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MATHEMATICAL ANALYSIS OF A DETERMINISTIC MODEL OF ZIKA VIRUS DISEASE DYNAMICS.

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Abstract

In this study, we developed a mathematical model for the spread of Zika virus disease. We established the existence and positivity of solutions to the model, Existence and stability analysis of the equilibrium states of the model and evaluated the basic reproduction number of the model. The feasible set for the model equations is given by $\Omega = \{ (S_{H,} I_H, R_H, S_{A,} I_A) \} \in \Re_+^5 : S_H, I_H, R_H, S_A, I_A \geq 0$ *;* $N_H \leq \frac{\Lambda_H}{\mu_H}, N_A \leq \frac{\Lambda_A}{\mu_A + u_2}$ *. The stability analysis of the Disease Free Equilibrium State (DFE) of the model shows that it will be stable if* $(\mu_H + \mu_0 + \gamma_H) < A_2$ *..*

KEYWORDS: *Zika Virus, Existence of solutions, Equilibrium states, Stability Analysis and Basic Reproduction Number.*

Introduction

Zika virus disease (ZIKV) is from the family Flaviviridae and genus Flavivirus (Aubry *et al*., 2017). The disease is mainly spread to humans by the bites of infected Aedes Aegypti mosquitoes (Ioos *et al*., 2014). However, the non-vector borne spread (that is, materno fetal and sexual transmission and transmission via blood transfusion) has also been reported (Musso, *et al*, (2015). Six more confirmed and probable cases of a sexual transmission of the infection in the United

States (US) were reported by the CDC on February 26, 2016 (Hills ,2016) and Europe's first case of a sexually transmitted Zika virus was diagnosed in France in February 2016 (Mansuy *et al*., 2016) . Zika is also transmitted by sexual contacts, blood transfusion, and from mother to fetus (causing microcephaly in a child) (Gatherer & Kohl (2016).

The mosquitoes responsible for the disease transmissions are, well-known in tropical and subtropical regions these mosquitoes also transmit dengue fever, chikungunya, yellow fever, and Japanese encephalitis (Gao *et al*., 2016). On 6th July 2016, World Health Organization reported evidence of Zika virus from 65 countries (WHO, 2016). The disease which was first discovered in 1947 in a febrile sentinel rhesus monkeys (Dick *et al*., 1952). And from a pool of Aedes Africanus mosquitoes in the Zika forest in Uganda during a yellow fever study (Dick *et al*., 1952). The virus was first identified in humans five years later in 1952 using neutralizing antibody testing in sera from East Africa (Momoh and Fügenschuh, 2017) and it was first isolated in a human in Uganda (Simpson, 1964). The first symptomatic case of the Zika fever in a human was recorded in Nigeria in 1954 (Macnamara, 1954). Since 1950s, it has been known to occur within a narrow equatorial belt from Africa to Asia. It spreads eastward across the Pacific Ocean, Eastern Polynesia, New Caledonia, the Cook Islands, and Easter Island (Onuorah *et al*., 2016).

Recently, infectivity has been out broken fast in Africa, the Americas and Asia from the time when the first case was recounted from Pacific in 2007 (Ding *et al*., 2016). It has caused multiple epidemics throughout the 21st century. In 2014 there were more than 30,000 reported cases in French Polynesia and it was projected that up to 94% of the population there had been infected. The most recent outbreak began in 2015 in Brazil and was officially labeled a Public Health Emergency of International Concern by the World Health Organization (WHO) on February 1, 2016 (WHO, 2016). And in the year 2015 Mexico, Central America, the Carribean and South America where the disease outbreak has reached pandemic levels. As of February 2015 there was evidence that the infection in pregnant women can cause abnormal brain development in their fetuses, which may result in miscarriage and Microcephaly (Oliveira *et al*., 2016) . Three deaths from Zika virus disease (one newborn, one 16-year-old and one adult) have been reported, the first known occurrences, reported by European

center for disease control (ECDC). The strong possibility exists of sexual transmission in two cases (Foy *et al*., 2011; Musso *et al*., 2015).Perinatal transmission in two cases (Besnard *et al*., 2014).

