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Stability Analysis of the Mathematical Modelling of Transmission and Control of Rabies Incorporating Vaccination Class

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Abstract

Rabies is a viral disease of nervous system that is often transmitted to human beings through the bite or scratch of rabid animals. The uprising of in-security globally has forced several people to get dogs in their houses. In this paper the mathematical model of rabies transmission and control was formulated by incorporating vaccination class. The Disease Free Equilibrium (DFE) state of the model was obtain and used to compute the basic reproduction number R_0. *Local stability analysis of the DFE was carried out using Jacobian Matrix techniques. The DFE is locally asymptotically stable if* $R_0 < 1$.

Keywords: Rabies, Mathematical model, stability, analysis, vaccination.

INTRODUCTION

Rabies is a deadly zoonotic viral disease that spread to human beings from the saliva of infected animals. The virus transmission is usually through a bite of a pet. Rabies is almost 100% fatal at the appearance of symptoms. Domestic dogs are responsible for almost 99% of rabies virus transmission to humans. Rabies also affects both domestic and wild animals. It is essential to carry out public enlightenment on dog actions and bite prevention for both children and adults, (WHO, 2020).

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Thongtha and Modnak (2021) formulated a mathematical model that described the dynamics of rabies virus transmission between dogs and humans. They also carried out equilibrium state analysis and optimal control theory was applied to seek vaccination cost minimization of rabies outbreak. Musaili and Chepkwony (2020) modified SIR model of infectious diseases with the system of ordinary differential equations to consider the spread of rabies virus in dogs incorporating public health enlightenment as a control measure. They calculated the reproduction number R_0 and obtained both the Disease free and endemic equilibrium points. Eze *et al*. (2020) presented an SEIR and SEIV model to describe the transmission dynamics of rabies virus in dogs and humans. They computed the basic reproduction number, the disease free and endemic equilibrium points. They also obtained a control solution for the model which predicts that using pre-exposure prophylaxis in both dogs and humans and public education is the best way of eliminating deaths from rabies. It was shown in their results that pre-exposure prophylaxis and post-exposure prophylaxis in humans with use of vaccination in the dog population can lead to total elimination of the disease. Asamoah *et al.* (2017) examined an optimal way of eradicating rabies transmission from dogs into the human population, using pre-exposure prophylaxis (vaccination) and post-exposure prophylaxis (treatment) due to public education. They obtain the disease-free equilibrium, the endemic equilibrium, the stability, and the sensitivity analysis of the optimal control model. They used Latin hypercube sampling (LHS), the forward-backward sweep scheme and the fourth-order Runge-Kutta numerical method to predict that the global alliance for rabies control aimed at eliminating deaths from canine rabies by 2030 is attainable through mass vaccination of susceptible dogs and continuous use of pre- and post-exposure prophylaxis in humans. Keller *et al.* (2013) studied the spread of raccoon rabies in New York State. They used finite elements for the space discretization of a partial differential equation (PDE) model to establish a fine spatial grid and locally varied the diffusion coefficient. Rabies epidemics cycles with a period of 3-6 years in dog populations in Africa, was modelled using susceptible, exposed, infectious and vaccinated model with an intervention response variable, and showed significant synchrony (Hampson *et al*., 2007). A standard SEIR mathematical model for dogs in Ghana was formulated. Both SEIR models with vaccination and without vaccination were formulated with ordinary differential equations (Addo, 2012).

Most of the above reviewed literatures did not incorporate the vaccination class into the populations of dogs and humans. Some of them only considered dog population with just three or four classes excluding vaccination class that is the key to control the transmission of rabies virus. They computed the basic reproduction number but they did not carry out the simulation. In this paper the vaccination classes were incorporated into standard SEIR models of both human and dog population. The equilibrium points of the model were determined and the Basic Reproduction Number R_0 was computed using next generation matrix. Local stability analysis of the Disease Free Equilibrium (DFE) was carried out and is stable if $R_0 < 1$. The Basic Reproduction Number R_0 was simulated graphically with some parameters of the model. The graphical representations revealed the parameters that will spread and control the rabies virus.

