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Stability Analysis of Endemic Equilibrium Points of Malaria and Dengue Fever Co-infection Model

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Abstract- Malaria-dengue co-infection is becoming a public health challenge with the growing report of the co-infection. Much has been done on analyzing malaria, dengue, and other infection but much has not been done to study the co-infection of malaria and dengue fever. A mathematical model to understand the transmission of malaria and dengue infection was formulated using a system of ordinary differential equations. We computed the basic reproduction number and establish the equilibria point. The endemic equilibrium point was further investigated. The result shows that with the reproduction number greater than one, the endemic equilibrium point was found to be locally asymptotically stable and globally asymptotically stable.

Keywords- Malaria, Dengue Fever, Co-infection, Endemic Equilibrium, Stability Analysis

I. INTRODUCTION

Malaria is transmitted via the bites of the disease carrier anopheles mosquito. It is brought about by five distinct types of *Plasmodium*. However, *Plasmodium falciparum* is the most predominant in the continent and causes the most elevated death rate evoked by the disease [1]. World Health Organization (WHO) in 2017, reported that 219 million cases of malaria happened worldwide with *Plasmodium falciparum* and *vivax* parasite presenting high health challenge. Within the WHO African Region that has the highest incidence of malaria worldwide, *P. falciparum* represent 99.7% of calculated cases whereas *P. vivax* result for 74.1% of malaria cases within the WHO Region of Americas [2].

Dengue, a communicable disease brought about by any of DENVs 1–4, is a vector-borne disease transmitted by the female *Aedes* mosquito. Dengue is highly prevalent in tropical areas, showing the vector distribution, *Aedes aegypti* mosquitoes. 33% of the globe is in danger [3]. Infection with DENV brings about mild asymptomatic dengue fever (DF) to serious dengue fever hemorrhagic fever (DHF) and dengue fever shock syndrome (DSS) and can turn lethal [4]. Dengue Fever and Malaria are the most predominant arthropod-borne diseases with world instance of 390 million and 214 million yearly, respectively. Severe Malaria is a co-infection of Dengue and Malaria in a person [5, 6].

The paper aims to analyze the local and global stability of the endemic points of the co-infection model. In investigating the local stability of the endemic points the author applied the central manifold theorem while the global stability was proven by constructing a suitable Lyapunov function.

The remaining part of the paper is as follows: section 2 presented some related works. Section 3 is the Methodology, here we defined the model assumptions, outlined the model parameters and variables. Section 4, consists of the model analysis. Section 5, is the discussion and conclusion.

II. RELATED WORKS

Bakare and Nwozo [7] studied a mathematical model to explore malaria and schistosomiasis co-infection. Schistosomiasis also is known as snail fever or bilharziasis is a parasitic disease. The model consists of the human, vector, and snail population. Amoah-Mensah et al. [8] in their work proposed a mathematical model to investigate the transmission of Malaria and Zika in malaria-endemic areas. The model was analyzed to compute the two equilibria. The model consists of nine (9) compartments. The sensitivity analysis from the work shows that improving the recovery rate of both diseases is the best approach to control and eliminate the disease. Aldila and Agustin [9] formulated a mathematical model to understand the spread of dengue and chikungunya in a closed population. The model consists of nine compartments wherein the human population is made up of five compartments while the mosquito population is made up of four compartments. Bonyah et al. [10] presented a co-infection model for dengue-zika disease. In this work, the computation was done to establish the basic reproduction numbers and the equilibrium point was analyzed. Ogunmiloro [11] formulated a mathematical model to study the co-infection of malaria and toxoplasmosis in tropical regions. In this work, the basic reproduction number was obtained, the local, global stability, and sensitivity analysis was carried out. Duncan, Owuor, and Okaka [12] carried the stability analysis of the endemic equilibrium of an Ebola disease model. In [13] Xia, Yicang and Hui proved the conditions for global stability of the endemic equilibrium of a SIR model. Ashezua, Udoo, and Ikpakyegh [14] investigated the analysis of the Endemic Equilibrium of an Infection Age-structured HIV/AIDS disease. Deephi, Radhika, and Praneeth [15] using Big data analytics investigate Epidemic Diseases