In this study we formulate and analyse a mathematical model of Zika virus infection incorporating control strategies of treatment and insecticide.

Materials and Methods

Model Formulation

We formulate a mathematical model of Zika virus infection. The model incorporated the use of control strategies. The model contains two populations, which are human and Aedes mosquitoes with three and two compartments respectively. We examine the susceptible-infected-recovered model to explore the dynamics of transmission of Zika to human. The three compartments, namely: susceptible human (S_H), infected human (I_H) and the recovered human (R_H). The other two compartments for aedes mosquitoes are susceptible aedes mosquitoes (S_A) and infected aedes (I_A).

Model Diagram

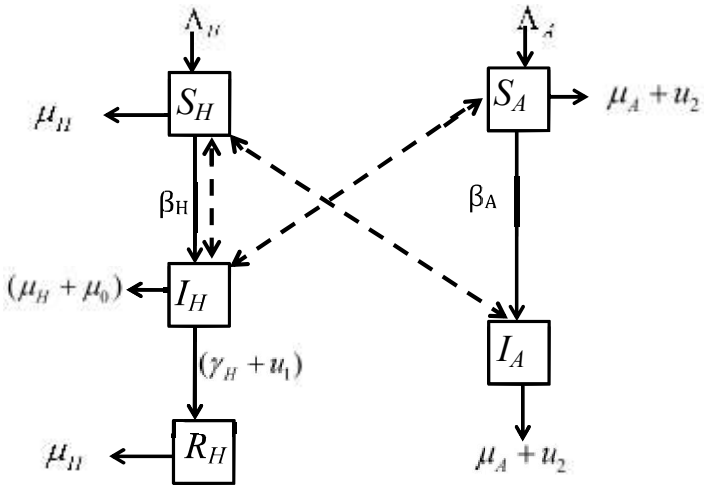

Figure 2.1: Schematic diagrams on the transmission of Zika virus infection

Model Assumptions:

1. We consider two population groups, the human with variable population size and the Aedes mosquito's population.

2. Only adult female Aedes mosquitoes were considered in the model, since they need human blood for egg production.
3. All new-born are susceptible in both populations. The infection of a susceptible human occurs when the individual is bitten by an infectious Aedes mosquito or when they have sexual contact with infected humans. The infected individual after a period of time becomes infectious. Susceptible Aedes mosquitoes become infected when an infectious human is bitten by a susceptible Aedes mosquito, the infected Aedes mosquito become infectious after a period of time.
4. Exposed humans and mosquitoes cannot transmit the disease, thus they are excluded in this model.
5. There is natural recovery γ_H

Model Description.

Susceptible individuals are recruited at a rate Λ_H and acquire Zika virus through contact with infectious Aedes at a rate $\beta\varepsilon\phi$, where β is the transmission probability per bite, ε is the per capita biting rate of Aedes, ϕ is the contact rate of vector per human per unit time and ϕ_1 is the transmission probability after sexual interaction between susceptible human and infected human.

Susceptible individuals move to the infectious class as a result of Aedes bite and human –human interaction (sexual interaction and blood transfusion). When the disease is fatal, infected individuals die at a rate μ_0, while μ_H is the natural death rate. Susceptible Aedes are generated at a per capita rate Λ_A and acquire infectivity through contacts with infected humans at a rate $\beta_1\varepsilon\phi$, where β_1 is the probability for an Aedes to get infected by an infectious human. Aedes are assumed to suffer death due to natural causes at a rate μ_A. Newly-infected Aedes progress to the class of infectious mosquitoes at a rate $\beta_1\varepsilon\phi$.

