Southeast-Asian J. of Sciences, Vol. 7, No. 1 (2019) pp. 71-79

EFFECT OF CONTROL MEASURES ON THE TRANSMISSION MODEL OF NIPAH VIRUS DISEASE

Wutinan Songprasert*
Patcharawadee Kliangmanee and **Unchulee Natakuatung**

Dept. of Mathematics, Fac. of Science and Technology,
Suratthani Rajabhat University, Surat Thani, Thailand, 84100,
e-mail: W.Songprasert39@gmail.com

Abstract

The objectives of this study were to propose mathematical model of Nipah Virus Disease with effect of control measures on the transmission model Nipah Virus Disease, and to investigate the transmission model of Nipah Virus Disease. The standard modeling method is applied for model analysis. In this study, there were two control measures, the awareness rate to protect disease (u_1) and the recovery rate of humans by treatment (u_2).

In the proposed model, the human population was divided into three compartments, susceptible human (S), infectious human (I), and recovered human (R). The results showed that there were two equilibrium points; disease free equilibrium and endemic equilibrium point. The qualitative results depended on the basic reproductive number R_0.

We obtained the basic reproductive number by using the next generation method. Stabilities of the model are determined by Routh-Hurwitz criteria. If $R_0 < 1$, with $u_1 = 0.96$ and $u_2 = 0.74$, then the disease free equilibrium point is local asymptotically stable, but if $R_0 > 1$ with $u_1 = 0.50$ and $u_2 = 0.35$, then the endemic equilibrium point is local asymptotically stable. The graphical representations are provided to qualitatively support the analytical results. It concluded that if the effective of awareness rate to protect disease (u_1) and the recovery rate of

* Corresponnding author.
Key words: Equilibrium point, Basic reproductive number, Nipah Virus Disease, Control measures.
2010 AMS Classification: 35Q30

humans by treatment (u_2) increases, then the spread of this disease is reduced.

1. Introduction

Nipah is a zoonotic virus that can spread from animals to humans through the contact of saliva or contaminated tissues. This virus has a natural host in fruit bats and can be transmitted to other domesticated animals such as pigs and then to humans.

Those infected with the Nipah virus will suffer acute brain inflammation, and even if the patients survive, the encephalitis from the virus can resume within two years, while patients who have pneumonia can also spread the virus through droplets from sneezing, allowing human-to-human transmission. One infected patient can spread the disease quickly to more than 30 people [1].

Nipah virus is an emerging pathogen first identified in 1999 in Malaysia, with cases also seen in Singapore, in an outbreak of acute encephalitis in pigs and humans. Since then, human Nipah virus outbreaks have been reported in India and Bangladesh. While no new outbreaks have been reported in Malaysia and Singapore, repeated outbreaks have been noted in Bangladesh almost every year since 2001 in select districts with occasional outbreaks in neighboring India [2].

From 1998 to 2015, there have been at least 600 cases of Nipah virus human infections, with case fatalities in later outbreaks in India and Bangladesh ranging between 43 and 100%. Human to human transmission is particularly notable in the outbreaks in India and Bangladesh, accounting for 75% and 51% of cases, respectively. Nipah virus infection has both a neurological and respiratory disease presentation. Respiratory involvement differs in prevalence between the outbreak in Malaysia (29%) and Bangladesh (75%). Relapsing Nipah virus encephalitis distinct from acute Nipah virus encephalitis has been described and is estimated to occur in < 10 of survivors. Around 7 to 9 percent of the fruit bat population in Thailand was found to host the Nipah virus, though they only spread the virus during a specific time of the year from April to June. The virus in Thai bats has 99 per cent genetic resemblance to the strain causing the current outbreak in India. Although Nipah virus has caused only a few outbreaks, it infects a wide range of animals and causes severe disease and death in people, making it a public health concern [3].

Mathematical models have become important tools in analyzing the spread and control of infectious disease. In 2012, Biswas [4] studied the dynamics of Nipah virus by formulated and analyzed SIR model. Sultana et al. [5] formulated a dynamic model of Nipah virus infections with variable size population

and two control strategies where creating awareness and treatment are considered as controls. From the simulations it was monitored that the optimal combination of treatment and creating awareness is very prominent for disease elimination.

