4 years. On day 360, male gonorrhea was just under 0.10 in the no-migration scenario, but was already close to 0.20 in the likely-migration scenario and close to 0.30 in the extreme-migration scenario.

The next set of results show specific characteristics of migration and how they affect female gonorrhea prevalence. Migration processes that we consider include the percent of the male population that migrates, migrant sexual behavior, the rate of migrant turnover, return-migrant sexual behavior, and the sexual behavior of female migrant partners.

- Insert Figure 7 about Here -

Figure 7A shows the relationship between the proportion of migrants in the male population and female gonorrhea prevalence. Again, the likely-migration scenario assumes 50% of return migrants exhibit core characteristics and migrant turnover is every 120 days, while the extreme scenario assumes 100% of return migrants exhibit core characteristics and migrant turnover is every 30 days. However, these models show the change in female gonorrhea prevalence when the proportion of migrants in the total male population varies between 0% (no migration) to 50%.

Also seen in Figure 6A, female gonorrhea prevalence (averaged over the last 5 years) is around 0.40 when no migration is included in the model. The association between the proportion of migrants in the population and female gonorrhea prevalence depends on the migration scenario; the slope is much steeper assuming extreme-migration. With 30% of the male population migrating—which is the likely scenario—female gonorrhea prevalence increases to 0.43 under other likely assumptions, and to 0.50

under extreme-migration assumptions. With 50% of the male population migrating, female prevalence increases to 0.45 and 0.54, respectively.

Migrant turnover or circular migration has also been noted in recent literature as a significant determinant of disease transmission. Figure 7B shows the relationship between rate of migrant turnover and female gonorrhea prevalence for two migration scenarios: likely and extreme. The likely-migration scenario assumes 30% migrants, with 50% return-migrants exhibiting core-sexual activity group characteristics—more sexual partners, shorter relationships, and more sexual encounters. The extreme scenario assumes 50% migrants, with 100% of return migrants exhibiting core characteristics. Rate of turnover varies from every 30 days to once a year.

Female gonorrhea prevalence is markedly higher when migrant turnover is once a month. Recall that female gonorrhea prevalence is 0.40 with the absence of migration. Assuming a likely-migration scenario, female prevalence would have increased to 0.47 if turnover was every 30 days, 0.434 if turnover was every 120 days (which is the default assumption), and to 0.432 if migration were only once a year. The shape of the relationship is the same but the values are higher in the extreme-migration scenario. Female gonorrhea prevalence is quite high at 0.54 if migrant turnover was once a month and it drops to 0.50 with turnover once a year. Migrant turnover plays a significant role in the rate and scale of disease transmission, but much more so at higher levels.

Risky migrant sexual behavior has been blamed for the association between migration and disease transmission; the generally agreed-upon assumption is that migrants feel anonymous and free from social norms while migrating, thus engage in risky sexual behavior such as encounters with prostitutes, numerous sexual partners and concurrent partners. In the present model, migrants have sex with prostitutes once a week while migrating. Gonorrhea prevalence in prostitutes is set at 0.75 in the model; therefore migrants have a high risk of infection. Figure 7C shows the relationship between migrant behavior—frequency of sex with prostitutes—and female gonorrhea prevalence.

Female gonorrhea prevalence in the likely-migration scenario is 0.43 when migrants have sex with prostitutes once a week; this represents the default set of assumptions. When migrants have sex with prostitutes more often, they return home with more infections and female gonorrhea prevalence increases. If migrants have daily sexual encounters with prostitutes, female gonorrhea prevalence ranges from 0.47 in the likely-migration scenario to 0.61 in the extreme scenario. On the other hand, female gonorrhea prevalence decreases to 0.41 and 0.47 if migrants visited a prostitute once every 2 weeks. Thus far, migrant behavior has the largest impact on female gonorrhea prevalence compared with the other migration processes modeled.

Some literature has suggested that migrants are selected for their risky sexual behavior. Other work, after showing that migrants exhibit risky sexual behavior after returning home, has suggested that return migrant behavior changes through the process of migration. Although the mechanisms of behavior change differ, both hypotheses suggest that return migrants act differently than non-migrants. Figure 7D shows the relationship between return migrant sexual behavior and female gonorrhea prevalence.

Assumptions of return migrant behavior are important when modeling migration and disease transmission. Figure 7D shows the results of two migration scenarios with three estimates of return migrant behavior: 20% of return migrants are core or the migrant population is simply a representative sub-sample of the entire population where, 50% of return migrants exhibit core characteristics, and 100% of return migrants exhibit core characteristics. Recall that in the present model a core male has more frequent sexual encounters, has shorter relationships, and is more likely to choose a core female as a partner. All of these characteristics lead to a higher risk of infection. Female gonorrhea prevalence under the likely-migration assumption varies from 0.41 when 20% of return migrants exhibit core characteristics, to 0.43 when 50% of return migrants exhibit core characteristics—the default likely-migration assumption, to 0.47 when 100% of return-migrants exhibit core-sexual activity group behavior. The same relationship between return-migrant behavior and female gonorrhea prevalence is seen in the extreme-migration scenario. Female prevalence increases from 0.48 to 0.54.

Lastly, female behavior has been suggested to be an important determinant of the relationship between male migration and disease transmission (Lurie *et al*., 2003). The present model assumes that women do not stay abstinent while their partners are away; rather they are allowed to switch partners once their current partner migrates. When women in the model are not allowed to switch partners when their partner migrates, female gonorrhea prevalence decreases from 0.43 to 0.36 (results shown in Figure 8) under assumptions of likely-migration. In this scenario, male migration becomes protective in terms of disease transmission. The detrimental effect from migrants returning home with newly acquired infections is outweighed by the reduction of disease transmission in female partners while they are gone. This result demonstrates the significance of female behavior in determining disease transmission.