We incorporate control strategies (treatment and insecticide) in to the model , where `treatment is represented by u_1 and use of insecticide represented by u_2.

This leads to the following SIR-SI model.

Model Equation

$$\frac{dS_H}{dt} = \Lambda_H - (\beta \varepsilon \phi I_A + \phi_1 I_H + \mu_H) S_H \quad (2.1)$$

$$\frac{dI_H}{dt} = (\beta \varepsilon \phi I_A + \phi_1 I_H) S_H - (\mu_H + \mu_0 + \gamma_H + u_1) I_H \quad (2.2)$$

$$\frac{dR_H}{dt} = (\gamma_H + u_1) I_H - \mu_H R_H \quad (2.3)$$

$$\frac{dS_A}{dt} = \Lambda_A - (\beta_1 \varepsilon \phi I_H + \mu_A + u_2) S_A \quad (2.4)$$

$$\frac{dI_A}{dt} = \beta_1 \varepsilon \phi I_H S_A - (\mu_A + u_2) I_A \quad (2.5)$$

Basic properties of the Zika virus model

Invariant Region

The total human population sizes N_H and total vector population N_A can be determined by $N_H = S_H + I_H + R_H$ and $N_A = S_A + I_A$ or from the differential equation model

$$\begin{aligned} dN_H &= \frac{dS_H}{dt} + \frac{dI_H}{dt} + \frac{dR_H}{dt} \\ &= \Lambda_H - \mu_H N_H - \mu_0 I_H \end{aligned} \quad (3.1)$$

and

$$\frac{dN_A}{dt} = \frac{dS_A}{dt} + \frac{dI_A}{dt} \qquad = \Lambda_A - \mu_A N_A + u_2 \quad (3.2)$$

Assuming this disease does not kills $\mu_0 = 0$ thus From (3.1)

$$\frac{dN_H}{dt} = \Lambda_H - \mu_H N_H - \mu_0 I_H \le \Lambda_H - \mu_H N_A$$

Lemma 3.1 The model equations (2.1) to (2.5) has solution which are contained in the feasible domain

$\Omega = \Omega_H \times \Omega_A$ Cooke and Van Driessche, (1996)

Proof :

Let $(S_{H,}I_{H,}R_{H,}S_{A,}I_{A})\in\Re_{+}^{5}$ be any solution of the system with non-negative initial conditions

Since

$$\frac{dN_H}{dt}\leq\Lambda_{H}-\mu_{H}N_{H}$$

From equation (3.1)

Hence, by the standard comparison theorem (Lakshmikantham *et al.*, 1988) it can be shown that

$0\leq N_{H}\leq\frac{\Lambda_{H}}{\mu_{H}},$ so that

$$\Lambda_{H}-\mu_{H}N_{H}\geq K\ell^{-\mu_{H}^{'}} \qquad (3.3)$$

where K is constant

Thus, all possible solutions of the human population of the model equations (2.1) to (2.5) are in the region.

$$\Omega_{H}=\left\{(S_{H,}I_{H,}R_{H})\in\Re_{+}^{3}:N_{H}\leq\frac{\Lambda_{H}}{\mu_{H}}\right\} \qquad (3.4)$$

Similarly, all possible solutions of the -mosquitos' population of the model equations (2.1) to (2.5) are in the region.

$$\Omega_{A}=\{S_{A},I_{A})\in\Re_{+}^{2}:N_{A}\leq\frac{\Lambda_{A}}{\mu_{A}+u_{2}} \qquad (3.5)$$

Thus, the feasible set for the model equations (2.1) to (2.5) is given by

$$\Omega=\{\ (S_{H,}I_{H},R_{H},S_{A,}I_{A})\in\Re_{+}^{5}:S_{H},I_{H},R_{H},S_{A},I_{A}\geq0;\ N_{H}\leq\frac{\Lambda_{H}}{\mu_{H}},N_{A}\leq\frac{\Lambda_{A}}{\mu_{A}+u_{2}} \qquad (3.6)$$

This is a positively invariant set under the flow induced by the model equation

Therefore the model equations (2.1) to (2.5) are epidemiologically significant and mathematically well posted in the domain. Thus, in this domain, it is sufficient to consider the dynamics of the flow generated by the model equations (2.1) to (2.5). In addition, the usual existence, uniqueness and continuation of results hold for the system (Hethcote, 2000).

