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Modeling the transmission dynamics of an avian influenza: qualitative and quantitative analysis

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Abstract
Background: *Annually, avian influenza causes high morbidity and mortality rate predominately among the immunodeficiency persons worldwide. Treatment and vaccination remain the optimal strategies in curbing the spread of avian influenza infection.*
Methods: *In this paper, a mathematical model of the dynamics of influenza infection is formulated and both qualitative and quantitative analyses are carried out extensively.*
Results: *The qualitative analysis of the model is given in terms of the basic reproduction number, equilibria points and their stability analyses. The disease dies out whenever the basic reproduction number is less than a unit. The disease free equilibrium (DFE) is locally asymptotically stable provided $R_0 < 1$ and unstable if otherwise. The endemic equilibrium only occurs whenever the disease threshold is greater than a unit. The endemic equilibrium, E_2^* is locally, globally asymptotically stable under certain condition. Numerical solution shows that vaccination and treatment of the susceptible and the infected individuals respectively have high impact for eradicating the disease. The non-linear incidence as a force of infection with parameter, θ has a great impact for reducing the pandemic of influenza disease.*
Conclusion: *Vaccination of susceptible individuals and treatment of infected individuals are imperative for curbing the spread of an avian influenza infection. Modeling style or structure especially the type of force of infection adopt for modeling an avian influenza disease depends on whether the disease can easily be put under control.*
Key word: *Avian Influenza, modeling, basic reproduction number, equilibrium, numerical solution.*

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I. Introduction

Avian influenza is a highly cytopathic, contagious and acute respiratory disease caused by an influenza virus infection[6,8]. The mode of transmission is through direct contact such as hand shake or by airborne virus[8]. The virus has seven internal proteins (nucleoprotein (NP), three polymerase proteins (PA, PB1 and PB2), two matrix proteins (M1 and M2) and nonstructural proteins (NS2)) and two external glycoproteins, hemagglutimin (HA) and neuraminidase (NA)[6].

During the 20th century, three global pandemics occurred. The "Spanish flu" of 1918 -1919, infected nearly one third of the entire human population[12]. During the global pandemic, more than 500,000 people died in the USA and approximately 50 million people died worldwide[12].

Infection of the respiratory tract with an influenza virus has a symptom ranging from mild non-febrile illness to severe disease and complications, including pneumonia, shock, renal failure, encephalopathy and multiorgan dysfunction[4,13]. However, mortality rates, clinical symptoms and basic reproduction numbers (outbreak thresholds) vary greatly between influenza type[3].

Influenza can be prevented by getting vaccination each year. However, given that the virus mutates rapidly, a vaccine made for one year may not be useful in the following year. More so, antigenic drift in the virus may occur after the year's vaccine has been formulated rendering the vaccine less protective, and hence, out breaks can easily occur[2].

Mathematical modeling has proven to be a valuable tool in the understanding the dynamics of influenza infection disease which helps in clarifying and testing hypotheses finding the smallest number of factors sufficient to explain the biological phenomena and analyzing experimental results[1].

In order to better understand and explore the dynamics of infectious diseases, various mathematical models have been used on their epidemiological behaviours and implemented useful control and preventive measure for the disease eradication[1,9]. Numerous mathematical models are

designed for avian influenza virus[3,5,7,10,11]. Recently, Muhammad *et al.*[9] in 2019 studied the transmission dynamics of avian influenza with saturation and psychological effect.

In the transmission of infectious disease, saturated incidence rate plays an important role. In most of the avian influenza models the incidence rate is considered the mass action from bi-linear interactions, which is increasing and unbound[9]. The adoption of the saturated incidence rate present a different result entirely.

II. Model Formulation and Analysis

A dynamical mathematical model of avian influenza virus infection is proposed which put into consideration on the vaccination of susceptible individuals and the treatment of the infected individuals. Most influenza disease mathematical model follow SEIR model for human disease transmission. On the other hand, the carrier (bird) population has SIR model dynamics. It should be noted that influenza model sometimes capture human population only without explicitly show the carrier model. In view of this, we compartmentalized our model into five state variables of human population namely, susceptible individuals (S(t)), vaccinated individuals (V(t)), exposed individuals (E(t)), infected individuals (I(t)) and recovered individuals (R(t)). The following assumptions are important for the formulation of our model equations. We considered the force of infection to follow non-linear incidence rate, the recruitment rate of the population is constant; a non-autonomous model is considered due to the time dependence of each state variable, a fraction of recovered individuals loss immunity and re-entered into the susceptible population. We define the parameters of the model as given in Table 2.1.

Table 2.1: Description and Interpretation of Parameters of the Model Equations

Parameter	*Interpretation*
Λ	Recruitment rate of human population
μ	Natural death rate
δ	Disease induced death rate
$\psi_1(t)$	Vaccination rate of the susceptible individual
$\sigma = (1 - \xi)$	Degree of protection where ξ is the vaccine efficacy
$\psi_2(t)$	Treatment of the infected individual
γ	Natural recovery rate of the infected individuals
k	Progression rate from exposed to infectious
δ	Rate at which recovered individual loss immunity and become susceptible
$1 + \theta I(t)$	Inhibition effect from the behavioural increase
$\lambda(t)$	The force of infection which represent the transmission rate of the disease

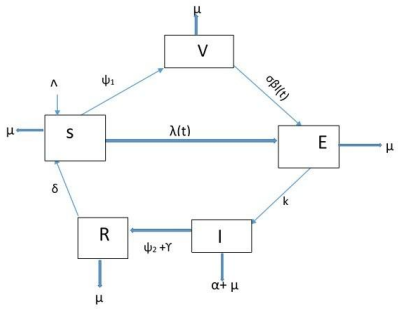

Fig. 2.1: Flow diagram of the model equations

Putting into consideration the variables, parameters and the assumptions stated above we arrived at our model equations as follow:

$$\begin{aligned}
\frac{dS}{dt} &= \Lambda - \lambda(t)S(t) - (\psi_1(t) + \mu)S(t) + \delta R(t) \\
\frac{dV}{dt} &= \psi_1(t)S(t) - \beta\ I(t)V(t) - \mu V(t) \\
\frac{dE}{dt} &= \beta\ I(t)V(t) + \lambda(t)S(t) - kE(t) - \mu E(t) \\
\frac{dI}{dt} &= kE(t) - (\alpha + \mu + \gamma + \psi_2(t))I(t) \\
\frac{dR}{dt} &= \psi_2(t)I(t) + \gamma I(t) - (\delta + n\mu)R(t)
\end{aligned} \qquad (2.1)$$

with

$$\lambda(t) = \frac{\beta\ I(t)}{(1 + \theta I(t))}$$

and

$$N(t) = S(t) + V(t) + E(t) + I(t) + R(t)$$

2 Analysis of the Model Equations

In order to gain more insight into the influenza dynamics, we seek to carryout the following qualitative analysis of the model equations in this section as analyzed in the order of the following subheadings:

2.1 Positive Invariant of the Model Equations

In this sub-section, we show the positive invariant of the five state variables in model equations (2.1). To accomplish this, we establish the following theorem

Theorem 2.1

The closed set

$$D = \{(S(t), V(t), E(t), I(t), R(t)) \in \Re_+^5 : N(t) \leq \frac{\Lambda}{\mu}\}$$

is positively invariant and attract all positive solutions of the model equations.

