AUSTRALIAN JOURNAL OF BASIC AND APPLIED SCIENCES

ISSN:1991-8178 EISSN: 2309-8414
Journal home page: www.ajbasweb.com

Mathematical Model for the Dynamic Transmission of Rabies with Control Measures

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ARTICLE INFO

Article history:
Received 3 March 2016
Accepted 2 May 2016
published 26 May 2016

Keywords:
Mathematical model, Rabie, Control measures, Stability, Equilibrium points, Basic reproductive number.

ABSTRACT

The objectives of this research were to develop and analyze the mathematical model for the dynamic transmission of rabies with control measures. The SEIR model is modified from Donkoh, Kabo-Bah and Asiedu (2014) model by adding control measures; isolation and eradication. The standard method is used to analyze the stability of the model. Routh-Hurwitz criteria is used for determining the stabilities of the model. We obtained the basic reproductive numbers by using the next generation method and finding the spectral radius. It was found that there are two equilibrium points; disease free and endemic equilibrium point. The qualitative results are depended on a basic reproductive numbers. If the basic reproductive number is less than one, the disease free equilibrium is local asymptotically stable, meaning that the disease will died out but if the basic reproductive number is greater than one, the endemic equilibrium will be local asymptotically stable, meaning that the disease will persist in the community. The numerical simulations are presented to illustrate the results. In addition, we show that control measures with isolation and eradication are the methods for controlling the disease.

INTRODUCTION

Rabies is an acute and fatal zoonotic disease, is caused by a member of the *Rhabdoviridae* family, genus *Lyssavirus* (Wunner, 2002 and 2007). Rabies may affect all mammals including humans, is transmitted with the bite and virus-containing saliva of an infected host (CDC, 2010). In most African and Asian countries dogs continue to be the main hosts and are responsible for least 55,000 human deaths per year worldwide from rabies (WHO, 2010, Knobel *et al*., 2005). Rabies transmission in dogs can be prevented vaccination but it has large economic costs. The other methods are used for dog population control: temporary birth control and permanent birth control (WHO, 2010).

In Thailand, rabies was first recorded in 1912, and it is also still a public health problem. The number of people exposed to animal bites varies from 300,000 – 400,000 per year and it estimated that 17,000 – 25,000 patients need application of rabies immune-globulin due to third degree exposure. Although the number of human rabies deaths is decreasing, an increase in the number of patients receiving post-exposure prophylaxis has been observed in the past decade. As many as 400,000 patients received vaccination due to dog bites. Dog bites represent a huge financial burden to the government that must provide post-exposure prophylaxis to those who have been bitten. The Thai private and public sectors spend at least US$ 10 million per year on post-exposure rabies prophylaxis (QSMI, MOPH 2005).

To Cite This Article: Kittiyanee Sornsong, Surapol Naowarat and Prasit Thongjaem., Mathematical Model for the Dynamic Transmission of Rabies with Control Measures. ***Aust. J. Basic & Appl. Sci.,*** *10(11): 169-175, 2016*

Mathematical models have become an important tool for understanding the spread and control of disease. This study provides a model introduction to the process of disease trans-mission, how this deterministic model can be represented mathematically and how this mathematical representation can be used to analyze the emergent dynamics of observed epidemics. Computer simulations are used to confirm study results by setting parameters and initial conditions (Hethcote, 2005) Most rabies model has focused on disease dynamics and control. One of the first rabies models has been given by Anderson *et al*. (1981). The simple susceptible-exposed-infectious-removed (SEIR) models of fox rabies in Europe, and ultimately this has led to effective disease eradication and containment strategies which are generally based on oral vaccination of foxes. The mathematical models now have been developed to incorporate dynamics in biological organization and interaction including the ability to incorporate environmental stochasticity and landscape heterogeneity (Smith *et al*., 2002, Russell *et al*., 2006) among coupled subpopulations of hosts linked across season (George, 2011) ecological gradients and proven predictive of spread in novel locations with tools, control measures (Smith and Cheeseman, 2002, Sterner and Smith. 2006, and optimal control (Coyne *et al*., 1989).

