Modeling the Transmission Dynamics on the Spread of Hantavirus Infection

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ABSTRACT

The transmission of Hantavirus infection is important but not much effort has been carried out by researchers to study the transmission of Hantavirus infection. The transmission of Hantavirus to humans occurs mainly through rodent bites and scratches of infected rodents. In this paper, we develop a model that tracks the dynamics of Hantavirus infection in the human and rodent populations. The existence of the disease-free and endemic equilibrium points for the uniqueness of the solution to the model is confirmed and the basic reproduction number is developed. Several numerical simulations were carried out and the results are discussed.

Keywords: Hantavirus infection, transmission dynamics, infectious disease, mathematical model, vector-host

INTRODUCTION

Hantaviruses are carried by rodents and can be transmitted via aerosolized excreta to humans beings, causing hemorrhagic fever with renal syndrome or Hantavirus pulmonary syndrome. The Hantavirus is transmitted horizontally between rodents through intraspecific aggressive behaviors, such as biting and scratching. Horizontal transmission occurs between rodents of the same species and spread to human. MacInnis et al. (2006) states that the horizontal transmission means that all rodents are born susceptible in that the infection does not propagate to the offspring through birth. The virus does not affect the life-span of the rodent and they are just carriers of the infection.

In 1993, an outbreak of HPS occurred in the South West corner of USA resulting in a high mortaility rate. A basic mathematical model was developed by Abramson and Kenkre (2002) to simulate the spread of the virus and it was found to be able to replicate some features of the infection such as the sporadic disappearance of the infection and the existence of refugias for the rodents when environmental conditions are not favourable for the rodents (lack of water, food, and shelter). Considerable work has been done on modeling of Hantavirus infection, using simple mathematical model based on systems of differential equation can be found in Abramson et al. (2003), Giuggioli et al. (2006), Peixoto and Abramson (2006), Abdul Karim et al. (2009), Goh et al. (2009), Yusof et al. (2010), Rida et al. (2012), Yusof et al. (2014) and Yusof et al. (2018a, 2018b).

As a group, rodents are probably the predominant natural reservoirs for pathogens that cause disease in humans (Ostfeld and Mills, 2007). The vector-host infectious diseases, such as hemorrhagic fever with renal syndrome (or epidemic nephritis and Hantavirus cardiopulmonary syndrome, are transmitted by rodents of several species. Rodents may spread Hantavirus to humans if: (1) a rodent with the virus bites someone, the virus may be spread to that person but this transmission is rare (2) they touch something that has been contaminated with rodent urine,

droppings, or saliva, and then touch their nose or mouth (3) they eat food contaminated by urine, droppings, or saliva from an infected rodent.

Vector-host epidemic diseases such as plague (spread by direct contamination) and these mentioned in this paper, have great influence on the health of human beings. Human health can be affected by rodents either directly or indirectly through disease transmission. The direct transmission category typically includes both the deposition of rodents via bites and scratches and deposition into urine and feces of rodents that enter other individuals through mucous membranes (e.g., inhalation) (Ostfeld and Mills, 2007).

According to Ostfeld and Mills (2007), the mode transmission zoonotic pathogens (i.e. Hantavirus) in human and rodent populations are the same as inhalation of viral aerosols or virus-contaminated dust. The force of transmission are dependent on the population density (or size) of the rodent reservoir, the frequency of infection in the rodent reservoir and the density of infected individuals in the reservoir population.

Recently there has been some effort in the mathematical modeling of the vector-host epidemic transmission dynamics. Li et al. (2011) develop the simple vector-host model for the transmission dynamics of the vector-host disease and obtained the basic reproductive number, R_0. They estimated the basic reproductive number, R_0, of the vector-host model using the next-generation method. Kong et al. (2011) introduce a vector-host epidemic model to investigate the effect of two different control strategies (i.e. medical treatment and pesticide) on the transmission of the vector-host diseases. They discuss the sensitivity of the reproduction number R_0 with respect to the model parameters which determines the model robustness to the parameter values. The results showed that the basic reproduction number is most sensitive to the biting rate of the mosquitoes so personal protection or mosquitos' reduction would be more effective measures.

In a real ecosystem, rodents share the environment with others species. Rodents can cause illness in human population through bites and scratches. Each bites and scratches of rodents that occur assist the spread of the infection to humans. The humans can become sick if they are bitten and scratched by an infected rodent. Generally, when the population of rodent falls the spread of Hantavirus disease will drop in the human population and the increase in rodent population will cause the disease to rapidly grow in the human population. The issue aimed to study is the effect if the host is a human population. In this paper, the influence of bites and scratches of infected rodent on Hantavirus transmission to human population are investigated.

In this paper, a basic vector-host model with direct and vector transmissions is developed and analyzed. The host dynamics is described by susceptible-infected-susceptible (SIS) model while the vector dynamics is described by susceptible-infected (SI) model (Cai and Li, 2010). According to Mackean (1995), a host is an organism in which pathogens live and reproduce. A vector is the transmitter of disease-causing organisms that carry the pathogens from one host to another (Jovanović and Krstić, 2012) and it picks up the infection from an organism in the reservoir (Green et al., 1990). It is assumed that there is no immunity in the vector and host populations.

The first objective of this study is to develop a mathematical model of the transmission dynamics i.e. human infection model and conduct an analysis. The second objective is to conduct numerical experiments on the transmission dynamic model that has been developed.