In this present study, we have proposed and analyzed epidemic model to study the effect of two control measures, the awareness rate to protect disease and the recovery rate of humans by treatment, on the transmission of Nipah virus. The remainder of the paper is organized as follows. In section 2, we formulate the propose model. In section 3, we analyze the model by using the standard method, to determine both disease free and endemic equilibrium point, derive the basic reproductive number and investigate the stability of the model. In section 4, we simulate numerical results, which confirm our theoretical results. Finally, we conclude our study in section 5.

2. Model Formulation

For this study, we formulated (SIR) model (Susceptible-Infected-Recovered) for the transmission of Nipah Virus Disease. Let $S(t), I(t)$ and $R(t)$ denote the susceptible, the infected, and the recovered human population, respectively. The Nipah Virus Disease model is combined the system of human populations. The diagram of the transmission of the Nipah Virus Disease as shown in Fig.1.

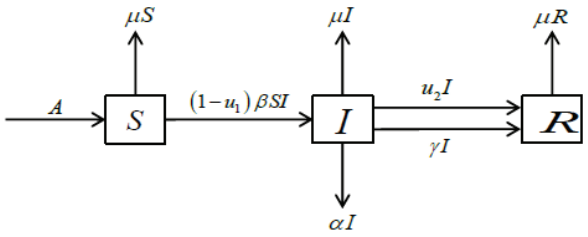

Fig. 1 Diagram of the transmission of the Nipah Virus Disease

We define: $S(t)$ is the number susceptible human population at time t, $I(t)$ is the number infected human population at time t, $R(t)$ is the number recovered human population at time t.

The dynamical model can be represented by the following system of differential equations as follows,

$$\frac{dS}{dt} = A - (1-u_1)\beta SI - \mu S \tag{1}$$

$$\frac{dI}{dt} = (1-u_1)\beta SI - (u_2+\gamma+\alpha+\mu)I \tag{2}$$

$$\frac{dR}{dt} = (u_2 + \gamma)I - \mu R \tag{3}$$

with $N = S + I + R$,

$$\frac{dN}{dt} = A - \mu N - \alpha I \tag{4}$$

where A is the birth rate of human population, β is the transmission rate of human-to-human, μ is the natural death rate of human population, α is the natural death rate of Nipah Virus Disease, $\gamma$is the recovery rate of human population, u_1 is the awareness rate to protect disease, u_2 is the recovery rate of humans by treatment and N is the total number of human population.

3. Model Analysis

Equilibrium point:

By using the standard method for analyzing our model, this system has two equilibrium points; disease free equilibrium point and endemic equilibrium point. We obtained these by setting the right hand side of equations, (1)-(4) to zero. Doing this, we obtain

1. Disease Free Equilibrium (DFE) denoted by $E_0(S, I, R, N)$. In the case of the absence of the disease, that is $I = 0$, we obtained $S = \frac{A}{\mu},\ R = 0,\ N = \frac{A}{\mu}$. Thus, $E_0(S, I, R, N) = \left(\frac{A}{\mu}, 0, 0, \frac{A}{\mu}\right)$

2. Endemic Equilibrium (EE) denoted by $E_1(S^*, I^*, R^*, N^*)$. In the case where the disease is present, that is $I^* > 0$, we obtained

$$I^* = \frac{(1-u_1)\beta A - \mu(u_2 + \gamma + \alpha + \mu)}{(1-u_1)(u_2 + \gamma + \alpha + \mu)\beta},\ S^* = \frac{A}{(1-u_1)\beta I^* + \mu},$$

$$R^* = \frac{(u_2 + \gamma)I^*}{\mu},\ N^* = \frac{A - \alpha I^*}{\mu}$$

Thus, $E_1(S^*, I^*, R^*, N^*) = \left(\frac{A}{(1-u_1)\beta I^* + \mu}, I^*, \frac{(u_2+\gamma)I^*}{\mu}, \frac{A-\alpha I^*}{\mu}\right)$.