Remark 1: In the theorem, we think of the solution space as having five dimensions, so that at any point of time *t*, we have a vector of solutions with five elements (standing for the state variables); real and positive solutions, hence the plus sign in $\Re_+^5$

We therefore prove Theorem (2.1). Generally, it implies thus:

Proof.

$$\frac{dN}{dt} = \Lambda - \mu N(t) - \alpha I(t)$$

By a standard comparison theorem, we see that

$$\frac{dN}{dt} = \lambda - \mu N(t),$$

which yields (by the method of integrating factor)

$$N(t) \leq N(0)e^{-\mu t} + \frac{\Lambda}{\mu}(1 - e^{-\mu t}),$$

To be specific, if $N(0) \leq \frac{\Lambda}{\mu}$, then $N(t) \leq \frac{\Lambda}{\mu}$. Hence, D is positively invariant and an attractor so that no solution path leaves through any boundary of D.

2.2 Disease Free Equilibrium (DFE) Analysis

Under this sub-section, we carryout the equilibrium state of our model(2.1) when there is no disease in the population of interest. To investigate this, we simply substitute $E(t) = I(t) = R(t) = 0$ and $\frac{dS}{dt} = \frac{dV}{dt} = \frac{dE}{dt} = \frac{dI}{dt} = \frac{dR}{dt} = 0$ in model (2.1) and obtain

$$\Lambda - (\psi_1(t) + \mu)S(t) = 0 \qquad (2.2)$$

$$\psi_1(t)S(t) - \mu V(t) = 0 \qquad (2.3)$$

Solving equations (2.2) and (2.3) simultaneously, we have

$$S(t) = \frac{\Lambda}{\psi_1(t) + \mu}$$

and

$$V(t) = \frac{\psi_1(t)\Lambda}{\mu\psi_1(t) + \mu}$$

Thus, the DFE of the model (2.1) is given by

$$E_1 = (S^*(t), V^*(t), E^*(t), I^*(t), R^*(t))$$
$$= \left(\frac{\Lambda}{\psi_1(t)+\mu}, \frac{\psi_1(t)\Lambda}{\mu\psi_1(t)+\mu}, 0, 0, 0\right)$$

2.3 Analysis of Basic Reproduction Number (R_0)

To calculate the basic reproduction number, we divide system (2.1) into appearance of infection and transfer of infection as matrix $F_i(x)$ and $V_i(x)$ where $F_i(x)$ be the rate of appearance of new infections in compartment i and $V_i(x)$ be the difference between the transfer rate of individuals out of compartment i by all other means[14].

Thus, the $F_i(x)$ and $V_i(x)$ of model (2.1) is shown below:

Let x_0 be the DFE of model (2.1). Thus, we have the following partitioned derivatives,

$$DF(x_0) = \begin{pmatrix} F & 0 \\ 0 & 0 \end{pmatrix}$$

$$DV(x_o) = \begin{pmatrix} V & 0 \\ J_3 & J_4 \end{pmatrix}$$

Where F and V are MxN matrices defined by

$$F = \left(\frac{\partial F_i}{\partial x_j(x_o)}\right)$$

and

$$V = \left(\frac{\partial V_i}{\partial x_j(x_o)}\right)$$

$1 \leq 1, j \leq m$

Here,the partial derivatives of F_i and V_i are with respect to the infected classes only. The basic reproduction number is defined as

$$R_o = \rho(FV^{-1})$$

Where ρ is the spectral radius of FV^{-1}(by spectral radius we mean the maximum eigenvalue of $FV-1$)

Theorem 2.2

Consider the disease transmission model (2.1) with $f(x)$ satisfying the stability conditions if x_0 is a *DFE* of the model,the x_o is locally asymptotically stable if $R_0<1$, but unstable if $R_0>1$. For the purpose of easy access and clarity, we shall rewrite model (2.1) as follows:

$$\begin{aligned}
\frac{dS}{dt} &= \Lambda - \lambda(t)S(t) - (\psi_1(t)+\mu)S(t) + \delta R(t) \\
\frac{dV}{dt} &= \psi_1(t)S(t) - \beta\ \ I(t)V(t) - \mu V(t) \\
\frac{dE}{dt} &= \beta\ \ I(t)V(t) + \lambda(t)S(t) - kE(t) - \mu E(t) \\
\frac{dI}{dt} &= kE(t) - (\alpha+\mu+\gamma+\psi_2(t))I(t) \\
\frac{dR}{dt} &= \psi_2(t)I(t) + \gamma I(t) - (\delta+\mu)R(t)
\end{aligned} \qquad (2.4)$$

with

$$\lambda(t) = \frac{\beta\ \ I(t)}{(1+\theta I(t))}$$

Thus, F and V are given as

$$F = \begin{pmatrix} \beta\ \ I(t)V(t) + \lambda(t)S(t) \\ 0 \end{pmatrix}$$

and

$$V = \begin{pmatrix} (k+\mu)E(t) \\ -kE(t) + (\alpha+\mu+\gamma+\psi_2(t))I(t) \end{pmatrix}$$

Since we have only two infected classes, $E(t)$ and $I(t)$. It follows that $m = 2$.