MODEL FORMULATION

The basic model of Abramson and Kenkre (2002) proposed a single rodent species without movement. Here the total population rodents are divided into two groups, one is susceptible and another is infected. The model is:

$$\frac{dr_s}{dt} = br - cr_s - \frac{r_s r}{k} - ar_s r_i$$

$$\frac{dr_i}{dt} = -cr_i - \frac{r_i r}{k} + ar_s r_i$$

where r_s and r_i are the populations of susceptible and infected rodents, respectively, where $r(t) = r_s(t) + r_i(t)$ is the total population of rodents. We shall refer to this model as the basic *AK* model.

The value br represents the births of rodents, all of them born vulnerable to the infection at a rate proportional to the total population assuming that all rodents contribute equally to the reproduction process. The value c represents the natural death rate. The infection does not cause deaths among rodents. The value $-\frac{r_s r}{k}$ or $-\frac{r_i r}{k}$ represents a limitation process in the rodent population growth due to competition for resources shared between r_s and r_i. In the basic model, parameter k depends on time and is a "environmental parameter". Higher values of the environmental parameter k represents higher availability of water, food, shelter and other resources for the rodents' use to thrive. According to Campbell et al. (2008), k is the maximum number of rodents which can be accommodated within a defined space or habitat and environment that can support them over an indefinite period of time. It is determined by the availability of nutrients, water, shelter and breeding sites. If k is increased the number of the population tends to increase to take advantage. $ar_s r_i$ represents the number of susceptible rodents that get infected due to an encounter with an infected rodent (e.g. bites from fights) at a rate a (assumed constant). The value a is known as the "aggression parameter". Kenkre et al. *(2007)* states that rodents do not die, nor are impaired, from contraction of the virus. There is no "vertical transmission" of the disease, i.e., there are no rodents are born infected from parents who are infected. Further, humans get the virus from the rodent but, in turn, have no feedback effects on the rodent in the infection process.

According to Abramson and Kenkre (2002), there is a critical value of the environmental parameter $\left(k_c = \dfrac{b}{a(b-c)} \right)$ that separates two distinctive regimes. If the environmental parameter k is smaller than k_c, r_i tends to zero and the infection dies away. If $k > k_c$, the infection thrives since there is an increase in resources. As the environmental parameter will vary with time, the system will undergo transitions from one state to another.

Our model is developed based on the following vector-host model introduced by Li et al. (2011)

$$\frac{dv}{dt} = c(1 - v)$$

$$\frac{dh}{dt} = \psi - \mu h$$

where v and h are the total population of vector and host, respectively, $v(t) = v_s(t) + v_i(t)$ is the total population of vector and $h(t) = h_s(t) + h_i(t)$ is the total population of host. The meaning of terms of Li et al. (2011) model is as follows:

The parameter ψ represents the host birth, μ represents the host death rate, γ represents the host recovery rate and c is the vector birth and death rate.

The model of vector-host model developed Li et al. (2011) is of the form:

$$\frac{dv_s}{dt} = c - cv_s - \beta_{v_s} v_s h_i$$

$$\frac{dv_i}{dt} = \beta_{v_s} v_s h_i - cv_i$$

$$\frac{dh_s}{dt} = \psi - \mu h_s + \gamma h_i - \beta_{h_s} h_s v_i$$

$$\frac{dh_i}{dt} = \beta_{h_s} h_s v_i - (\mu + \gamma)h_i$$

where v_s, v_i, h_s and v_i are proportions of susceptible vectors, infected vectors, susceptible hosts and infected hosts, respectively and β_{v_s} and β_{h_s} are disease transmission terms. Wonham et al. (2006) states that the disease-transmission term represents the contact between host individuals in directly transmitted diseases, or between host and vector individuals in host-vector diseases.

According to Li et al. (2011), there is a disease basic reproductive number $\left(R_0 = \sqrt{\dfrac{\beta_{v_s} \beta_{h_s}}{c(\mu + \gamma)}} \right)$ that separates two distinctive regimes where the basic reproductive number, R_0, is defined as the average number of secondary infections that single infectious host can generate in a totally susceptible population of hosts and vectors. If $R_0 < 1$, the virus is cleared and the disease dies out whereas if $R_0 > 1$, the virus persists in the host. R_0 is often used as a measure of disease strength to estimate the effectiveness of control measures (Li et al., 2011).

In our present paper, the model of Li et al. (2011) is extended by assuming that the host is a human population and the rodent population is a vector. Numerical experiments are conducted and the results analysed.

HUMAN INFECTION

Our model is developed based on the following basic vector-host model introduced by Li et al. (2011)

$$\frac{dv}{dt} = c(1 - v)$$

$$\frac{dh}{dt} = \psi - \mu h$$

where v and h are populations of vectors and hosts, respectively. For the population of vector, c is the vector birth and death rate, and $v(t) = v_s(t) + v_i(t)$ is the total population of vector.

Meanwhile for the host population, ψ is the host birth, μ is the host death rate and $h(t) = h_s(t) + h_i(t)$ is the total population of host.

From Li et al. model, the host population is maintained and the host is a human population is assumed. Further, the population of the vector is modified by replacing with the Abramson and Kenkre model. In this model, the disease spread occurs through contacts between humans and the infection between humans and infected rodents are considered. The rodent is identified by the variable r, and the human population by h. Therefore, the result is the human infection model as follows

$$\frac{dr}{dt} = (b - c)r - \frac{r^2}{k}$$
$$\frac{dh}{dt} = \psi - \mu h$$

where b is birth rate, c is the natural death rate, k is the environmental parameter, r is the population of rodents, h is the population of human, the parameter ψ represents the human birth and μ is the human death rate.