Basic Reproductive Number: The basic reproductive number (R_0) (threshold condition in epidemiology) is the number of secondary infections induced by an infected individual into the total susceptible population [6]. By using the next generation method and used spectral radius [7]. Doing this, we rewrite the system in matrix form.

$$\frac{dX}{dt} = F(X) - V(X),\ X = (S, I, R, N)^T$$

and obtain,

$$F(X) = \begin{bmatrix} 0 \\ (1-u_1)\beta SI \\ 0 \\ 0 \end{bmatrix} \quad \text{and} \quad V(X) = \begin{bmatrix} -A + (1-u_1)\beta SI + \mu S \\ (u_2+\gamma+\alpha+\mu)I \\ -(u_2+\gamma)I + \mu R \\ -A + \mu N + \alpha I \end{bmatrix}$$

Finding the Jacobian matrix of $F(X)$ and $V(X)$ evaluated at $E_0(\frac{A}{\mu}, 0, 0, \frac{A}{\mu})$, we obtain:

$$F(E_0) = \begin{bmatrix} 0 & 0 & 0 & 0 \\ 0 & \frac{(1-u_1)\beta A}{\mu} & 0 & 0 \\ 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 \end{bmatrix} \text{ and } V(E_0) = \begin{bmatrix} \mu & \frac{(1-u_1)\beta A}{\mu} & 0 & 0 \\ 0 & u_2+\gamma+\alpha+\mu & 0 & 0 \\ 0 & -u_2-\gamma & \mu & 0 \\ 0 & \alpha & 0 & \mu \end{bmatrix}$$

Finding FV^{-1}, we get

$$FV^{-1} = \begin{bmatrix} 0 & 0 & 0 & 0 \\ 0 & \frac{(1-u_1)\beta A}{\mu(u_2+\gamma+\alpha+\mu} & 0 & 0 \\ 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 \end{bmatrix}$$

The spectral radius of FV^{-1} is denoted by $\rho(FV^{-1})$, thus,

$$\rho(FV^{-1}) = \frac{(1-u_1)\beta A}{\mu(u_2+\gamma+\alpha+\mu)}$$

We obtained the basic reproductive number as shown,

$$R_0 = \frac{(1-u_1)\beta A}{\mu(u_2+\gamma+\alpha+\mu)}$$

Stability Analysis

In this section, we show the stability of the model at both disease free equilibrium and endemic equilibrium. First, we show that the system (1)-(4) is local asymtotically stable. The stability of this system as shown in the follow Theorem.

Theorem 1. *The disease free equilibrium of the system (1)-(4) at the equilibrium E_0, is local asymptotically stable if $R_0 < 1$, and unstable if $R_0 > 1$.*

Proof. Since $R_0 < 1$, we have the Jacobian matrix of the system (1)-(4) at

$E_0 = \left(\frac{A}{\mu}, 0, 0, \frac{A}{\mu}\right)$ is

$$J_0 = \begin{bmatrix} -\mu & \frac{-(1-u_1)\beta A}{\mu} & 0 & 0 \\ 0 & \frac{(1-u_1)\beta A - \mu(u_2+\gamma+\alpha+\mu)}{\mu} & 0 & 0 \\ 0 & u_2+\gamma & -\mu & 0 \\ 0 & -\alpha & 0 & -\mu \end{bmatrix}$$

The eigenvalues of the Jacobian matrix J_0 are obtained by solving $\det(J_0 - \lambda I) = 0$. From this, we obtain the characteristic equation,

$$(\lambda+\mu)(\lambda+\mu)(\lambda+\mu)\left(\lambda + \frac{\mu(u_2+\gamma+\alpha+\mu)+(1-u_1)\beta A}{\mu}\right) = 0.$$

From the characteristic equation, we see that four eigenvalues are $\lambda_1 = -\mu < 0,\ \lambda_2 = -\mu < 0,\ \lambda_3 = -\mu < 0,\ \lambda_4 = -\frac{\mu(u_2+\gamma+\alpha+\mu)+(1-u_1)\beta A}{\mu} < 0.$ □

Theorem 2. *The endemic equilibrium of the system (1)-(4) at the equilibrium E_1, is local asymptotically stable if $R_0 > 1$, and unstable if $R_0 < 1$.*

