ABSTRACT

Leptospirosis is a bacterial zoonotic disease caused by spirochaetes of the genus Leptospira that affects humans and a wide range of animals, including mammals, birds, amphibians, and reptiles. Illness can range from mild to severe. In this study, we use mathematical models to study the behavior of the transmission of Leptospires disease. This model is formulated by considering the rates of change for human and rats. The human is divided into juvenile and adult groups. Each group is separated into susceptible, infectious and recovered classes. The rat is separated into susceptible and infectious classes. The dynamical analysis method is used for analyzing this modified model. Two equilibrium points are found and the conditions for stability of these two equilibrium points are established. We confirm these results by using numerical results.

1. INTRODUCTION

Leptospirosis (also known as Weil's disease, canicola fever, canefield fever, nanukayami fever, 7-day fever and many more), an infectious disease that affects humans and animals is considered the most common zoonosis in the world [1]. Well is credited with first described leptospirosis as a unique disease process in 1886, 30 years before Inada and colleagues identified the causal organism. The genus Leptospira belongs to the Leptospiraceae family of the order Spirochaetales. The nomenclature system used to organize leptospires, making review of the literature often confusing. The traditional system divided the genus into 2 species: the pathogenic Leptospira interrogans and the nonpathogenic Leptospira biflexa. These species were divided further into serogroups, serovars, and strains, based on shared antigens. L. interrogans include more than 250 serovars.

Symptoms of leptospirosis are high fever, headache, chills, muscle aches, conjunctivitis (red eyes), diarrhea, vomiting, and kidney or liver problems (which may include jaundice), anemia and, sometimes, rash. Symptoms may last from a few days to several weeks. Deaths may occur but they are rareness. For some cases, the infections can be mild and without obvious symptom [2]-[6]. Most outbreaks are depending on season and these are often linked to environmental factors, to animals and to agricultural and occupational cycles [7].

Mathematical models used here (a deterministic model consisting of a set of differential equations) have a long tradition in the study of wildlife diseases. For the majority of models, the primary motivation is to predict the impact of intervention by either culling or vaccination and a universal motivation is a better understanding of the dynamics of infection [8]. In 2006, J.Holt and et al. introduced a mathematical model of infection in an African rodent of Tanzania [9]. Recently, W.Triampo and et al. considered a deterministic SIR (S = Susceptible, I = Infected, R = Recovered) model for the transmission of leptospirosis in the Thai population [10]. SIR model can be used to describe the transmission dynamics of many infectious diseases. Modification of the SIR model must make it applicable to a particular disease [11]. From the data of Leptospirosis cases during 1997 and 2006 [12], we pick the year which give the highest outbreak (year 2000) to see the age distribution of the disease. We can see that the most cases are adult humans as shown in figure 1.

Figure 1. Reported cases of Leptospirosis per 1,000,000 population, Thailand, 2000.

In this paper, we modify the model of Leptospirosis by introducing the age structure of the human population into the SIR model.
2. MATHEMATICAL MODEL

In this study, the model is based on the following assumptions. The total human populations have constant sizes, which are classified into two groups, adult and juvenile populations. The human has constant size and it is divided into three classes, susceptible, infectious and recovered populations. The rat is divided into two groups, susceptible and infectious populations, with the rats never recover from the infection.

The model considers the rate of change for eight variables:

- $S'_A$ is the number of susceptible adult human,
- $I'_A$ is the number of infective adult human,
- $R'_A$ is the number of recovered adult human,
- $S'_J$ is the number of susceptible juvenile human,
- $I'_J$ is the number of infective juvenile human,
- $R'_J$ is the number of recovered juvenile human,
- $S'_M$ is the number of susceptible rat,
- $I'_M$ is the number of infective rat.

The rates of change for human and rat populations are given by

\[
\begin{align*}
\frac{dS'_A}{dt} &= \lambda_H N_A - \mu_H S'_A - \gamma_J S'_J I'_M - \beta S'_A J, \\
\frac{dI'_A}{dt} &= \beta S'_A I'_J + \beta R'_A - \gamma_A S'_A I'_M - \mu_H S'_A, \\
\frac{dR'_A}{dt} &= \gamma J S'_J I'_M - \mu_H I'_A - \beta I'_A - \gamma I'_A, \\
\frac{dI'_J}{dt} &= \gamma J S'_J I'_M - \mu_H I'_J - \beta I'_J - \gamma I'_J, \\
\frac{dR'_J}{dt} &= \gamma J S'_J I'_M - \mu_H I'_J - \beta I'_J - \gamma I'_J, \\
\frac{dS'_M}{dt} &= \lambda_M N_M - \mu_M S'_M - \gamma_M S'_M I'_M, \\
\frac{dI'_M}{dt} &= \gamma M S'_M I'_M - \mu_M I'_M - \mu_H I'_J - \gamma I'_M, \\
\frac{dR'_M}{dt} &= \gamma I'_J - \beta R'_J - \mu_H R'_A, \\
\end{align*}
\]

where $N_H$ is the number of the human population,
- $N_J$ is the number of the adult human,
- $N_J$ is the number of the juvenile human,
- $N_M$ is the number of rats,
- $\lambda_H$ is the constant birth rate of the human,
- $\lambda_M$ is the constant birth rate of rats,
- $\mu_H$ is the constant death rate of the human,
- $\mu_M$ is the constant death rate of rats,
- $\beta$ is the constant rate of population change from juvenile to adult,
- $\gamma$ is the constant rate at which an infected human recovers,
- $\gamma_J$ is the transmission probability from rat to adult,
- $\gamma_J$ is the transmission probability from rat to juvenile,
- $\gamma_M$ is the transmission probability from rat to rat,

with the three conditions

\[
\begin{align*}
S'_J + I'_J + R'_J &= N_A, \\
S'_A + I'_A + R'_A &= N_M.
\end{align*}
\]