Suppose an internal classification of the rodent model is used where r_s is the susceptible rodent, r_i is the infected rodent and that r is the total rodent population

$$r(t) = r_s(t) + r_i(t).$$

while h_s is the susceptible human, h_i is the infected human and that h is the total human population

$$h(t) = h_s(t) + h_i(t)$$

The model of human infection is given by

$$\left. \begin{aligned} \frac{dr_s}{dt} &= br - cr_s - \frac{r_s r}{k} - ar_s h_i \\ \frac{dr_i}{dt} &= -cr_i - \frac{r_i r}{k} + ar_s h_i \\ \frac{dh_s}{dt} &= \psi - \mu h_s + \gamma h_i - \beta r_i h_s \\ \frac{dh_i}{dt} &= \beta r_i h_s - (\mu + \gamma)h_i \end{aligned} \right\} \qquad \ldots(1)$$

where r_s and r_i are the population of susceptible and infected rodents, respectively, h_s and h_i represent the population of susceptible and infected humans, respectively at any time t and $r(t) = r_s(t) + r_i(t)$ is the total population of rodents. The parameter a is the transmission rate from rodents to humans, ψ represents the human birth, μ represents the human death rate, γ represents the human recovery rate and β is the transmission rate from humans to rodents.

MODEL ANALYSIS

In this analysis we follow the approach of Mukherjee (2012), Cai and Li (2010), Cai et al. (2013), Wonham et al. (2006) and Xiao and Chen (2002). The equilibrium values for susceptible rodent, infected rodent, susceptible human and infected human populations, r_s, r_i, h_s and h_i respectively, are obtained by letting $\dfrac{dr_s}{dt} = 0$, $\dfrac{dr_i}{dt} = 0$, $\dfrac{dh_s}{dt} = 0$ and $\dfrac{dh_i}{dt} = 0$ in human infection model of the model (1). Then, the result are two equilibrium of the model (1), namely $E_0\left(R*, 0, H*, 0\right)$ where

$$R* = k(b - c) \quad \text{and} \quad H* = \frac{\psi}{\mu} \quad \text{and} \quad E_1(r_s*, r_i*, h_s*, h_i*) \quad \text{where} \quad h_s* = h_i* - \frac{\psi}{\mu} \quad,$$

$$r_s* = k(b - c) - \frac{\mu(\mu + \gamma)h_i*}{\beta(\mu h_i* - \psi)} \text{ and } r_i* = \frac{\mu(\mu + \gamma)h_i*}{\beta(\mu h_i* - \psi)} .$$

Next the dynamics of model (1) in the neighborhood of each equilibrium are considered. The Jacobian matrix of model (1) at the equilibrium $E_1\left(r_s*, r_i*, h_s*, h_i*\right)$ is given by

$$J\left(r_s*, r_i*, h_s*, h_i*\right) = \begin{bmatrix} b - c - \dfrac{1}{k}(2r_s* + r_i*) - ah_i* & b - \dfrac{r_s*}{k} & 0 & -ar_s* \\ -\dfrac{r_i*}{k} + ar_i* & -c - \dfrac{1}{k}(r_s* + 2r_i*) & 0 & ar_s* \\ 0 & -\beta h_s* & -\mu - \beta r_i* & \gamma \\ 0 & \beta h_s* & \beta r_i* & -(\mu + \gamma) \end{bmatrix}$$

When $J\left(R*, 0, H*, 0\right) = 0$, then the Jacobian matrix of model (1) at E_0 takes the form of

$$J\left(R*, 0, H*, 0\right) = \begin{bmatrix} b - c - \dfrac{2r_s*}{k} & b - \dfrac{r_s*}{k} & 0 & -ar_s* \\ 0 & -c - \dfrac{r_s*}{k} & 0 & ar_s* \\ 0 & -\beta h_s* & -\mu & \gamma \\ 0 & \beta h_s* & 0 & -(\mu + \gamma) \end{bmatrix}$$

The characteristic equation of the disease-free equilibrium E_0 of the model (1) is

$$\left(-b + c - \lambda\right)\left(-b - \lambda\right)\left[\lambda^2 + \left(c(1 - k) + kb + \mu + \gamma\right)\lambda + \left(c(1 - k) + kb\right)(\mu + \gamma) - \frac{\beta adk(b - c)}{\mu}\right] = 0 .$$ There are

four eigenvalues of the corresponding characteristic equation to equilibrium E_0. Two of the eigenvalues $-(b - c)$ and $-\mu$ have negative real part.

The other two eigenvalues can be obtained by solving the quadratic equation

$$\lambda^2 + A\lambda + B = 0$$
where $A = c(1 - k) + kb + \mu + \gamma$

$$B = (c(1-k)+kb)(\mu+\gamma) - \frac{\beta adk(b-c)}{\mu}.$$

Both roots of this quadratic equation have negative real parts if and only if its coefficients are positive ($A > 0$ and $B > 0$). So, all of the eigenvalues of the characteristic equation are negative real parts if $b > \frac{1}{k}(c(k-1)-\mu-\gamma)$ and $b > \frac{\beta ad(b-c)}{\mu(\mu+\gamma)} + \frac{c}{k}(k-1)$. Therefore, the disease-free equilibrium E_0 of the model (1) is locally asymptotically stable.

Theorem 1.1: If $R_0 < 1$, the disease-free equilibrium point $E_0(R^*, 0, H^*, 0)$ of the model (1) is globally asymptotically stable.