We should note that at the *DFE*, $E^*(t) = I^*(t) = R^*(t) = 0$, $X \in (S(t), V(t), E(t), I(t), R(t))$

$$S^*(t) = \frac{\Lambda}{\psi_1(t)+\mu}, V^*(t) = \frac{\psi_1(t)\Lambda}{\mu(\psi_1(t)+\mu)} \qquad (2.5)$$

putting these into $M = \frac{\partial F}{\partial X}(E_1) = \begin{pmatrix} 0 & \beta\ V(t) + \beta\ S(t) \\ 0 & 0 \end{pmatrix}$, consideration, we have (2.6)

and

$$N = \frac{\partial V}{\partial X} \begin{pmatrix} k+\mu & 0 \\ -k & \alpha+\mu+\gamma+\psi_2(t) \end{pmatrix} \quad (2.7)$$

Therefore,

!

$$N^{-1} = \begin{pmatrix} \frac{1}{k+\mu} & 0 \\ \frac{k}{(k+\mu)(\alpha+\gamma+\mu+\psi_2)} & \frac{1}{\alpha+\gamma+\mu+\psi_2} \end{pmatrix} \quad (2.8)$$

Thus, calculating the eigenvalues of equation (2.8), we have,

$$MN^{-1} = \begin{pmatrix} \frac{k\left(\frac{\beta\ \Lambda}{\mu+\psi_1} + \frac{\beta\ \sigma\psi_1\Lambda}{\mu(\mu+\psi_1)}\right)}{(k+\mu)(\alpha+\gamma+\mu+\psi_2)} & \frac{\beta\ \Lambda}{\mu+\psi_1} + \frac{\beta\ \sigma\psi_1\Lambda}{\mu(\mu+\psi_1)} \\ 0 & \frac{\alpha+\gamma+\mu+\psi_2}{0} \end{pmatrix}$$

More so, the dominant eigenvalue is the basic reproduction number. Therefore,

$$R_0 = \lambda_2 = \frac{\beta\ \ k\Lambda\,(\mu + \sigma\psi_1)}{\mu(k+\mu)\,(\mu+\psi_1)\,(\alpha+\gamma+\mu+\psi_2)}$$

2.4 Local Asymptotic Stability of the Disease Free Equilibrium

In this sub-section, we investigate the local asymptotic stability (LAS) of our model(2.1) in the case where there is no disease in a population of interest. To do this, we linearized our model equations with the corresponding equilibrium, E_1. We first rewrite model (2.1) as follow:

$$f_1 = \Lambda - \lambda(t)S(t) - (\psi_1(t) + \mu)S(t) + \delta R(t)$$
$$f_2 = \psi_1(t)S(t) - \sigma\beta I(t)V(t) - \mu V(t)$$
$$f_3 = \sigma\beta I(t)V(t) + \lambda(t)S(t) - kE(t) - \mu E(t) \quad (2.9)$$
$$f_4 = kE(t) - (\alpha + \mu + \gamma + \psi_2(t))I(t)\ f_5 = \psi_2(t)I(t) + \gamma I(t) - (\mu + \delta)R(t)$$

Differentiating (2.9) with respect to $S(t)$,$V(t)$,$E(t)$,$I(t)$ and $R(t)$, we have

$$\frac{\partial f_1}{\partial S} = \frac{\beta\ \ I(t)}{1+\theta I(t)} - \mu - \psi_1(t), \frac{\partial f_1}{\partial V} = 0, \frac{\partial f_1}{\partial E} = 0, \frac{\partial f_1}{\partial I} = \frac{S(t)I(t)\beta\ \ \theta}{(1+\theta I(t))^2} - \frac{S(t)\beta}{1+\theta I(t)},$$
$$\frac{\partial f_1}{\partial R} = \delta, \frac{\partial f_2}{\partial S} = \psi_1(t), \frac{\partial f_2}{\partial V} = -\mu - I(t)\beta\ \ \sigma, \frac{\partial f_2}{\partial E} = 0, \frac{\partial f_2}{\partial I} = \sigma(t), \frac{\partial f_2}{\partial R} = 0,$$
$$\frac{\partial f_3}{\partial S} = \frac{\beta\ \ I(t)}{1+\theta I(t)}, \frac{\partial f_3}{\partial V} = \beta\ \ I(t), \frac{\partial f_3}{\partial E} = -(k+\mu), \frac{\partial f_3}{\partial I} = \beta\ \ V(t) + \frac{S(t)I(t)\beta\ \ \theta}{(1+\theta I(t))^2} + \frac{S(t)\beta}{1+\theta I(t)}$$
$$\frac{\partial f_3}{\partial R} = 0, \frac{\partial f_4}{\partial S} = 0, \frac{\partial f_4}{\partial V} = 0, \frac{\partial f_4}{\partial E} = k, \frac{\partial f_4}{\partial I} = -(\alpha+\mu+\gamma+\psi_2(t), \frac{\partial f_4}{\partial R} = 0,$$
$$\frac{\partial f_5}{\partial S} = 0, \frac{\partial f_5}{\partial V} = 0, \frac{\partial f_5}{\partial E} = 0, \frac{\partial f_5}{\partial I} = \psi_2(t) + \gamma, \frac{\partial f_5}{\partial R} = -(\mu+\delta).$$

,

Using the above linearized system, we obtain the general Jacobian matrix of the model (2.1) and is given by

$$J = \begin{pmatrix} -\lambda - G3 + G6 & 0 & 0 & G_4 & \delta \\ \psi 1 & \lambda - \square - I(t)\beta_\sigma & 0 & V(t)\beta_\sigma & 0 \\ G_6 & I(t)\beta_\sigma & -k-\lambda-\mu & G_5 & 0 \\ 0 & 0 & k & -\lambda - \mathrm{G}_1 & 0 \\ 0 & 0 & 0 & G_2 & -\lambda - \square \end{pmatrix}$$

(2.10)

with

$G_1 = \alpha+\mu+\gamma+\psi_2(t), G_2 = \psi_2(t)+\gamma, G_3 = \psi_1(t)+\mu, G_4 = \frac{S(t)I(t)\beta\ \ \theta}{(1+\theta I(t))^2} - \frac{S(t)\beta}{1+\theta I(t)}, G_5 = \beta\ \ V(t) + \frac{S(t)I(t)\beta\ \ \theta}{(1+\theta I(t))^2} + \frac{S(t)\beta}{1+\theta I(t)}$