Positivity of Solution

$\{S_{\mathrm{H}}(0), S_{\mathrm{A}}(0) > 0, (\mathrm{I}_{\mathrm{H}}(0), \mathrm{I}_{\mathrm{A}}(0), R_H(0))\} \in \Omega$

Then the solution set $\{S_{\mathrm{H}}, S_{\mathrm{A}}, R_{\mathrm{H}}, \mathrm{I}_{\mathrm{H}}, \mathrm{I}_{\mathrm{A}}\}$ (t) of the model system (2.1) to (2.5) is positive for all t >0 (Cooke and Den Driessche 1996)

Proof: The first equation of the model (3.6) gives

$$\frac{dS_H}{dt} = \Lambda_H - (\beta_H + \phi_1 \mathrm{I}_H + \mu_H) S_H \geq -(\beta_H + \phi_1 \mathrm{I}_H + \mu_H) S_H$$

$$\frac{dS_H}{dt} \geq -(\beta_H + \phi_1 I_H + \mu_H) S_H$$

Separating the variables and integrating both sides

$$\int \frac{dS_H}{S_H} \geq -\int (\beta_H + \phi_1 I_H + \mu_H) dt$$

$$S_H(t) \geq S_H(0) e^{-(\beta_H + \phi_1 I_H + \mu_H)t + c}$$

$$S_H(t) \geq S_H(0) e^{-(\beta_H + \phi_1 I_H + \mu_H)t} \qquad (3.7)$$

$$S_H(t) \geq S_H(0) e^{-(\beta_H + \phi_1 I_H + \mu_H)t} > 0$$

$$S_H(t) \geq S_H(0)$$

$$S_H(t) \geq 0$$

Similarly, it can be shown that $S_{\mathrm{A}}(t), R_H(t), \mathrm{I}_H(t), \mathrm{I}_{\mathrm{A}}(t) > 0$

This completes the proof; furthermore, it is necessary to show that region Ω is positively invariant so that it suffices the dynamics of the above system.It follows that

$$\begin{cases} \dfrac{dN_H}{dt} = \Lambda_{HN} - \mu_H N_H - \mu_0 \mathrm{I}_H \leq \Lambda_H - \mu_H N_H \\ \dfrac{dN_{\mathrm{A}}}{dt} = \Lambda_{\mathrm{A}} - N_{\mathrm{A}} \mu_{\mathrm{A}} + u_2 \end{cases} \qquad (3.8)$$

Applying the (Brikhoff and Rota,1982)theorem on differential inequality and separating the equation (3.8) yields

$$\frac{dN_H}{\Lambda_H - \mu_H N_H} \leq dt \qquad (3.9)$$

Integrating both sides of equation (3.19) gives

$$\int \frac{dN_H(t)}{\Lambda_H - \mu_H N_H(t)} \leq \int dt$$

$$\Rightarrow \frac{1}{\mu_H} \ln(\Lambda_H - \mu_H N_H(t)) \leq t + c$$

$$\Rightarrow \ln(\Lambda_H - \mu_H N_H(t)) \leq \mu_H (t + c)$$

Therefore

$$\Lambda_H - \mu_H N_H(t)) \leq Ae^{-\mu_H(t+c)} \tag{3.10}$$

Similarly the Aedes mosquito population yields

$$\Lambda_A - N_A \mu_A + u_2(t)) \leq Be^{-\mu_A(t+c)} \tag{3.11}$$

Where A and B are constant, using the initial condition $N_H(t) = N_H(0)$ and $N_A(t) = N_A(0)$ this yield

$$\begin{cases} A = \Lambda_H - \mu_H N_H(0) \\ B = \Lambda_A - \mu_A + u_2 N_A(0) \end{cases} \tag{3.12}$$