Proof: We define a Lyapunov function as follows

$$W(r_s, r_i, h_s, h_i) = \frac{b(\mu+\gamma)}{aR^*}\left[\left(r_s - R^* - R^* \log\frac{r_s}{R^*}\right) + r_i\right] + \left(h_s - H^* - H^* \log\frac{h_s}{H^*}\right) + h_i$$

By directly calculating the derivative of W along the solution of model (1), we obtain

$$\frac{dW}{dt} = \frac{b(\mu+\gamma)}{aR^*}\left[\left(1 - \frac{R^*}{r_s}\right)\frac{dr_s}{dt} + \frac{dr_i}{dt}\right] + \left(1 - \frac{H^*}{h_s}\right)\frac{dh_s}{dt} + \frac{dh_i}{dt}$$

$$\frac{dW}{dt} = \frac{b(\mu+\gamma)}{aR^*}\left(1 - \frac{R^*}{r_s}\right)\left(br - cr_s - \frac{r_s r}{k} - ar_s h_i\right) +$$

$$\frac{b(\mu+\gamma)}{aR^*}\left(-cr_i - \frac{r_i r}{k} + ar_s h_i\right) + \left(1 - \frac{H^*}{h_s}\right)(\psi - \mu h_s + \gamma h_i - \beta r_i h_s) +$$

$$(\beta r_i h_s - (\mu+\gamma)h_i)$$

Using $h_i = h - h_s$, $R^* = r$ and $H^* = h$, we have

$$\frac{dW}{dt} = \frac{b(\mu+\gamma)}{ar}\left(1 - \frac{r}{r_s}\right)\left(br - cr_s - \frac{r_s r}{k} - ar_s(h - h_s)\right) +$$

$$\frac{b(\mu+\gamma)}{ar}\left(-cr_i - \frac{r_i r}{k} + ar_s(h - h_s)\right) +$$

$$\left(1 - \frac{h}{h_s}\right)(\psi - \mu h_s - \gamma(h_s - h) - \beta r_i h_s) +$$

$$(\beta r_i h_s - (\mu+\gamma)(h - h_s))$$

$$= \frac{b(\mu+\gamma)}{ar}\left(\frac{r_s - r}{r_s}\right)\left(br - cr_s - \frac{r_s r}{k}\right) - \frac{b(\mu+\gamma)}{ar}\left(\frac{r_s - r}{r_s}\right)(ar_s(h - h_s))$$

$$+ \frac{b(\mu+\gamma)}{ar}\left(-cr_i - \frac{r_i r}{k}\right) - \frac{b(\mu+\gamma)}{ar}(ar_s(h_s - h)) +$$

$$\left(\frac{h_s - h}{h_s}\right)(\psi - \mu h_s - \gamma(h_s - h)) - \left(\frac{h_s - h}{h_s}\right)(\beta r_i h_s) + \beta r_i h_s - (\mu + \gamma)(h - h_s)$$

$$= -\frac{\gamma}{h_s}(h_s - h)^2 - (h_s - h)(\beta r_i - \gamma) + \left(\frac{h_s - h}{h_s}\right)\psi +$$

$$\frac{b(\mu + \gamma)}{ar}\left(\frac{r_s - r}{r_s}\right)\left(br - cr_s - \frac{r_s r}{k}\right) + \frac{b}{r}(\mu + \gamma)r_s(h_s - h) -$$

$$\frac{b(\mu + \gamma)}{a}\left(\frac{r_i}{k}\right) - \frac{b(\mu + \gamma)}{ar}\left(c - \frac{\beta a r h_s}{b(\mu + \gamma)}\right)r_i$$

$$= -\frac{\gamma}{h_s}(h_s - h)^2 - (h - h_s)(\beta r_i - \gamma) - \left(\frac{h_s - h}{h_s}\right)\psi +$$

$$\frac{b(\mu + \gamma)}{ar}\left(\frac{r_s - r}{r_s}\right)\left(br - cr_s - \frac{r_s r}{k}\right) + \frac{b}{r}(\mu + \gamma)(h_s - h) -$$

$$\frac{b(\mu + \gamma)}{a}\left(\frac{r_i}{k}\right) - \frac{cb(\mu + \gamma)}{ar}\left(1 - \frac{1}{c}\left(\frac{\beta a r h_s}{b(\mu + \gamma)}\right)\right)r_i$$

$$= -\frac{\gamma}{h_s}(h_s - h)^2 - (h - h_s)(\beta r_i - \gamma) - \left(\frac{h_s - h}{h_s}\right)\psi +$$

$$\frac{b(\mu + \gamma)}{ar}\left(\frac{r_s - r}{r_s}\right)\left(br - cr_s - \frac{r_s r}{k}\right) + \frac{b}{r}(\mu + \gamma)(h_s - h) -$$

$$\frac{b(\mu + \gamma)}{a}\left(\frac{r_i}{k}\right) - \frac{cb(\mu + \gamma)}{ar}\left(1 - \frac{1}{c}R\right)r_i \leq 0$$

where $R = \dfrac{\beta a r h}{b(\mu + \gamma)}$ is threshold parameter and the quantity $R_0 = \sqrt{R}$ is called the a disease basic

reproductive number. If the disease-free equilibrium (DFE) is $\left(k(b - c), 0, \dfrac{\psi}{\mu}, 0\right)$, then the disease

basic reproductive number is $\sqrt{\dfrac{\beta a \psi k(b - c)}{b\mu(\mu + \gamma)}}$.

Following the work of Vargas-De-León and Castro Hernández (2008), the proof of Theorem 1.1 is completed.