6. Discussion & conclusion

Unexpectedly, male migration did not have a very large affect on gonorrhea prevalence rates once they stabilized. When the model assumed migration rates and sexual behavior parameters as was seen on Yap in 1930, female prevalence rates were near 0.43 (as expected). When no migration was allowed, female prevalence only dropped 3 percentage points to 0.40. Similar associations were seen with male gonorrhea prevalence rates. Here, we assumed that migration would also increase overall male prevalence rates because migrants would return home with newly acquired infections, pass them to women, and then become reinfected. However the results of the model show that male gonorrhea prevalence would have only been 2 percentage points lower in Yap if there were no labor migration, from 0.21 to 0.19. Again, if assumptions of male migration were more extreme, migration could have contributed to an 11 percentage point increase in male gonorrhea prevalence, raising rates to 0.30.

The reason why migration did not contribute to a greater increase in gonorrhea prevalence rates is because of the combination of short infectious periods and high transmission probabilities. With time and without treatment, prevalence rates quickly increase and the effect from introduced infections from migrants is overshadowed by the epidemic.

If duration is sufficiently short, an infection brought home by a migrant may be gone before it was passed on. To test this theory, we run the model with assumptions of duration of infection twice as long as the usual assumptions. Here, female duration is set at 120 days, and male duration is 60 days. As expected, overall prevalence rates are much higher when duration of infection is longer. However, migration seems to play an even smaller role in these models. Female prevalence is 0.725 with no migration, rises less than a percentage point to 0.730 with likely-migration assumptions, and jumps only slightly to 0.776 with extreme migration assumptions. Changes in male gonorrhea prevalence are similar: rates range from 0.400 with no migration, to 0.406 with likely-migration, and to 0.491 with extreme migration assumptions (data not shown). Duration of infection alone does not seem to be an important determinant in the relationship between migration and disease transmission.

However, we see the typically expected association between migration and disease prevalence when we combine long disease duration with very low transmission probabilities. Figure 8 illustrates results from the same microsimulation model, the only difference is that disease duration is permanent and transmission probability per sex act is set at 0.0011; these parameters are set to resemble HIV transmission (Gray et al. 2001). Here, migration seems to play a very significant role in determining disease prevalence at any point in the model. After twenty years, female disease prevalence is 0.07 under the no-migration scenario, 0.18 under the likely-migration scenario, and 0.25 under the extreme-migration scenario.

- Insert Figure 8 about Here -

Migration might not contribute to large changes in gonorrhea prevalence rates in the current model because gonorrhea is extremely easily transmitted, and no treatment was available. When the disease reaches epidemic proportions, the ease in transmission simply overwhelms any great contribution from introduced disease cases brought by return migrants. Recall that when the disease is first introduced and rates are increasing—in the first four years of the model—the trajectory of prevalence rates varies quite a bit with and without assumptions of migration. This is where migration has a large and significant impact on gonorrhea transmission and prevalence rates.

If gonorrhea infections were quickly cured with antibiotics, then an epidemic like that seen in Yap would not occur. In this circumstance, transmission from non-migrant to non-migrant would not be nearly as important as it is in the current model. New infections introduced to the home-population by migrants would have a much larger impact. The process of migration would continually add new infections to the pool when otherwise current infections would be treated and transmission would be kept to a minimum. We get a glimpse of this phenomenon in the first four years of the model. Gonorrhea prevalence rates were not yet high among non-migrants in the population, and in the scenarios where migration occurred, prevalence was significantly higher.

Previous models of population mobility and infectious disease have shown the relationship between two or more cities connected by migration and the resulting disease prevalence in each. These studies suggest that if migration exists between many cities with at least one of them at an endemic disease level, then all connected cities eventually will be at an endemic level. Of course, if a disease-free city becomes connected with a city with disease, migration will be directly or indirectly responsible for 100% of the resulting disease cases. However, they do not specifically model the role of migration on disease prevalence over time.

Most empirical work on migration and STDs has simply shown that migrants suffer disproportionately from STDs and carry infections home; therefore they suggest that migration affects prevalence rates. This paper clarifies the relationship with regard to gonorrhea. Migrants carry infections home, and migration is responsible for a quick increase in gonorrhea prevalence rate. But over time the role of migration in gonorrhea prevalence, without other treatment, is not very significant.

Not very often does one hear of a gonorrhea epidemic as severe as was seen in Yap during the Japanese occupation. This historical situation—a severe epidemic, an isolated community, and labor migration—provides a telling, yet quite simple example that suggests that labor migration plays an important role in disease dissemination. The microsimulation model suggests that new infections brought into Yap via labor migration played a very large role in the initial rate of increase of gonorrhea prevalence, and could have increased overall gonorrhea prevalence by 3 percentage points. However, under alternative conditions, migration could have increased prevalence rates by 11 percentage points. The model presented in this paper provides a first step in quantifying the effect of labor migration on disease spread. Perhaps a more important contribution, at least in policy terms, are the results from breaking down migration into five important characteristics: 1) percent of migrants in a population, 2) risky migrant behavior that translates to higher risk of infection, 3) the rate of migrant turnover, 4) migrant selectivity or return-migrant sexual behavior, and 5) female sexual behavior while migrant partners are away.

