

ON STABILITY ANALYSIS OF CO-INFECTION MODEL ON MALARIA AND ZIKA VIRUS

ABSTRACT

The article formulates a model to study the spread of Co-infection of Malaria and Zika virus diseases. Under the model, individual diseases were studied and analyzed separately to determine their basic reproduction numbers and their equilibrium points. Stability analysis on the individual disease models shows that the equilibrium points are locally and globally asymptotically stable, while the combined model is only locally asymptotically stable but not globally asymptotically stable for the disease free equilibrium point. The endemic equilibrium point of the co-infection model of Malaria and Zika virus also show that they are both locally and globally asymptotically stable.

Impact of the individual on each other were also studied and analysed. The analysis shows that an increase in malaria cases results in decrease in Zika virus case in the community and an increase in Zika virus cases results in decrease of malaria cases in the community.

KEYWORDS-Coinfection, Reproduction number, local stability, global stability etc.

INTRODUCTION

Zika virus disease is caused by a virus which is transmitted mostly by female *Aedes aegypti* mosquito (Varandani, 2016) which is also responsible for the transmission of chikungunya and dengue fever. The disease was initially discovered in a monkey in the Zika forest of Uganda in 1947 (Omprakash, 2017) however much attention was not given to it until recently when it started causing harm to expectant mothers in the Americas. Mothers in this part of the world were producing microcephaly babies (children with abnormal small head and other neurological disorders), and this caught the attention of the World Health Organization (WHO). The alarming rate of the incidence in Brazil and other parts of the world forced the world health organization to declare the virus as the international emergence concerned. The incidence of Zika virus disease is spreading and this is partly due to the fact that there is neither cure nor vaccine.

Mode of transmission of Zika virus : Only female *Aedes aegypti* mosquito bites an infected human. She has to bite during the viremic stage- that is in the first several days of infection, when the virus is still circulating in the human's blood. The mosquito takes up the virus, stores it in her gut and salivary glands, and then transmits it when she bites another uninfected human. (Jeneen 2016) As part of the mode of transmission, there has been an evidence that Zika virus can be contracted through casual sex with an infected person according to Centre for Disease and preventive Control (CDC).

In the light of this, it is very important to know the key parameters in the transmission of the disease and come out with the measures to combat the menace.

Malaria and Mode of transmission: In another development Malaria is an old disease that was first studied by Ross in the late 1800's (Kamal et al, 2012). Malaria is a vector borne disease which is caused by a female Anopheles mosquito. There are four species of parasites namely: plasmodium falciparum, plasmodium vivax, plasmodium ovale and plasmodium malariae infects human.

Among the parasites, plasmodium falciparum is considered as deadly. (Ducrota et al, 2008). Plasmodium falciparum is known to be the type of species that is believed to cause human infections in Africa (Lawi G.O et al, 2011). The disease continues to be a major problem in sub-Saharan Africa, Asia, Central and South America and furthermore the Middle East. Almost 40% of the world's population settles in endemic areas. (Mwantobe, 2014). The disease is caused by plasmodium parasite and is transmitted between humans through the bite of the female anopheles mosquito. It kills about 700,000 to 2.7 million people yearly, 75% of whom are African children (Chnitis, 2005). The parasites develop into the body of human between 10-18 days, then is passed on when the mosquito injects saliva while feeding. In the human body malaria parasites migrate to the liver, where they grow and multiply. As time goes on the parasites find its way in the blood stream and continue to develop in the red blood cells. At this stage the infected individuals begin to show symptoms like fever, chills, sweating, headaches and other flu-like conditions. The infection can sometimes produce even more severe reactions including kidney failure and death, especially if not treated for a period of time. (Mosquito World, 2017)

In this research, the idea is to propose a mathematical model for the transmission dynamics of both Zika virus and malaria, which is co-infection. A considerable amount of work, has been done on co-infections of various diseases, however, there is none on malaria-Zika co-infection. Some of the works done on co-infections are: a deterministic mathematical model for hepatitis B and tuberculosis by Bowong et al. (2010). Bhunu et al. also formulated and analyzed a deterministic model for hepatitis C virus and HIV/AIDS in 2013 in order to assess their impact on the dynamics of each disease in the presence of treatment. Mushayabasa S. et al. designed a mathematical model to explore the co-infection of gonorrhea and HIV in the presence of

antiretroviral therapy and gonorrhea treatment in 2010. The model in this paper is a system of ordinary nonlinear differential equations. The model is described, formulated and analysed below.

1.2 DIFFERENCE BETWEEN ZIKA VIRUS AND MALARIA

Zika virus and Malaria are both mosquito borne diseases, and since the rise of Zika first in Brazil and now extending to other parts of the world, a lot of questions are being asked as about the differences between Zika virus and Malaria (Marchione, 2016) .The major differences is the manner we combat the two diseases because they are spread by two different types of mosquitoes species namely female anopheles for malaria and female aedes aegypti for zika virus. Female anopheles mosquito bite at night and at dawn and can give you the malaria. This can be prevented by sleeping in the mosquito insecticide net. On the contrary, the aedes aegypti mosquito bite during the day time (Landman, 2016) which makes prevention more complex to deal with . However, to avoid been bitten by the female aedes aegypti mosquito having the virus, the medical experts suggest that using insect repellent and protective clothing can also help in a way.(Ivanovich,2016) .Since zika virus can be transmitted through sexual intercourse there is the need for us to abstain or consistently use condom

The paper has been organized as follows, Section 2 deals with the description of the model, Section 3 deals with the analysis of Co-infection Malaria and Zika virus model ,Malaria model only ,Zika virus only ,Section 4 deals with the impact of Malaria on Zika virus and the vice versa.the paper is concluded in with relevant discussion .

2.0 MODEL FORMULATION AND DESCRIPTION

This model subdivides human population into six compartments namely: susceptible (S_h) , infectious malaria (I_m) , infectious zika (I_z) , both malaria and zika infectious (I_{mz}) , recovered from malaria only (R_m) and recovered from zika only (R_z) and the female

95 mosquito population is also partition into three compartments, that is, susceptible (S_m),
 96 infectious female Anopheles mosquito (I_v), infectious female aedes aegypti mosquito (I_a).

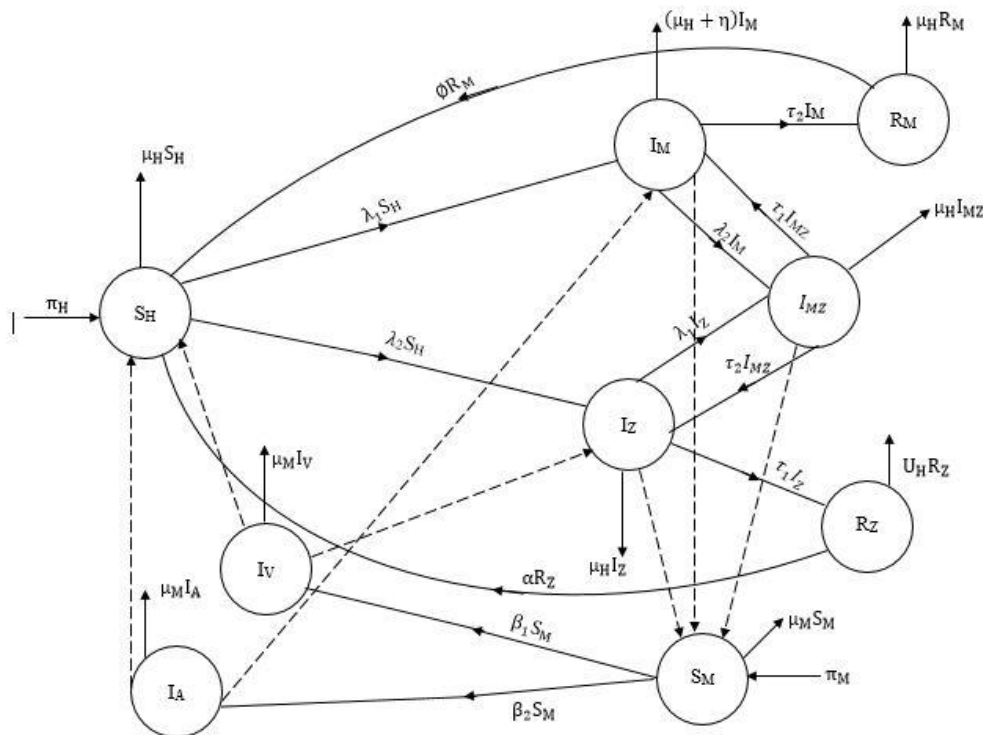
97 Individuals who are susceptible to infection (S_h), individuals infected with malaria(I_m),
 98 individuals infected with zika virus(I_z), individuals infected with both malaria and zika virus
 99 infectious (I_{mz}), individuals who recover from malaria only (R_m) and individuals who
 100 recover from zika only (R_z). This means that

$$N_h = S_h + I_m + I_z + I_{mz} + R_m + R_z \dots \dots \dots (1)$$

101 and

$$N_m = S_m + I_v + I_a \dots \dots \dots (2)$$

FLOW CHART FOR ZIKA AND MALARIA



Human beings are recruited into their population at the rate Π_h and the mosquitoes are also recruited at the rate Π_m . When an infected female anopheles mosquito bites an individual in the (S_h) compartment and becomes infectious, then the individual moves to (I_m) compartment when he or she has malaria infection, and into (I_z) , when it is zika infection. Those in (I_m) and (I_z) can be infected with either malaria or zika virus. If those in (I_m) are infected with zika then they move to (I_{mz}) compartment, and those in the (I_z) compartment move to (I_{mz}) compartment when they are infected with malaria. If an individual in the (I_{mz}) compartment recovers from only malaria, then he or she moves to (I_z) . and If an individual in the (I_{mz}) compartment recovers from only zika, then he or she moves to (I_m) compartment. Those in (I_m) and (I_z) compartment moves to R_m and R_z respectively after recovering from malaria only and zika virus only. Further more individual in R_m and R_z compartment also move to (S_h) at the rates of $\emptyset$ and α respectively for reinfection. The individual in the human population exits their population at the per capita natural death rate (μ_h) in each compartment and they can also exit the human population through the disease induced death rate at (I_m) compartment. Our attention is now on the mosquito. The mosquito (S_m) compartment moves to (I_v) or (I_a) compartment when they bite human in either (I_m) or (I_z) compartment and becomes infectious at rates β_1 and β_2 respectively. Mosquitoes in the (I_v) and (I_a) compartment remains in the (I_v) and (I_a) compartment until they die because the mosquitoes do not recover from either the plasmodium parasite infection or the zika virus infection. Mosquito exit their population through per capita natural death rate in each compartment. Both human and mosquitoes follow the logistic model for population growth.

he compartmental model describes the dynamics of the co-infection model of malaria and zika virus in human and mosquito population. The recruitment rate for susceptible human and mosquito populations are denoted by Π_h and Π_m , probability of female aedes aegypti mosquito getting infected with zika virus denoted by σ_a , probability of female Anopheles mosquito getting infected with malaria parasite denoted by β_v , probability of human getting infected with malaria is β_h , probability of human getting infected by zika virus is (σ) , rate at which individual return to susceptible after recovering from zika virus α , recovery rate for zika virus only is τ_1 , recovery rate of malaria is τ_2 , Natural death rate for human is μ_h , Natural death rate for mosquito is μ_m , malaria induced death rate is η . Susceptible

human becomes infected with malaria when he or she is bitten by anopheles mosquito, then he or she then moves to the malaria infectious compartment. Then, the infectious malaria individual either recovers and moves to recovery compartment for malaria only or get bitten by aedes aegypti mosquito and moves to co-infection compartment after getting zika virus. Also, susceptible human becomes infected with zika when an individual is bitten by female aedes aegypti mosquito, then the individual moves to the zika infectious compartment. Then, the infectious zika individual either recovers from zika depending on the strength of one's immune system and moves to recovery compartment for zika only or get bitten by female Anopheles mosquito and moves to co-infection compartment after getting malaria. Note that the disease is self-limiting meaning ability to recover depending on the strength of one's immune system.