MATERIALS AND METHODS

Model Formulation

In this model, two populations are considered; dog and human. We divide each of the population into five compartments; susceptible, exposed, infected, vaccinated and recovered,

with dog population denoted by $S_1(t), E_1(t), I_1(t), V_1(t)$, and $R_1(t)$, and human population denoted by $S_2(t), E_2(t), I_2(t), V_2(t)$, and $R_2(t)$, respectively.

The dog population, σ_1 represent the recruitment rate of dogs, some of the dogs in the population are given Pre Exposure Prophylaxis (PREP) vaccine represented by ϕ_1. The susceptible dogs get in contact with infected dogs at rate α_1 to get expose to rabies. Some of the dogs that got exposed may develop clinical rabies represented by $\tau_1\varsigma_1$ which make them move to the infected class while others may not develop clinical rabies represented by $\tau_1(1-\varsigma_1)$. Those dogs with clinical rabies have a small chance of surviving which leads to death due to the infection at rate δ_1 and those that were attended to immediately after being exposed to are vaccinated at rate ϕ_1 and they were confirmed totally free from rabies move to recovered class at rate γ_1 and after sometime a loss of vaccine immunity can occur at rate θ_1 and they became susceptible. All dogs in the model have natural mortality rate μ_1

The human population, σ_2 represent the recruitment rate of humans. The susceptible humans get in contact with infected dogs at rate α_2 to get expose to rabies. Some of the humans that got exposed may develop clinical rabies represented by $\tau_2\varsigma_2$ which make them move to the infected class while others may not develop clinical rabies represented by $\tau_2(1-\varsigma_2)$. Those humans with clinical rabies have a small chance of surviving which leads to death due to the infection at rate δ_2 and those that were attended to immediately after being exposed to by washing the bite with soap and water at rate ψ_2 and are vaccinated at rate ϕ_2 and they were confirmed totally free from rabies move to recovered class at rate γ_2 and after sometime a loss of vaccine immunity can occur at rate θ_2 and they became susceptible. All humans in the model have natural mortality rate μ_2. All parameters are positive.

The model flow diagram is shown in figure 1. The arrow from infected dog to the susceptible human shows the infected dog infects the susceptible human.