III. METHODOLOGY

3.1 Model Formulation

In this model, the human population denoted by N_h is divided into eight classes which are susceptible humans (S_h), individuals exposed to malaria only (E_{hm}), individuals infected with malaria only (I_{hm}), individuals exposed to dengue fever only (E_{hd}), individuals infected with only dengue fever (I_{hd}), individuals exposed to malaria and dengue fever co-infection (E_{md}), individuals infected with malaria and dengue fever co-infection (I_{md}), individuals that recovered from malaria and dengue fever (R_h). The vector population includes the Malaria Parasite non-carrier vectors (S_m), Malaria parasite carrier vectors (I_m), Dengue virus non-carrier vectors (S_d), and Dengue fever carrier vectors (I_d). Individuals are recruited through a constant Λ_h. Susceptible individuals are infected with dengue fever through contact with infectious vector at a rate α_d, infected with malaria at a rate α_m, individuals who recover from malaria returns to the susceptible class at a rate of γ_h, susceptible individual has a natural death rate of μ_h. The class of individuals exposed to malaria only are generated by susceptible individuals infected with malaria only and reduced by the rate of contracting dengue fever at a rate α_d, the rate of progression to the malaria only infected class κ_1 and natural death rate μ_h. The class of individuals infected with malaria (I_{hm}) is increased by κ_1 rate of progression from malaria exposed class, reduced by the rate of contacting dengue fever at a rate α_d, disease-induced death rate δ_1, malaria only recovery rate θ_1, and natural death rate μ_h. Individuals that are exposed to dengue fever only are generated by individuals infected with dengue fever at a rate α_d, reduced by the natural death rate μ_h, rate of progression to infected class for dengue fever only at rate, κ_2 and the rate at which susceptible individuals contact malaria only. Individuals with dengue fever only (I_{hd}) is generated by individuals that progressed from the exposed class (E_{hd}) at the rate κ_2. It is also reduced by disease-induced death rate δ_2, recovery rate from dengue fever only θ_2 and the rate of contacting malaria only. The population of individuals exposed to malaria and dengue fever co-infection (E_{md}) is increased by rate of acquiring malaria through contact with the parasite carrier vectors and dengue fever through contact with dengue virus carrier vectors, but reduced by natural death rate and rate of progression to infected malaria and dengue fever co-infection class κ_3. The infected malaria and dengue fever co-infection class (I_{md}) is increased by κ_3 and reduced by the natural death rate, co-infection recovery rate θ_3 and disease-induced death rate δ_3. The recovery class (R_h) is generated by the individuals who recovery from malaria only at the rate θ_1, individuals who recovers from dengue fever only at the rate θ_2, individuals who recover from both diseases at the rate θ_3, and reduced by natural death rate and individuals who return to susceptible class after recovery at the rate γ_h. The Malaria parasite non-carrier vector population (S_m) is generated by a constant Λ_m, reduced by the vector natural death rate μ_m and the rate at which the non-carrier vector acquires malaria parasite through contact with exposed and infected individuals with malaria only and co-infection of malaria and dengue fever given as α_{vm}. The Malaria parasite carrier vector population is generated by the rate at which the non-carrier vector acquires malaria through contact with exposed and infected individuals with malaria only and co-infection of malaria and dengue fever and the natural death rate μ_m. The Dengue virus non-carrier vector population (S_d) is generated by a constant Λ_d, reduced by the vector natural death rate μ_d, and the rate at which the Dengue virus non-carrier vector acquires dengue virus through contact with exposed and infected individuals with dengue fever only and co-infection of malaria and dengue fever given as α_{vd}. The Dengue virus carrier vector class (I_d) is increased by the rate at which Dengue virus non-carrier vector acquires dengue virus through contact with exposed and infected individuals with dengue fever only and co-infection of malaria and dengue fever and reduced by the vectors natural death rate μ_d .

3.2 Model Assumptions

Assumptions made in the formulation of the equations includes:

1. Recruitment into the susceptible population is constant
2. The recovery population include those jointly infected with Malaria and Dengue fever only
3. Recovery from Dengue fever is permanent.