3.0 Confection Model For Malaria And Zika Virus

$$\left. \begin{aligned} \frac{dS_h}{dt} &= \Pi_h + \phi R_m + \alpha R_z - \mu_h S_h - \lambda_1 S_h - \lambda_2 S_h \\ \frac{dI_m}{dt} &= \lambda_1 S_h - \lambda_2 I_m - (\mu_h + \eta + \tau_2) I_m + \tau_1 I_{mz} \\ \frac{dI_z}{dt} &= \lambda_2 S_h - \lambda_1 I_z - (\mu_h + \tau_1) I_z + \tau_2 I_{mz} \\ \frac{dI_{mz}}{dt} &= \lambda_2 I_m + \lambda_1 I_z - (\mu_h + \tau_1 + \tau_2) I_{mz} \\ \frac{dR_m}{dt} &= \tau_2 I_m - (\phi + \mu_h) R_m \\ \frac{dR_z}{dt} &= \tau_1 I_z - (\mu_h + \alpha) R_z \\ \frac{dS_m}{dt} &= \Pi_m - \mu_m S_m - \beta_1 S_m - \beta_2 S_m \\ \frac{dI_v}{dt} &= \beta_1 S_m - \mu_m I_v \\ \frac{dI_a}{dt} &= \beta_2 S_m - \mu_m I_a \end{aligned} \right\} \dots\dots\dots (3)$$

With the force of infection

$$\lambda_1 = \frac{\beta_h I_v}{N_h}, \lambda_2 = \frac{\sigma I_a}{N_h}, \beta_1 = \frac{\beta_v (I_m + I_{mz})}{N_h}, \beta_2 = \frac{\sigma_a (I_z + I_{mz})}{N_h} \dots\dots\dots (4)$$

3.2 Stability Analysis Of Co-Infection Model : Disease free equilibrium (DFE) of the disease model is the steady state solution of the disease where there is no infection or disease (malaria) in the

150 population. The disease free equilibrium can be determined by putting the right hand side of
 151 equation (5) to be equal to zero. That is $\{I_m = I_z = I_{mz} = I_v = I_a = R_m = R_z = 0\}$

152
 153

$$154 \quad E_{mz}^* = (S_h, I_m, I_z, I_{mz}, R_m, R_z, S_m, I_v, I_a) = \left(\frac{\Pi_h}{\mu_h}, 0, 0, 0, 0, 0, \frac{\Pi_m}{\mu_m}, 0, 0 \right) \dots \dots \dots (5)$$

155 **3.3. Basic Reproduction Number (R_{mz})**–The basic reproduction number is the average number of
 156 secondary cases generated in a wholly susceptible population by a typical infective individual.

157 We identify the matrices F and V for the new infection terms and the remaining transfer terms at
 158 the disease free equilibrium using the next generation operator method

159 as described by (P. van den Driessche and J. Watmough, 2002) respectively

$$160 \quad F = \begin{pmatrix} \frac{\beta_h I_v S_h}{N_h} + \frac{\sigma I_a I_m}{N_h} \\ \frac{\sigma I_a S_h}{N_h} - \frac{\beta_h I_v I_z}{N_h} \\ \frac{\sigma I_a I_m}{N_h} + \frac{\beta_h I_v I_z}{N_h} \\ \frac{\beta_v (I_m + I_{mz})}{N_h} \\ \frac{\sigma_a (I_z + I_{mz})}{N_h} \end{pmatrix} \text{ and } V = \begin{pmatrix} (\mu_h + \eta + \tau_2) I_m - \tau_1 I_{mz} \\ (\mu_h + \tau_1) I_z - \tau_2 I_{mz} \\ (\mu_h + \tau_1 + \tau_2) I_{mz} \\ \mu_m I_v \\ \mu_m I_a \end{pmatrix}$$

161 The Jacobian matrix of F and V are given as

162

$$163 \quad F^1 = \begin{pmatrix} -\frac{\sigma I_a}{N_h} & 0 & 0 & \frac{\beta_h S_h}{N_h} & -\frac{\sigma I_m}{N_h} \\ 0 & -\frac{\beta_h I_v}{N_h} & 0 & -\frac{\beta_h I_z}{N_h} & \frac{\sigma S_h}{N_h} \\ \frac{\sigma I_a}{N_h} & \frac{\beta_h I_v}{N_h} & 0 & \frac{\beta_h I_z}{N_h} & \frac{\sigma I_m}{N_h} \\ \frac{\beta_v S_m}{N_h} & 0 & \frac{\beta_v S_m}{N_h} & 0 & 0 \\ 0 & \frac{\sigma_a S_m}{N_h} & \frac{\sigma_a S_m}{N_h} & 0 & 0 \end{pmatrix}$$

164 and

$$165 \quad V = \begin{vmatrix} (\mu_h + \eta + \tau_2) & 0 & -\tau_1 & 0 & 0 \\ 0 & (\mu_h + \tau_1) & -\tau_2 & 0 & 0 \\ 0 & 0 & (\mu_h + \tau_1 + \tau_2) & 0 & 0 \\ 0 & 0 & 0 & \mu_m & 0 \\ 0 & 0 & 0 & 0 & \mu_m \end{vmatrix}$$

166

167 The Jacobian matrix at the disease free equilibrium E_{mz}^* of the co-infection model where

$$168 \quad 0 \leq N_h \leq \frac{\Pi_h}{\mu_h} \text{ and } 0 \leq N_m \leq \frac{\Pi_m}{\mu_m}$$

169

$$170 \quad F = \begin{vmatrix} 0 & 0 & 0 & \beta_h & 0 \\ 0 & 0 & 0 & 0 & \sigma \\ 0 & 0 & 0 & 0 & 0 \\ \frac{\beta_v \Pi_m \mu_h}{\Pi_h \mu_m} & 0 & \frac{\beta_v \Pi_m \mu_h}{\Pi_h \mu_m} & 0 & 0 \\ 0 & \frac{\sigma_a \Pi_m \mu_h}{\Pi_h \mu_m} & \frac{\sigma_a \Pi_m \mu_h}{\Pi_h \mu_m} & 0 & 0 \end{vmatrix} \Rightarrow F = \begin{vmatrix} 0 & 0 & 0 & A_1 & 0 \\ 0 & 0 & 0 & 0 & A_2 \\ 0 & 0 & 0 & 0 & 0 \\ A_3 & 0 & A_3 & 0 & 0 \\ 0 & A_4 & A_4 & 0 & 0 \end{vmatrix}$$

171 Where

172

$$173 \quad A_1 = \beta_h, A_2 = \sigma, A_3 = \frac{\beta_v \Pi_m \mu_h}{\Pi_h \mu_m}, A_4 = \frac{\sigma_a \Pi_m \mu_h}{\Pi_h \mu_m}$$

$$174 \quad \text{and } V = \begin{vmatrix} (\mu_h + \eta + \tau_2) & 0 & -\tau_1 & 0 & 0 \\ 0 & (\mu_h + \tau_1) & -\tau_2 & 0 & 0 \\ 0 & 0 & (\mu_h + \tau_1 + \tau_2) & 0 & 0 \\ 0 & 0 & 0 & \mu_m & 0 \\ 0 & 0 & 0 & 0 & \mu_m \end{vmatrix} \Rightarrow V = \begin{vmatrix} B_1 & 0 & -B_2 & 0 & 0 \\ 0 & B_3 & -B_4 & 0 & 0 \\ 0 & 0 & B_5 & 0 & 0 \\ 0 & 0 & 0 & B_6 & 0 \\ 0 & 0 & 0 & 0 & B_6 \end{vmatrix}$$

175 Where

176

$$177 \quad B = (\mu_h + \eta + \tau_2), B_2 = \tau_1, B_3 = (\mu_h + \tau_1), B_4 = \tau_2, B_5 = (\mu_h + \tau_1 + \tau_2), B_6 = \mu_m$$

178 V Inverse (V^{-1})

179
$$V^{-1} = \begin{vmatrix} \frac{1}{B_1} & 0 & -\frac{B_2}{B_1 B_5} & 0 & 0 \\ 0 & \frac{1}{B_3} & -\frac{B_4}{B_3 B_5} & 0 & 0 \\ 0 & 0 & \frac{1}{B_5} & 0 & 0 \\ 0 & 0 & 0 & \frac{1}{B_6} & 0 \\ 0 & 0 & 0 & 0 & \frac{1}{B_6} \end{vmatrix}$$

180

181

182 Finding $F^1 V^{-1} = \begin{vmatrix} 0 & 0 & 0 & A_1 & 0 \\ 0 & 0 & 0 & 0 & A_2 \\ 0 & 0 & 0 & 0 & 0 \\ A_3 & 0 & A_3 & 0 & 0 \\ 0 & A_4 & A_4 & 0 & 0 \end{vmatrix} \begin{vmatrix} \frac{1}{B_1} & 0 & -\frac{B_2}{B_1 B_5} & 0 & 0 \\ 0 & \frac{1}{B_3} & -\frac{B_4}{B_3 B_5} & 0 & 0 \\ 0 & 0 & \frac{1}{B_5} & 0 & 0 \\ 0 & 0 & 0 & \frac{1}{B_6} & 0 \\ 0 & 0 & 0 & 0 & \frac{1}{B_6} \end{vmatrix}$

183
$$= \begin{vmatrix} 0 & 0 & 0 & \frac{A_1}{B_6} & 0 \\ 0 & 0 & 0 & 0 & \frac{A_2}{B_6} \\ 0 & 0 & 0 & 0 & 0 \\ \frac{A_3}{B_1} & 0 & \frac{A_3(B_1 + B_2)}{B_1 B_5} & 0 & 0 \\ 0 & \frac{A_4}{B_3} & \frac{A_4(B_3 + B_4)}{B_3 B_5} & 0 & 0 \end{vmatrix}$$

184

185 Determining the eigenvalues $FV^{-1} - I\lambda$ we have

$$186 \quad FV - I\lambda = \begin{vmatrix} -\lambda & 0 & 0 & \frac{A_1}{B_6} & 0 \\ 0 & -\lambda & 0 & 0 & \frac{A_2}{B_6} \\ 0 & 0 & -\lambda & 0 & 0 \\ \frac{A_3}{B_1} & 0 & \frac{A_3(B_1+B_2)}{B_1B_5} & -\lambda & 0 \\ 0 & \frac{A_4}{B_3} & \frac{A_4(B_3+B_4)}{B_3B_5} & 0 & -\lambda \end{vmatrix} \Rightarrow FV - I\lambda = \begin{vmatrix} -\lambda & 0 & 0 & C_1 & 0 \\ 0 & -\lambda & 0 & 0 & C_2 \\ 0 & 0 & -\lambda & 0 & 0 \\ C_3 & 0 & C_4 & -\lambda & 0 \\ 0 & C_5 & C_6 & 0 & -\lambda \end{vmatrix}$$

187 Where

$$188 \quad C_1 = \frac{A_1}{B_6}, C_2 = \frac{A_2}{B_6}, C_3 = \frac{A_3}{B_1}, C_4 = \frac{A_3(B_1+B_2)}{B_1B_5}, C_5 = \frac{A_4}{B_3}, C_6 = \frac{A_4(B_3+B_4)}{B_3B_5}$$

$$189 \quad \lambda = \begin{cases} 0 \\ \sqrt{C_1C_3} = \sqrt{\frac{A_1A_3}{B_1B_6}} = \sqrt{\frac{\beta_h\beta_v\Pi_m\mu_h}{(\mu_h + \eta + \tau_2)\Pi_h\mu_m^2}} \\ \sqrt{C_2C_5} = \sqrt{\frac{A_2A_4}{B_3B_6}} = \sqrt{\frac{\sigma\sigma_a\Pi_m\mu_h}{(\mu_h + \tau_1)\Pi_h\mu_m^2}} \\ -\sqrt{C_1C_3} = -\sqrt{\frac{A_1A_3}{B_1B_6}} = -\sqrt{\frac{\beta_h\beta_v\Pi_m\mu_h}{(\mu_h + \eta + \tau_2)\Pi_h\mu_m^2}} \\ -\sqrt{C_2C_5} = -\sqrt{\frac{A_2A_4}{B_3B_6}} = -\sqrt{\frac{\sigma\sigma_a\Pi_m\mu_h}{(\mu_h + \tau_1)\Pi_h\mu_m^2}} \end{cases}$$

190 The basic reproduction number of Coinfection model Malaria and Zika Virus is denoted by R_{mz} and is
191 given as

$$192 \quad R_{mz} = 0, \pm \sqrt{\frac{\beta_h\beta_v\Pi_m\mu_h}{(\mu_h + \eta + \tau_2)\Pi_h\mu_m^2}}, \pm \sqrt{\frac{\sigma\sigma_a\Pi_m\mu_h}{(\mu_h + \tau_1)\Pi_h\mu_m^2}}. \text{ Here we consider the dominant eigenvalues.}$$

193 Therefore the dominant eigenvalue is given by

$$194 \quad R_{mz} = \max \left\{ \sqrt{\frac{\beta_h\beta_v\Pi_m\mu_h}{(\mu_h + \eta + \tau_2)\Pi_h\mu_m^2}}, \sqrt{\frac{\sigma\sigma_a\Pi_m\mu_h}{(\mu_h + \tau_1)\Pi_h\mu_m^2}} \right\}$$

195 Where we have $R_{mz} = \max \{R_{ma}, R_{zv}\}$. Representing

$$196 \quad R_{ma} = \sqrt{\frac{\beta_h \beta_v \Pi_m \mu_h}{(\mu_h + \eta + \tau_2) \Pi_h \mu_m^2}} \text{ and } R_{zv} = \sqrt{\frac{\sigma \sigma_a \Pi_m \mu_h}{(\mu_h + \tau_1) \Pi_h \mu_m^2}} \dots\dots\dots(6)$$

197 R_{ma} is the average number of secondary malaria infections in human or female anopheles mosquito
 198 population caused by a single infective human or mosquito introduced into a wholly susceptible
 199 population. In the same way , R_{zv} is the average number of secondary Zika virus infections in human or
 200 mosquito population caused by a single infective human or female aedes aegypti mosquito introduced
 201 into a wholly susceptible population.