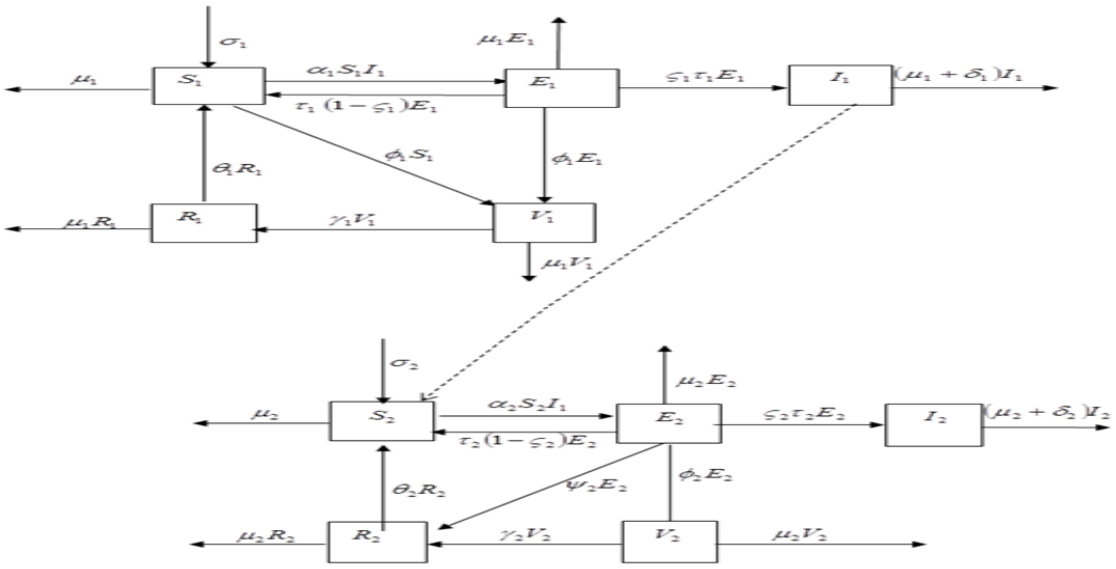

Figure 1: Schematic Diagram of the Model

The equations of the model are formulated from the schematic diagram above.

$$\frac{dS_1(t)}{dt} = \sigma_1 - \alpha_1 S_1 I_1 + \tau_1(1-\varsigma_1)E_1 + \theta_1 R_1 - (\mu_1 + \phi_1)S_1 \quad (1)$$

$$\frac{dE_1(t)}{dt} = \alpha_1 S_1 I_1 - (\mu_1 + \tau_1 + \phi_1)E_1 \quad (2)$$

$$\frac{dI_1(t)}{dt} = \tau_1 \lambda_1 E_1 - (\mu_1 + \delta_1)I_1 \quad (3)$$

$$\frac{dV_1(t)}{dt} = \phi_1 S_1 + \phi_1 E_1 - (\mu_1 + \gamma_1)V_1 \quad (4)$$

$$\frac{dR_1(t)}{dt} = \gamma_1 V_1 - (\theta_1 + \mu_1)R_1 \quad (5)$$

$$\frac{dS_2(t)}{dt} = \sigma_2 - \alpha_2 S_2 I_1 + \tau_2(1-\varsigma_2)E_2 + \theta_2 R_2 - \mu_2 S_2 \quad (6)$$

$$\frac{dE_2(t)}{dt} = \alpha_2 S_2 I_1 - (\mu_2 + \tau_2 + \phi_2 + \psi_2)E_2 \quad (7)$$

$$\frac{dI_2}{dt} = \tau_2 \lambda_2 E_2 - (\mu_2 + \delta_2)I_2 \quad (8)$$

$$\frac{dV_2}{dt} = \phi_2 E_2 - (\mu_2 + \gamma_2)V_2 \quad (9)$$

$$\frac{dR_2(t)}{dt} = \gamma_2 V_2 + \psi_2 E_2 - (\theta_2 + \mu_2)R_2 \quad (10)$$

Equilibrium State of the Model

At equilibrium the time derivatives are equal to zero, i.e.;

$$\frac{dS_1}{dt} = \frac{dE_1}{dt} = \frac{dI_1}{dt} = \frac{dV_1}{dt} = \frac{dR_1}{dt} = \frac{dS_2}{dt} = \frac{dE_2}{dt} = \frac{dI_2}{dt} = \frac{dV_2}{dt} = \frac{dR_2}{dt} = 0 \quad (11)$$

Disease Free Equilibrium State

Let $E^0 = (S_1, E_1, I_1, V_1.R_1, S_2, E_2, I_2, V_2.R_2) = (S_1^0, E_1^0, I_1^0, V_1^0.R_1^0, S_2^0, E_2^0, I_2^0, V_2^0, R_2^0)$ (12)

be the DFE point

Substituting equation (12) into (1) to (10) equates to zero and solve gives

$$E^0 = (S_1^0, E_1^0, I_1^0, V_1^0.R_1^0, S_2^0, E_2^0, I_2^0, V_2^0, R_2^0) = \left(\begin{array}{c} \frac{\sigma_1 K_4 K_5}{K_1 K_4 K_5 - \phi_1 \gamma_1 \theta_1}, 0, 0, \frac{\sigma_1 \phi_1 K_5}{K_1 K_4 K_5 - \phi_1 \gamma_1 \theta_1}, \\ \frac{\sigma_1 \phi_1 \gamma_1}{K_1 K_4 K_5 - \phi_1 \gamma_1 \theta_1}, \frac{\sigma_2}{\mu_2}, 0, 0, 0, 0 \end{array} \right) \quad (13)$$