,

$G_6 = \frac{\beta\ \ I(t)}{1+\theta I(t)}$ On substituting the equilibrium, E_1 of the system (2.1) in (2.10), we get

$$J(E_1) = \begin{pmatrix} -\lambda - \square - \psi 1 & 0 & 0 & \beta S^* & \delta \\ \psi 1 & \lambda - \square & 0 & \beta_\sigma V^* & 0 \\ 0 & 0 & -k - \lambda - \mu & \beta S^* + \beta_\sigma V^* & 0 \\ 0 & 0 & k & -\alpha - \gamma - \lambda - \square - \psi_2 & 0 \\ 0 & 0 & 0 & \gamma + \psi_2 & -\lambda - \square \end{pmatrix}$$

(2.11)

Using Mathematica Software to evaluate the eigenvalues of equation (2.11), we have

$$(-\lambda - \mu)^2(-\lambda - \mu - \psi_1(t))(-k(S^*(t)\beta + V^*(t)\beta\sigma) + (-k - \lambda - \mu)(-\alpha - \gamma - \lambda - \psi_2(t))) = 0. \quad (2.12)$$

From equation (2.12), we have $\lambda_{1,2} = -(\mu+\delta)$, $\lambda_3 = -(\mu+\psi_2(t))$ and λ_4,λ_5 can be obtain from the remaining quadratic equation (2.12) which is given as

$$\lambda^2 + (k + \alpha + \gamma + \psi_2(t))\lambda + k(\alpha + \gamma + \mu + \psi_2(t)) + \mu(\alpha + \gamma + \mu + \psi_2(t)) - \frac{k\beta(\sigma\psi_1(t)\Lambda + \beta\Lambda\mu)}{\mu(\psi_1(t) + \mu)} = 0 \quad (2.13)$$

Or

$$\lambda^2 + (k + \alpha + \gamma + \psi_2(t))\lambda + \psi_2(t)(k + \mu) + (k + \mu)(\alpha + \gamma + \mu)(1 - R_0) = 0 \quad (2.14)$$

Remark 2: The model (2.1) is locally asymptotically stable provided $R_0 < 1$ and unstable if otherwise.

2.5 Disease Endemic Equilibrium

Disease endemic equilibrium (DEE) only occurs when the basic reproduction number R_0 is greater than a unit. Whenever this occurred, the disease evade a population and persist for a long time. We therefore seek to investigate the DEE of model (2.1), $E_2 = (S^{**}(t), V^{**}(t), E^{**}(t), I^{**}(t), R^{**}(t))$ by equating the left hand sides of the model (2.1) to zero and then solve for each state variable as follows:

$$\Lambda - \lambda(t)S(t) - (\psi_1(t) + \mu)S(t) + \delta R(t) = 0 \quad (2.15)$$

$$\psi_1(t)S(t) - \sigma\beta I(t)V(t) - \mu V(t) = 0 \quad (2.16)$$

$$\sigma\beta I(t)V(t) + \lambda(t)S(t) - kE(t) - \mu E(t) = 0 \quad (2.17)$$

$$kE(t) - (\alpha + \mu + \gamma + \psi_2(t))I(t) = 0 \quad (2.18)$$

$$\psi_2(t)I(t) + \gamma I(t) - \mu R(t) = 0 \quad (2.19)$$

We solve for each state variable of equations (2.15) – (2.19) and we obtain

$$S(t) = \frac{\mu\Lambda + \delta G_2 I^{**}(t)}{\mu(\lambda^{**}(t) + G_3)}$$

$$V(t) = \frac{\psi_1(t)(\mu\Lambda + \delta G_2 I^{**}(t))}{\mu(\lambda^{**}(t) + G_3)(\beta I^{**}(t) + \mu)}$$

$$E(t) = \frac{G_1 I^{**}(t)}{k}$$

$$R(t) = \frac{G_1 I^{**}(t)}{\mu + \delta}$$

Substituting $S(t), V(t)$ and $E(t)$ in equation (2.17), we have

$$(k\lambda^{**}(t)\mu\sigma G_1 + \beta\lambda^{**}(t)\mu^2\sigma G_1 + \beta\mu^2\sigma G_1 G_2)I^{**}(t) - \mu^3\lambda^{**}(t)G_1 - k\lambda^{**}(t)\mu^2$$

$$G_1 - k\mu^2 G_1 G_3 - \mu^3 G_1 G_3 + k\lambda^{**}(t)\Lambda\mu\sigma + k\delta\lambda^{**}(t)\mu G_2 + \frac{k\Lambda\mu\beta}{1 + \theta I^{**}(t)} = 0 \quad (2.20)$$

Whenever the disease inhibition rate is too low, then $\theta \to 0$. Thus, we have $\lambda^{**}(t) \to \beta I^{**}(t)$ and equation (2.20) becomes

$$a_1 I^{**2}(t) + a_2 I^{**}(t) + a_3 = 0 \quad (2.21)$$

where

$a_1 = \beta^2\sigma\mu G_1(k + \mu)$

$a_2 = k\beta\mu\sigma G_1 G_3 + \beta\mu^2\sigma G_1 G_2 + k\beta^2\Lambda\mu\sigma + k\delta\beta\mu G_2 - \mu^3\beta G_1$ $a3 = k\mu 2G1G3 + \mu 3G1G3 - k\Lambda\mu 2\beta$

The roots of equation (2.20) always have either one negative root and one positive root or two positive roots. It should be noted that whenever the roots are one positive and one negative, the negative root should be ignored, then model (2.1) has only one endemic equilibrium but whenever two positive roots occurred, then model (2.1) has two endemic equilibria.

Theorem 3.3

The non-negative equilibrium, E_2^* of model (2.1) exists and is unique provided $R_0 > 1$.

2.6 Local Asymptotic Stability of the Disease Endemic Equilibrium

Here, we seek to analyze the local asymptotic stability of the disease endemic equilibrium (DEE). To do this we claim the following result

Theorem 2.4

The disease endemic equilibrium, E_2^* is locally asymptotically stable provided $R_0 > 1$.