202 **3.4.Local Stability Of Disease Free Equilibrium Point For Co-Infection Model**

203 To determine the local stability of the disease free equilibrium of the co-infection model of
 204 equation (3) the following theorem is considered.

205 **Theorem1.1:**

206 The disease free equilibrium point is locally asymptotically stable if
 207 $R_0 < 1 (R_{ma} < 1 \text{ and } R_{zv} < 1)$ and unstable if $R_0 > 1$.

208 **Proof**

209 The Jacobian matrix of the system (5) is given as

$$J = \begin{bmatrix} -\left(\mu_H + \frac{\beta_h I_v}{N_h} + \frac{\sigma I_a}{N_h}\right) & 0 & 0 & 0 & \phi \\ \frac{\beta_h I_v}{N_h} & -\left(\mu_h + \eta + \tau_2 + \frac{\sigma I_a}{N_h}\right) & 0 & \tau_1 & 0 \\ \frac{\sigma I_a}{N_h} & 0 & -\left(\mu_h + \tau_1 + \frac{\beta_h I_v}{N_h}\right) & \tau_2 & 0 \\ 0 & \frac{\sigma I_a}{N_h} & \frac{\beta_h I_v}{N_h} & -(\mu_h + \tau_1 + \tau_2) & 0 \\ 0 & \tau_2 & 0 & 0 & -(\mu_h + \phi) \\ 0 & 0 & \tau_1 & 0 & 0 \\ 0 & -\frac{\beta_v S_m}{N_h} & -\frac{\sigma_a S_m}{N_h} & -\frac{(\beta_v + \sigma_a)}{N_h} & 0 \\ 0 & \frac{\beta_v S_m}{N_h} & 0 & \frac{\beta_v S_m}{N_h} & 0 \\ 0 & 0 & \frac{\sigma_a S_m}{N_h} & \frac{\sigma_a S_m}{N_h} & 0 \end{bmatrix}$$

$$-\left(\mu_h + \alpha\right) \begin{bmatrix} \alpha & 0 & -\beta_h & -\sigma \\ 0 & 0 & \beta_h & \frac{-\sigma I_m}{N_h} \\ 0 & 0 & \frac{-\beta_h I_z}{N_h} & \sigma \\ 0 & 0 & \frac{\beta_h I_z}{N_h} & \frac{\sigma I_m}{N_h} \\ 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 \\ 0 & -\left[\frac{\beta_v (I_m + I_{mz}) + \sigma_a (I_z + I_{mz})}{N_h} + \mu_m\right] & 0 & 0 \\ 0 & \frac{\beta_v (I_m + I_{mz})}{N_h} & -\mu_m & 0 \\ 0 & \frac{\sigma_a (I_z + I_{mz})}{N_h} & 0 & -\mu_m \end{bmatrix}$$

At the disease free equilibrium,

$E_{mz}^* = (S_h^*, I_m^*, I_z^*, I_{mz}^*, R_m^*, R_z^*, S_m^*, I_v^*, I_a^*) = \left(\frac{\Pi_h}{\mu_h}, 0, 0, 0, 0, 0, \frac{\Pi_m}{\mu_m}, 0, 0 \right)$, the Jacobian matrix is given

as

$$J = \begin{pmatrix} -\mu_H & 0 & 0 & 0 & \phi & \alpha & 0 & -\beta_h & -\sigma \\ 0 & -(\mu_h + \eta + \tau_2) & 0 & \tau_1 & 0 & 0 & 0 & \beta_h & 0 \\ 0 & 0 & -(\mu_h + \tau_1) & \tau_2 & 0 & 0 & 0 & 0 & \sigma \\ 0 & 0 & 0 & -(\mu_h + \tau_1 + \tau_2) & 0 & 0 & 0 & 0 & 0 \\ 0 & \tau_2 & 0 & 0 & -(\mu_h + \phi) & 0 & 0 & 0 & 0 \\ 0 & 0 & \tau_1 & 0 & 0 & -(\mu_h + \alpha) & 0 & 0 & 0 \\ 0 & -\frac{\beta_v \Pi_m \mu_h}{\Pi_h \mu_m} & -\frac{\sigma_a \Pi_m \mu_h}{\Pi_h \mu_m} & -\frac{(\beta_v + \sigma_a) \Pi_m \mu_h}{\Pi_h \mu_m} & 0 & 0 & -\mu_m & 0 & 0 \\ 0 & \frac{\beta_v \Pi_m \mu_h}{\Pi_h \mu_m} & 0 & \frac{\beta_v \Pi_m \mu_h}{\Pi_h \mu_m} & 0 & 0 & 0 & -\mu_m & 0 \\ 0 & 0 & \frac{\sigma_a \Pi_m \mu_h}{\Pi_h \mu_m} & \frac{\sigma_a \Pi_m \mu_h}{\Pi_h \mu_m} & 0 & 0 & 0 & 0 & -\mu_m \end{pmatrix} \quad ..(7)$$

The diagonal entries $-\mu_h$ and $-\mu_m$ of (a_{11}) and (a_{77}) are the two of the eigenvalue of the Jacobian matrix. This means that two columns and their respective rows can be avoided. Hence the 9×9 Jacobian matrix of (7) is reduce to 7×7 matrix. (Seidu et al, 2015)

$$J = \begin{pmatrix} -(\mu_h + \eta + \tau_2) & 0 & \tau_1 & 0 & 0 & \beta_h & 0 \\ 0 & -(\mu_h + \tau_1) & \tau_2 & 0 & 0 & 0 & \sigma \\ 0 & 0 & -(\mu_h + \tau_1 + \tau_2) & 0 & 0 & 0 & 0 \\ \tau_2 & 0 & 0 & -(\mu_h + \phi) & 0 & 0 & 0 \\ 0 & \tau_1 & 0 & 0 & -(\mu_h + \alpha) & 0 & 0 \\ \frac{\beta_v \Pi_m \mu_h}{\Pi_h \mu_m} & 0 & \frac{\beta_v \Pi_m \mu_h}{\Pi_h \mu_m} & 0 & 0 & -\mu_m & 0 \\ 0 & \frac{\sigma_a \Pi_m \mu_h}{\Pi_h \mu_m} & \frac{\sigma_a \Pi_m \mu_h}{\Pi_h \mu_m} & 0 & 0 & 0 & -\mu_m \end{pmatrix} \quad(8)$$

Again the diagonal entries $-(\mu_m + \phi)$ and $-(\mu_h + \alpha)$ of (a_{44}) and (a_{55}) are the two of the eigenvalue of the Jacobian matrix. This means that two columns and their respective rows can be avoided. Hence the 7×7 Jacobian matrix of (8) is reduce to 5×5 matrix.

$$J = \begin{vmatrix} -(\mu_h + \eta + \tau_2) & 0 & \tau_1 & \beta_h & 0 \\ 0 & -(\mu_h + \tau_1) & \tau_2 & 0 & \sigma \\ 0 & 0 & -(\mu_h + \tau_1 + \tau_2) & 0 & 0 \\ \frac{\beta_v \Pi_m \mu_h}{\Pi_h \mu_m} & 0 & \frac{\beta_v \Pi_m \mu_h}{\Pi_h \mu_m} & -\mu_m & 0 \\ 0 & \frac{\sigma_a \Pi_m \mu_h}{\Pi_h \mu_m} & \frac{\sigma_a \Pi_m \mu_h}{\Pi_h \mu_m} & 0 & -\mu_m \end{vmatrix} \dots\dots\dots (9)$$

$$J = \begin{vmatrix} -A_1 & 0 & A_2 & A_3 & 0 \\ 0 & -A_4 & A_5 & 0 & A_6 \\ 0 & 0 & -A_7 & 0 & 0 \\ A_8 & 0 & A_8 & -A_9 & 0 \\ 0 & A_{10} & A_{10} & 0 & -A_9 \end{vmatrix} \dots\dots\dots (10)$$

$$A_1 = \mu_h + \eta + \tau_2, A_2 = \tau_1, A_3 = \beta_h, A_4 = \mu_h + \tau_1, A_5 = \tau_2, A_6 = \sigma, A_7 = \mu_h + \tau_1 + \tau_2,$$

$$A_8 = \frac{\beta_v \Pi_m \mu_h}{\Pi_h \mu_m}, A_9 = \mu_m, A_{10} = \frac{\sigma_a \Pi_m \mu_h}{\Pi_h \mu_m}$$

Here, elementary row transformation(Sirajo et al ,2013)is performed on equation (10) and this leads equation (11) as follows

$$J = \begin{vmatrix} -A_1 & 0 & A_2 & A_3 & 0 \\ 0 & -A_4 & A_5 & 0 & A_6 \\ 0 & 0 & -A_7 & 0 & 0 \\ 0 & 0 & 0 & (A_7 A_3 A_8 - A_7 A_1 A_9) & 0 \\ 0 & 0 & 0 & 0 & (A_7 A_6 A_{10} - A_7 A_4 A_9) \end{vmatrix} \dots\dots\dots (11)$$

From matrix (11) we find the eigenvalues $J - I\lambda$.

$$J - I\lambda = \begin{vmatrix} -(A_1 + \lambda) & 0 & A_2 & A_3 & 0 \\ 0 & -(A_4 + \lambda) & A_5 & 0 & A_6 \\ 0 & 0 & -(A_7 + \lambda) & 0 & 0 \\ 0 & 0 & 0 & (A_7 A_3 A_8 - A_7 A_1 A_9 - \lambda) & 0 \\ 0 & 0 & 0 & 0 & (A_7 A_6 A_{10} - A_7 A_4 A_9 - \lambda) \end{vmatrix} = 0 \dots\dots\dots (12)$$

$$\Rightarrow -(A_1 + \lambda_1) = 0, -(A_4 + \lambda_2) - (A_7 + \lambda_3) = 0$$

$$\Rightarrow \lambda_1 = -A_1, \lambda_2 = -A_4, \lambda_3 = -A_7,$$

Also for λ_4 and λ_5 we consider the following manipulation

$$\text{For } \lambda_4 < 0, R_{ma} < 1$$

$$(A_7 A_3 A_8 - A_7 A_1 A_9 - \lambda_4) = 0$$

$$A_7 A_3 A_8 - A_7 A_1 A_9 - \lambda_4 = 0$$

$$\lambda_4 = A_7 A_3 A_8 - A_7 A_1 A_9$$

$$\Rightarrow \lambda_4 = -A_7 A_1 A_9 \left[1 - \frac{A_7 A_3 A_8}{A_7 A_1 A_9} \right]$$

$$\Rightarrow \lambda_4 = -A_7 A_1 A_9 \left[1 - \frac{A_3 A_8}{A_1 A_9} \right]$$

$$\Rightarrow \lambda_4 = -A_7 A_1 A_9 [1 - R_{ma}^2]$$

And also for $\lambda_5 < 0, R_{zv} < 1$

$$(A_7 A_6 A_{10} - A_7 A_4 A_9 - \lambda_5) = 0$$

$$A_7 A_6 A_{10} - A_7 A_4 A_9 - \lambda_5 = 0$$

$$\lambda_5 = A_7 A_6 A_{10} - A_7 A_4 A_9$$

$$\Rightarrow \lambda_5 = -A_7 A_4 A_9 \left[1 - \frac{A_7 A_6 A_{10}}{A_7 A_4 A_9} \right]$$

$$\Rightarrow \lambda_5 = -A_7 A_4 A_9 \left[1 - \frac{A_6 A_{10}}{A_4 A_9} \right]$$

$$\Rightarrow \lambda_5 = -A_7 A_4 A_9 [1 - R_{zv}^2]$$

Finally, since all the eigenvalues of the Jacobian matrix of equation (12) are all negative, the disease free equilibrium point is locally asymptotically stable when $R_0 < 1$ ($R_{ma} < 1$ and $R_{zv} < 1$).

3.5 .GLOBAL STABILITY AT THE DISEASE FREE EQUILIBRIUM FOR COINFECTION MODEL:

Here in this section we try to prove the global stability of the disease free equilibrium.