2. Model Formulation:

Our SEIR model was developed from the rabies model given in Donkoh, Kabo-Bah and Asiedu (2014) and adding control measures; isolation and eradication. The population is divided into four sub-classes. There are the susceptible class (S), exposed class (E), infected class (I), and recovered class (R). We denote the total numbers of dogs by N(t)and classify each of the numbers of dogs by S(t), E(t), I(t), and R(t), respectively, so that $S(t)+E(t)+I(t)+R(t)=N(t)$. The transmission dynamics associated with these sub-classes are illustrated in **Fig.1.**

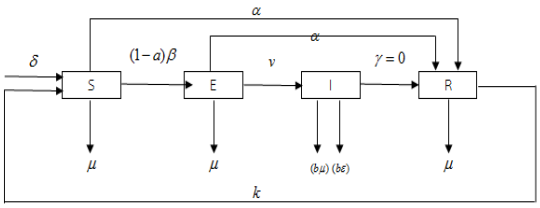

Fig. 1: Flow chart showing rabies model with control measures.

The dynamics of flow chart are described by the following ordinary differential equations:

$$\frac{dS}{dt} = \delta + kR - (1-a)\beta SI - (\alpha + \mu)S \quad (1)$$

$$\frac{dE}{dt} = (1-a)\beta SI - (\alpha + \mu + v)E \quad (2)$$

$$\frac{dI}{dt} = vE - (\mu b + \varepsilon b)I \quad (3)$$

$$\frac{dR}{dt} = \alpha S + \alpha E - (\mu + k)R \quad (4)$$

The parameters for the model are defined as δ is the birth rate of dogs, β is the transmission co-efficient between dogs, v is the latency (incubation) rate in dogs, μ is the death rate in dogs, ε is the disease induced mortality of dogs, α is the vaccination rate , k is the waning immunity in dogs, a is the interaction between dogs, so the control measures by isolation is $(1-a)$ and b is the control measures by eradication.

In this model, we assume infectious dogs $I(t)$ can infect susceptible dogs $S(t)$ by bite. The transmission rate between $S(t)$ and $I(t)$ is β where β is the number of dogs that a susceptible dog comes across per unit time. After being bitten by dogs, so we suppose infected dogs will not infect susceptible dogs. In fact rabies has an incubation period (from weeks to months). But since there is no rabies virus in saliva during the incubation period, they are not capable of transmitting the disease, until the virus had reached the brain. The susceptible dog is protected with control measures by isolation $(1-a)$. The birth numbers of dogs per unit time are δ. Vaccination is often applied to seemingly healthy dogs $S(t)$ and dogs bitten by dogs $E(t)$ where α is the vaccination rate. However, there is a protection period for rabies vaccine. Thus, we import loss rates of immunity (v). After a dog infected is appeared rabies infection, rabies is always fatal rate (γ). There is a control measures from the infected dogs by eradication. Natural death rates are μ and disease-related death rates are ε and the recovered dogs $R(t)$ can transfer to be the susceptible dogs $S(t)$ with the waning immunity rate k.

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3. ***Analysis of the Model:***

Equilibrium Points:

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

Disease Free Equilibrium Point (E_0 ***):***

In the absence of the disease in the community, that is $E = I = 0$, we obtained, $E_0(S, E, I, R) = E_0(\frac{(\mu+k)\delta}{\mu^2+(\alpha+k)\mu}, 0, 0, \frac{\alpha\delta}{\mu^2+(\alpha+k)\mu})$.

Endemic Equilibrium Point (E_1 ***):***

In case the disease is presented in the community, $I \neq 0$, we obtained, $E_1(S^*, E^*, I^*, R^*)$

$$S^* = \frac{(\alpha+\mu+\nu)(\mu b+\varepsilon b)}{(1-a)\beta\nu}$$

$$E^* = \frac{\delta(1-a)\beta\nu - (\alpha(k-1)+\mu)(\alpha+\mu+\nu)(\mu b+\varepsilon b)}{(1-a)\beta\nu(\mu+k)(\alpha+\mu+\nu) - \alpha(1-a)\beta\nu)}$$

$$I^* = \frac{\delta(1-a)\beta\nu^2 - (\alpha\nu(k-1)+\mu\nu)(\alpha+\mu+\nu)(\mu b+\varepsilon b)}{(\mu b+\varepsilon b)(1-a)\beta\nu(\mu+k)(\alpha+\mu+\nu) - \alpha(1-a)\beta\nu)}$$

$$R^* = \frac{1}{\mu+k}\left(\frac{\alpha(\alpha+\mu+\nu)(\mu b+\varepsilon b)-\mu}{(1-a)\beta\nu(\mu+k)} + \frac{\alpha\delta}{(\mu+k)(\alpha+\mu+\nu)-\alpha}\right)$$

Local Asymptotically Stability*:*

The local stability of each equilibrium point is determined from the Jacobian matrix of the system of equations (1)-(4) by considering the signs of real parts of all eigenvalualues. The eigenvalualues (λ) are the solutions of the characteristic equation $\det(J - \lambda I) = 0$. Where J is the Jacobian matrix at equilibrium point, I is the identity matrix dimension 4×4 .Equilibrium point is locally stability, when all eigenvalualues are negative real part.