Substituting equation (3.12) in to (3.10) - (3.11) gives

$$\begin{cases} (\Lambda_H - \mu_H N_H(t)) \leq (\Lambda_A - \mu_H N_H(0))e^{-\mu_H(t+c)} \\ (\Lambda_A - \mu_A + u_2 N_A(t)) = (\Lambda_A - \mu_A N_A(0))e^{-\mu_A(t+c)} \end{cases} \tag{3.13}$$

Making $N_H(t)$ and $N_A(t)$ the subject of formula in (3.13) gives,

$$\begin{cases} N_H(t) \leq \frac{\Lambda_H}{\mu_H} - \left[\frac{\Lambda_A - \mu_A + u_2 N_A(0)}{\mu_H}\right] e^{-\mu_H t} \\ N_A(t) = \frac{\Lambda_A}{\mu_A + u_2} - \left[\frac{\Lambda_A - \mu_A + u_2 N_A(0)}{\mu_A + u_2}\right] e^{-\mu_A t} \end{cases} \tag{3.14}$$

$$N_H(t) \leq \frac{\Lambda_H}{\mu_H}(1 - e^{-\mu_H t}) + N_H(0)e^{(-\mu_H t)} \quad \text{and} \quad N_A \leq \frac{\Lambda_A}{\mu_A + u_2} 1 - e^{(-\mu_A t)} + N_A(0)e^{(-\mu_A t)} \tag{3.15}$$

In particular, if $N_H(0) < \frac{\Lambda_H}{\mu_H}$ then $N_H(0) \leq \frac{\Lambda_H}{\mu_H}$, $N_A(0) < \frac{\Lambda_A}{\mu_A + u_2}$ if $N_A(0) \leq \frac{\Lambda_A}{\mu_A + u_2}$ then

Therefore Ω is positively invariant if $N_H(0) > \frac{\Lambda_H}{\mu_H}$ and $N_A(0) > \frac{\Lambda_A}{\mu_A + u_2}$, then either the solution enters Ω in finite time or $N_H(t)$ approaches $\frac{\Lambda_H}{\mu_H}$ and $N_A(t)$ approaches $\frac{\Lambda_A}{\mu_A + u_2}$ asymptotically, and the affected variable I_H and I_A approaches zero. In this region, the model can be considered as being epidemiologically and mathematically well-posed (Hethcote, 2000).

3.6 The Equilibrium states of the model

At the equilibrium state;

$$\frac{dS_H}{dt} = \frac{dI_H}{dt} = \frac{dR_H}{dt} = \frac{dS_A}{dt} = \frac{dI_A}{dt} = 0$$

Let $S_H = x_1, I_H = x_2, R_H = x_3, S_A = x_4, I_A = x_5$

Then from(2.1) to (2.5)

$$\Lambda_A - (\beta_1 \varepsilon \phi x_2 + \mu_A + u_2)x_4 = 0 \tag{3.16}$$

$$(\beta \varepsilon \phi x_5 + \phi_1 x_2)x_1 - (\mu_H + \mu_0 + \gamma_H + u_1)x_2 = 0 \tag{3.17}$$

$$(\gamma_H + u_1)x_2 - \mu_H x_3 = 0 \tag{3.18}$$

$$\Lambda_A - (\beta_1 \varepsilon \phi x_2 + \mu_A + u_2)x_4 = 0 \tag{3.19}$$

$$\beta_1 \varepsilon \phi x_2 x_4 - (\mu_A + u_2)x_5 = 0 \tag{3.20}$$

Solving these system of equation simultaneously gives

$$(x_1, x_2, x_3, x_4 x_5) = \left(\frac{\Lambda_H}{\mu_H}, 0, 0 \frac{\Lambda_A}{\mu_A}, 0\right) \tag{3.21}$$