Theorem 1.2:

The DFE (E_{mz}) of system of equation is globally asymptotically stable if $R_{mz} < 1$ and unstable if $R_{mz} > 1$

Proof : We divide the model into two submodels thus the infectious class and uninfected class by A and B . A is defined by $A = (I_m, I_z, I_{mz}, I_v, I_a)$ where we have individual infected with malaria, individual infected with zika virus, individual infected with both malaria and zika virus, infectious anopheles mosquitoes and individual infected with zika virus. In addition, B is also defined by $B = (S_h, R_m, R_z, S_m)$ which represents the susceptible individuals, individual recovered from malaria, individual recovered from zika virus, and number of susceptible mosquitoes. The above description can be represented as

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$$\left. \begin{aligned} \frac{dA}{dt} &= \chi(A, B) \\ \frac{dB}{dt} &= \gamma(A, B) \end{aligned} \right\} \dots\dots\dots(13)$$

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268 Where we define the two valued functions as $\chi(A, B)$ (dimension 5) and $\gamma(A, B)$ (dimension 4)
269 are given by

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271

272

$$\left. \begin{aligned} \chi(A, B) &= \left[\begin{aligned} &\frac{\beta_h I_v}{N_h} S_h - \frac{\sigma I_a}{N_h} I_m - (\mu_h + \eta + \tau_2) I_m + \tau_1 I_{mz}, \frac{\sigma I_a}{N_h} S_h - \frac{\beta_h I_v}{N_h} I_z - (\mu_h + \tau_1) I_z + \tau_2 I_{mz}, \\ &\frac{\sigma I_a}{N_h} I_m + \frac{\beta_h I_v}{N_h} I_z - (\mu_h + \tau_1 + \tau_2) I_{mz}, \frac{\beta_v (I_m + I_{mz})}{N_h} S_m - \mu_m I_v, \frac{\sigma_a (I_z + I_{mz})}{N_h} S_m - \mu_m I_a \end{aligned} \right]^T \\ \gamma(A, B) &= \left[\begin{aligned} &\Pi_h + \alpha R_z + \phi R_m - \mu_h S_h - \lambda_1 S_h - \lambda_2 S_h, \tau_2 I_m - (\phi + \mu_h) R_m \\ &\tau_1 I_z - (\mu_h + \alpha) R_z, \Pi_m - \mu_m S_m - \beta_1 S_m - \beta_2 S_m \end{aligned} \right]^T \end{aligned} \right\} \dots\dots\dots(14)$$

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where T is the transpose . Now the reduced form of the system : $\frac{dB}{dt} = \gamma(0, B)$

276

$$\left. \begin{aligned} \frac{dS_h}{dt} &= \Pi_h + \alpha R_z + \phi R_m - \mu_h S_h - \lambda_1 S_h - \lambda_2 S_h \\ \frac{dR_m}{dt} &= \tau_2 I_m - (\phi + \mu_h) R_m \\ \frac{dR_z}{dt} &= \tau_1 I_z - (\mu_h + \alpha) R_z \\ \frac{dS_m}{dt} &= \Pi_m - \mu_m S_m - \beta_1 S_m - \beta_2 S_m \end{aligned} \right\} \dots\dots\dots(15)$$

277

278

$B^* = (S_h^*, R_m^*, R_z^*, S_m^*) = \left(\frac{\Pi_h}{\mu_h}, 0, 0, \frac{\Pi_m}{\mu_m} \right)$ is globally asymptotically stable equilibrium point for the

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reduced form of the system $\frac{dB}{dt} = \gamma(0, B)$. To see this we solve the second and the third equations of

equation (18) to yield this result. $R_m(t) = R_m(0)e^{-(\mu_h + \phi)t}$; it turns to zero as $t \rightarrow \infty$ and

$R_z(t) = R_z(0)e^{-(\mu_h + \alpha)t}$; also turns to zero as $t \rightarrow \infty$, again the last equation of equation (31)

$S_m(t) = \frac{\Pi_m}{\mu_m} + \left\{ S_m(0) - \frac{\Pi_m}{\mu_m} \right\} e^{-\mu_m t}$ which turns to $\frac{\Pi_m}{\mu_m}$ as $t \rightarrow \infty$. lastly substitute second and third

equations of equation (31) in equation (1) of equation (31) gives

$$S_h(t) = \Pi_h + \phi \left\{ R_m(0) e^{-(\mu_h + \phi)t} \right\} + \alpha \left\{ R_z(0) e^{-(\mu_h + \alpha)t} \right\} - \mu_h \left\{ \frac{\Pi_h}{\mu_h} + \left[S_h(0) - \frac{\Pi_h}{\mu_h} \right] \right\} e^{\mu_h t} \rightarrow \frac{\Pi_h}{\mu_h}$$

as $t \rightarrow \infty$. This asymptotic dynamics is independent of initial conditions in Ω . Hence the convergence of the solution (31) is global in Ω . Truly $\chi(A, B)$ satisfies the following two conditions given as H_2 in (Carlos Castillo et al, 2002) namely

1. $\chi(0, B) = 0$ and

2. $\chi(A, B) = TA - \bar{\chi}(A, B), \bar{\chi}(A, B) \geq 0$ on Ω (16)

$$T = D_A \chi(0, B^*) = \begin{pmatrix} -\left(\mu_h + \eta + \tau_2 + \frac{\sigma I_a}{N_h} \right) & 0 & \tau_1 & \beta_h & \frac{\sigma I_m}{N_h} \\ 0 & -\left(\frac{\beta_h I_v}{N_h} + \mu_h + \tau_1 \right) & \tau_2 & -\frac{\beta_h I_z}{N_h} & \sigma \\ \frac{\sigma I_a}{N_h} & \frac{\beta_h I_v}{N_h} & -(\mu_h + \tau_1 + \tau_2) & \frac{\beta_h I_z}{N_h} & \frac{\sigma I_m}{N_h} \\ \frac{\beta_v S_m}{N_h} & 0 & \frac{\beta_v S_m}{N_h} & 0 & 0 \\ 0 & \frac{\sigma_a S_m}{N_h} & \frac{\sigma_a S_m}{N_h} & 0 & 0 \end{pmatrix}$$

At $I_m = I_z = I_{mz} = I_v = I_a = 0$

At $I_m = I_z = I_{mz} = I_v = I_a = 0$

$$T = D_A \chi(0, B^*) = \begin{pmatrix} -(\mu_h + \eta + \tau_2) & 0 & \tau_1 & \beta_h & 0 \\ 0 & -(\mu_h + \tau_1) & \tau_2 & 0 & \sigma \\ 0 & 0 & -(\mu_h + \tau_1 + \tau_2) & 0 & 0 \\ \frac{\beta_v S_m}{N_h} & 0 & \frac{\beta_v S_m}{N_h} & 0 & 0 \\ 0 & \frac{\sigma_a S_m}{N_h} & \frac{\sigma_a S_m}{N_h} & 0 & 0 \end{pmatrix}$$

294 And

295

$$296 \quad \hat{\chi}(A, B) = \begin{pmatrix} \hat{\chi}_1(A, B) \\ \hat{\chi}_2(A, B) \\ \hat{\chi}_3(A, B) \\ \hat{\chi}_4(A, B) \\ \hat{\chi}_5(A, B) \end{pmatrix} = \begin{pmatrix} \beta_h I_v \left(1 - \frac{S_h}{N_h}\right) + \lambda_2 I_m \\ \lambda_2 I_a \left(1 - \frac{S_h}{N_h}\right) + \lambda_1 I_z \\ -(\lambda_1 I_z + \lambda_2 I_m) \\ \frac{\beta_v (I_m + I_{mz})}{N_h} \left(1 - \frac{S_m}{N_m}\right) \\ \frac{\sigma_a (I_z + I_{mz})}{N_h} \left(1 - \frac{S_m}{N_m}\right) \end{pmatrix}$$

297 Since $\hat{\chi}_3(A, B) < 0$ and does not completely satisfy the two conditions stated in equation (16), the
298 disease free equilibrium may not globally asymptotically stable.

299

300 **3.6 Existence of endemic equilibrium point of the Coinfection Malaria and Zika virus** Endemic
301 equilibrium point is the steady state solution where the disease (malaria and zika virus) exists in the
302 population. In other words, the disease is rampant in the population. We denote the endemic
303 equilibrium point of the coinfection model by E_{mz}^{**} and is given by

$$304 \quad E_{mz}^{**} = (S_h^{**}, I_m^{**}, I_z^{**}, I_{mz}^{**}, R_m^{**}, R_z^{**}, S_m^{**}, I_v^{**}, I_a^{**})$$

305 **3.7. Global Stability Of Endemic Equilibrium of coinfection (Malaria And Zika) model:** Here in this
306 section we try to prove the global stability of the endemic equilibrium.

307

308 **Theorem 1.3.**

309 **If** $R_{ma} > 1$ then the unique endemic equilibrium E_{mz}^{**} of System (3) is globally stable in the interior of
310 Ω .

311

312 **Proof**

313 This can be determined by constructing Logarithmic Lyapunov function $L(t)$ such that

314 $S_h \leq S_h^{**}, I \leq I_m^{**}, I \leq I_z^{**}, I \leq I_{mz}^{**}, R \leq R_m^{**}, R \leq R_z^{**}, S \leq S_m^{**}, I \leq I_v^{**}$ and $I \leq I_a^{**}$ and $L(t)$ is given as

$$\begin{aligned}
 L(t) = & \frac{1}{(\mu_h + \lambda_1 + \lambda_2)} \left(S_h^* S_h - S_h - S_h^* \ln \frac{S_h}{S_h^*} \right) + \frac{1}{(\mu_h + \eta + \tau_2 + \lambda_2)} \left(I_m^* I_m - I_m - I_m^* \ln \frac{I_m}{I_m^*} \right) \\
 & + \frac{1}{(\mu_h + \lambda_1 + \tau_1)} \left(I_z^* I_z - I_z - I_z^* \ln \frac{I_z}{I_z^*} \right) + \frac{1}{(\mu_h + \tau_1 + \tau_2)} \left(I_{mz}^* I_{mz} - I_{mz} - I_{mz}^* \ln \frac{I_{mz}}{I_{mz}^*} \right) \\
 & + \frac{1}{(\phi + \mu_h)} \left(R_m^* R_m - R_m - R_m^* \ln \frac{R_m}{R_m^*} \right) + \frac{1}{(\mu_h + \alpha)} \left(R_z^* R_z - R_z - R_z^* \ln \frac{R_z}{R_z^*} \right) \\
 & \frac{1}{(\mu_m + \beta_1 + \beta_2)} \left(S_m^* S_m - S_m - S_m^* \ln \frac{S_m}{S_m^*} \right) + \frac{1}{\mu_m} \left(I_v^* I_v - I_v - I_v^* \ln \frac{I_v}{I_v^*} \right) + \frac{1}{\mu_h} \left(I_a^* I_a - I_a - I_a^* \ln \frac{I_a}{I_a^*} \right) \dots\dots\dots (17)
 \end{aligned}$$

we take the derivative of $L(t)$ with respect to the state variables which is given as

$$\begin{aligned}
 \frac{dL}{dS_h} &= \frac{1}{(\mu_h + \lambda_1 + \lambda_2)} \left(S_h^* - 1 - \frac{1}{S_h} \right) = \frac{1}{(\mu_h + \lambda_1 + \lambda_2)} \left(\frac{S_h^* S_h - S_h - 1}{S_h} \right) \\
 \frac{dL}{dI_m} &= \frac{1}{(\mu_h + \lambda_2 + \tau_2 + \eta)} \left(I_m^* - 1 - \frac{1}{I_m} \right) = \frac{1}{(\mu_h + \lambda_2 + \tau_2 + \eta)} \left(\frac{I_m^* I_m - I_m - 1}{I_m} \right) \\
 \frac{dL}{dI_z} &= \frac{1}{(\mu_h + \lambda_1 + \tau_1)} \left(I_z^* - 1 - \frac{1}{I_z} \right) = \frac{1}{(\mu_h + \lambda_1 + \tau_1)} \left(\frac{I_z^* I_z - I_z - 1}{I_z} \right) \\
 \frac{dL}{dI_{mz}} &= \frac{1}{(\mu_h + \tau_1 + \tau_2)} \left(I_{mz}^* - 1 - \frac{1}{I_{mz}} \right) = \frac{1}{(\mu_h + \tau_1 + \tau_2)} \left(\frac{I_{mz}^* I_{mz} - I_{mz} - 1}{I_{mz}} \right) \\
 \frac{dL}{dR_m} &= \frac{1}{(\mu_h + \phi)} \left(R_m^* - 1 - \frac{1}{R_m} \right) = \frac{1}{(\mu_h + \phi)} \left(\frac{R_m^* R_m - R_m - 1}{R_m} \right) \\
 \frac{dL}{dR_z} &= \frac{1}{(\mu_h + \alpha)} \left(R_z^* - 1 - \frac{1}{R_z} \right) = \frac{1}{(\mu_h + \alpha)} \left(\frac{R_z^* R_z - R_z - 1}{R_z} \right) \\
 \frac{dL}{dS_m} &= \frac{1}{(\mu_h + \beta_1 + \beta_2)} \left(S_m^* - 1 - \frac{1}{S_m} \right) = \frac{1}{(\mu_h + \beta_1 + \beta_2)} \left(\frac{S_m^* S_m - S_m - 1}{S_m} \right) \\
 \frac{dL}{dI_v} &= \frac{1}{\mu_m} \left(I_v^* - 1 - \frac{1}{I_v} \right) = \frac{1}{\mu_m} \left(\frac{I_v^* I_v - I_v - 1}{I_v} \right) \\
 \frac{dL}{dI_a} &= \frac{1}{\mu_m} \left(I_a^* - 1 - \frac{1}{I_a} \right) = \frac{1}{\mu_m} \left(\frac{I_a^* I_a - I_a - 1}{I_a} \right)
 \end{aligned}$$