Then, a disease basic reproductive number R_0 is calculated as follows:
The infected equations r_i and h_i can be rewritten in matrix form, separating new infections terms (f) from vital dynamics term (v):

$$\frac{d}{dt}\begin{bmatrix} r_i \\ h_i \end{bmatrix} = f - v = \begin{bmatrix} ar_s h_i \\ \beta r_i h_s \end{bmatrix} - \begin{bmatrix} cr_i + \dfrac{r_i(r_s + r_i)}{k} \\ (\mu + \gamma)h_i \end{bmatrix}$$

Calculating the respective linearized matrices at the disease-free equilibrium (DFE) gives:

$$F = \begin{bmatrix} 0 & ar_s \\ \beta h_s & 0 \end{bmatrix}, \quad V = \begin{bmatrix} c + \dfrac{r_s + 2r_i}{k} & 0 \\ 0 & \mu + \gamma \end{bmatrix}$$

The disease-free equilibrium (DFE) is $\left(k(b-c), 0, \dfrac{\psi}{\mu}, 0 \right)$. The result of the matrices is

$$F = \begin{bmatrix} 0 & ak(b-c) \\ \dfrac{\beta \psi}{\mu} & 0 \end{bmatrix}, \quad V = \begin{bmatrix} b & 0 \\ 0 & \mu + \gamma \end{bmatrix}$$

Thus,

$$V^{-1} = \begin{bmatrix} \dfrac{1}{b} & 0 \\ 0 & \dfrac{1}{\mu + \gamma} \end{bmatrix}$$

and the next generation matrix is

$$FV^{-1} = \begin{bmatrix} 0 & ak(b-c) \\ \dfrac{\beta \psi}{\mu} & 0 \end{bmatrix} \begin{bmatrix} \dfrac{1}{b} & 0 \\ 0 & \dfrac{1}{\mu + \gamma} \end{bmatrix} = \begin{bmatrix} 0 & \dfrac{ak(b-c)}{(\mu + \gamma)} \\ \dfrac{\beta \psi}{b\mu} & 0 \end{bmatrix}.$$

Finally, a disease basic reproductive number R_0 is given as the dominant eigenvalue of FV^{-1}:

$$R_0 = \sqrt{\dfrac{\beta a \psi \, k(b-c)}{b\mu(\mu + \gamma)}}$$

The coexistent steady value E_1 is studied. The corresponding characteristic equation of the above variational matrix is

$$\lambda^4 + A\lambda^3 + B\lambda^2 + C\lambda + D = 0$$

where $A = -(a_{11} + a_{22} + a_{33} + a_{44})$,

$B = a_{11}a_{22} + a_{11}a_{33} + a_{11}a_{44} + a_{22}a_{33} + a_{22}a_{44} + a_{33}a_{44} - a_{24}a_{42}$,

$C = a_{11}a_{24}a_{42} + a_{24}a_{33}a_{42} - a_{11}a_{22}a_{33} - a_{11}a_{22}a_{44} - a_{11}a_{33}a_{44} - a_{22}a_{33}a_{44}$,

$D = a_{11}a_{22}a_{33}a_{44} + a_{14}a_{21}a_{32}a_{43} - a_{12}a_{21}a_{34}a_{43} - a_{11}a_{24}a_{33}a_{42}$

$a_{11} = b - c - \dfrac{1}{k}(2r_s * + r_i *) - ah_i *$, $\quad a_{12} = b - \dfrac{r_s *}{k}$, $\quad a_{13} = 0$, $a_{14} = -ar_s *$, $a_{21} = -\dfrac{r_i *}{k} + ah_i *$,

$a_{22} = -c - \dfrac{1}{k}(r_s * + 2r_i *)$, $a_{23} = 0$, $a_{24} = ar_s *$, $a_{31} = 0 *$, $\quad a_{32} = -\beta h_s *$, $a_{33} = -\mu - \beta r_i *$,

$a_{34} = \gamma$, $a_{41} = 0$, $\quad a_{42} = \beta h_s *$, $\quad a_{43} = \beta r_i *$, $a_{44} = -(\mu + \gamma)$.

Following the work of Lashari and Zaman (2011), the equilibrium E_1 is locally asymptotically stable if all roots of characteristic equation of model (1) have negative real parts. If the parameter

$A > 0$, $B > 0$, $C > 0$, $D > 0$ and $ABC > C^2 + A^2 D$ are chosen, then the equilibrium E_1 is locally asymptotically stable.

Theorem 1.2: If $R_0 > 1$, the endemic equilibrium point $E_1(r_s*, r_i*, h_s*, h_i*)$ is globally asymptotically stable.

Proof: We define a Lyapunov function as follows

$$L(r_s, r_i, h_s, h_i) = C_1\left(r_s - r_s* - r_s*\log\frac{r_s}{r_s*}\right) + C_2\left(r_i - r_i* - r_i*\log\frac{r_i}{r_i*}\right) +$$

$$C_3\left(h_s - h_s* - h_s*\log\frac{h_s}{h_s*}\right) + C_4\left(h_i - h_i* - h_i*\log\frac{h_i}{h_i*}\right)$$

where C_1, C_2, C_3 and C_4 are positive constants to be chosen later.