as the Disease Free Equilibrium State and

$$x_1 = (\mu_H + \mu_0 + \gamma_H + u_1) / (-1 + \beta \varepsilon \phi)(\mu_H^2 + (\mu_0 + \gamma_H + u_1)\mu_H - \Lambda_H \phi_1)$$
$$\mu_A^2 + u_2 + \Lambda_H \beta_1 \varepsilon^3 \phi^3 \beta^2 \mu_A + u_2 + \Lambda_H \Lambda_A \beta \phi^2 \varepsilon^2 \beta_1)(\phi_1$$
$$(\mu_H^2 + (\mu_0 + \gamma_H + u_1)\mu_H - \Lambda_H \phi_1)$$
$$(-1 + \beta \varepsilon \phi)\mu_A^2 + u_2 + \phi_1 \Lambda_H \beta \varepsilon^3 \phi^3 \beta^2 \mu_A + u_2 + \Lambda_A \beta_1 \phi^2 \varepsilon^2 (\varepsilon \phi \beta \mu_H^2) +$$
$$\varepsilon \phi \beta (\mu_0 + \gamma_H + u_1)\mu_H - \Lambda_H \phi_1 (-1 + \beta \varepsilon \phi) \beta) \tag{3.22}$$

$$x_2 = \frac{\mu_A^2 x_1 \phi_1 - \mu_A^2 \mu_H - \mu_A^2 \mu_0 - \mu_A^2 \gamma_H + u_1 + x_1 \beta_1 \varepsilon^3 \phi^3 \beta^2 \mu_A + x_1 \beta_1 \varepsilon^2 \phi^2 \beta \Lambda_A}{\beta_1 \varepsilon^2 \phi^2 \beta \mu_A (-x_1 \phi_1 + \mu_H + \mu_0 + \gamma_H + u_1)} \quad (3.23)$$

$$x_3 = \frac{\gamma_H + u_1(-\mu_A^2 \mu_H^2 - \mu_A^2 (\mu_0 + \gamma_H + u_1)\mu_H + \Lambda_H (\mu_A^2 \phi_1 + \Lambda_A \beta \phi^2 \varepsilon^2 \beta_1 + \beta_1 \varepsilon^3 \phi^3 \beta^2 \mu_A)}{\mu_A \varepsilon^2 \beta_1 \phi^2 (\mu_H^2 + (\mu_0 + \gamma_H + u_1)\mu_H - \Lambda_H \phi_1)\beta \mu_H} \quad (3.24)$$

$$x_4 = \frac{\Lambda_A (\mu_H^2 + \mu_0 + \gamma_H + u_1)\mu_H - \Lambda_H \phi_1)\phi \mu_A \varepsilon \beta}{(-1 + \beta \varepsilon \phi)(\mu_H^2 + (\mu_0 + \gamma_H + u_1)\mu_H - \Lambda_H \phi_1)\mu_A^2 + \Lambda_H \beta_1 \varepsilon^3 \phi^3 \beta^2 \mu_A + \Lambda_H \Lambda_A \beta \phi^2 \varepsilon^2 \beta_1} \quad (3.25)$$

$$x_5 = \Lambda_A (-\mu_A^2 \mu_H^2 - \mu_A^2 (\mu_0 + \gamma_H + u_1)\mu_H + \Lambda_H \phi_1) \mu_A^2 + \Lambda_A$$
$$\beta_1 \varepsilon^3 \phi^3 \beta^2 \mu_A + \Lambda_H \Lambda_A \beta \phi^2 \varepsilon^2 \beta_1)/(\mu_A$$
$$(-1 + \beta \varepsilon \phi)(\mu_H^2 + (\mu_0 + \gamma_H + u_1)\mu_H - \Lambda_H \phi_1)\mu_A^2 + \Lambda_H \beta_1 \varepsilon^3 \phi^3 \beta^2 \mu_A + \Lambda_H \Lambda_A \beta \phi^2 \varepsilon^2 \beta_1) \quad (3.26)$$

as the endemic equilibrium state.