where,

$$\left. \begin{array}{l} K_1 = (\mu_1 + \phi_1), K_2 = (\mu_1 + \tau_1 + \phi_1), K_3 = (\mu_1 + \delta_1), K_4 = (\mu_1 + \gamma_1) \\ K_5 = (\theta_1 + \mu_1), K_6 = (\mu_2 + \tau_2 + \phi_2 + \psi_2), K_7 = (\mu_2 + \delta_2) \\ K_8 = (\mu_2 + \gamma_2), K_9 = (\theta_2 + \mu_2) \end{array} \right\} \quad (14)$$

Equation (13) is the Disease Free Equilibrium DFE point of the model

Basic Reproduction Number (R_0)

In this model, the next generation matrix method as described by Driessche and Watmough (2002) is used to get the basic reproduction number R_0. Basic reproduction number $(R_0) = \rho(FV^{-1})$, where $f_i(x)$ be the rate of appearance of new infections in compartment i, V_i^+ the rate of transfer of individuals into compartment i by all other means and V_i^- the rate of transfer of individuals out of compartment i.

$$f = \begin{pmatrix} \alpha_1 S_1 I_1 \\ 0 \\ \alpha_2 S_2 I_1 \\ 0 \end{pmatrix} \tag{15}$$

The jacobian matrix of F evaluated at the disease free equilibrium point is given by

F=$\left(\frac{\partial f_i(E^0)}{\partial x_j}\right)$, where $x_j = E_1, I_1, E_2, I_2$ for j=1, 2, 3, 4 and E^0 is the disease free equilibrium.

The Jacobian matrix of (15) evaluated at the disease free equilibrium point is given

$$F = \begin{pmatrix} 0 & \frac{\alpha_1 \sigma_1 K_4 K_5}{K_1 K_4 K_5 - \phi_1 \gamma_1 \theta_1} & 0 & 0 \\ 0 & 0 & 0 & 0 \\ 0 & \frac{\alpha_2 \sigma_2}{\mu_2} & 0 & 0 \\ 0 & 0 & 0 & 0 \end{pmatrix} \tag{16}$$

The rate of transfer of individuals in and out of the infectious compartment i is given by the matrix,

$$V_i = \begin{pmatrix} K_2 E_1 \\ K_3 I_1 - \tau_1 \varsigma_1 E_1 \\ K_6 E_2 \\ K_7 I_2 - \tau_2 \varsigma_2 E_2 \end{pmatrix} \tag{17}$$

The Jacobian matrix of (17) evaluated at the disease free equilibrium point is given by,

$$V = \begin{pmatrix} K_2 & 0 & 0 & 0 \\ -\tau_1 \varsigma_1 & K_3 & 0 & 0 \\ 0 & 0 & K_6 & 0 \\ 0 & 0 & -\tau_2 \varsigma_2 & K_7 \end{pmatrix} \tag{18}$$

where $x_j = E_1, I_1, E_2, I_2$ for j=1, 2, 3, 4 and x_0 is the disease free equilibrium

The inverse of V is computed using guass Jordan method

$$V^{-1} = \begin{pmatrix} \frac{1}{K_2} & 0 & 0 & 0 \\ \frac{\tau_1 \varsigma_1}{K_2 K_3} & \frac{1}{K_3} & 0 & 0 \\ 0 & 0 & \frac{1}{K_6} & 0 \\ 0 & 0 & \frac{\tau_2 \varsigma_2}{K_6 K_7} & \frac{1}{K_7} \end{pmatrix} \tag{19}$$