321 We then find the derivative of $L(t)$ with respect to the state variables. Thus

$$\begin{aligned}
 322 \quad \frac{dL}{dt} &= \frac{\partial L}{\partial S_h} \frac{dS_h}{dt} + \frac{\partial L}{\partial I_m} \frac{dI_m}{dt} + \frac{\partial L}{\partial I_z} \frac{dI_z}{dt} + \frac{\partial L}{\partial I_{mz}} \frac{dI_{mz}}{dt} + \frac{\partial L}{\partial R_m} \frac{dR_m}{dt} + \frac{\partial L}{\partial R_z} \frac{dR_z}{dt} + \frac{\partial L}{\partial S_m} \frac{dS_m}{dt} + \frac{\partial L}{\partial I_v} \frac{dI_v}{dt} + \frac{\partial L}{\partial I_a} \frac{dI_a}{dt} \\
 323 \quad \frac{dL}{dt} &= \frac{1}{(\mu_h + \lambda_1 + \lambda_2)} \left(\frac{S_h^* S_h - S_h - 1}{S_h} \right) [-(\mu_h + \lambda_1 + \lambda_2) S_h] \\
 &+ \frac{1}{(\mu_h + \lambda_2 + \tau_2 + \eta)} \left(\frac{I_m^* I_m - I_m - 1}{I_m} \right) [-(\mu_h + \lambda_2 + \tau_2 + \eta) I_m] \\
 &+ \frac{1}{(\mu_h + \lambda_1 + \tau_1)} \left(\frac{I_z^* I_z - I_z - 1}{I_z} \right) [-(\mu_h + \lambda_1 + \tau_1) I_z] \\
 &+ \frac{1}{(\mu_h + \tau_1 + \tau_2)} \left(\frac{I_{mz}^* I_{mz} - I_{mz} - 1}{I_{mz}} \right) [-(\mu_h + \tau_1 + \tau_2) I_{mz}] \\
 &+ \frac{1}{(\mu_h + \phi)} \left(\frac{R_m^* R_m - R_m - 1}{R_z} \right) [-(\mu_h + \phi)] \\
 &+ \frac{1}{(\mu_h + \alpha)} \left(\frac{R_z^* R_z - R_z - 1}{R_z} \right) [-(\mu_h + \alpha)] \\
 324 \quad &+ \frac{1}{(\mu_h + \beta_1 + \beta_2)} \left(\frac{S_m^* S_m - S_m - 1}{S_m} \right) [-(\mu_h + \beta_1 + \beta_2)] \\
 &+ \frac{1}{\mu_m} \left(\frac{I_v^* I_v - I_v - 1}{I_v} \right) [-\mu_m] \\
 &+ \frac{1}{\mu_m} \left(\frac{I_a^* I_a - I_a - 1}{I_a} \right) [-\mu_m]
 \end{aligned}$$

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326

$$\begin{aligned}
 &\Rightarrow \frac{dL}{dt} = -(S_h^* S_h - S_h - 1) - (I_m^* I_m - I_m - 1) - (I_z^* I_z - I_z - 1) - (I_{mz}^* I_{mz} - I_{mz} - 1) - (R_m^* R_m - R_m - 1) \\
 &\quad - (R_z^* R_z - R_z - 1) - (S_m^* S_m - S_m - 1) - (I_v^* I_v - I_v - 1) - (I_a^* I_a - I_a - 1) \\
 &\Rightarrow \frac{dL}{dt} = -S_h^* S_h + S_h + 1 - I_m^* I_m + I_m + 1 - I_z^* I_z + I_z + 1 - I_{mz}^* I_{mz} + I_{mz} + 1 - R_m^* R_m + R_m + 1 - R_z^* R_z + R_z + 1 \\
 &\quad - S_m^* S_m + S_m + 1 - I_v^* I_v + I_v + 1 - I_a^* I_a + I_a + 1 \\
 &\Rightarrow \frac{dL}{dt} = 1 + 1 + 1 + 1 + 1 + 1 + 1 + 1 + 1 + S_h(1 - S_h^*) + I_m(1 - I_m^*) + I_z(1 - I_z^*) + I_{mz}(1 - I_{mz}^*) \\
 &\quad + R_m(1 - R_m^*) + R_z(1 - R_z^*) + S_m(1 - S_m^*) + I_v(1 - I_v^*) + I_a(1 - I_a^*) \\
 &\Rightarrow \frac{dL}{dt} = 9 + S_h(1 - S_h^*) + I_m(1 - I_m^*) + I_{mz}(1 - I_{mz}^*) + I_z(1 - I_z^*) + R_m(1 - R_m^*) + R_z(1 - R_z^*) \\
 &\quad + S_m(1 - S_m^*) + I_v(1 - I_v^*) + I_a(1 - I_a^*) \leq 0
 \end{aligned}$$

Theorem 1.4

If a function is positive definite on the entire state space, and has the additional property that $|V(x)| \rightarrow \infty$ as $\|x\| \rightarrow \infty$, and if its derivative $\dot{V}$ is negative definite on the entire state space, then the equilibrium point at the origin is globally asymptotically stable (Bonyah, 2014).

Therefore $\dot{V} \leq 0$ and by the LaSalle's Extension (LaSalle's, 1976), it implies that the omega limit set of each solution lies in an invariant set contained in Ω . The only invariant set contained in Ω is the singleton E_{ma}^{**} . This shows that each solution which intersects R_+^5 limits to the endemic equilibrium and that trivial equilibrium is globally asymptotically stable in the invariant feasible region. This ends the proof of global stability.

3.8. Malaria only model: Here, we consider the malaria model only

$$\left. \begin{aligned}
 \frac{dS_h}{dt} &= \Pi_h + \phi R_m - \mu_h S_h - \lambda_1 S_h \\
 \frac{dI_m}{dt} &= \lambda_1 S_h - (\mu_h + \eta + \tau_2) I_m \\
 \frac{dR_m}{dt} &= \tau_2 I_m - (\phi + \mu_h) R_m \\
 \frac{dS_m}{dt} &= \Pi_m - \mu_m S_m - \beta_1 S_m \\
 \frac{dI_v}{dt} &= \beta_1 S_m - \mu_m I_v
 \end{aligned} \right\} \dots\dots\dots (18)$$

$$\lambda_1 = \frac{\beta_h I_v}{N_h} \text{ and } \beta_1 = \frac{\beta_v I_m}{N_h}$$

Insect the force of infection into (34) gives

Now the disease free equilibrium point of malaria is given as

$$E_{ma}^* = (S_h^*, I_m^*, R_m^*, S_m^*, I_v^*) = \left(\frac{\Pi_h}{\mu_h}, 0, 0, \frac{\Pi_m}{\mu_m}, 0 \right) \dots \dots \dots (19)$$

3.9. Basic Reproduction Number for Malaria only (R_{ma})

Rewriting the system (18) starting from the infected disease I_m, I_v and uninfected classes ;

$$\left. \begin{aligned} \frac{dI_m}{dt} &= \frac{\beta_h I_v}{N_h} S_h - (\mu_h + \eta + \tau_2) I_m \\ \frac{dI_v}{dt} &= \frac{\beta_v I_m}{N_h} S_m - \mu_m I_v \\ \frac{dR_m}{dt} &= \tau_2 I_m - (\phi + \mu_h) R_m \\ \frac{dS_h}{dt} &= \Pi_h + \phi R_m - \mu_h S_h - \frac{\beta_h I_v}{N_h} S_h \\ \frac{dS_m}{dt} &= \Pi_m - \mu_m S_m - \frac{\beta_v I_m}{N_h} S_m \end{aligned} \right\} \dots \dots \dots (20)$$

We identify the matrices F and V for the new infection terms and the remaining transfer terms at the disease free equilibrium using the next generation operator method as described by (P.van den Driessche and J.Watmough,2002) respectively

$$f = \begin{vmatrix} \frac{\beta_h I_v}{N_h} S_h \\ \frac{\beta_v I_m}{N_h} S_m \end{vmatrix} \text{ and } v = \begin{vmatrix} (\mu_h + \eta + \tau_2) I_m \\ \mu_m I_v \end{vmatrix}$$

The Jacobian matrix of F and V are given as

$$F = \begin{vmatrix} 0 & \beta_h \\ \frac{\beta_v \Pi_m \mu_h}{\Pi_h \mu_m} & 0 \end{vmatrix} \text{ and } V = \begin{vmatrix} (\mu_h + \eta + \tau_2) & 0 \\ 0 & \mu_m \end{vmatrix}$$

Inverse of V^1 (inverse V^{-1})

$$V^{-1} = \frac{1}{\mu_m (\mu_h + \eta + \tau_2)} \begin{vmatrix} \mu_m & 0 \\ 0 & (\mu_h + \eta + \tau_2) \end{vmatrix} = \begin{vmatrix} \frac{1}{(\mu_h + \eta + \tau_2)} & 0 \\ 0 & \frac{1}{\mu_m} \end{vmatrix}$$

$$F^1 V^{-1} = \begin{vmatrix} 0 & \beta_h \\ \frac{\beta_v \Pi_m \mu_h}{\Pi_h \mu_m} & 0 \end{vmatrix} \begin{vmatrix} \frac{1}{(\mu_h + \eta + \tau_2)} & 0 \\ 0 & \frac{1}{\mu_m} \end{vmatrix}$$

$$F^1 V^{-1} = \begin{vmatrix} 0 & \frac{\beta_h}{\mu_m} \\ \frac{\beta_v \Pi_m \mu_h}{\Pi_h \mu_m (\mu_h + \eta + \tau_2)} & 0 \end{vmatrix}$$

The basic reproduction number of malaria only is denoted by (R_{ma}) and is given as

$$R_{ma} = \sqrt{\frac{\beta_h \beta_v \Pi_m \mu_h}{\Pi_h \mu_m^2 (\mu_h + \eta + \tau_2)}} \dots \dots \dots (21)$$

3.10. Local Stability Of Disease Free Equilibrium Point for Malaria only

Theorem1.5:

The disease free equilibrium point is locally asymptotically stable if $\mathfrak{R}_{ma} < 1$ and unstable if $\mathfrak{R}_{ma} > 1$.

$$J(E_{ma}) = \begin{vmatrix} -\mu_h & 0 & \phi & 0 & \beta_h \\ 0 & -(\mu_h + \eta + \tau_2) & 0 & 0 & \beta_h \\ 0 & \tau_2 & -(\mu_h + \phi) & 0 & 0 \\ 0 & -\frac{\beta_v \Pi_m \mu_h}{\Pi_h \mu_m} & 0 & -\mu_m & 0 \\ 0 & \frac{\beta_v \Pi_m \mu_h}{\Pi_h \mu_m} & 0 & 0 & -\mu_m \end{vmatrix} \dots \dots \dots (22)$$

The diagonal entries $-\mu_h$ and $-\mu_m$ are the two of the eigenvalus of the Jacobian matrix. This means that two columns and their corresponding rows can be excluded . Hence we have

$$J(E_{ma}) = \begin{vmatrix} -(\mu_h + \eta + \tau_2) & 0 & \beta_h \\ \tau_2 & -(\mu_h + \phi) & 0 \\ \frac{\beta_v \Pi_m \mu_h}{\Pi_h \mu_m} & 0 & -\mu_m \end{vmatrix}$$

The diagonal entry $-(\mu_h + \phi)$ is one of the eigenvalues of the Jacobian matrix. Hence we have

$$J(E_{ma}) = \begin{pmatrix} -(\mu_h + \eta + \tau_2) & \beta_h \\ \frac{\beta_v \Pi_m \mu_h}{\Pi_h \mu_m} & -\mu_m \end{pmatrix} \dots \dots \dots (23)$$

From equation (23) we obtain

$$\det(J) = \mu_m (\mu_h + \eta + \tau_2) - \frac{\beta_h \beta_v \Pi_m \mu_h}{\Pi_h \mu_m}$$

$$\text{tr}(J) = -(\mu_h + \eta + \tau_2 + \mu_m) < 0$$

Consider

$$\det(J) = \mu_m (\mu_h + \eta + \tau_2) - \frac{\beta_h \beta_v \Pi_m \mu_h}{\Pi_h \mu_m}$$

Dividing the terms by gives

$$\det = \frac{\mu_m (\mu_h + \eta + \tau_2)}{\mu_m (\mu_h + \eta + \tau_2)} - \frac{\beta_h \beta_v \Pi_m \mu_h}{(\mu_h + \eta + \tau_2) \Pi_h \mu_m^2} = 1 - R_{ma}^2 \dots \dots \dots (24)$$

if $R_{ma} < 1$ in (24), then the determinant is greater than zero ($\det > 0$).