Proof. We shall prove this by linearizing model (2.1) at E_2^* equilibrium using Jacobian method. We then substitute the E_2^* equilibrium into the general Jacobian matrix obtained previously to obtain

$$J(E2*)\begin{pmatrix} -\lambda - G3 + G6 & 0 & 0 & G_4 & \delta \\ \psi 1 & \lambda - \square - I^{**}(t)\beta_\sigma & 0 & V^{**}(t)\beta_\sigma & 0 \\ G_6 & I^{**}(t)\beta_\sigma & -k-\lambda-\mu & G_5 & 0 \\ 0 & 0 & k & -\lambda - G_1 & 0 \\ 0 & 0 & 0 & G_2 & -\lambda - \square \end{pmatrix} \quad (2.22)$$

with

$G_1 = \alpha + \mu + \gamma + \psi_2(t),\ G_2 = \psi_2(t) + \gamma, G_3 = \psi_1(t) + \mu,\ G_4 = \frac{S^{**}(t)I**(t\square\ \theta}{(1+\theta I^{**}(t))^2} - \frac{S^{**}(t\square}{1+\theta I^{**}(t)},\ G_5 = \beta\ V^{**}(t) + \frac{S^{**}(t)I**(t\square\ \theta}{(1+\theta I^{**})^2} + \frac{S^{**}(t\square}{1+\theta I^{**}(t)},\ G_6 = \frac{\beta\ I^{**}(t)}{1+\theta I^{**}(t)}$

The characteristic equation of the equation (2.22) can be written as:

$$\lambda^5 + b_1\lambda^4 + b_2\lambda^3 + b_3\lambda^2 + b_4\lambda + b_5 = 0 \quad (2.23)$$

where

$b_1 = G_1 + G_3 - G_6 + k + 3\mu + \beta\sigma I^{**}(t)$

$b_2 = G_1k + G_3k - G_5k - G_6k + 3G_1\mu + 3G_3\mu - 3G_6\mu + \beta G_1\sigma I^{**}(t) + \beta G_3\sigma I^{**}(t) - \beta G_6\sigma I^{**}(t) + G_1G_3 - G_1G_6 + 2k\mu + \beta k\sigma I^{**}(t) + 3\mu^2 + 2\beta\mu\sigma I^{**}(t)$

$b_3 = 2G_1k\mu + 2G_3k\mu - 2G_5k\mu - 2G_6k\mu + \beta G_1k\sigma I^{**}(t) + \beta G_3k\sigma I^{**} - \beta G_5k\sigma I^{**}(t) - \beta G_6k\sigma I^{**}(t) + G_1G_3k - G_3G_5k - G_1G_6k - G_4G_6k + G_5G_6k + 3G_1\mu^2 + 3G_3\mu^2 - 3G_6\mu^2 + 3G_1G_3\mu - 3G_1G_6\mu + 2\beta G_1\mu\sigma I^{**}(t) + 2\beta G_3\mu\sigma I^{**}(t) - 2\beta G_6\mu\sigma I^{**}(t) + \beta G_1G_3\sigma I^{**}(t) - \beta G_1G_6\sigma I^{**}(t) + k\mu^2 + \beta k\mu\sigma I^{**}(t) - \beta^2k\sigma^2I^{**}(t)V^{**}(t) + \mu^3 + \beta\mu^2\sigma I^{**}(t)$

$b_4 = G_1k\mu^2 - \delta G_2G_6k + G_3k\mu^2 - G_5k\mu^2 - G_6k\mu^2 + 2G_1G_3k\mu - 2G_3G_5k\mu - 2G_1G_6k\mu - 2G_4G_6k\mu + 2G_5G_6k\mu + \beta G_1k\mu\sigma I^{**}(t) + \beta G_3k\mu\sigma I^{**}(t) - \beta G_5k\mu\sigma I^{**}(t) - \beta G_6k\mu\sigma I^{**}(t) - \beta G_4k\sigma I^{**}(t)\psi_1 + \beta G_1G_3k\sigma I^{**}(t) - \beta G_3G_5k\sigma I^{**}(t) - \beta G_1G_6k\sigma I^{**}(t) - \beta G_4G_6k\sigma I^{**}(t) + \beta G_5G_6k\sigma I^{**}(t) - \beta^2G_3k\sigma^2I^{**}(t)V^{**}(t) + \beta^2G_6k\sigma^2I^{**}(t)V^{**} + G_1\mu^3 + G_3\mu^3 - G_6\mu^3 + 3G_1G_3\mu^2 - 3G_1G_6\mu^2 + \beta G_1\mu^2\sigma I^{**}(t) + \beta G_3\mu^2\sigma I^{**}(t) - \beta G_6\mu^2\sigma I^{**}(t) + 2\beta G_1G_3\mu\sigma I^{**}(t) - 2\beta G_1G_6\mu\sigma I^{**}(t) - \beta^2k\mu\sigma^2I^{**}(t)V^{**}(t)$

$b_5 = G_1G_3k\mu^2 - \delta G_2G_6k\mu - G_3G_5k\mu^2 - G_1G_6k\mu^2 - G_4G_6k\mu^2 + G_5G_6k\mu^2 - \beta\delta G_2G_6k\sigma I^{**}(t) + \beta G_1G_3k\mu\sigma I^{**}(t) - \beta G_3G_5k\mu\sigma I^{**}(t) - \beta G_1G_6k\mu\sigma I^{**}(t) - \beta G_4G_6k\mu\sigma I^{**}(t) + \beta G_5G_6k\mu\sigma I^{**}(t) - \beta^2G_3k\mu\sigma^2I^{**}(t)V^{**}(t) + \beta^2G_6k\mu\sigma^2I^{**}(t)V^{**}(t) + G1G3\mu3 - G1G6\mu3 + \beta G1G3\mu2\sigma I**(t) - \beta G1G6\mu2\sigma I**(t)$

Theorem 2.5

The equilibrium, E_2^* is locally asymptotically stable provided the coefficients of the characteristic equation (2.23) satisfies the following Routh Hurwitz stability conditions:

1. $b_i (i = 1,2,...,5) > 0$
2. $b_1b_2 > b_3$
3. $b1b2b3 > b23 + b21b4$
4. $b1b2b3b4 + b1b2b5 + 2b1b4b5 > b23b4 + b21b24 + b1b22b5 + b25$

2.7 Global stability analysis of the disease endemic equilibrium

In this section, we present the global stability of the model (2.1) at E_2^* equilibrium. We assume that the drug efficacy $\xi \to 1$ and then $\sigma \to 0$. We give the following theorem by following:

Theorem 2.6

If $R_0 > 1$, then, the endemic equilibrium, E_2^* of the model (2.1) is globally asymptotically stable on Ω. Proof. At a steady state, system (2.1) at E_2^* gives

$$\Lambda = \frac{\beta I^{**}(t)S^{**}(t)}{1+\theta I^{**}(t)} + (\psi_1(t)+\mu)S^{**}(t) + \delta R^{**}(t)$$

$$k+\mu = \frac{\beta I^{**}(t)S^{**}(t)}{1+\theta I^{**}(t)E^{**}(t)}$$

$$\frac{(k+\mu)(\alpha+\mu+\gamma+\psi_2(t)}{k} = \frac{\beta I^{**}(t)S^{**}(t)}{1+\theta I^{**}(t)I^{**}(t)} \quad (2.24)$$