- Insert Figure 9 about Here -

This paper has demonstrated the relative importance of these characteristics of the migration process in disease transmission. Figure 9 illustrates model results from likely- and extreme-assumptions of migration for five migration processes. Migrant behavior seems to be the most important characteristic of migration in terms of its relative contribution to increased female gonorrhea prevalence. The more prostitutes migrants visit, the more infections they bring home; and this contributes to higher gonorrhea prevalence, up to 0.61. The proportion of migrants and return migrant behavior are the next most important determinants of gonorrhea transmission. They both can raise gonorrhea prevalence from 0.43 to 0.53 in the present model. A higher proportion of migrants mean more gonorrhea cases will be introduced, but it also implies that male partners will be migrants more often, exposing more women to disease. Migrant selectivity, or return migrant behavior, is also important in determining the rate of disease transmission. If all migrants behave like core men after migration, gonorrhea transmission will increase. Assumptions of migrant turnover lead to a 7 percentage point increase in the model; a higher rate of turnover simply allows more disease cases to be introduced to the population. Lastly, female behavior can account for an 8 percentage point decrease in gonorrhea prevalence.

Effects of migration on population health are incredibly difficult to disentangle; however, the issue is more important today than ever. Mobility as faster, easier, and cheaper, and STDs like HIV/AIDS, gonorrhea and syphilis are spreading quickly and amounting to be the most important international health problem today. Numerous exogenous factors influence the rate of STD transmission through labor migration, and there is no way to account for them all. In fact, the breakdown of traditional values associated with migration might be a much stronger factor in the relationship between migration and disease transmission than the actual number of infections a migrant carries home. Much more work needs to be done to understand the context of migration and disease transmission, what determinants are the most important, and what can be done to slow down the process.

Table 1: List of parameters used in microsimulation model of gonorrhea transmission, with estimates and sources from past literature.

parameter	point estimate	source
demography module		
N	2000 (%50 women)	
Age	15-45 years	South Seas Government (1920-1937)
Proportion of migrants**	0 - 50%	Cassels (2004 fieldwork); South Seas Government (1920-1937)
Rate of migrant turnover**	once/month - once/year	Cassels (2004 fieldwork)
Migrant selection**	20 - 100%	Brockerhoff & Biddlecom (1999); Chirwa (1997)
Runtime	20 years	
sexual behavior module		
% core women	20%	Barnes & Holmes (1984); Potterat et al. (1985); Rothenberg (1983)
% core men	20%	
Probability sex act/day	Poisson dist., μ = 0.15 - 0.314	Kramer & Reynolds (1981); Korenromp *et al*. (2000)
# of sexual partners per month	1 - 6	Kramer & Reynolds (1981)
Age-preference matrix	(see Table 2)	Korenromp et al. (2000)
Mixing parameter: e	0.6	Aral et al. (1999); Garnett & Anderson (1993)
waiting time between relationships	(1/30)*exp(-t/30)	Korenromp et al. (2000)
Probability relationship dissolves	20% every 15-30 days	Kramer & Reynolds (1981)
transmission module		
P(transmission: male-female)	0.5	Hethcote & Yorke (1984); Barnes & Holmes (1984); Swinton *et al*. (1992)
P(transmission: female-male)	0.2	Hethcote & Yorke (1984); Barnes & Holmes (1984); Swinton *et al*. (1992)
P(prostitute = infected)	0.75	Anderson (Croonian lecture…)
Age-specific gonorrhea variation	(see Figure 5)	South Seas Government (1920-1937)
%infected (core) at start of model	2%	
%infected (non-core) at start of model	1%	
natural history/disease module		
average duration of disease (women)	60 days	Hethcote & Yorke (1984)
average duration of disease (men)	30 days	Hethcote & Yorke (1984)

** Key migration parameter. The values of these paramers vary in the model in order to measure sensitivity in gonorrhea prevalence.

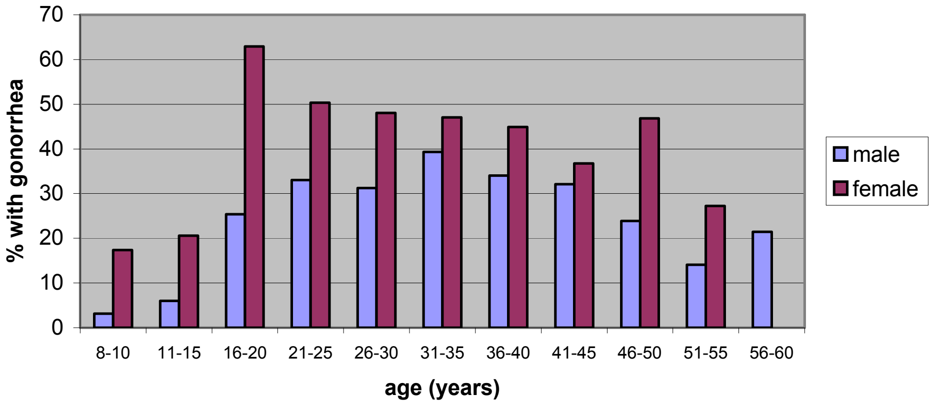
Table 2: Age preference matrices for a female/male (age groups in rows) selecting a new male/female partner (age group in columns).

Female age-group	Male age group							
	15-19	20-24	25-29	30-34	35-39	40-44	45-49	50+
15-19	0.4	0.3	0.2	0.1				
20-24	0.1	0.2	0.35	0.25	0.1			
25-29		0.1	0.2	0.35	0.25	0.1		
30-34			0.1	0.2	0.35	0.25	0.1	
35-39				0.1	0.2	0.35	0.25	0.1
40-44					0.1	0.3	0.35	0.25

Male age-group	Female age group							
	15-19	20-24	25-29	30-34	35-39	40-44	45-49	50+
15-19	0.9	0.1						
20-24	0.7	0.2	0.1					
25-29	0.35	0.4	0.2	0.05				
30-34	0.1	0.25	0.4	0.2	0.05			
35-39		0.1	0.25	0.4	0.2	0.05		
40-44			0.1	0.25	0.4	0.2	0.05	
45+				0.1	0.25	0.4	0.2	0.05

Source: Korenromp *et al* (2000)

Figure 1: Age distribution of men and women with gonorrhea on the main island of Yap in 1930.