The Jacobian matrix at E_0, we get

$$J_0 = \begin{bmatrix} -D_1 & 0 & -D_3 & k \\ 0 & -D_2 & D_3 & 0 \\ 0 & \nu & -D_4 & 0 \\ \alpha & \alpha & 0 & -D_5 \end{bmatrix}$$

with

$$D_1 = \alpha+\mu, \quad D_2 = \alpha+\mu+\nu, \quad D_3 = \frac{(1-a)\beta(\mu+k)\delta}{\mu^2+(\alpha+k)\mu},$$

$$D_4 = (\mu+\varepsilon)b, \quad D_5 = \mu+k.$$

The eigenvalualues of the J_0 are obtained by solving $\det(J_0 - \lambda I) = 0$. From Eqn. (1)-(4), we obtain the characteristic equation.

$$\lambda^4 + a_1\lambda^3 + a_2\lambda^2 + a_3\lambda + a_4 = 0$$

Where

$$a_1 = D_1 + D_2 + D_4 + D_5,$$

$$a_2 = D_2D_5 + D_1D_5 + D_4D_5 + D_1D_4 + D_2D_4 + D_1D_2 - k\alpha,$$

$$a_3 = D_1D_4D_5 + D_2D_4D_5 + D_1D_2D_5 + D_1D_2D_4 - k\alpha D_2 - k\alpha D,$$

$$a_4 = D_1D_2D_4D_5 - k\alpha D_2D_4 - \nu\alpha D_2.$$

with

$$D_1 = \alpha+\mu, \quad D_2 = \alpha+\mu+\nu, \quad D_3 = \frac{(1-a)\beta(\mu+k)\delta}{\mu^2+(\alpha+k)\mu},$$

$$D_4 = (\mu+\varepsilon)b, \quad D_5 = \mu+k.$$

From the characteristic equation, the eiganvalues are the solutions of $\lambda^4 + a_1\lambda^3 + a_2\lambda^2 + a_3\lambda + a_4 = 0$. The roots of this equation are negative if the coefficients satisfied the four conditions of the Routh – Hurwitz criteria(Allen. 2006). For them to be negative, we need $a_1 > 0, a_3 > 0, a_4 > 0, a_1a_2a_3 > a_3^2 + a_1^2a_4$.

The Jacobian matrix of the systems at the endemic equilibrium E_1 is

$$J = \begin{vmatrix} -D_1 & 0 & -D_4 & k \\ D_2 & -D_3 & D_4 & 0 \\ 0 & v & -D_5 & 0 \\ \alpha & \alpha & 0 & -D_6 \end{vmatrix}$$

$$D_1 = \frac{(1-a)\beta\delta(1-a)\beta v^2 - (\alpha v(k-1)+\mu v)(\alpha+\mu+v)(\mu b+\varepsilon b)}{(\mu b+\varepsilon b)(1-a)\beta v(\mu+k)(\alpha+\mu+v)-\alpha(1-a)\beta v)} + \alpha + \mu,$$

$$D_2 = \frac{(1-a)\beta\delta(1-a)\beta v^2 - (\alpha v(k-1)+\mu v)(\alpha+\mu+v)(\mu b+\varepsilon b)}{(\mu b+\varepsilon b)(1-a)\beta v(\mu+k)(\alpha+\mu+v)-\alpha(1-a)\beta v)},$$

$$D_3 = \alpha+\mu+v,$$

$$D_4 = \frac{(1-a)\beta(\alpha+\mu+v)(\mu b+\varepsilon b)}{(1-a)\beta v},$$

with $D_5 = \mu b+\varepsilon b, \quad D_6 = \mu + k.$

The eigenvalualues of the J_1 are obtained by solving $\det(J_1 - \lambda I) = 0$. We obtain the characteristic equation.