Basic Reproduction Number

The basic reproduction number, often expressed as the average number of human infected by an index case, is a vital threshold making use of the infected compartments of the model equations. This is given as the spectral radius (ρ) of the next generation matrix, $R_0 = \rho(FV^{-1})$ Where F is the rate of arrival of new infection in to the class that is infected and V is the transmission of persons out of the compartment that is infected.

$$\frac{dI_H}{dt} = (\beta \varepsilon \phi I_A + \phi_1 I_H) S_H - (\mu_H + \mu_0 + \gamma_H + u_1) I_H \quad (3.27)$$

$$\frac{dI_A}{dt} = \beta_1 \varepsilon \phi I_H S_A - (\mu_A + u_2) I_A \quad (3.28)$$

From(3.27) to(3.28) we obtained the following

$$F = \begin{bmatrix} \frac{\phi_1 \Lambda_H}{\mu_H} & \frac{\beta \varepsilon \phi \Lambda_H}{\mu_H} \\ \frac{\beta_1 \varepsilon \phi \Lambda_H}{\mu_A + u_2} & 0 \end{bmatrix} \quad (3.29)$$

$$V = \begin{bmatrix} \mu_H + \mu_0 + \gamma_H + u_1 & 0 \\ 0 & \mu_A + u_2 \end{bmatrix} \quad (3.30)$$

$$V^{-1} = \begin{bmatrix} \dfrac{1}{\mu_H + \mu_0 + \gamma_H + u_1} & 0 \\ 0 & \dfrac{1}{\mu_A + u_2} \end{bmatrix} \tag{3.31}$$

$$FV^{-1} = \begin{bmatrix} \dfrac{\phi_1 \lambda_H}{\mu_H(\mu_H + \mu_0 + \gamma_H + u_1)} & \dfrac{\beta\varepsilon\phi\Lambda_H}{\mu_H\mu_A + u_2} \\ \dfrac{\beta_1\varepsilon\phi\Lambda_H}{\mu_A + u_2(\mu_H + \mu_0 + \gamma_H + u_1)} & 0 \end{bmatrix}$$

$$R_0 = FV^{-1} = \begin{bmatrix} \dfrac{\phi_1 \lambda_H}{\mu_H(\mu_H + \mu_0 + \gamma_H + u_1)} - \lambda & \dfrac{\beta\varepsilon\phi\Lambda_H}{\mu_H\mu_A + u_2} \\ \dfrac{\beta_1\varepsilon\phi\Lambda_H}{\mu_A + u_2(\mu_H + \mu_0 + \gamma_H + u_1)} & -\lambda \end{bmatrix} \tag{3.32}$$

Therefore the basic reproduction number is

$$R_0 = \lambda = \frac{1}{2}\frac{\left(\mu_A + u_2\theta_1\Lambda_H + \sqrt{4}\sqrt{\left(\frac{1}{4}\mu_A^2 + u_2\theta_1^2 + \beta\theta^2\varepsilon^2\beta_1\Lambda_A\mu_H(\mu_H + \mu_0 + \gamma_H + u_1)\right)\Lambda_H}\right.}{\mu_H(\mu_H + \mu_0 + \gamma_H + u_1)\mu_A + u_2} \tag{3.33}$$

Stability Analysis of the Disease free Equilibrium (DFE)