The next generated matrix FV^{-1} is given by;

$$FV^{-1}=\begin{pmatrix} \dfrac{\alpha_1\sigma_1\tau_1\varsigma_1K_4K_5}{K_2K_3\left(K_1K_4K_5-\phi_1\gamma_1\theta_1\right)} & \dfrac{\alpha_1\sigma_1K_4K_5}{K_3\left(K_1K_4K_5-\phi_1\gamma_1\theta_1\right)} & 0 & 0 \\ 0 & 0 & 0 & 0 \\ \dfrac{\alpha_2\sigma_2\tau_1\varsigma_1}{\mu_2K_2K_3} & \dfrac{\alpha_2\sigma_2}{\mu_2K_3} & 0 & 0 \\ 0 & 0 & 0 & 0 \end{pmatrix} \tag{20}$$

$\rho\left(FV^{-1}\right)$ is the dominant eigenvalue of the $\left(FV^{-1}\right)$ matrix.

$$\left.\begin{aligned} &\left|FV^{-1}-\lambda I\right|=0 \\ &\begin{vmatrix} \dfrac{\alpha_1\sigma_1\tau_1\varsigma_1K_4K_5}{K_2K_3\left(K_1K_4K_5-\phi_1\gamma_1\theta_1\right)}-\lambda & \dfrac{\alpha_1\sigma_1K_4K_5}{K_3\left(K_1K_4K_5-\phi_1\gamma_1\theta_1\right)} & 0 & 0 \\ 0 & -\lambda & 0 & 0 \\ \dfrac{\alpha_2\sigma_2\tau_1\varsigma_1}{\mu_2K_2K_3} & \dfrac{\alpha_2\sigma_2}{\mu_2K_3} & -\lambda & 0 \\ 0 & 0 & 0 & -\lambda \end{vmatrix}=0 \end{aligned}\right\} \tag{21}$$

Then, $R_0=\dfrac{\alpha_1\sigma_1\tau_1\varsigma_1K_4K_5}{K_2K_3\left(K_1K_4K_5-\phi_1\gamma_1\theta_1\right)}$ (22)

Local Stability of Disease Free Equilibrium Point.

Theorem: The disease free equilibrium point is said to be locally asymptotically stable, if all the eigenvalues of the Jacobian matrix at DFE are negative or unstable otherwise.

Proof:

The Jacobian matrix of the system of equations at disease free equilibrium is;

$$J\left(E^0\right)=\begin{bmatrix} -A_1 & \tau_1\left(1-\varsigma_1\right) & -M & 0 & \theta_1 & 0 & 0 & 0 & 0 & 0 \\ 0 & -A_2 & M & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & \tau_1\varsigma_1 & -A_3 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ \phi_1 & \phi_1 & 0 & -A_4 & o & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & \gamma_1 & -A_5 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & \dfrac{-\alpha_2\sigma_2}{\mu_2} & 0 & 0 & -\mu_2 & \tau_2\left(1-\varsigma_2\right) & 0 & 0 & \theta_{h2} \\ 0 & 0 & \dfrac{\alpha_2\sigma_2}{\mu_2} & 0 & 0 & 0 & -A_6 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & \tau_2\varsigma_2 & -A_7 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & \phi_2 & 0 & -A_8 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & \psi_2 & 0 & \gamma_2 & -A_9 \end{bmatrix} \tag{23}$$

Where,

$$M=\frac{\alpha_1\sigma_1\left(\theta_1+\mu_1\right)\left(\mu_1+\gamma_1\right)}{\left(\mu_1^2+\gamma_1\mu_1\right)\left(\theta_1+\mu_1+\phi_1\right)+\phi_1\mu_1\theta_1}$$

Reducing equation (23) to upper triangular matrix and the characteristic equation gives,

$$\left|J\left(E^{0}\right)-\lambda I\right|=0$$

$$\begin{vmatrix} -A_1-\lambda & \tau_1(1-\varsigma_1) & -M & 0 & \theta_d & 0 & 0 & 0 & 0 & 0 \\ 0 & -A_2-\lambda & M & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & -A_3-\lambda & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & -A_4-\lambda & o & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & -A_5-\lambda & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & -\mu_h-\lambda & \tau_2(1-\varsigma_2) & 0 & 0 & \theta_h \\ 0 & 0 & 0 & 0 & 0 & 0 & -A_6-\lambda & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 & -A_7-\lambda & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & -A_8-\lambda & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & -A_9-\lambda \end{vmatrix} = 0 \quad (24)$$