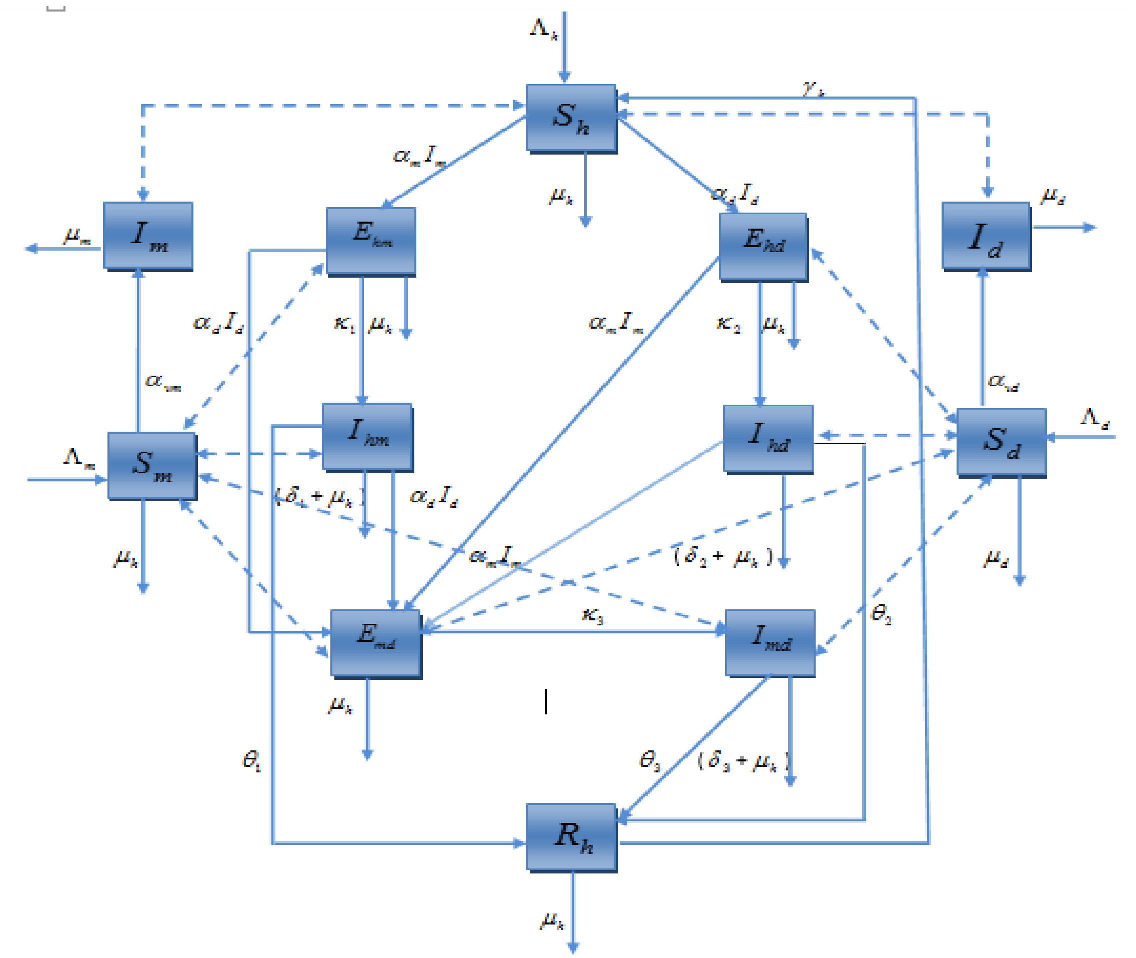

Figure 1. Schematic Representation of the Model

The equations governing the co-infection dynamics is given as,

$$\frac{dS_h}{dt} = \Lambda_h + \gamma_h R_{hm} - (\alpha_d I_d + \alpha_m I_m)S_h - \mu_h S_h \quad (1)$$

$$\frac{dE_{hm}}{dt} = \alpha_m I_m S_h - (\alpha_d I_d + \kappa_1 + \mu_h)E_{hm} \quad (2)$$

$$\frac{dI_{hm}}{dt} = \kappa_1 E_{hm} - (\alpha_d I_d + \delta_1 + \theta_1 + \mu_h)I_{hm} \quad (3)$$

$$\frac{dE_{hd}}{dt} = \alpha_d I_d S_h - (\alpha_m I_m + \kappa_2 + \mu_h)E_{hd} \quad (4)$$

$$\frac{dI_{hd}}{dt} = \kappa_2 E_{hd} - (\alpha_m I_m + \delta_2 + \theta_2 + \mu_h)I_{hd} \quad (5)$$

$$\frac{dE_{md}}{dt} = \alpha_d I_d E_{hm} + \alpha_d I_d I_{hm} + \alpha_m I_m E_{hd} + \alpha_m I_m I_{hd} - (\kappa_3 + \mu_h) E_{md} \quad (6)$$

$$\frac{dI_{md}}{dt} = \kappa_3 E_{md} - (\delta_3 + \theta_3 + \mu_h) I_{md} \quad (7)$$

$$\frac{dR_{hm}}{dt} = \theta_1 I_{hm} + \theta_2 I_{hd} + \theta_3 I_{md} - (\gamma_h + \mu_h) R_{hm} \quad (8)$$

$$\frac{dS_m}{dt} = \Lambda_m - \alpha_{vm}(E_{hm} + I_{hm} + E_{md} + I_{md}) S_m - \mu_m S_m \quad (9)$$

$$\frac{dI_m}{dt} = \alpha_{vm}(E_{hm} + I_{hm} + E_{md} + I_{md}) S_m - \mu_m I_m \quad (10)$$

$$\frac{dS_d}{dt} = \Lambda_d - \alpha_{vd}(E_{hd} + I_{hd} + E_{md} + I_{md}) S_d - \mu_d S_d \quad (11)$$

$$\frac{dI_d}{dt} = \alpha_{vd}(E_{hd} + I_{hd} + E_{md} + I_{md}) S_d - \mu_d I_d \quad (12)$$