Since the trace is negative ($\text{tr} < 0$) and $\det > 0$ if $R_{ma} < 1$, then the disease free is locally asymptotically stable.

3.11.Global stability on DFE Malaria only(E_{ma}) : Here in this section we try to prove the global stability of the disease free equilibrium.

Theorem 1.6:

The DFE(E_{ma}) of system of equation(20) is globally asymptotically stable if $R_{ma} < 1$ and unstable if $R_{ma} > 1$

roof :We start the proof by dividing (20) into two sub-models ,that is ,the infectious class and uninfected class which are denoted as W and V respectively .The variables W and V are defined as, $W = (I_m, I_v)$ and $V = (S_h, R_m, S_m)$ respectively. Therefore the model (20) can be written as

$$\left. \begin{aligned} \frac{dW}{dt} &= E(V, W) \\ \frac{dV}{dt} &= F(V, W) \end{aligned} \right\} \dots\dots\dots (25)$$

The two valued functions $E(V, W)$ (dimension 2) and $F(V, W)$ (dimension 3) are given by

$$\left. \begin{aligned} E(V, W) &= \left(\frac{\beta_h I_v}{N_h} S_h - (\eta + \mu_h + \tau_2) I_m, \frac{\beta_v I_m}{N_h} S_m - \mu_m I_v \right)^T \\ F(V, W) &= \left(\Pi_h + \phi R_m - \mu_h S_h - \frac{\beta_h I_m}{N_h} S_h, \tau_2 I_m - (\phi + \mu_h) R_m, \Pi_m - \mu_m S_m - S_m \beta_1 \right)^T \end{aligned} \right\} \dots\dots\dots (26)$$

Where T is transpose .Now consider the reduced system: $\frac{dV}{dt} = F(V, 0)$

$$\left. \begin{aligned} \frac{dS_h}{dt} &= \Pi_h + \phi R_m - \mu_h S_h \\ \frac{dR_m}{dt} &= \tau_2 I_m - (\mu_h + \phi) R_m \\ \frac{dS_m}{dt} &= \beta_1 S_m - \mu_m I_v \end{aligned} \right\} \dots\dots\dots (27)$$

$V^* = (S_h^*, R_m^*, S_m^*) = \left(\frac{\Pi_h}{\mu_h}, 0, \frac{\Pi_m}{\mu_m} \right)$ is a globally asymptotically stable equilibrium point for the reduced

system $\frac{dV}{dt} = F(V, 0)$. To see this ,solve the second equation in (27) to obtain

$R_m(t) = R_m(0)e^{-(\mu_h + \phi)t}$; it turns to zero as $t \rightarrow \infty$. In the same way , the last equation

gives $S_m(t) = \frac{\Pi_m}{\mu_m} + \left\{ S_m(0) - \frac{\Pi_m}{\mu_m} \right\} e^{\mu_m t}$ which turns to $\frac{\Pi_m}{\mu_m}$ as $t \rightarrow \infty$ Finally, the first

equation of (27) gives

$$S_h(t) = \frac{\Pi_h}{\mu_h} + \frac{\phi}{\mu_h} \left\{ R_m(0)e^{-(\mu_h + \phi)t} \right\} - \left\{ \frac{\Pi_h}{\mu_h} + \left[S_h(0) - \frac{\Pi_h}{\mu_h} \right] \right\} e^{\mu_h t} \rightarrow \frac{\Pi_h}{\mu_h} \text{ as } t \rightarrow \infty . \text{ This}$$

asymptotic dynamics is independent of initial conditions in Ω .Hence the convergence of the solution (27) is global in Ω . Clearly $E(V, W)$ satisfies the following two conditions given as H_2 in (Carlos Castillo et al,2002) .namely

1) $E(V, 0) = 0$ and

2) $E(V, W) = AW - \bar{E}(V, W), \bar{E}(V, W) \geq 0$ on Ω where

$$A = D_W E(V^*, 0) = \begin{pmatrix} -(\eta + \mu_t + \tau_2) & \beta_h \\ \frac{\beta_v S_m}{N_h} & -\mu_m \end{pmatrix} \text{ and}$$

417

$$418 \quad \bar{E}(V, W) = \begin{pmatrix} \bar{E}_1(V, W) \\ \bar{E}_2(V, W) \end{pmatrix} = \begin{pmatrix} \beta_h I_v \left[1 - \frac{S_h}{N_h} \right] \\ \beta_v I_m \left[1 - \frac{S_m}{N_h} \right] \end{pmatrix}$$

419 Since the terms in $\bar{E}(V, W)$ are nonnegative and the conditions H_2 given in (Carlos Castillo et
420 al,2002) also satisfied,we can conclude that the disease free equilibrium of malaria is globally
421 asymptotically stable.

422

423 **3.12. Existence of endemic equilibrium point for Malaria only :**endemic equilibrium point is
424 the steady state solution where the disease (malaria) is present in the population.In order words
425 ,the disease is rampant in the population. We denote the endemic equilibrium point by E_{ma}^{**} and
426 is given by

$$427 \quad E_{ma}^{**} = (S_h^{**}, I_m^{**}, R_m^{**}, S_m^{**}, I_v^{**}) \dots \dots \dots (28)$$

428 To evaluate E_{ma}^{**} , we solve the model (20) by equating it to zero.

429 Let

430

$$431 \quad A_1 = \beta_h, A_2 = \frac{\beta_v S_m}{N_h}, A_3 = (\mu_h + \eta + \tau_2), A_4 = \mu_m, A_5 = (\phi + \mu_h)$$

432

433 This gives the result as follows

434

$$S_h^{**} = \frac{(N_h A_1 A_2 A_4 A_5^2 \Pi_h - R_{ma}^2 A_4^2 A_5 N_h \Pi_h \phi \tau_2 + N_h \alpha \tau_2 (R_{ma}^2 - 1) A_4^2 A_5 \Pi_h)}{A_1 A_2 A_4 A_5^2 (R_{ma}^2 - 1) \Pi_h + \mu_h N_h A_4 (A_1 A_2 A_5 - R_{ma}^2 A_4 \tau_2 \phi)}$$

$$I_m^{**} = \frac{(R_{ma}^2 - 1) A_4 A_5 \Pi_h}{A_1 A_2 A_5 - R_{ma}^2 A_4 \tau_2 \phi}$$

$$435 \quad R_{ma}^2 = \frac{(R_{ma}^2 - 1) A_4 A_5 \Pi_h \tau_2}{A_1 A_2 A_5^2 - R_{ma}^2 A_4 A_5 \tau_2 \phi}$$

$$S_m^{**} = \frac{\Pi_m (A_1 A_2 A_5 - R_{ma}^2 A_4 \tau_2 \phi) - (R_{ma}^2 - 1) A_2 A_4 A_5 \Pi_h}{A_1 A_2 A_5^2 - R_{ma}^2 A_4 A_5 \tau_2 \phi}$$

$$I_v^{**} = \frac{(R_{ma}^2 - 1) A_2 A_4 A_5 \Pi_h}{A_1 A_2 A_4 A_5 - R_{ma}^2 A_4^2 \tau_2 \phi}$$

436

437 On the existence of the endemic equilibrium the following results are obtained:

438 **Theorem1.7:**

439 System (20) has a unique endemic equilibrium E_{ma}^{**} point when $R_{ma} > 1$.

440

3.13. Global Stability Of Endemic Equilibrium Of Malaria model only : Here in this section we try to prove the global stability of the endemic equilibrium of Malaria model only .

Theorem 1.8:

If $R_{ma} > 1$ then the unique endemic equilibrium E_{ma}^{**} of System (20) globally stable in the interior of Ω .

Proof

This can be determined by constructing Logarithmic Lyapunov function $L(t)$ such that

$S_h \leq S_h^*, I \leq I_m^*, R \leq R_m^*, S \leq S_m^*$ and $I \leq I_v^*$ and $L(t)$ is given as

$$L(t) = \frac{1}{(\mu_h + \lambda_1)} \left(S_h^* S_h - S_h - S_h^* \ln \frac{S_h}{S_h^*} \right) + \frac{1}{(\mu_h + \eta + \tau_2)} \left(I_m^* I_m - I_m - I_m^* \ln \frac{I_m}{I_m^*} \right) +$$

$$\frac{1}{(\mu_h + \beta_1)} \left(R_m^* R_m - R_m - R_m^* \ln \frac{R_m}{R_m^*} \right) + \frac{1}{(\mu_h + \phi)} \left(S_m^* S_m - S_m - S_m^* \ln \frac{S_m}{S_m^*} \right) + \frac{1}{\mu_h} \left(I_v^* I_v - I_v - I_v^* \ln \frac{I_v}{I_v^*} \right) \dots (29)$$

we take the derivative of $L(t)$ with respect to the state variables which is given as

$$\frac{dL}{dS_h} = \frac{1}{(\mu_h + \lambda_1)} \left(S_h^* - 1 - \frac{1}{S_h} \right) = \frac{1}{(\mu_h + \lambda_1)} \left(\frac{S_h^* S_h - S_h - 1}{S_h} \right)$$

$$\frac{dL}{dI_m} = \frac{1}{(\mu_h + \eta + \tau_2)} \left(I_m^* - 1 - \frac{1}{I_m} \right) = \frac{1}{(\mu_h + \eta + \tau_2)} \left(\frac{I_m^* I_m - I_m - 1}{I_m} \right)$$

$$\frac{dL}{dR_m} = \frac{1}{(\mu_h + \phi)} \left(R_m^* - 1 - \frac{1}{R_m} \right) = \frac{1}{(\mu_h + \phi)} \left(\frac{R_m^* R_m - R_m - 1}{R_m} \right)$$

$$\frac{dL}{dS_m} = \frac{1}{(\mu_h + \beta_1)} \left(S_m^* - 1 - \frac{1}{S_m} \right) = \frac{1}{(\mu_h + \beta_1)} \left(\frac{S_m^* S_m - S_m - 1}{S_m} \right)$$

$$\frac{dL}{dI_v} = \frac{1}{\mu_h} \left(I_v^* - 1 - \frac{1}{I_v} \right) = \frac{1}{\mu_h} \left(\frac{I_v^* I_v - I_v - 1}{I_v} \right)$$

We then find the derivative of $L(t)$ with respect to the state variables. Thus

$$\frac{dL}{dt} = \frac{\partial L}{\partial S_h} \frac{dS_h}{dt} + \frac{\partial L}{\partial I_m} \frac{dI_m}{dt} + \frac{\partial L}{\partial R_m} \frac{dR_m}{dt} + \frac{\partial L}{\partial S_m} \frac{dS_m}{dt} + \frac{\partial L}{\partial I_v} \frac{dI_v}{dt}$$

$$\frac{dL}{dt} = \frac{1}{(\mu_h + \lambda_1)} \left(\frac{S_h^* S_h - S_h - 1}{S_h} \right) [-(\mu_h + \lambda_1) S_h]$$

$$+ \frac{1}{(\mu_h + \eta + \tau_2)} \left(\frac{I_m^* I_m - I_m - 1}{I_m} \right) [-(\mu_h + \eta + \tau_2) I_m]$$

$$\begin{aligned}
 & + \frac{1}{(\mu_h + \phi)} \left(\frac{R_m^* R_m - R_m - 1}{R_m} \right) [-(\mu_h + \phi) R_m] \\
 & + \frac{1}{(\mu_h + \beta_1)} \left(\frac{S_m^* S_m - S_m - 1}{S_m} \right) [-(\mu_h + \beta_1) S_m] + \frac{1}{\mu_h} \left(\frac{I_v^* I_v - I_v - 1}{I_v} \right) [-\mu_h I_v] \\
 \Rightarrow \frac{dL}{dt} & = - (S_h^* S_h - S_h - 1) - (I_m^* I_m - I_m - 1) - (R_m^* R_m - R_m - 1) - (S_m^* S_m - S_m - 1) - (I_v^* I_v - I_v - 1) \\
 \Rightarrow \frac{dL}{dt} & = -S_h^* S_h + S_h + 1 - I_m^* I_m + I_m + 1 - R_m^* R_m + R_m + 1 - S_m^* S_m + S_m + 1 - I_v^* I_v + I_v + 1 \\
 \Rightarrow \frac{dL}{dt} & = 1 + 1 + 1 + 1 + 1 + S_h (1 - S_h^*) + I_m (1 - I_m^*) + R_m (1 - R_m^*) + S_m (1 - S_m^*) + I_v (1 - I_v^*) \leq 0
 \end{aligned}$$

Theorem 1.13

If a function is positive definite on the entire state space, and has the additional property that $|V(x)| \rightarrow \infty$ as $\|x\| \rightarrow \infty$, and if its derivative V is negative definite on the entire state space, then the equilibrium point at the origin is globally asymptotically stable (Bonyah, 2014).

Therefore $\dot{V} \leq 0$ and by the LaSalle's Extension (LaSalle's, 1976), it implies that the omega limits set of each solution lies in an invariant set contained in Ω . The only invariant set contained in Ω is the singleton E_{ma}^{**} . This shows that each solution which intersects R_+^5 limits to the endemic equilibrium and that trivial equilibrium is globally asymptotically stable in the invariant feasible region. This ends the proof of global stability.