Source: (South Seas Government 1920-1937)

Figure 2: An example of migrant gonorrhea prevalence over the course of a year. The chance that a migrant is infected depends on when he returned home, the duration of gonorrhea, and his behavior once home.

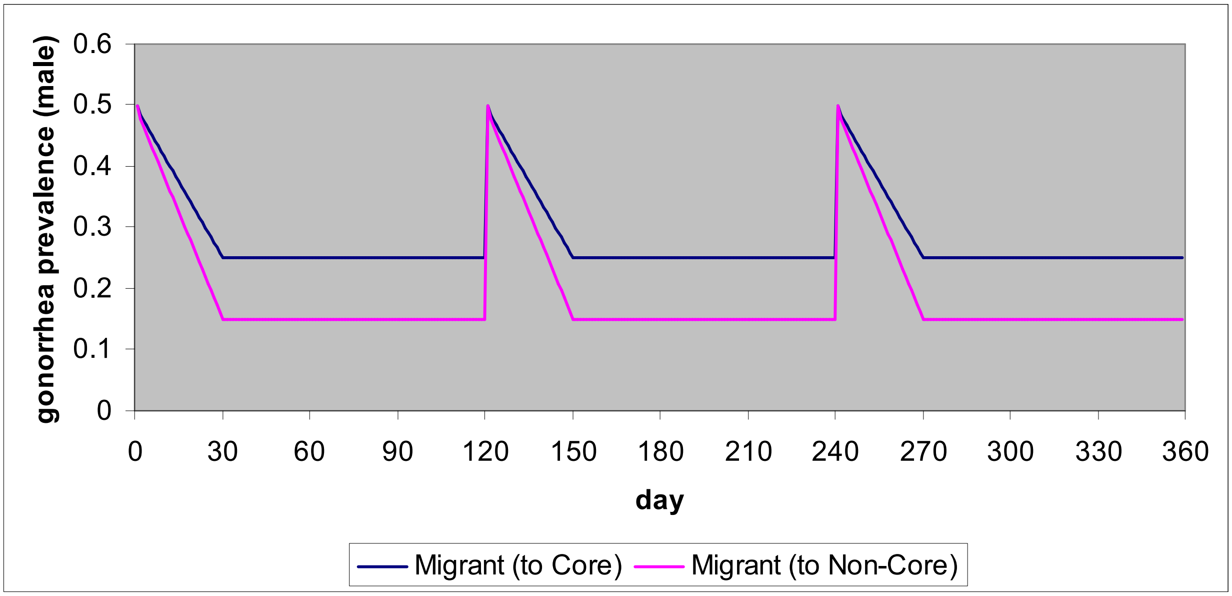


Figure 3: Relationship and infection status timeline for hypothetical woman #146.