The determinant of equation (24) gives;

$$\left[\begin{matrix}(-A_1-\lambda_1)(-A_2-\lambda_2)(-A_3-\lambda_3)(-A_4-\lambda_4)(-A_5-\lambda_5) \\ (-\mu_h-\lambda_6)(-A_6-\lambda_7)(-A_7-\lambda_8)(-A_8-\lambda_9)(-A_9-\lambda_{10})=0\end{matrix}\right] \quad (25)$$

Therefore,

$\lambda_1=-A_1$ or $\lambda_2=-A_2$ or $\lambda_3=-A_3$ or $\lambda_4=-A_4$ or $\lambda_5=-A_5$

or $\lambda_6=-\mu_h$ or $\lambda_7=-A_6$ or $\lambda_8=-A_7$ or $\lambda_9=-A_8$ or $\lambda_{10}=-A_9$

(26)

From equation (26)

$\lambda_1,\lambda_2,\lambda_3,\lambda_4,\lambda_5,\lambda_6,\lambda_7,\lambda_8,\lambda_9,\lambda_{10}<0$

Hence, the disease free equilibrium point is locally asymptotically stable.

RESULT AND DISCUSSIONS

The figures 2 to 6 is graphical simulation of the Basic Reproduction Number and some selected parameters of the model.

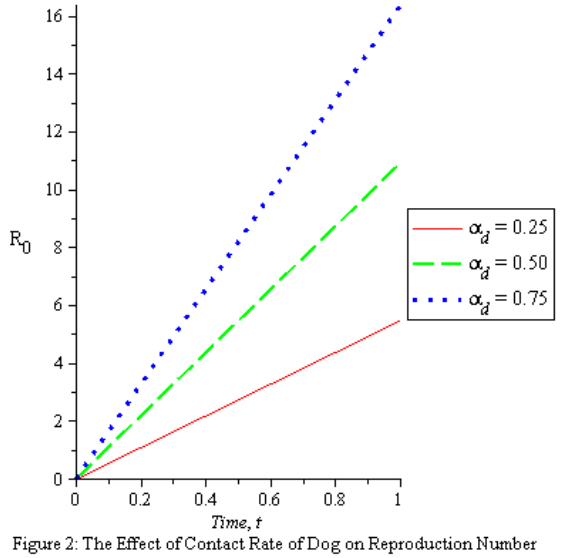

Figure 2: The Effect of Contact Rate of Dog on Reproduction Number

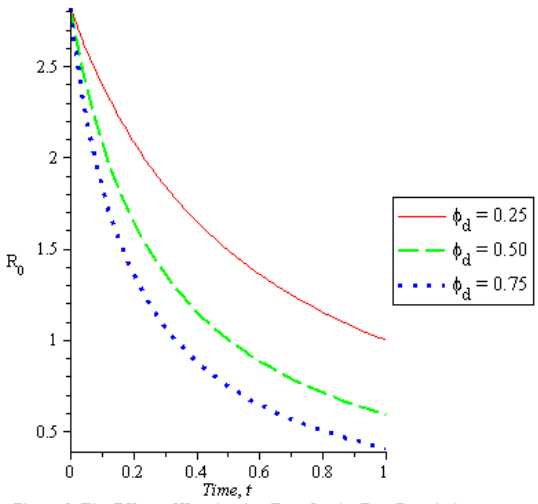

Figure 3: The Effect of Vaccination Rate for the Dog Populations on Reproduction Number