Proof. Since $R_0 > 1$, we have the Jacobian matrix of the system (1)-(4) at $E_1(S^*, I^*, R^*, N^*)$ is

$$J_1 = \begin{bmatrix} -(1-u_1)\beta I^* - \mu & -(1-u_1)\beta S^* & 0 & 0 \\ (1-u_1)\beta I^* & (1-u_1)\beta S^* - (u_2+\gamma+\alpha+\mu) & 0 & 0 \\ 0 & u_2+\gamma & -\mu & 0 \\ 0 & -\alpha & 0 & -\mu \end{bmatrix}$$

where S^*, I^*, R^*, N^* are given by equation (4). The characteristic equation of Jacobian matrix at E_1, given by equations (1)-(4), becomes

$$(\lambda+\mu)(\lambda+\mu)(\lambda^2 + B_1\lambda + B_2) = 0$$

where $a_1 = (1-u_1)\beta I^* - \mu,\ a_2 = (1-u_1)\beta S^*,\ a_3 = (1-u_1)\beta I^*,\ a_4 = u_2+\gamma+\alpha+\mu,\ a_5 = u_2+\gamma,\ B_1 = a_1 - a_2 + a_4,\ B_2 = a_2a_3 - a_1(a_2 - a_4).$

From the characteristic equation, we see that two eigenvalues are $\lambda_1 = -\mu < 0,\ \lambda_2 = -\mu < 0$ The other two are the solution of quadratic equation $\lambda^2 + B_1\lambda + B_2 = 0$. The roots of this equation will be negative if two conditions satisfied with the Routh-Hurwitz criteria [8], $B_1 > 0$ and $B_2 > 0$. □

Numerical Results

The parameters used in the numerical simulation results are given in Table 1.

Table.1 parameter values in numerical simulations at disease free state.

Parameters	Descriptions	Values Unit	References
A	Birth rate of human population	0.03 per day	[5]
β	Transmission rate of human-to-human	0.5	Assumed
μ	Natural death rate of human population	0.002 per day	[5]
α	Natural death rate of Nipah Virus Disease	0.01 per day	[5]
γ	Recovery rate of human population	0.005 per day	[5]
u_1	Awareness rate to protect disease	0.96	Assumed
u_2	Recovery rate of humans by treatment	0.74	Assumed

Stability of disease free state: Using the values of parameters as shown in Table.1. We obtained the eigenvalues and the basic reproductive number as follows,

$$\lambda_1 = -0.002,\ \lambda_2 = -0.002, \lambda_3 = -0.002,\ \lambda_4 = -0.457,\ R_0 = 0.3963011890 < 1.$$

Since all eigenvalues are to be negative and the basic reproductive number is less than one, the disease free equilibrium state, E_0, will be local asymptotically stable, as shown in Fig 2.

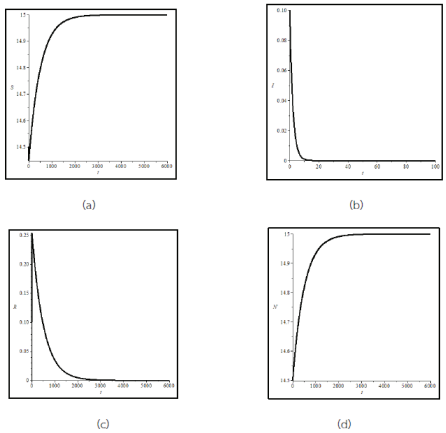

Fig 2. Time series of (a) Susceptible population (S), (b) Infected population (I), (c) Recovered population (R) and (d) Total population (N) with the values of parameters
$A = 0.03, \beta = 0.5, \mu = 0.002, \alpha = 0.01, \gamma = 0.005, u_1 = 0.96, u_2 = 0.74, R_0 = 0.3963011890 < 1$.

We see that the solutions approach to the disease free equilibrium $E_0 = (15, 0, 0, 15)$.