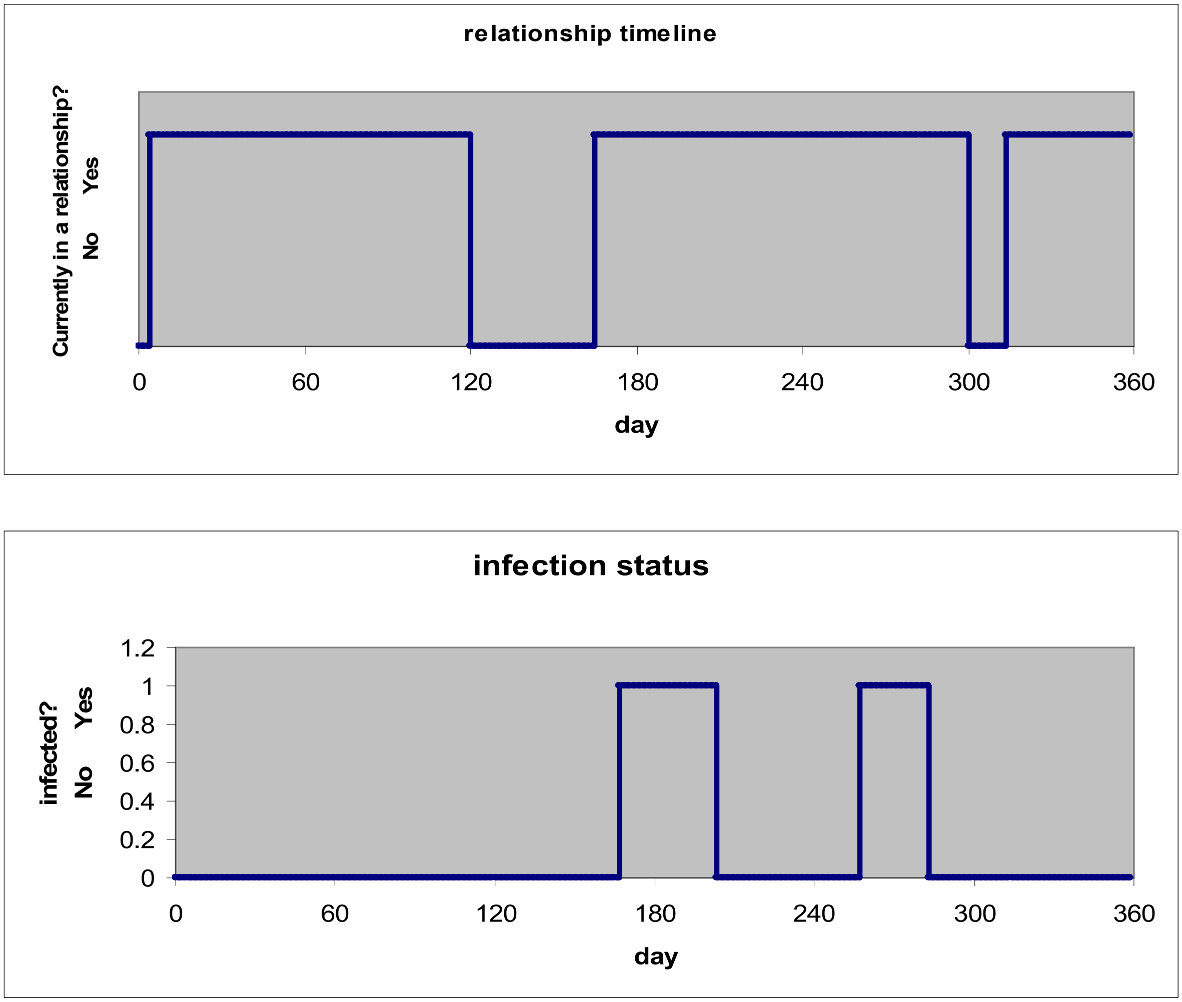


Figure 4a and 4b: Sex partner distribution for core and non-core individuals.

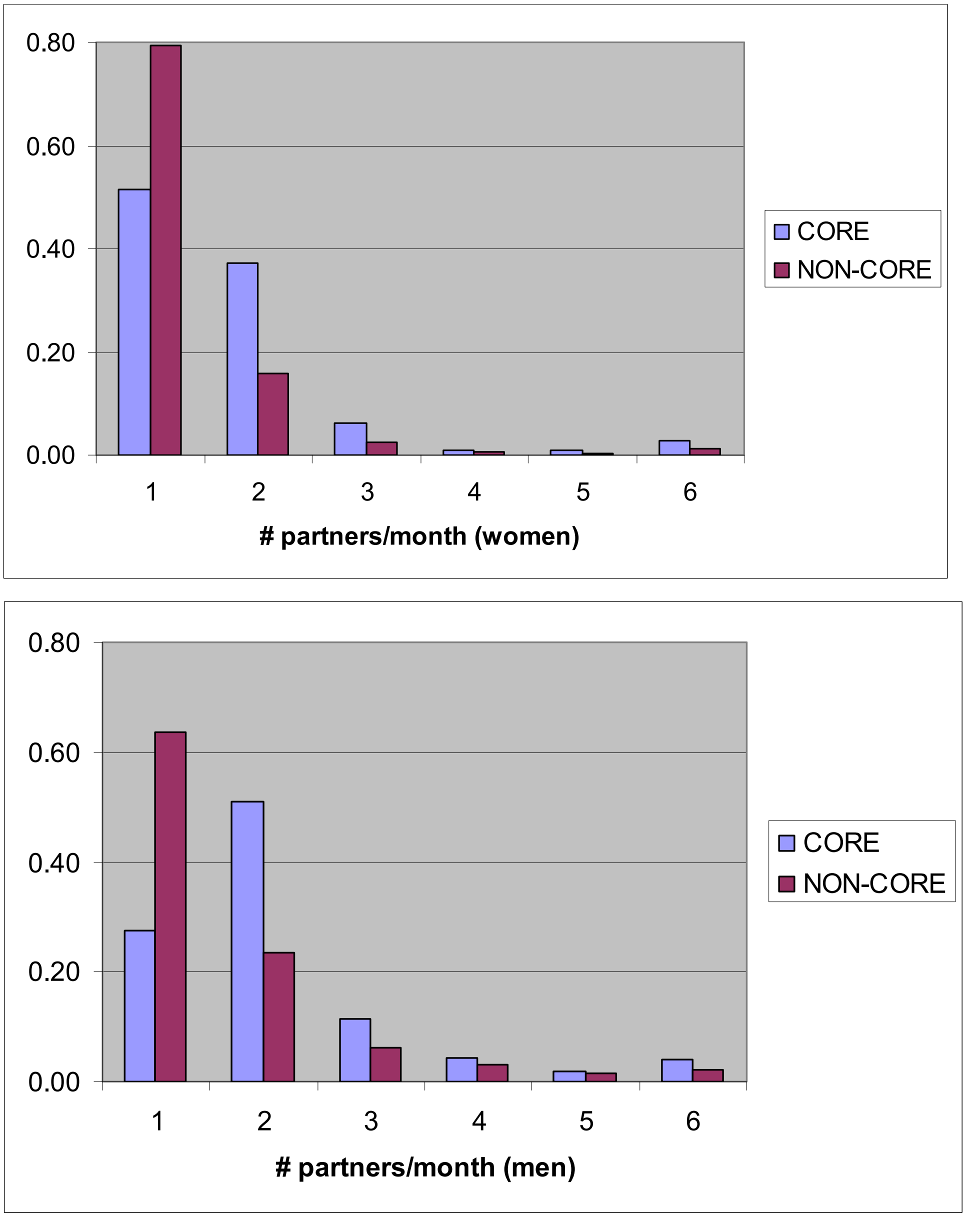
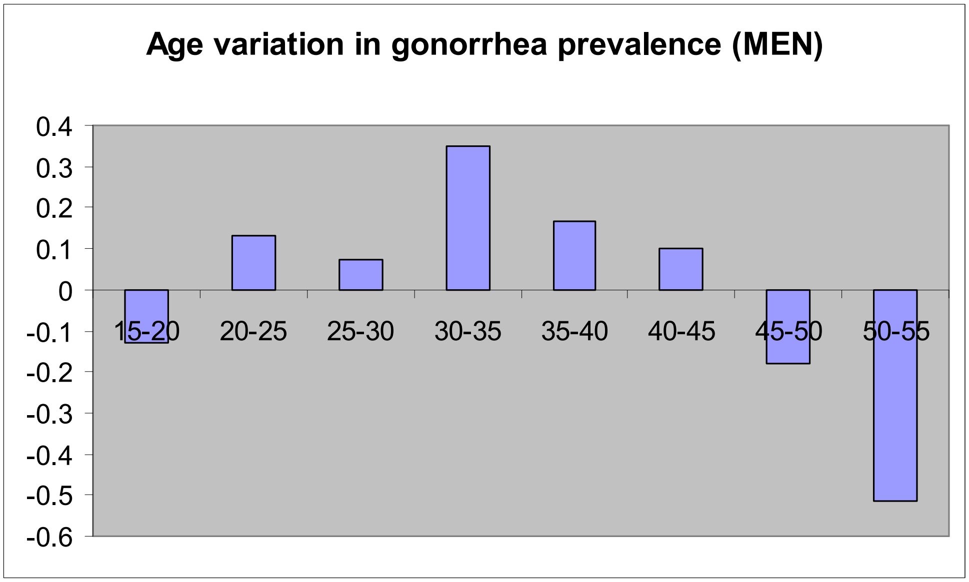