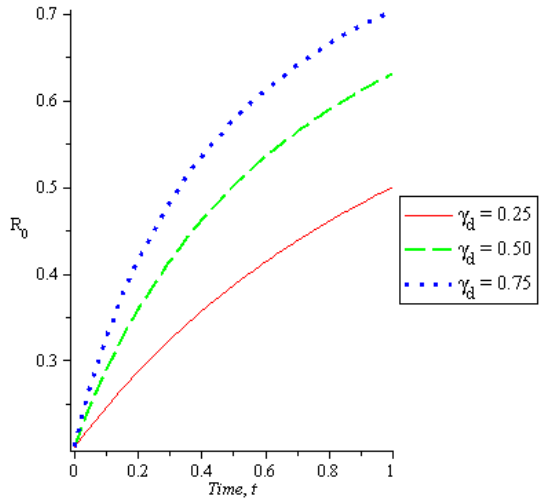

Figure 4: The Effect of Recovery Rate of Dog Populations on Reproduction Number

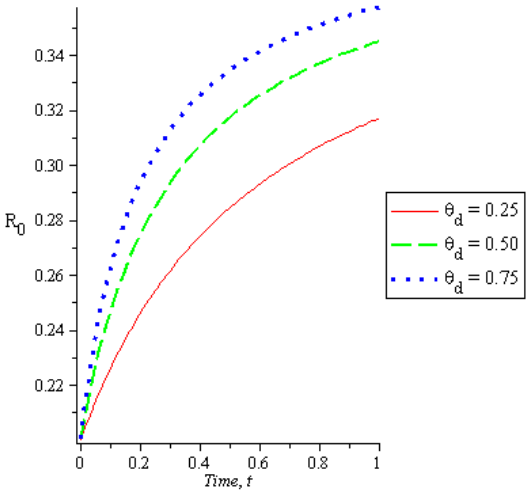

Figure 5: The Effect of Loss of Vaccine Immunity in the Dog Populations on Reproduction Number

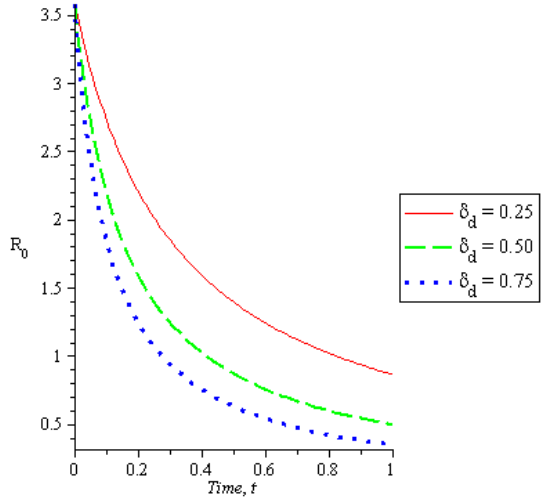

Figure 6: The Effect of Disease-Induced Death Rate of Dog Populations on Reproduction Number

Figure 2 shows that, the increase in contact rate of dogs with time increases the reproduction number. This shows that no matter how small is the contact of the infected dog with the susceptible dog or human will spread the transmission of rabies. Figure 3 reveal that, as vaccination rate for the dog increases with time, the reproduction number decreases. This implies that the vaccination is the best to curb the transmission of the rabies. In figure 4 it is shown that as recovery rate of dog increase with time the basic reproduction number increases. This implies that, the treatment of rabies cannot control the transmission. It is observed from figure 5 that the higher the loss of vaccination immunity rate the higher the basic reproduction number. Figure 6 revealed that, the increase in disease-induced death rate of dog decreases the reproduction number. This implies that the more the dogs with rabies are killed or died the less the transmission.

CONCLUSION

The mathematical model of rabies was formulated by incorporating vaccination. There are two equilibrium states that exist in the model; Disease Free Equilibrium (DFE) and Endemic Equilibrium. The local stability analysis shows that DFE is stable if $R_0 < 1$. This implies that rabies can be eradicated from the population if the dogs are vaccinated. It was observed from the Basic reproduction number that, all the parameters are that of dog even though the model

involve both the dog and human populations, this shows once the dog are handled well rabies can be eradicated from the population.

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