Stability of endemic state: we change the value of the awareness rate to protect disease to $u_1 = 0.50$, the recovery rate of humans by treatment $u_2 = 0.35$ and keep the other values of parameters to be those given in Table 1. We obtain the eigenvalues and the basic reproductive number as follows, $\lambda_1 = \lambda_2 = -0.002$, $\lambda_3 = -0.01011798365 + 0.08161858127i$, $\lambda_4 = -0.01021798365 - 0.08161858127i$, $R_0 = 10.21798365 > 1$.

Since the real part of all eigenvalues are to be negative and the basic reproductive number is greater than one, the endemic equilibrium state, 1 E , will be local asymptotically stable as shown in Fig. 3.

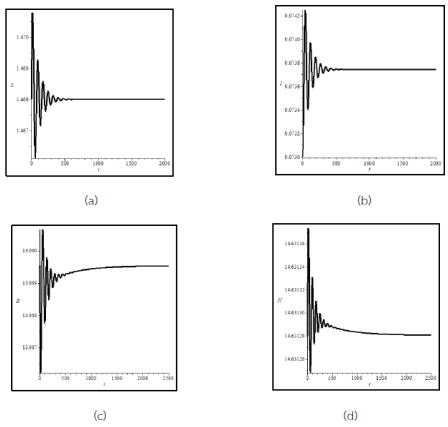

Fig.3. Time series of (a) Susceptible population (S), (b) Infected population (I), (c) Recovered population (R) and (d) Total population (N) with the values of parameters:
$A = 0.03, \beta = 0.5, \mu = 0.002, \alpha = 0.01, \gamma = 0.005, u_1 = 0.50, u_2 = 0.35, R_0 = 10.21798365 > 1$.

The state variables approach to endemic equilibrium
$E_1 = (1.468,\ 0.07374386921,\ 13.08953678,\ 14.63128065.)$

Conclusion

In this study, we proposed mathematical model of Nipah Virus Disease with the effect of control measures on the transmission model Nipah Virus Disease and analyzed the analytical results by using standard modeling method. The basic reproductive number is obtained through the use of spectral radius of the next generation matrix. The basic reproductive number is $R_0 = \frac{(1-u_1)\beta A}{\mu(u_2+\gamma+\alpha+\mu)}$. The basic reproductive number is the threshold condition for determining the stability of the equilibrium point of the model which are shown in Fig. 2 and 3. Our simulation result shown that R_0 were 0.3963011890 and 10.21798365 when $u_1 = 0.96,\ u_2 = 0.74$ and $u_1 = 0.50,\ u_2 = 0.35$, respectively. It is seen that the infected human will decrease when the effective of awareness rate to protect disease (u_1) and the recovery rate of humans by treatment (u_2) is increased.

ACKNOWLEDGEMENT The author is grateful to the Department of Mathematics, Faculty of Science and Technology, Suratthani Rajabhat University for providing the facilities to carry out the research and to thank Surapol Naowarat for valuable suggestions.

References

[1] WHO. (2018). Nipah virus. Available [http://www.who.int/news-room/fact-sheets/detail/nipah-virus].

[2] WHO, *WHO Target Product Profile for Nipah virus Vaccine,* Available [http://www.who.int/blueprint/priority-diseases/key-action/Nipah_virus_vaccineTPP.] (2017).

[3] P. Rujivanarom, *Caution urged to prevent outbreak of Nipah virus,* Available [http://www.nationmultimedia.com/detail/national/30346549] (2018).

[4] H. A. Biswas, *Model and control strategy of the deadly nipah virus (NiV) infections in Bangladesh,* Khulna University, Khulna, RRBS **6**(12) (2012), 370-377.

[5] J. Sultana and C.N. Podder, *Mathematical Analysis of Nipah Virus Infections Using Optimal Control Theory,* Journal of Applied Mathematics and Physics, **4**(2016), 1099-1111.

[6] R.M. Anderson and R.M. May, "Infectious Disease in Human : Dynamics and Control", Oxford University Press, Oxford, 1991.

[7] V.D. Driessche and J. Watmough, *Reproductive number and sub-threshold endemic equilibrium for compartment models of disease transmission,* Math. Biosci., **180** (2002), 29-48.

[8] L.J.S. Alen, "An Introduction to Mathematical Biology", Pearson/Prince Hall, Upper Saddle River, New Jersey, 2006.