Figure 5a and 5b: Age-specific deviation in mean gonorrhea prevalence.



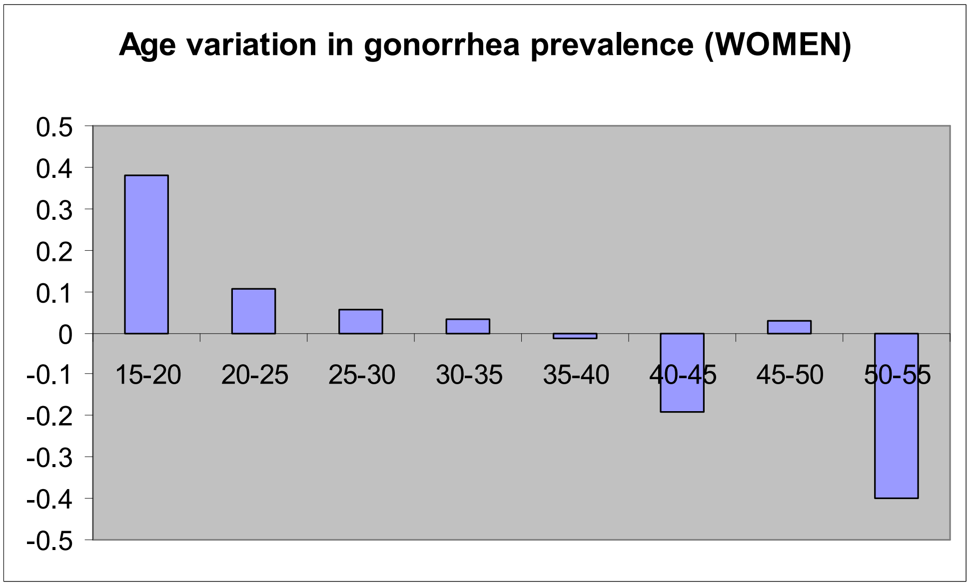
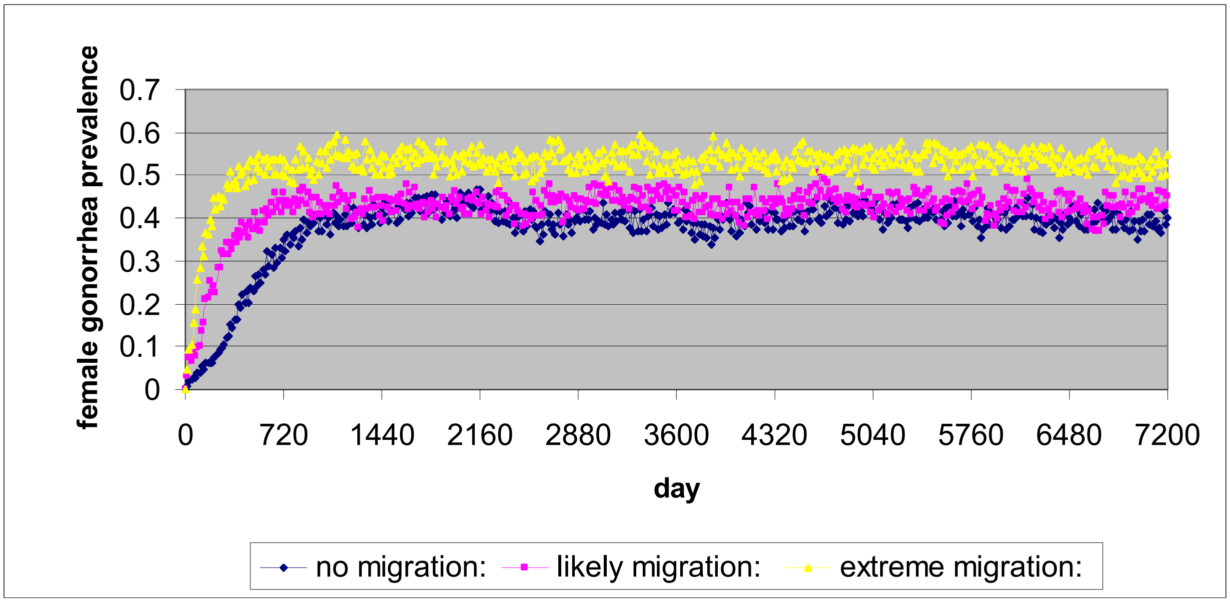


Figure 6A and 6B: Female and male gonorrhea prevalence over time under three migration scenarios.