Differentiating L with respect to t along the solutions of model (7.1), we get

$$\frac{dL}{dt} = C_1\left(1 - \frac{r_s*}{r_s}\right)\frac{dr_s}{dt} + C_2\left(1 - \frac{r_i*}{r_i}\right)\frac{dr_i}{dt} + C_3\left(1 - \frac{h_s*}{h_s}\right)\frac{dh_s}{dt} + C_4\left(1 - \frac{h_i*}{h_i}\right)\frac{dh_i}{dt}$$

Choosing $C_1 = C_2 = \beta r_i * h_s *$ and $C_3 = C_4 = ar_s * h_i *$, then

$$\frac{dL}{dt} = \beta r_i * h_s *\left(1 - \frac{r_s*}{r_s}\right)\left(br - cr_s - \frac{r_s r}{k} - ar_s h_i\right) +$$

$$\beta r_i * h_s *\left(1 - \frac{r_i*}{r_i}\right)\left(-cr_i - \frac{r_i r}{k} + ar_s h_i\right) +$$

$$ar_s * h_i *\left(1 - \frac{h_s*}{h_s}\right)\left(\psi - \mu h_s + \gamma h_i - \beta r_i h_s\right) +$$

$$ar_s * h_i *\left(1 - \frac{h_i*}{h_i}\right)\left(\beta r_i h_s - (\mu + \gamma)h_i\right)$$

Using $h_i = h - h_s$, $h_i* = h* - h_s*$, $br = cr_s* + \frac{1}{k}\left(r_s*^2 + r_s* r_i*\right) + ar_s* h_i*$,

$c = \frac{1}{k}\left(r_s* + r_i*\right) - \frac{ar_s* h_i*}{r_i*}$, $\gamma h = (\mu + \gamma)h_s* + \beta r_i* h_s* - \psi$ and $(\mu + \gamma) = \frac{\beta r_i* h_s*}{h_i*}$,

$\dfrac{dL}{dt}$ can further be written as

$$\frac{dL}{dt} = \beta r_i * h_s *\left(1 - \frac{r_s*}{r_s}\right)\left(c(r_s - r_s*) + ar_s * h_i * - ar_s h_i\right) + \frac{1}{k}\left(r_s*^2 + r_s* r_i* + r_s^2 + r_s r_i\right)$$

$$\beta r_i * h_s *\left(1 - \frac{r_i*}{r_i}\right)\left(-cr_i - \frac{1}{k}\left(r_i^2 + r_s\right) + ar_s h_i\right) +$$

$$ar_s * h_i *\left(1 - \frac{h_s*}{h_s}\right)\left(-(\mu + \gamma)(h_s - h_s*) + \beta r_i * h_s * - \beta r_i h_s\right) +$$

$$ar_s * h_i * \left(1 - \frac{h_i *}{h_i}\right)\left(\beta r_i h_s - (\mu + \gamma)h_i\right)$$

We expand $\dfrac{dL}{dt}$ about $E_1\left(r_s *, r_i *, h_s *, h_i *\right)$ and obtain

$$\frac{dL}{dt} = -c\beta r_i * h_s * \frac{(r_s - r_s *)^2}{r_s} - a(\mu + \gamma)r_s * h_i * \frac{(h_s - h_s *)^2}{h_s} -$$

$$a\beta\, r_s * r_i * h_s * h_i * \left(\frac{r_s *}{r_s} + \frac{r_s r_i * h_i}{r_s * r_i * h_i *} + \frac{r_i *}{r_i} + \frac{r_i h_i * h_i}{r_i * h_i h_s *} - 4\right) + \text{H.O.T}$$

where H.O.T. stands for terms that are higher than quadratic.
Since the arithmetic mean is greater than or equal to the geometric mean, we have

$$\frac{r_s *}{r_s} + \frac{r_s r_i * h_i}{r_s * r_i * h_i *} + \frac{r_i *}{r_i} + \frac{r_i h_i * h_i}{r_i * h_i h_s *} \geq 4, \ \forall\, r_s, r_i, h_s, h_i \geq 0$$

Thus, we have

$$\frac{dL}{dt} \leq 0.$$

Following the work of Vargas-De-León and Castro Hernández (2008) and Cai and Li (2010), we complete the proof of Theorem 1.2.

There are two equilibrium of human infection model, namely $E_0\left(R*, 0, H*, 0\right)$ and $E_1\left(r_s *, r_i *, h_s *, h_i *\right)$. In an environment free of the disease, the disease-free equilibrium is $E_0\left(R*, 0, H*, 0\right)$ when $R_0 < 1$. For $R_0 > 1$, there is an additional equilibrium $E_1\left(r_s *, r_i *, h_s *, h_i *\right)$ which is called endemic equilibrium, where all population survive. It is clear that the disease will always persist in the environment. The most sensitive parameter for $h_i *$ and $r_i *$ are environmental parameter, k. Change in the value of k is directly related to change in $h_i *$ and $r_i *$. With higher values for environmental parameter k, the spread of disease in human population increases.

NUMERICAL EXPERIMENTS AND DISCUSSION OF RESULTS

In this paper, the human infection model is solved using Runge-Kutta fourth order scheme. The parameter $a = 0.1$, $b = 1.0$, $c = 0.5$ are chosen as they were used by Abramson and Kenkre (2002). Note the k_c will then be $k_c = 20$. Meanwhile the model parameters used by Li et al. (2011) were used in the experiments, viz. $\psi = 6.75$, $\mu = 0.15$, $\beta = 0.03$, $\gamma = 3.075$. The value $k = 10$, which means the environmental condition is adverse, will eliminate the infection. Nevertheless, the value of $k = 800$ is used which implies the environmental condition is favourable and thus the infection will thrive. The value of environmental condition, $(k = 800)$, chosen is very high to ensure the competition for resources shared between susceptible and infected rodents are low when higher resources are available. The duration of the simulation results is 20 years. We now study what happens the human and rodent populations for different environmental parameter (k) in our model of human infection.