Recall that at the equilibrium states,

$$\Lambda_H - (\beta\varepsilon\phi x_5 + \phi_1 x_2 + \mu_H)x_1 = 0$$
$$(\beta\varepsilon\phi x_5 + \phi_1 x_2)x_1 - (\mu_H + \mu_0 + \gamma_H + u_1)x_2 = 0$$

$$(\gamma_H + u_1)x_2 - \mu_H x_3 = 0 \quad \Lambda_A - (\beta_1\varepsilon\phi x_2 + \mu_A + u_2)x_4 = 0 \quad \beta_1\varepsilon\phi x_2 x_4 - (\mu_A + u_2)x_5 = 0$$

The characteristic equation is given by $|j - I\lambda|$ = 0

$$\Rightarrow \begin{bmatrix} -A_1 - \lambda & -A_2 & 0 & 0 & -A_3 \\ 0 & A_2 - (\mu_H + \mu_0 + \gamma_H + u_1) - \lambda & 0 & 0 & A_3 \\ 0 & \gamma_H + u_1 & -\mu_H - \lambda & 0 & 0 \\ 0 & -A_5 & 0 & -(u_2 + \mu_A) - \lambda & 0 \\ 0 & A_5 & 0 & u_2 & -\mu_A - u_2 - \lambda \end{bmatrix} = 0$$

Where

$$A_1 = \left(\beta \varepsilon \phi x_5 + \phi_1 x_2 + \mu_H\right), A_2 = \phi_1 x_1, A_3 = \beta \varepsilon \phi x_1, A_4 = \beta \varepsilon \phi x_5 + \phi_1 x_2, A_5 = \beta_1 \varepsilon \phi x_4 \quad (4.1)$$

$$\Rightarrow$$

$$(-A_1 - \lambda)A_2(-(\mu_H + \mu_0 + \gamma_H + u_1) - \lambda)(-\mu_H - \lambda)((-u_2 + \mu_A) - \lambda)(\mu_A - u_2 - \lambda) = 0 \quad (4.2)$$

Either ; $-A_1 - \lambda = 0$ or $A_2(-(\mu_H + \mu_0 + \gamma_H + u_1) - \lambda) = 0$ or $(-\mu_H - \lambda) = 0$ or $(-u_2 + \mu_A) - \lambda) = 0$ (4.3)

Therefore;

$\lambda_1 = A_1$ $\lambda_2 = (\mu_H + \mu_0 + \gamma_H + u_1) - A_2$, $\lambda_3 = -\mu_H$ and $\lambda_4 = -(u_2 + \mu_A)$ (4.4)

From (4.4)

λ_1 , , λ_3 and $\lambda_4 < 0$ λ_2 will be negative if and only if $(\mu_H + \mu_0 + \gamma_H + u_1) < A$

Hence, the DFE is stable if $(\mu_H + \mu_0 + \gamma_H + u_1) < A$

otherwise unstable.

Conclusion

we have developed and analysed a mathematical model for the spread of Zika virus disease. We established the existence and positivity of solutions to the model, Existence and stability analysis of the equilibrium states of the model and evaluated the basic reproduction number of the model. The feasible set for the model equations is given by $\Omega = \{$ ($S_{\mathrm{H}}, \mathrm{I}_{\mathrm{H}}, R_{\mathrm{H}}, S_{\mathrm{A}}, \mathrm{I}_{\mathrm{A}}) \} \in \Re_+^5 : S_{\mathrm{H}}, \mathrm{I}_{\mathrm{H}}, R_{\mathrm{H}}, S_{\mathrm{A}}, \mathrm{I}_{\mathrm{A}} \geq 0$; $\mathrm{N}_{\mathrm{H}} \leq \frac{\Lambda_{\mathrm{H}}}{\mu_{\mathrm{H}}}, \mathrm{N}_{\mathrm{A}} \leq \frac{\Lambda_{\mathrm{A}}}{\mu_{\mathrm{A}} + u_2}$. The stability analysis of the Disease Free Equilibrium State (DFE) of the model shows that it will be stable if $(\mu_H + \mu_0 + \gamma_H) < A_2$.

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