$$\lambda^4 + a_1\lambda^3 + a_2\lambda^2 + a_3\lambda + a_4$$

Where

$$a_1 = D_1 + D_3 + D_5 + D_6$$

$$a_2 = D_3D_5 + D_1D_5 + D_5D_6 + D_1D_3 + D_6D_3 + D_1D_6 - v$$

$$a_3 = D_1D_3D_5 + D_3D_5D_6 + 2D_1D_3D_6 - D_1D_4v - D_6D_4v - D_2D_4v$$

$$a_4 = D_2D_4D_6v + k\alpha vD_4 + D_1D_4D_6v + D_1D_3D_5D_6$$

With

$$D_1 = \frac{(1-a)\beta\delta(1-a)\beta v^2 - (\alpha v(k-1)+\mu v)(\alpha+\mu+v)(\mu b+\varepsilon b)}{(\mu b+\varepsilon b)(1-a)\beta v(\mu+k)(\alpha+\mu+v)-\alpha(1-a)\beta v)} + \alpha + \mu,$$

$$D_2 = \frac{(1-a)\beta\delta(1-a)\beta v^2 - (\alpha v(k-1)+\mu v)(\alpha+\mu+v)(\mu b+\varepsilon b)}{(\mu b+\varepsilon b)(1-a)\beta v(\mu+k)(\alpha+\mu+v)-\alpha(1-a)\beta v)},$$

$$D_3 = \alpha+\mu+v,$$

$$D_4 = \frac{(1-a)\beta(\alpha+\mu+v)(\mu b+\varepsilon b)}{(1-a)\beta v},$$

$$D_5 = \mu b+\varepsilon b,$$

$$D_6 = \mu + k.$$

From the characteristic equation, the eiganvalues are the solutions of $\lambda^4 + a_1\lambda^3 + a_2\lambda^2 + a_3\lambda + a_4$. The roots of this equation are negative if the coefficients satisfied the four conditions of the Routh – Hurwitz criteria(Allen. 2006). For them to be negative, we need $a_1 > 0, a_3 > 0,\ a_4 > 0, a_1a_2a_3 > a_3^2 + a_1^2a_4$.

Basic Reproductive Number ***(R_0):***

We obtained a basic reproductive number by using the next generation method (6) Rewriting the equations (1)-(4) in matrix form

$$\frac{dX}{dt} = F(X) - V(X) \tag{5}$$

Where $F(X)$ is the non-negative matrix of new infection terms and $V(X)$ is the non – singular matrix of remaining transfer terms.

Letting

$$X = \begin{bmatrix} S \\ E \\ I \\ R \end{bmatrix}, \quad . \tag{6}$$

$$F(X) = \begin{bmatrix} 0 \\ (1-a)\beta SI \\ 0 \\ 0 \end{bmatrix},$$

$$V(x) = \begin{bmatrix} (1-a)\beta SI + \alpha S + \mu S - kR - \delta \\ \alpha E + \mu E + \nu E \\ (\mu+\varepsilon)bI - \nu E \\ \mu R + kR - \alpha S - \alpha E \end{bmatrix}$$

And letting

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$$F=\left[\frac{\partial F_i(E_0)}{\partial X_i}\right] \text{ and } V=\left[\frac{\partial V_i(E_0)}{\partial X_i}\right] \tag{7}$$

For all $i, j=1,2,3,4$ be the Jacobian matrix of $F(X)$ and $V(X)$ at E_0 . The basic reproductive number (R_0) is the number of secondary case generate by a primary infectious case (6) or basic reproductive number is a measure of the power of an infection disease to a susceptible population. It can be evaluated through the formula

$$\rho(FV^{-1}) \tag{8}$$

Where FV^{-1} is called the next generation matrix and $\rho(FV^{-1})$ is the sprectral radius (largest eiginvalue) of FV^{-1}.

For our model, the Jacobian matrix becomes

$$F(E_0)=\begin{bmatrix} 0 & 0 & 0 & 0 \\ 0 & 0 & \frac{(1-a)\beta(\mu+k)\delta}{\mu^2+(\alpha+k)\mu} & 0 \\ 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 \end{bmatrix} \text{ and}$$

$$V(E_0)=\begin{bmatrix} \alpha+\mu & 0 & \frac{(1-a)\beta(\mu+k)\delta}{\mu^2+(\alpha+k)\mu} & -k \\ 0 & \alpha+\mu+\nu & 0 & 0 \\ 0 & -\nu & \mu b+\varepsilon b & 0 \\ -\alpha & -\alpha & 0 & \mu+k \end{bmatrix}$$

Hence,

$$FV^{-1}=\begin{bmatrix} 0 & 0 & 0 & 0 \\ 0 & \frac{(1-a)\beta\nu(\mu+k)\delta}{(\alpha+\mu+\nu)(\mu b+\varepsilon b)(\mu^2+(\alpha+k)\mu)} & \frac{(1-a)\beta\nu(\mu+k)\delta}{(\mu b+\varepsilon b)(\mu^2+(\alpha+k)\mu)} & 0 \\ 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 \end{bmatrix}$$

Thus

$$\rho(FV^{-1})=\frac{(1-a)\beta\nu\delta(\mu+k)}{(\alpha+\mu+\nu)(\mu b+\varepsilon b)(\mu^2+\alpha\mu+k\mu)}$$

We get

$$R_0=\frac{(1-a)\beta\nu\delta(\mu+k)}{(\alpha+\mu+\nu)(\mu b+\varepsilon b)(\mu^2+\alpha\mu+k\mu)}$$

4 Numerical simulation:

In this section, we considered the dynamic of SEIR model with control measures at disease-free and an endemic states. The parameter values leading to disease free state are show in **Table 1.**

Table 1: The parameter values leading to disease free state.