Figures 1 shows the rodent and human populations for the case of adverse environmental conditions $(k = 10)$ when the human infection model is solved using the same initial values $(= 50)$ for r_s, r_i, h_s and h_i.
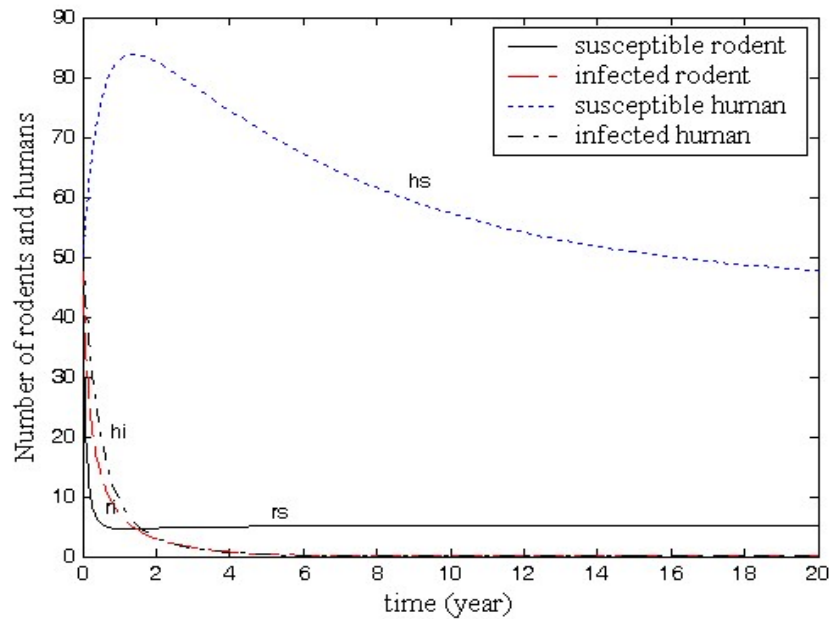

Figure 1: Values of r_s, r_i, h_s and h_i for human infection model with initial values $r_s = 50$, $r_i = 50$, $h_s = 50$ and $h_i = 50$.

Figure 1 shows that when resources such as water and food is low $(k(= 10) < k_c)$ and $R_0 (= 0.46) < 1$, the population of the infected rodents r_i and infected humans h_i will reduce to zero regardless of the initial values and both the infected populations phase are unstable. Both infected rodents and human populations does not survive, spurring a rapid growth in the susceptible human h_s due to the disease-free situation. The population of susceptible human h_s increases sharply initially and reaches a certain maximum before reducing and stabilizing at a steady value of 48. Since the infection does not survive, this reduces the population of susceptible rodents significantly before rising slightly and approaching a stable value when the infected rodent goes to extinction. Meanwhile, the susceptible rodent r_s will stabilize at a steady value of 5. The steady state values of susceptible human h_s is always higher than that the value of susceptible rodent r_s. Thus, the infection will die away in the ecosystem. If we consider the model (1) with parameters $a = 0.1$, $b = 1.0$, $c = 0.5$, $\psi = 6.75$, $\mu = 0.15$, $\beta = 0.03$ and $\gamma = 3.075$, the disease-free equilibrium point E_0 is $(5, 0, 48, 0)$. Consequently, the disease-free equilibrium point E_0 of the model (1) is globally asymptotically stable, which can be seen in Figure 1.

Figures 2 shows the rodent and human populations for the case of favourable environmental conditions $(k = 800)$ when human infection model is solved using the same initial values $(= 50)$ for r_s, r_i, h_s and h_i.
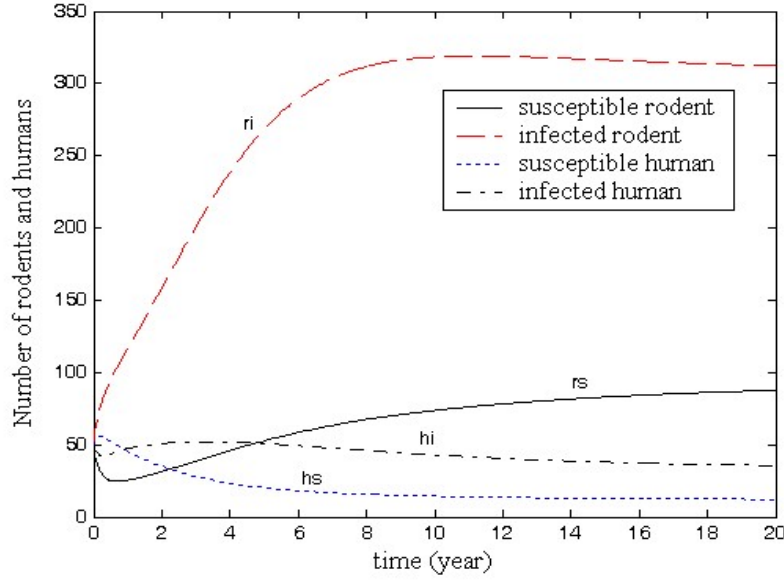
Figure 2: Values of r_s, r_i, h_s and h_i for human infection model with initial values $r_s = 50$, $r_i = 50$, $h_s = 50$ and $h_i = 50$.