Thus, we define the Lyapunov function as

$$Y(t) = [(S(t)-S^{**}(t)-S^{**}(t)log\frac{S(t)}{S^{**}(t))}+(E(t)-E^{**}(t)-E^{**}(t)log\frac{E(t)}{E^{**}(t)}+\frac{k+\mu}{k}(I(t)-I^{**}(t)-I^{**}(t)log\frac{I(t)}{I^{**}(t)}] \quad (2.25)$$

Taking the time derivative of equation (2.25) along the solution of the system (2.1), we have

$$\dot{Y} = (1-\frac{S^{**}(t)}{S(t)})\dot{S} + (1-\frac{E^{**}(t)}{E(t)})\dot{E} + (\frac{k+\mu}{k})(1-\frac{I^{**}(t)}{I(t)})\dot{I} \quad (2.26)$$

By direct substitution of equation (2.1) in (2.26), we obtain

$$\begin{aligned}(1-\frac{S^{**}(t)}{S(t)})\dot{S} &= (1-\frac{S^{**}(t)}{S(t)})[\Lambda - \frac{\beta I(t)}{(1+\theta I(t))}S(t) - (\psi_1(t)+\mu)S(t) + \delta R(t)] \\ &= (1-\frac{S^{**}(t)}{S(t)})[\frac{\beta I^{**}(t)}{(1+\theta I^{**}(t))}S^{**}(t) + (\psi_1(t)+\mu)S^{**}(t) \\ &- \delta R^{**}(t)] - \frac{\beta I(t)}{(1+\theta I(t))}S(t) - (\psi_1(t)+\mu)S(t) + \delta R(t)] \\ &= \frac{\beta I^{**}(t)S^{**}(t)}{1+\theta I^{**}(t)}(1-\frac{S^{**}(t)}{S(t)}) + (\psi_1(t)+\mu)S^{**}(t)(1-\frac{S^{**}(t)}{S(t)}) - \delta R^{**}(t)(1-\frac{S^{**}(t)}{S(t)}) \\ &- \frac{\beta I(t)S(t)}{1+\theta I(t)}(1-\frac{S^{**}(t)}{S(t)}) - (\psi_1(t)+\mu)S(t)(1-\frac{S^{**}(t)}{S(t)}) - \delta R(t)(1-\frac{S^{**}(t)}{S(t)}) \\ &= (\psi_1(t)+\mu)S^{**}(t)(2-\frac{S^{**}(t)}{S(t)}-\frac{S(t)}{S^{**}(t)}) + (1-\frac{S^{**}(t)}{S(t)})(\frac{\beta I^{**}(t)S^{**}(t)}{1+\theta I^{**}(t)} - \frac{\beta I(t)S(t)}{1+\theta I(t)})\end{aligned} \quad (2.27)$$

$$\begin{aligned}(1-\frac{E^{**}(t)}{E(t)})\dot{E} &= (1-\frac{E^{**}(t)}{E(t)})[\frac{\beta I(t)S(t)}{1+\theta I(t)} - (k+\mu)E(t)] \\ &= (1-\frac{E^{**}(t)}{E(t)})[\frac{\beta I(t)S(t)}{1+\theta I(t)} - \frac{\beta I^{**}(t)S^{**}(t)}{1+\theta I^{**}(t)}\frac{E(t)}{E^{**}(t)}] \\ &= \frac{\beta I(t)S(t)}{1+\theta I(t)} - \frac{\beta I^{**}(t)S^{**}(t)}{1+\theta I^{**}(t)}\frac{E(t)}{E^{**}(t)} - \frac{\beta I(t)S(t)}{1+\theta I(t)}\frac{E(t)}{E^{**}(t)} + \frac{\beta I^{**}(t)S^{**}(t)}{1+\theta I^{**}(t)}\end{aligned} \quad (2.28)$$

$$\begin{aligned}(\frac{k+\mu}{k})(1-\frac{I^{**}(t)}{I(t)})\dot{I} &= (\frac{k+\mu}{k})(1-\frac{I^{**}(t)}{I(t)})[kE(t) - (\alpha+\mu+\gamma+\psi_2(t))I(t)] \\ &= (k+\mu)(1-\frac{I^{**}(t)}{I(t)})E(t) - \frac{k+\mu}{k}(\alpha+\mu+\gamma+\psi_2(t)(1-\frac{I^{**}(t)}{I(t)})I(t) \\ &= \frac{\beta I^{**}(t)S^{**}(t)}{1+\theta I^{**}(t)}\frac{E(t)}{E^{**}(t)}(1-\frac{I^{**}(t)}{I(t)}) - \frac{\beta I^{**}(t)S^{**}(t)}{1+\theta I^{**}(t)}\frac{I(t)}{I^{**}(t)}(1-\frac{I^{**}(t)}{I(t)}) \\ &= \frac{\beta I^{**}(t)S^{**}(t)}{1+\theta I^{**}(t)}\frac{E(t)}{E^{**}(t)} - \frac{\beta I^{**}(t)S^{**}(t)}{1+\theta I^{**}(t)}\frac{E(t)}{E^{**}(t)}\frac{I^{**}(t)}{I(t)} \\ &- \frac{\beta I^{**}(t)S^{**}(t)}{1+\theta I^{**}(t)}\frac{I(t)}{I^{**}(t)} + \frac{\beta I^{**}(t)S^{**}(t)}{1+\theta I^{**}(t)}\end{aligned} \quad (2.29)$$

It follows from (2.27 – 2.29) that

$$\dot{Y} = (\psi_1(t) + \mu)S^{**}(t)\left(2 - \frac{S^{**}(t)}{S(t)} - \frac{S(t)}{S^{**}(t)}\right) + \frac{\beta}{1+\theta I^{**}(t)}\frac{I^{**}(t)S^{**}(t)}{}\left(3 - \frac{S^{**}(t)}{S(t)} - \frac{E(t)I^{**}(t)}{E^{**}I(t)} - \frac{I(t)}{I^{**}(t)}\right) + \frac{\beta}{1+\theta I(t)}\frac{I(t)S^{**}(t)}{}\left(1 - \frac{S(t)E^{**}(t)}{S^{**}(t)E(t)}\right)$$

(2.30) From equation (2.30), we have

$$\left(2 - \frac{S^{**}(t)}{S(t)} - \frac{S(t)}{S^{**}(t)}\right) \leq 0$$

$$\left(3 - \frac{S^{**}(t)}{S(t)} - \frac{E(t)I^{**}(t)}{E^{**}I(t)} - \frac{I(t)}{I^{**}(t)}\right) \leq$$

$$\left(1 - \frac{S(t)E^{**}(t)}{S^{**}(t)E(t)}\right) \leq 0 \quad 0 \quad (2.31)$$

Thus, the condition (2.31) implies that $\dot{Y} \leq 0$, for $(S(t),V(t),E(t),I(t),R(t)) \in \Omega$. Then, the equilibrium, $E_2^*$is globally asymptotically stable on Ω.