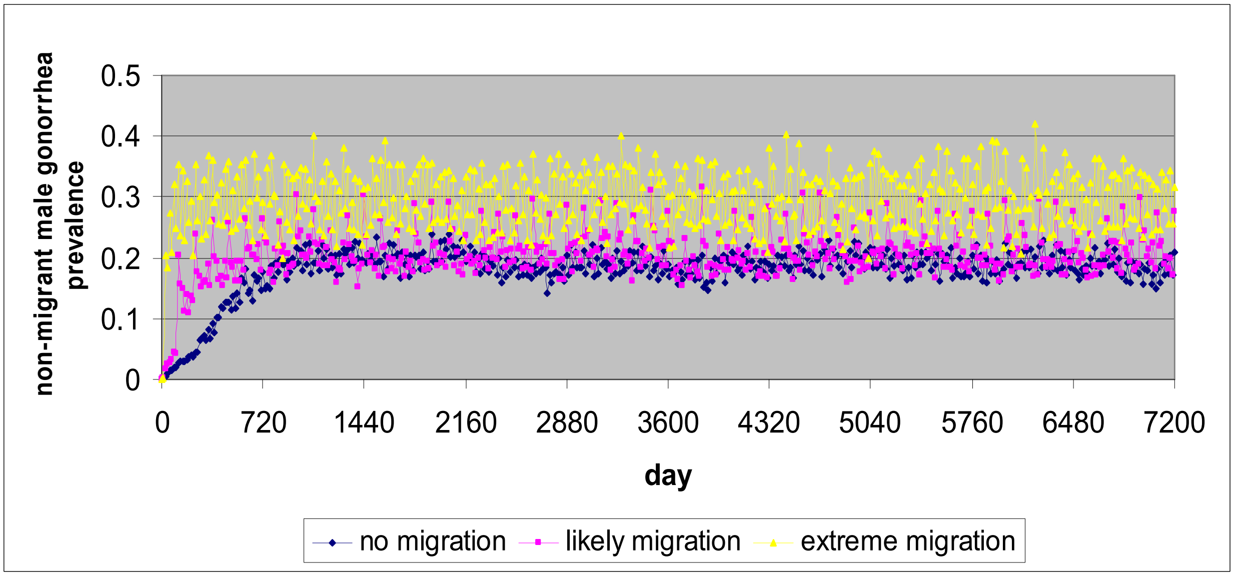
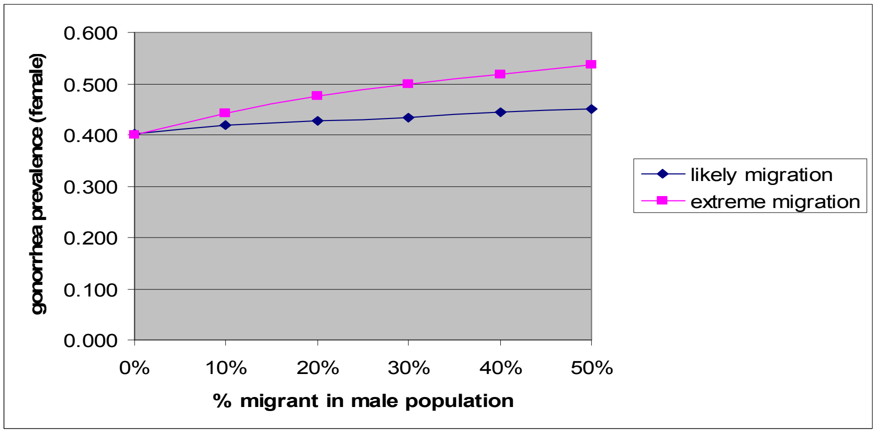
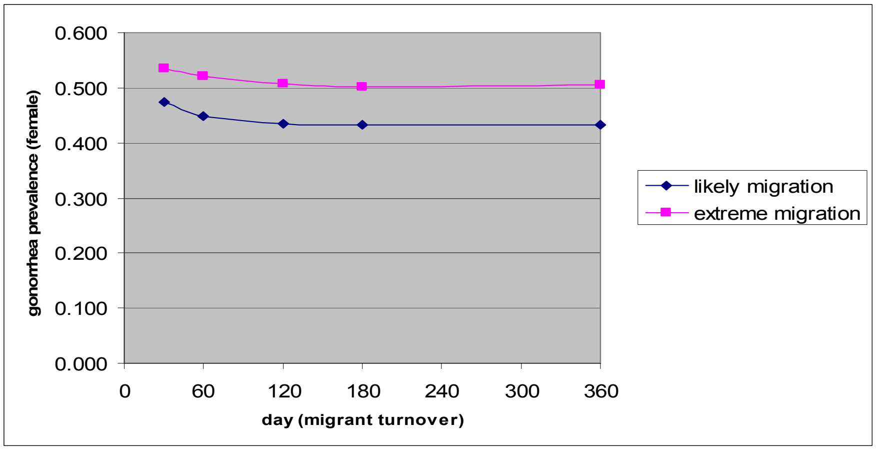


Figure 7: Four characteristics of migration and their affect on female gonorrhea prevalence.

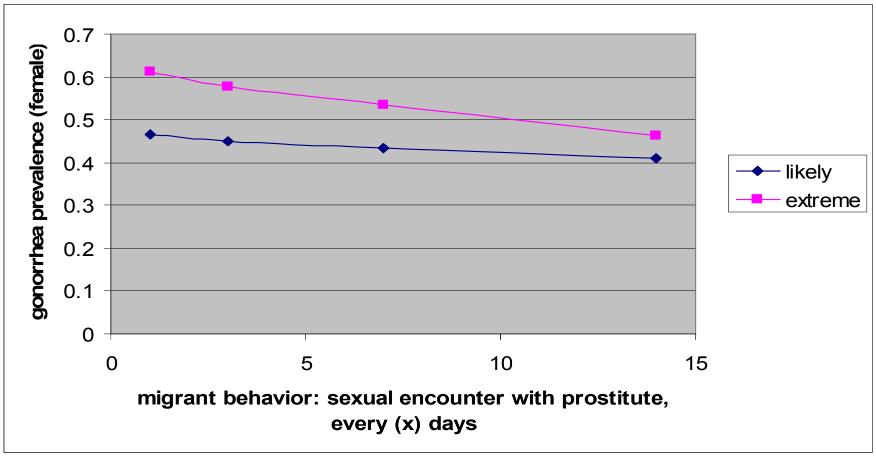
7A: Percent migrants in the total male population.