The graph of susceptible rodent r_s, infected rodent r_i, susceptible human h_s and infected human h_i over time with $k = 800$ $(k > k_c)$ and $R_0 (= 4.09) > 1$ is as given in Figure 2. Now, the population of the infected rodent r_i and infected human h_i will gradually increase and approach an equilibrium stable value for large value of environmental conditions $(k = 800)$ and $R_0 (= 0.46) > 1$. The infected rodent r_i will approach a stable value of 312. Since the infection was thriving, this has the affect of reducing the population of susceptible rodents r_s and susceptible human h_s drastically and approaches a stable value when the infected numbers starts to stabilize. Meanwhile the susceptible rodent r_s decrease sharply initially and reaches a certain minimum before showing signs of a very fast increase. This is due to the fact that both infected and susceptible rodents breed susceptible rodent. The susceptible rodent r_s will eventually stabilize at a steady value of 87. When r_i is very high, the virus can persist between new generations of susceptible rodent and human population. Humans could get infection from bites and scratches of infected rodent r_i and susceptible rodent r_s could acquire the disease from infected rodent r_i via fights. The infected human h_i will eventually stabilize at a steady value of 36. The susceptible human h_s will gradually disappear regardless of the initial values. The susceptible human h_s will approach a steady value of 12. The steady state values of infected rodent r_i is always higher than that the value of human and susceptible rodent r_s. When the environmental condition $k(800) > k_c$ is very high, Hantavirus can thrive between new generations of susceptible rodents and rodent populations breeding infected rodents. Consequences from the bites and scratches of infected rodent increased to allow the spread of infection from rodents to humans. These are the reasons that leads to infected rodents to increase in the population. In addition, the competition is very low between rodent population and the disease will persist in the human population when $k > k_c$ and $R_0 > 1$. The frequency of fighting decreased when the environment parameter is too high causing overcrowded population of rodent. The chronic infection occurs in rodent that do not die and infected rodent that do not heal. As a result the population spread infection in humans. This could be due to an increased frequency of bites and scratches when the population of infected rodent r_i

is too high and these infected rodents r_i transmit the disease to the human population. In case $k > k_c$ and $R_0 > 1$, Figure 2 shows that the stability of endemic equilibrium E_1. The system converges to the equilibrium $E_1 = (87, 312, 12, 36)$ where all four species coexist in the ecosystem. The endemic equilibrium E_1 of the model (1) is globally asymptotically stable.
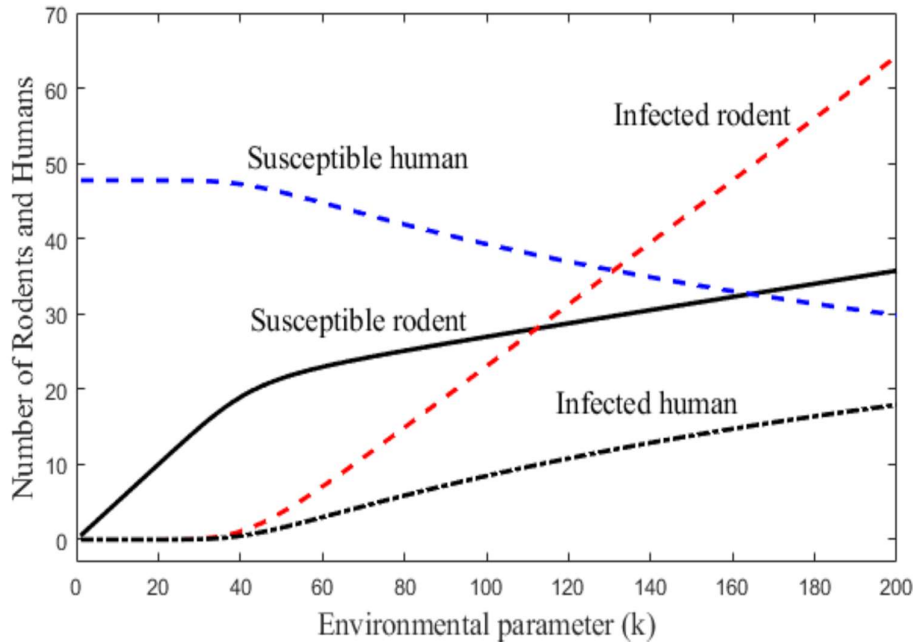

Figure 3. Bifurcation diagram of the rodent and human populations as a function of the environmental parameter (*k*). Model parameters are the same as in Figure 1 and Figure 2.

The bifurcation diagram (Figure 3) clearly demonstrates how the human infection model behaves with the increasing environmental parameter (*k*). From the figure, the result of the model show the rodents and infected human populations increase linearly while the susceptible human will gradually decreases linearly.

CONCLUSION

The focus in this paper has been to study the effect of human infection on the direct transmission of the spread of the Hantavirus infection. For such a situation, disease elimination would depend on the environmental parameter *k* of the ecosystem of the model. However, humans can become sick if they are bitten and scratched from an infected rodent.

The disease basic reproductive number of the human infection model $R_0 = \sqrt{\dfrac{\beta a \psi \, k(b-c)}{b \mu (\mu + \gamma)}}$

has been obtained. Then, the result of human infection model showed that the population of susceptible rodent r_s, infected rodent r_i, susceptible human h_s and infected human h_i will emerge to a stable point after a certain time interval. The infected human population does not survive below a critical environmental condition $(k < k_c)$ and $R_0 < 1$ and hence the disease does

not spread in human population. When the environmental condition is favourable $(k > k_c)$ and $R_0 > 1$, the disease persists in the human population. The result implies that an efficient way to halt the spread of rodent epidemic is by taking steps to reduce the environmental condition of the environment for the rodent population.

The stability of the model (1) is analysed for the disease-free and the endemic equilibrium (i.e. all population coexist). When $k < k_c$, the disease-free equilibrium for the human infection model is globally asymptotically stable so that the disease always dies out. This model predicts Hantavirus infection persists and the unique endemic equilibrium is globally asymptotically stable and the disease never dies out if $k > k_c$. Thus, the population size at the equilibrium state was much higher than it would have been in the presence of infection which indicates that the virus was able to control the rodent and human populations.

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