3.14. Zika virus model only

$$\left. \begin{aligned}
 \frac{dS_h}{dt} &= \Pi_h + \alpha R_z - \mu_h S_h - \lambda_2 S_h \\
 \frac{dI_z}{dt} &= \lambda_2 S_h - (\mu_h + \tau_1) I_z \\
 \frac{dR_z}{dt} &= \tau_1 I_z - (\mu_h + \alpha) R_z \\
 \frac{dS_m}{dt} &= \Pi_m - \mu_m S_m - \beta_2 S_m \\
 \frac{dI_a}{dt} &= \beta_2 S_m - \mu_m I_a
 \end{aligned} \right\} \dots \dots \dots (30).$$

With the force of infection

$$\lambda_2 = \frac{\sigma I_a}{N_h} \text{ and } \beta_2 = \frac{\sigma_a I_z}{N_h} \dots \dots \dots (31)$$

$$\left. \begin{aligned}
 \frac{dS_h}{dt} &= \Pi_h + \alpha R_z - \mu_h S_h - \frac{\sigma I_a}{N_h} S_h \\
 \frac{dI_z}{dt} &= \frac{\sigma I_a}{N_h} S_h - (\mu_h + \tau_1) I_z \\
 \frac{dR_z}{dt} &= \tau_1 I_z - (\mu_h + \alpha) R_z \\
 \frac{dS_m}{dt} &= \Pi_m - \mu_m S_m - \frac{\sigma_a I_z}{N_h} S_m \\
 \frac{dI_a}{dt} &= \frac{\sigma_a I_z}{N_h} S_m - \mu_m I_a
 \end{aligned} \right\} \dots\dots\dots (49)$$

The zika virus model only of model (30) has a disease free equilibrium point given as

$$E_{zv} = (S_h^*, I_z^*, R_z^*, S_m^*, I_a^*) = \left(\frac{\Pi_h}{\mu_h}, 0, 0, \frac{\Pi_m}{\mu_m}, 0 \right) \dots\dots\dots (32)$$

3.15.Local Stability Of Disease Free Equilibrium Point for Zika virus

Theorem1.14:

The disease free equilibrium point is locally asymptotically stable if $\mathfrak{R}_{zv} < 1$ and unstable if $\mathfrak{R}_{zv} > 1$.

$$J(E_{zv}) = \begin{vmatrix} -\mu_h & 0 & \alpha & 0 & \sigma \\ 0 & -(\mu_h + \tau_1) & 0 & 0 & \sigma \\ 0 & \tau_1 & -(\mu_h + \alpha) & 0 & 0 \\ 0 & -\frac{\sigma_a \Pi_m \mu_h}{\Pi_h \mu_m} & 0 & -\mu_m & 0 \\ 0 & \frac{\sigma_a \Pi_m \mu_h}{\Pi_h \mu_m} & 0 & 0 & -\mu_m \end{vmatrix} \dots\dots\dots (33)$$

The diagonal entries $-\mu_h$ and $-\mu_m$ are the two of the eigenvalue of the Jacobian matrix. This means that two columns and their corresponding rows can be excluded. Hence we have (Mwantobe,2014)

$$J(E_{zv}) = \begin{vmatrix} -(\mu_h + \tau_1) & 0 & \sigma \\ \tau_2 & -(\mu_h + \alpha) & 0 \\ \frac{\sigma_a \Pi_m \mu_h}{\Pi_h \mu_m} & 0 & -\mu_m \end{vmatrix}$$

Which also leads to

494

$$495 \quad J(E_{zv}) = \begin{pmatrix} -(\mu_h + \tau_1) & \sigma \\ \frac{\sigma \sigma_a \Pi_m \mu_h}{\Pi_h \mu_m} & -\mu_m \end{pmatrix} \dots \dots \dots (34)$$

496 which gives

$$497 \quad \det(J) = \mu_m (\mu_h + \tau_1) - \frac{\sigma \sigma_a \Pi_m \mu_h}{\Pi_h \mu_m} \text{ and}$$

$$498 \quad \text{tr}(J) = -(\mu_h + \tau_1 + \mu_m) < 0$$

499 Consider

$$500 \quad \det(J) = \mu_m (\mu_h + \tau_1) - \frac{\sigma \sigma_a \Pi_m \mu_h}{\Pi_h \mu_m} \dots \dots \dots (35)$$

501 Dividing the terms by gives

$$502 \quad \det(J) = \frac{\mu_m (\mu_h + \tau_1)}{\mu_m (\mu_h + \tau_1)} - \frac{\sigma \sigma_a \Pi_m \mu_h}{(\mu_h + \tau_1) \Pi_h \mu_m^2}$$

$$503 \quad \det(J) = \frac{\mu_m (\mu_h + \tau_1)}{\mu_m (\mu_h + \tau_1)} - \frac{\sigma \sigma_a \Pi_m \mu_h}{(\mu_h + \tau_1) \Pi_h \mu_m^2} = 1 - \frac{\sigma \sigma_a \Pi_m \mu_h}{(\mu_h + \tau_1) \Pi_h \mu_m^2} = 1 - R_{zv}^2 \dots \dots \dots (36)$$

504 if $R_{zv} < 1$ in (36), then the determinant is greater than zero ($\det > 0$).

505 since the trace is negative ($\text{tr} < 0$) and $\det > 0$ if $R_{zv} < 1$, then the disease free equilibrium point of

506 Zika virus is locally asymptotically stable

507 3.16 Global stability of disease free equilibrium of Zika Virus

508

509 **Theorem 1.15** : The DFE (E_{zv}) of system of equation (30) is globally asymptotically
510 stable if $R_{zv} < 1$ and unstable if $R_{zv} > 1$

511 Proof : We start the proof by dividing (30) into two sub-models, that is, the infectious class and
512 uninfected class which are denoted as χ and γ respectively. The variables χ and γ are

513 defined as, $\chi = (I_z, I_a)$ and $\gamma = (S_h, R_z, S_m)$ respectively. Therefore the model (30) can be
514 written as

515

516

517

$$518 \quad \left. \begin{aligned} \frac{d\chi}{dt} &= R(\chi, \gamma) \\ \frac{d\gamma}{dt} &= S(\chi, \gamma) \end{aligned} \right\} \dots \dots \dots (37)$$

519 The two valued functions $R(\chi, \gamma)$ (dimension 2) and $S(\chi, \gamma)$ (dimension 3) are given by

$$\left. \begin{aligned} R(\chi, \gamma) &= \left(\frac{\lambda_a I_z}{N_h} S_h - (\mu_h + \tau_1) I_z, \frac{\sigma_a I_z}{N_h} S_m - \mu_m I_a \right)^T \\ S(\chi, \gamma) &= \left(\Pi_h + \alpha R_z - \mu_h S_h - \frac{\lambda I_a}{N_h} S_h, \tau_1 I_z - (\alpha + \mu_h) R_z, \Pi_m - \mu_m S_m - S_m \frac{\sigma_a I_z}{N_h} \right)^T \end{aligned} \right\} \dots\dots\dots (38)$$

Where T is transpose .Now consider the reduced system: $\frac{d\gamma}{dt} = S(\chi, 0)$

$$\left. \begin{aligned} \frac{dS_h}{dt} &= \Pi_h + \alpha R_z - \mu_h S_h \\ \frac{dR_z}{dt} &= \tau_1 I_m - (\mu_h + \alpha) R_z \\ \frac{dS_m}{dt} &= \beta_2 S_m - \mu_m I_a \end{aligned} \right\} \dots\dots\dots (39)$$

$\gamma^* = (S_h^*, R_z^*, S_m^*) = \left(\frac{\Pi_h}{\mu_h}, 0, \frac{\Pi_m}{\mu_m} \right)$ is a globally asymptotically stable equilibrium point for the reduced

system $\frac{d\gamma}{dt} = S(\chi, 0)$. To see this ,solve the second equation in (39) to obtain

$R_z(t) = R_z(0)e^{-(\mu_h + \alpha)t}$; it turns to zero as $t \rightarrow \infty$. In the same way , the last equation in

equation (39)gives $S_m(t) = \frac{\Pi_m}{\mu_m} + \left\{ S_m(0) - \frac{\Pi_m}{\mu_m} \right\} e^{\mu_m t}$ which turns to $\frac{\Pi_m}{\mu_m}$ as $t \rightarrow \infty$ Finally, the

first equation of (39) gives

$$S_h(t) = \frac{\Pi_h}{\mu_h} - \left\{ \frac{\Pi_h}{\mu_h} + \left[S_h(0) - \frac{\Pi_h}{\mu_h} \right] \right\} e^{\mu_h t} \rightarrow \frac{\Pi_h}{\mu_h} \text{ as } t \rightarrow \infty . \text{ This asymptotic dynamics is}$$

independent of initial conditions in Ω .Hence the convergence of the solution (39) is global in Ω . Clearly

$R(\chi, \gamma)$ satisfies the following two conditions given as H_2 in (Carlos Castillo et al,2002) .namely

1) $R(\chi, 0) = 0$ and

2) $R(\chi, \gamma) = A\chi - \bar{R}(\chi, \gamma), \bar{R}(\chi, \gamma) \geq 0$ on Ω where

$$A = D_\chi R(\chi^*, 0) = \begin{pmatrix} -(\mu_t + \tau_1) & \sigma \\ \frac{\sigma_a S_m}{N_h} & -\mu_m \end{pmatrix} \text{ and}$$

$$R(\chi, \gamma) = \begin{pmatrix} \bar{R}_1(\chi, \gamma) \\ \bar{R}_2(\chi, \gamma) \end{pmatrix} = \begin{pmatrix} \sigma I_a \left[1 - \frac{S_h}{N_h} \right] \\ \sigma_a I_z \left[1 - \frac{S_m}{N_h} \right] \end{pmatrix}$$

Since the terms in $\bar{R}(\chi, \gamma)$ are nonnegative and the conditions H_2 given in (Carlos Castillo et al, 2002) also satisfied, we can conclude that the disease free equilibrium of zika virus is globally stable.

3.17. Global Stability Of Endemic Equilibrium point for Zika virus: Here in this section we try to prove the global stability of the endemic equilibrium.

Theorem 1.16:

If $R_{zv} > 1$ then the unique endemic equilibrium E_{zv}^{**} of System (30) is globally stable in the interior of Ω .

Proof

This can be determined by constructing Logarithmic Lyapunov function $L(t)$ such that

$S_h \leq S_h^*, I_z \leq I_z^*, R_z \leq R_z^*, S_m \leq S_m^*$ and $I_a \leq I_a^*$ and $L(t)$ is given as

$$L(t) = \frac{1}{(\mu_h + \lambda_2)} \left(S_h^* S_h - S_h - S_h^* \ln \frac{S_h}{S_h^*} \right) + \frac{1}{(\mu_h + \lambda_2)} \left(I_z^* I_z - I_z - I_z^* \ln \frac{I_z}{I_z^*} \right) + \frac{1}{(\mu_h + \alpha)} \left(R_z^* R_z - R_z - R_z^* \ln \frac{R_z}{R_z^*} \right) + \frac{1}{(\mu_h + \beta_2)} \left(S_m^* S_m - S_m - S_m^* \ln \frac{S_m}{S_m^*} \right) + \frac{1}{\mu_h} \left(I_a^* I_a - I_a - I_a^* \ln \frac{I_a}{I_a^*} \right) \dots (40)$$

we take the derivative of $L(t)$ with respect to the state variables which is given as

$$\frac{dL}{dS_h} = \frac{1}{(\mu_h + \lambda_2)} \left(S_h^* - 1 - \frac{1}{S_h} \right) = \frac{1}{(\mu_h + \lambda_2)} \left(\frac{S_h^* S_h - S_h - 1}{S_h} \right)$$

$$\frac{dL}{dI_z} = \frac{1}{(\mu_h + \tau_1)} \left(I_z^* - 1 - \frac{1}{I_z} \right) = \frac{1}{(\mu_h + \tau_1)} \left(\frac{I_z^* I_z - I_z - 1}{I_z} \right)$$

$$\frac{dL}{dR_z} = \frac{1}{(\mu_h + \alpha)} \left(R_z^* - 1 - \frac{1}{R_z} \right) = \frac{1}{(\mu_h + \alpha)} \left(\frac{R_z^* R_z - R_z - 1}{R_z} \right)$$

$$\frac{dL}{dS_m} = \frac{1}{(\mu_h + \beta_2)} \left(S_m^* - 1 - \frac{1}{S_m} \right) = \frac{1}{(\mu_h + \beta_2)} \left(\frac{S_m^* S_m - S_m - 1}{S_m} \right)$$

$$\frac{dL}{dI_a} = \frac{1}{\mu_h} \left(I_a^* - 1 - \frac{1}{I_a} \right) = \frac{1}{\mu_h} \left(\frac{I_a^* I_a - I_a - 1}{I_a} \right)$$