Remark 2: The occurrence of this condition implies that the influenza disease becomes endemic globally. When this happens, it will claim many lives and may also put the world into recession as similar to the novel corona virus disease 2019 (COVID 19 Pandemic).

III. Results

2.8 Solution of the Model Equations

In this section, we use the inbuilt MATLAB function ode 45 to solve the model equations above. The graphical user interface in the MATLAB version 7.5 was used for the solution method, simulation and visualization on graphs. We made use of the parameters of the model and their values from related literature and we assumed some parameters values that are not found in literature.

Table 3.1: Description and Interpretation of Parameters Values of the Model Equations

Parameter			Symbol	
Value				
Recruitment rate of human population			Λ	
1534				
Natural death rate			μ	
0.1917				
Disease induced death rate			δ	0.03
Vaccination rate of the susceptible individual		$\psi_1(t)$	0.9	
Degree of protection where ξ is the vaccine efficacy		$\sigma = (1 - \xi)$	0.699	
Treatment of the infected individual	$\psi_2(t)$	0.8		
Natural recovery rate of the infected individuals	γ	0.36		

Progressionratefromexposedtoinfectious	k	0.00015
Rateatwhichrecoveredindividuallossimmunityandbecomesusceptible	δ	0.01

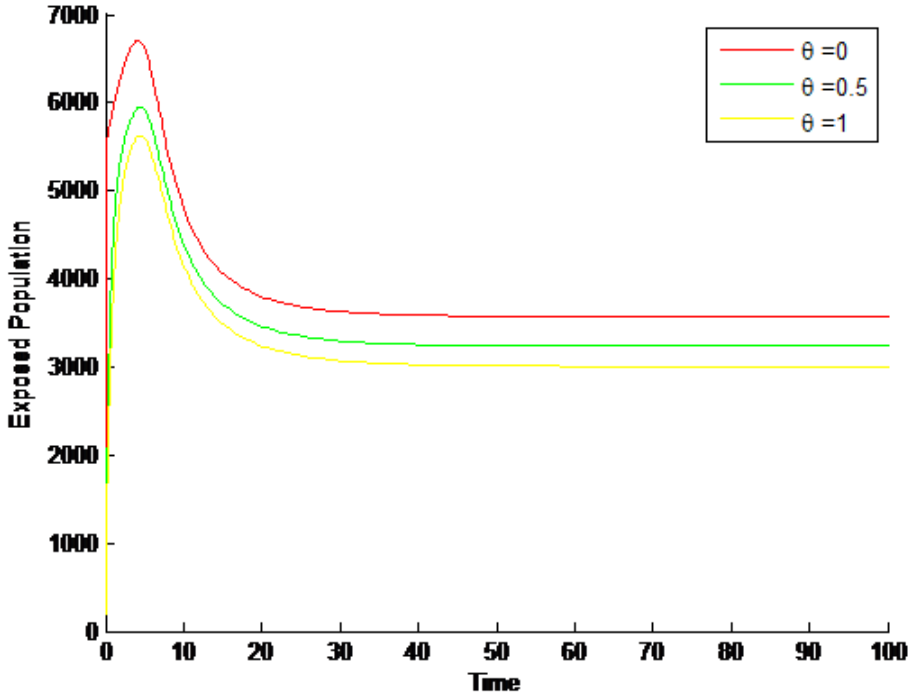

Fig. 2.2: Plot of exposed individuals over time

Fig. 2.2 shows the plot of exposed individuals over time at different rate of the saturated parameter, θ. From the graph, the exposed individuals population decrease when the saturated parameter, θ increased. It is easy to say that the saturated parameter, θ inhibits disease transmission.

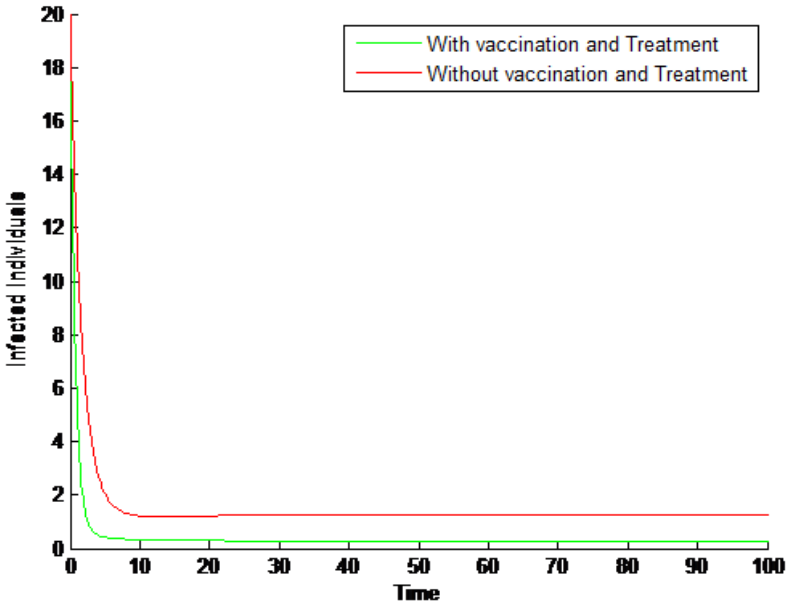

Fig. 2.3: Plot of infected individuals over time

Fig. 2.3 describes the infected population over time in the presence of vaccination and treatment and in the absence of vaccination and treatment. It can be clearly seen from the graph that administration of vaccine and treatment of infected individuals decrease the disease burden in the population.