7B: Rate of migrant turnover



7C: Migrant sexual behavior



7D: Return-migrant sexual behavior

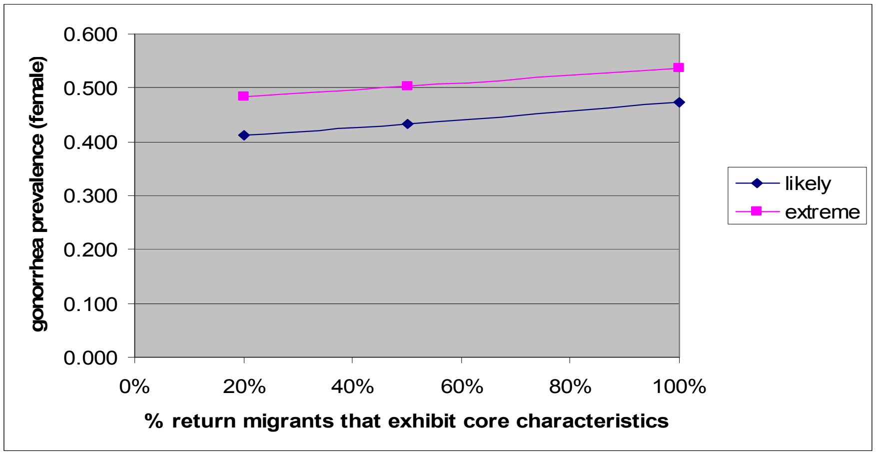


Figure 8: Female disease prevalence over time for three migration scenarios, given permanent disease duration and very low transmission probabilities.

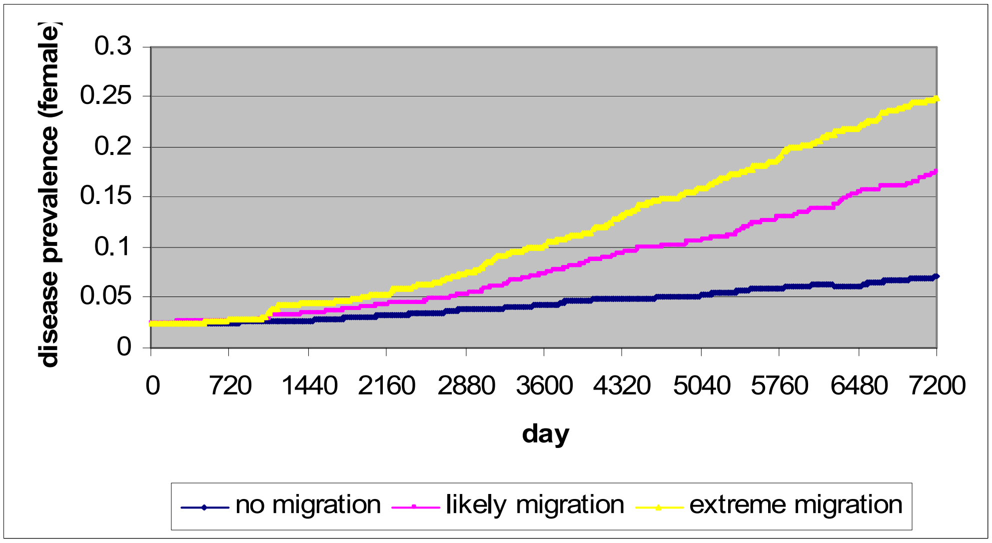
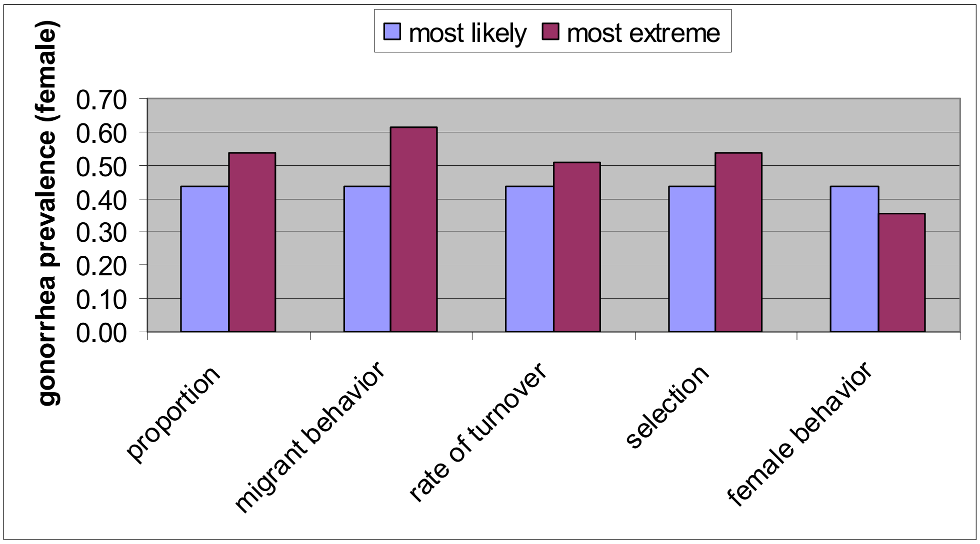


Figure 9: Relative contributions of 5 processes of migration to female gonorrhea prevalence.



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