We then find the product of the derivative of $L(t)$ with respect to the state variables. Thus

$$\frac{dL}{dt} = \frac{\partial L}{\partial S_h} \frac{dS_h}{dt} + \frac{\partial L}{\partial I_z} \frac{dI_z}{dt} + \frac{\partial L}{\partial R_z} \frac{dR_z}{dt} + \frac{\partial L}{\partial S_m} \frac{dS_m}{dt} + \frac{\partial L}{\partial I_a} \frac{dI_a}{dt}$$

$$\begin{aligned}
 \frac{dL}{dt} &= \frac{1}{(\mu_h + \lambda_2)} \left(\frac{S_h^* S_h - S_h - 1}{S_h} \right) [-(\mu_h + \lambda_2) S_h] \\
 &+ \frac{1}{(\mu_h + \tau_1)} \left(\frac{I_z^* I_z - I_z - 1}{I_z} \right) [-(\mu_h + \tau_1) I_z] \\
 &+ \frac{1}{(\mu_h + \alpha)} \left(\frac{R_z^* R_z - R_z - 1}{R_z} \right) [-(\mu_h + \alpha) R_z] \\
 &+ \frac{1}{(\mu_h + \beta_2)} \left(\frac{S_m^* S_m - S_m - 1}{S_m} \right) [-(\mu_h + \beta_2) S_m] \\
 &+ \frac{1}{\mu_h} \left(\frac{I_a^* I_a - I_a - 1}{I_a} \right) [-\mu_h I_a] \\
 \Rightarrow \frac{dL}{dt} &= - (S_h^* S_h - S_h - 1) - (I_z^* I_z - I_z - 1) - (R_z^* R_z - R_z - 1) - (S_m^* S_m - S_m - 1) - (I_a^* I_a - I_a - 1) \\
 \Rightarrow \frac{dL}{dt} &= -S_h^* S_h + S_h + 1 - I_z^* I_z + I_z + 1 - R_z^* R_z + R_z + 1 - S_m^* S_m + S_m + 1 - I_a^* I_a + I_a + 1 \\
 \Rightarrow \frac{dL}{dt} &= 1 + 1 + 1 + 1 + 1 + S_h (1 - S_h^*) + I_z (1 - I_z^*) + R_z (1 - R_z^*) + S_m (1 - S_m^*) + I_a (1 - I_a^*) \\
 \Rightarrow \frac{dL}{dt} &= 5 + S_h (1 - S_h^*) + I_z (1 - I_z^*) + R_z (1 - R_z^*) + S_m (1 - S_m^*) + I_a (1 - I_a^*) \leq 0
 \end{aligned}$$

Theorem1.167

If a function is positive definite on the entire state space, and has the additional property that $|V(x)| \rightarrow \infty$ as $\|x\| \rightarrow \infty$, and if its derivative $\dot{V}$ is negative definite on the entire state space, then the equilibrium point at the origin is globally asymptotically stable (Bonyah, 2014).

Therefore $\dot{V} \leq 0$ and by the LaSalle's Extension (LaSalle's, 1976), it implies that the omega limit set of each solution lies in an invariant set contained in Ω . The only invariant set contained in Ω is the singleton E_{zv}^{**} . This shows that each solution which intersects R_+^5 limits to the endemic equilibrium and that trivial equilibrium is globally asymptotically stable in the invariant feasible region. This ends the proof of global stability.

4.0. Impact Of Malaria On Zika Virus And Vice Versa

From the individual models, the basic reproduction numbers of Malaria only and Zika virus only models are denoted by R_{ma} and R_{zv} . From R_{ma} and R_{zv} , the basic reproduction number for the co-infection model is given as $R_{mz} = \max\{R_{ma}, R_{zv}\}$ where ,

$$R_{ma} = \sqrt{\frac{\beta_h \beta_v \Pi_m \mu_h}{(\mu_h + \eta + \tau_2) \Pi_h \mu_m^2}} \dots \dots \dots (41)$$

and

$$R_{zv} = \sqrt{\frac{\sigma \sigma_a \Pi_m \mu_h}{(\mu_h + \tau_1) \Pi_h \mu_m^2}} \dots \dots \dots (42)$$

To analysis the effect of Zika virus and malaria or vice versa ,we begin by first expressing R_{zv} in terms of R_{ma} .This idea is similar to (Okosun et al,2014) . We solve for μ_h from equation (42).Thus Squaring both sides of (41) gives

$$\begin{aligned} R_{ma}^2 &= \frac{\beta_h \beta_v \Pi_m \mu_h}{(\mu_h + \eta + \tau_2) \Pi_h \mu_m^2} \cdot \\ R_{ma}^2 \Pi_h \mu_m^2 (\mu_h + \eta + \tau_2) &= \beta_h \beta_v \Pi_m \mu_h \\ R_{ma}^2 \Pi_h \mu_m^2 \mu_h + R_{ma}^2 \Pi_h \mu_m^2 (\eta + \tau_2) &= \beta_h \beta_v \Pi_m \mu_h \\ R_{ma}^2 \Pi_h \mu_m^2 (\eta + \tau_2) &= \beta_h \beta_v \Pi_m \mu_h - R_{ma}^2 \Pi_h \mu_m^2 \mu_h \\ R_{ma}^2 \Pi_h \mu_m^2 (\eta + \tau_2) &= (\beta_h \beta_v \Pi_m - R_{ma}^2 \Pi_h \mu_m^2) \mu_h \\ \Rightarrow \mu_h &= \frac{R_{ma}^2 \Pi_h \mu_m^2 (\eta + \tau_2)}{(\beta_h \beta_v \Pi_m - R_{ma}^2 \Pi_h \mu_m^2)} \\ \Rightarrow \mu_h &= \frac{R_{ma}^2 Z_1}{Z_2 - Z_3 R_{ma}^2} \dots \dots \dots (43) \end{aligned}$$

$$Z_1 = \Pi_h \mu_m^2 (\eta + \tau_2) \cdot$$

$$Z_2 = \beta_h \beta_v \Pi_m$$

$$Z_3 = \Pi_h \mu_m^2$$

Substitute (43) into equation (42) gives

$$R_{zv} = \sqrt{\frac{(\sigma \sigma_a \Pi_m R_{ma}^2 Z_1)}{[R_{ma}^2 Z_1 + \tau_1 (Z_2 - Z_3 R_{ma}^2)] Z_3}} \dots \dots \dots (44)$$

Differentiate equation (64) partially with respect to R_{ma} gives

$$\frac{\partial R_{zv}}{\partial R_{ma}} = \frac{\tau_1 Z_1 \sqrt{\frac{\sigma \sigma_a \Pi_m R_{ma}^2 Z_1}{[\tau_1 Z_1 + (Z_1 - \tau_1 Z_3) R_{ma}^2]} \Pi_h \mu_m^2}}{\tau_1 Z_1 R_{ma} + (Z_1 - \tau_1 Z_3) R_{ma}^2} \dots \dots \dots (45)$$

Anytime (45) is strictly positive, it implies that malaria enhances zika virus infection, that is ,an increase in malaria cases results in an increase of zika virus cases in the community. If (45) is equal to zero ,malaria cases have no significant effect on the transmission dynamics of zika

virus. If (45) is less than zero , an increase in malaria cases results in decrease in zika virus case in the community.

In a similar way, we analysis the effect of malaria and Zika virus by solving for μ_h from equation (42).Thus Squaring both sides of (42) gives

$$\begin{aligned}
 R_{zv}^2 &= \frac{\sigma\sigma_a\Pi_m\mu_h}{(\mu_h + \tau_1)\Pi_h\mu_m^2} \\
 R_{zv}^2(\mu_h + \tau_1)\Pi_h\mu_m^2 &= \sigma\sigma_a\Pi_m\mu_h \\
 R_{zv}^2\Pi_h\mu_m^2\mu_h + R_{zv}^2\Pi_h\mu_m^2\tau_1 &= \sigma\sigma_a\Pi_m\mu_h \\
 R_{zv}^2\Pi_h\mu_m^2\tau_1 &= (\sigma\sigma_a\Pi_m - R_{zv}^2\Pi_h\mu_m^2)\mu_h \\
 \mu_h &= \frac{R_{zv}^2\Pi_h\mu_m^2\tau_1}{\sigma\sigma_a\Pi_m - R_{zv}^2\Pi_h\mu_m^2} \\
 \mu_h &= \frac{R_{zv}^2Z_4}{Z_5 - R_{zv}^2Z_6} \dots\dots\dots(46)
 \end{aligned}$$

Where

$$\begin{aligned}
 Z_4 &= \Pi_h\mu_m^2\tau_1 \\
 Z_5 &= \sigma\sigma_a\Pi_m \\
 Z_6 &= \Pi_h\mu_m^2
 \end{aligned}$$

Substitute (45) into equation (41) gives

$$\begin{aligned}
 R_{ma} &= \sqrt{\frac{\beta_h\beta_v\Pi_m\mu_h}{(\mu_h + \eta + \tau_2)\Pi_h\mu_m^2}} \\
 R_{ma} &= \sqrt{\frac{\beta_h\beta_v\Pi_m\left(\frac{R_{zv}^2Z_4}{Z_5 - R_{zv}^2Z_6}\right)}{\left(\left[\frac{R_{zv}^2Z_4}{Z_5 - R_{zv}^2Z_6}\right] + \eta + \tau_2\right)\Pi_h\mu_m^2}} \\
 R_{ma} &= \sqrt{\frac{\beta_h\beta_v\Pi_mR_{zv}^2Z_4}{\left(\left[R_{zv}^2Z_4 + (Z_5 - R_{zv}^2Z_6)(\eta + \tau_2)\right]\right)\Pi_h\mu_m^2}} \dots\dots\dots(47)
 \end{aligned}$$

Differentiate (67) partially with respect to R_{zv} , yields

$$\frac{\partial R_{ma}}{\partial R_{zv}} = \frac{(\eta + \tau_2) Z_5 \sqrt{\frac{\beta_h \beta_v \Pi_m R_{zv}^2 Z_4}{\left(\left[R_{zv}^2 Z_4 + (Z_5 - R_{zv}^2 Z_6) (\eta + \tau_2) \right] \right) \Pi_h \mu_m^2}}}{(\eta + \tau_2) (Z_5 - R_{zv}^2 Z_6) + R_{zv}^2 Z_4} \dots\dots\dots (48)$$

Also whenever (48) is greater than zero, an increase in zika virus cases results in an increase of malaria cases in the community. If (48) is equal to zero, this implies zika virus cases have no effect on the transmission dynamics of malaria .If (48) is less than zero ,an increase in zika virus cases results in decrease of malaria cases in the community .

The impact of malaria treatment on zika virus is evaluated by partially differentiating R_{ma} with respect to τ_1 gives

$$\frac{\partial R_{ma}}{\partial \tau_1} = \frac{(\eta + \tau_2) (Z_5 - R_{zv}^2 Z_6) \sqrt{\frac{\beta_h \beta_v \Pi_m R_{zv}^2 Z_4}{\left(\left[R_{zv}^2 Z_4 + (Z_5 - R_{zv}^2 Z_6) (\eta + \tau_2) \right] \right) \Pi_h \mu_m^2}}}{2 Z_4 \left[(\eta + \tau_1) (Z_5 - R_{zv}^2 Z_6) + R_{zv}^2 Z_4 \right]} \dots\dots\dots (49)$$

Whenever (49) is negative , R_{ma} is strictly a decreasing function of τ_1 ,so the treatment of zika virus will have a positive impact on the dynamics of malaria and zika virus co-infection .If (49) is positive ,then the treatment of zika virus will have a negative impact on the dynamics of malaria and zika virus co-infection.If (49) is zero then the treatment of zika virus will have no impact on the dynamics of malaria and zika virus co-infection.

CONCLUSION

In this article we formulated the co-infection model for Malaria and Zika virus diseases to describe the transmission dynamics of both infections happening concurrently or one after the other . The co-infection model was divided into two sub-models ,that is Malaria only model and Zika only model.Stability analysis was carried out on the three models ,that is the co-infection model and the two sub-models. The disease free equilibrium points for the sub-models are locally and globally asymptotically stable when their basic reproduction numbers are less than 1.($R_{ma} < 1$ and $R_{zv} < 1$). Also, their endemic equilibrium points are locally and globally asymptotically stable when their basic reproduction numbers are greater than 1.($R_{ma} > 1$ and $R_{zv} > 1$). However ,for the coinfection model the disease free equilibrium point is locally asymptotically stable when the basic reproduction number is less than 1($R_{mz} < 1$) but not globally asymptotically stable. For the endemic equilibrium point ,it is globally asymptotically stable when the basic reproduction number is greater than 1($R_{ma} > 1$). The impact of the sub-models on each other shows that when there is increase in malaria cases , it results in decrease in zika virus case in the community and the vice versa. On the whole, we hope that the model will give policy makers and scientists good insights as to how to control or eliminate each disease or both.

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