3. ANALYSIS OF THE MATHEMATICAL MODEL

3.1 Analytical Results

The equilibrium points are found by setting the right side of (3) equal to zero. This gives

1) The disease free equilibrium point $E_0 = (1, 0, 1, 0, 0)$ and
2) The endemic disease equilibrium point
The stability of each equilibrium point is determined from linearizing equations in (3) about the equilibrium point examining the eigenvalues of the resulting Jacobian matrix. We now consider the eigenvalues of the Jacobian matrix at each equilibrium point. If all eigenvalues for each equilibrium state have negative real parts then that equilibrium state is locally stable. The local stability of the disease free equilibrium $E_1$ is governed by the matrix

$$
\begin{pmatrix}
-(\mu_H + \beta) & 0 & 0 & \gamma_A N_M \\
0 & -(\mu_H + \beta + \gamma) & 0 & \gamma_N S_M \\
0 & 0 & -\mu_H & \gamma_N S_M \\
0 & 0 & 0 & -(\mu_H + \gamma)
\end{pmatrix}
$$

The eigenvalues are

$$
\lambda_1 = -\mu_H - \beta, \quad \lambda_2 = -\mu_H - \beta - \gamma, \quad \lambda_3 = -\mu_H, \quad \lambda_4 = -\mu_H - \gamma, \quad \lambda_5 = -\mu_H + \gamma N_M.
$$

It can be easily seen that $\lambda_1, \lambda_2, \lambda_3$ and $\lambda_4$ have negative real parts. $\lambda_5$ has negative real part when $\gamma_M N_M < \mu_H$.

Therefore the disease free equilibrium point is locally stable for $B_A < 1 \left( B_A = \frac{\gamma_M N_M}{\mu_H} \right)$.
Time series of the susceptible juvenile human, infectious juvenile human, susceptible adult human, infectious adult human and infectious rat population. The values of the parameter are

\[ \mu_H = \frac{1}{365 \times 70} \text{ day}^{-1}, \quad \mu_M = \frac{1}{365 \times 1.5} \text{ day}^{-1}, \]

\[ \gamma = \frac{1}{15} \text{ day}^{-1}, \quad \gamma_j = 0.001, \quad \gamma_M = 0.0000001, \]

\[ \gamma_A = 0.001, \quad N_J = 3000, \quad N_M = 50000, \quad N_A = 7000 \]

\[ \beta = 1, \quad B_A = 0.005475. \]

The fractions of populations approach to the free disease equilibrium point.

We show the time development of \( S, J, I, S_A, I_A, I_M \). The value of \( B_A = 0.005475 \) less than 1, the numerical solutions are shown in figure 2. Figure 3 shows the numerical solutions for \( B_A \) greater than 1. We will see that the numerical solutions approach to the disease free equilibrium points for \( B_A < 1 \). The numerical solutions oscillate to the endemic equilibrium points for \( B_A > 1 \).

4. DISCUSSION AND CONCLUSION

The mathematical model which we analyze in this study, the juvenile, adult human and rat population are assumed to have constant sizes. The basic reproductive number of this disease is

\[ R_0 = \frac{\gamma_M N_M}{\mu_M}. \]

It indicates the average number of secondary patients that one patient can produce if introduced into a susceptible person. After that, we consider the time series of juvenile, adult human and rat populations when the basic
reproductive numbers are difference. We show in figure 4.

Figure 4. Time series of the susceptible juvenile human, infectious juvenile human, susceptible adult human, infectious adult human and infectious rat population, respectively for $B_A > 1$

4a) $B_A = 2.7375$, the fractions of populations oscillate to the endemic disease equilibrium point $(0.0197602, 0.918977, 0.000000788954, 0.00586739, 0.992172)$

4b) $B_A = 574.5$, the fractions of populations oscillate to the endemic disease equilibrium point $(0.0000099978, 0.937409, 0.0000000391405, 0.00058674, 0.999961)$

Moreover, we compare the endemic equilibrium point for the transmission probability from rat to rat are difference. We can see in figure 5.
5a)  

Figure 5. Time series of the susceptible juvenile human, infectious juvenile human, susceptible adult human, infectious adult human and infectious rat population, respectively for the transmission probability from rat to rat are difference.  
5a) \( \gamma_f = 0.001, \gamma_d = 0.001, \gamma_m = 0.0000001 \), the fractions of populations oscillate to the endemic disease equilibrium point (0.0197602, 0.918977, 0.000000788954, 0.00586739, 0.992172).  
5b) \( \gamma_f = 0.001, \gamma_d = 0.001, \gamma_m = 0.001 \), the fractions of populations oscillate to the endemic disease equilibrium point (0.0196086, 0.919119, 0.000000782779, 0.00058674, 0.999999).

The transmission of leptospirosis for the different basic reproductive number, figure 4a) and figure 4b) equal to 2.7375 and 574.5, respectively. If the basic reproductive rate is higher, this means that one case can produce the greater number of secondary cases. The endemic equilibrium points for susceptible juvenile and susceptible adult humans decrease. The endemic equilibrium points for infectious juvenile, infectious adult humans and infectious rat increase.  

From figure 5, we can see that the value of basic reproductive number where the transmission probability from rat to rat are high then this number is high too. The endemic equilibrium points for infectious juvenile, infectious adult humans and infectious rat increase.

REFERENCES