Parameters	Description	Values (Month)$^{-1}$
δ	Birth rate of dogs	1.975
k	Waning immunity in dogs	0.1918
β	transmission co-efficient between dogs	0.30417
α	Vaccination rate co-efficient	0.2975
μ	Death rate in dogs	0.002293
ν	Latency (incubation) rate in dogs	0.0021429
ε	Disease induced mortality of dogs	0.0049167
a	commination between Dogs	0.9041
b	control measures by eradication	1.005

5 Discussion and Conclusion:

In this paper, we proposed a mathematical model for the dynamic transmission of rabies with control measures consisting of a system of four nonlinear differential equations. The model analysis shown that there were two equilibrium points; disease free and endemic equilibrium points. The qualitative results are depended on a basic reproductive numbers. From Fig. 3, we can see that when a=0.9 and b=0.01 we obtain R_0 = 1.1746, this mean that the rabies disease will occur in the community. But when the value of a=0.9041 and b=1.005 we obtain R_0 = 0.799431 this mean that the rabies disease will died out from the community as shown in Fig. 2. We can conclude that if we increased the isolation value of infected dogs and increased the eradication value of infected dogs then the number of infected dogs to be decrease as Okuonghae and Aihie, (2010) they used the isolation and immi-gration of infected human as control measures.

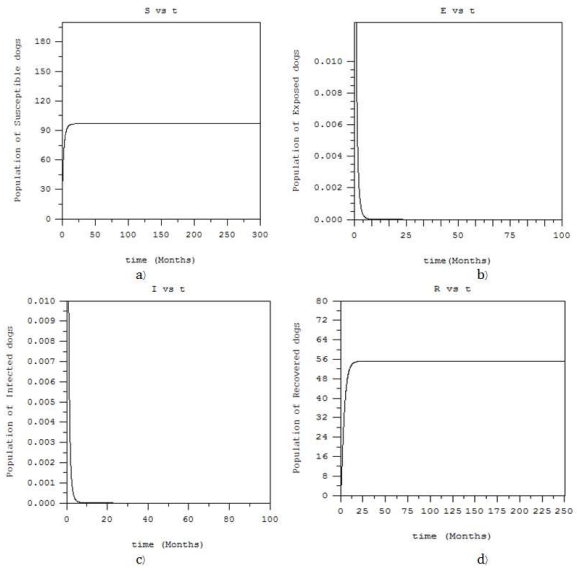

Fig. 2: Time series of (a) Susceptible dog population (S), (b) Exposed dog population (E), (c) Infected dog population (I) and (d) Recovered population dog (R). All the state variables approach their disease free state values $E_0(96.6537, 0, 0, 55.1835)$ as $a=0.9041, b=1.005$ and $R_0=0.799431<1$.

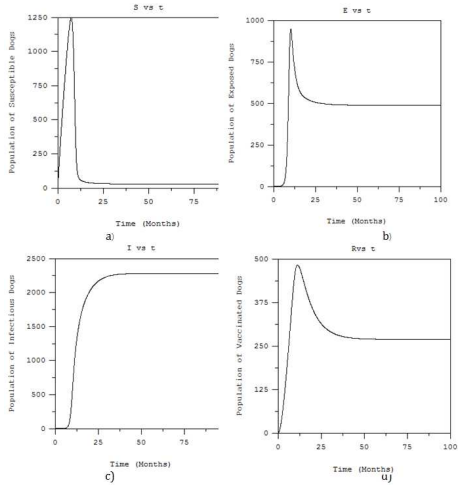

Fig. 3: Time series of (a) Susceptible dog population (S), (b) Exposed dog population (E), (c) Infected dog population (I), and (d) Recovered population dog (R). All the state variables approach their endemic state values $E_1(29.094, 488.211, 2275.200, 268.498)$ as $a=0.01, b=0.9$ and $R_0=1.17646>1$.

ACKNOWEDGMENTS

The authors would like to thank Department of Mathematics, Faculty of Science and Technology, Suratthani Rajabhat University for equipment support and the anonymous reviewers for their kind helpful comments.

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