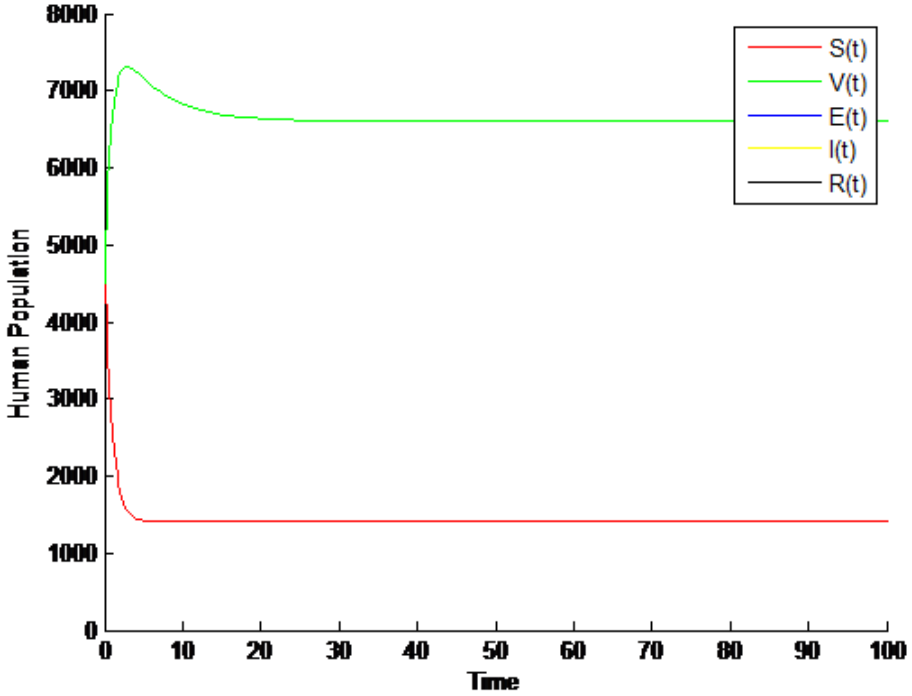

Fig. 2.4: Plot of E_1 equilibrium

Fig. 2.4 is a plot of the disease free equilibrium (DFE) state over time. From the graph, the susceptible population decreased as a result of protection majority of the susceptible individuals received through vaccination. The vaccinated individuals population increased and latter decreased a little. The small decrease of the vaccinated population is due to loss of immunity by subgroup of the population.

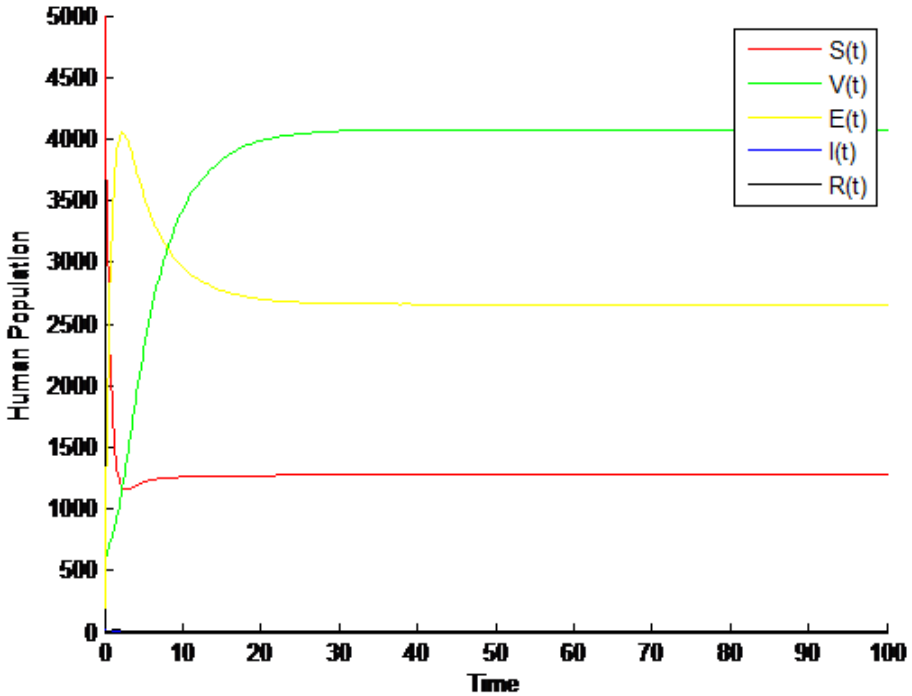

Fig. 2.5: Plot of E_2^* equilibrium

Fig. 2.5 shows the plot of the disease endemic equilibrium (DEE) state over time. From the graph, it is interesting to see that majority of the population were vaccinated and remain in the class due to the

development of immunity to the disease. We also observe that some susceptible population which were not given the vaccine and those that loss their immunity became exposed to the disease. **IV. Discussion**

We present a mathematical model on avian influenza with detailed analysis. We basically considered human population only and ignored the bird population as a result of our interest on the dynamics of influenza on human population. Initially, we presented a detailed mathematical results of the model equations. The results obtained show that the model is stable both locally and globally under some certain conditions. The stability results for disease free equilibrium is obtained when $R_0 < 1$. If $R_0 > 1$, we proved that the endemic equilibrium of the model is both locally, globally asymptotically stable under some certain conditions.

The numerical results of the model is obtained and is given in Figure 2.2 − 2.5. The numerical results validate that the transmission dynamics of the avian influenza which is determined by force of infections. It is observed that the parameter θ and β respectively show, the saturation effect and the contact between infective humans to susceptible humans do not change the stability of the equilibria and so that the outbreaks, as the infected humans do not spread the virus further.

However, the numerical results show that increasing the vaccination parameter and the treatment parameter decrease the exposed humans and the infected humans respectively and can help to control the disease.

V. Conclusion

In this study we have proposed a non-autonomous mathematical model that study the dynamics of an avian influenza with saturated incidence rate. The model exhibits two equilibria, namely, the disease free equilibrium (DFE) and the disease endemic equilibrium (DEE). The disease threshold that is, the basic reproduction number is computed using the next generation method. The DFE is locally asymptotically stable when $R_0 < 1$ and the endemic equilibrium is both locally and globally stable when $R_0 > 1$. The disease can be eradicated provided the efficacy of the vaccine is high and the administration is up to 80% - 90% of the susceptible individuals and the treatment of the infected individuals are seriously observed.

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