Table 1. Variables of the Model

Symbols	**Description**
S_h	Susceptible Humans
E_{hm}	Exposed Humans with Malaria
I_{hm}	Humans infected with Malaria only
E_{hd}	Exposed Humans with Dengue Fever
I_{hd}	Humans infected with Dengue Fever only
E_{md}	Exposed Humans jointly infected with Malaria and Dengue Fever
I_{md}	Humans jointly infected with Malaria and Dengue Fever
R_h	Humans Recovered from Malaria and Dengue Fever
S_m	Malaria Parasite carrier vectors
I_m	Malaria Parasite non-carrier vectors
S_d	Dengue virus non-carrier vectors
I_d	Dengue virus carrier vectors

Table 2. Parameters of the Model

Symbols	**Description**
Λ_h	Recruitment of Human Population
Λ_m	Recruitment of Malaria Parasite Vectors
Λ_d	Recruitment rate of Dengue Virus Vectors
θ_1	Recovery rate for Humans infected with Malaria only
θ_2	Recovery rate for Human infected with Dengue only
θ_3	Recovery rate for Human jointly infected with Malaria and Dengue
γ_h	Rate at which recovered becomes susceptible
κ_1	Rate at which E_{hm} becomes I_{hm}
κ_2	Rate at which E_{hd} becomes I_{hd}
κ_3	Rate at which E_{md} becomes I_{md}
α_m	Transmission rate of Malaria Parasite Vectors

α_d	Transmission rate of Dengue Virus Carrier Vectors
α_{vm}	Probability for Malaria Parasite Vectors to be infected
α_{vd}	Probability for Dengue Virus Vectors to be infected
δ_1	Disease induced death for I_{hm}
δ_2	Disease induced death for I_{hd}
δ_3	Disease induced death for I_{md}
μ_h	Human Natural death rate
μ_m	Death rate of Malaria Parasite Vectors
μ_d	Death rate of Dengue Virus Vectors

IV. MODEL ANALYSIS

4.1 Reproduction Number (R_0)

Reproduction number is the number of secondary infection generated by one infectious individual. The next-generation matrix is employed to compute the R_0, which is given as

$$R_0 = \max\{R_{0m}, R_{0d}\} \quad (13)$$

where

$$R_{0m} = \sqrt{\frac{\Lambda_h \Lambda_m \alpha_m \alpha_{vm}(z_1+\kappa_1)}{\eta_1 z_1 \mu_h \mu_m^2}} \quad (14)$$

and

$$R_{0d} = \sqrt{\frac{\Lambda_h \Lambda_d \alpha_d \alpha_{vd}(z_2+\kappa_2)}{\eta_2 z_2 \mu_h \mu_d^2}} \quad (15)$$

These are the reproduction number of malaria and dengue fever respectively.

4.2 Disease Free Equilibrium (DFE) and Endemic Equilibrium (EE) Points

DFE (ε_0) is when there is no disease in the population and it is given as

$$\varepsilon_0 = \left(S_h^0, E_{hm}^0, I_{hm}^0, E_{hd}^0, I_{hd}^0, E_{md}^0, I_{md}^0, R_{hm}^0, S_m^0, I_m^0, S_d^0, I_d^0\right)$$
$$= \left(\frac{\Lambda_h}{\mu_h}, 0,0,0,0,0,0,0, \frac{\Lambda_m}{\mu_m}, 0, \frac{\Lambda_d}{\mu_d}, 0\right) \quad (16)$$

The EE (ε_E) is when the diseases persist in the community. It is therefore given as

$$\varepsilon_E = \left(S_h^*, E_{hm}^*, I_{hm}^*, E_{hd}^*, I_{hd}^*, E_{md}^*, I_{md}^*, R_{hm}^*, , S_m^*, I_m^*, S_d^*, I_d^*\right) =$$
$$\left(\begin{array}{l}
\frac{Q_6}{Q_4+Q_5}, \frac{\alpha_m I_m Q_6}{(\alpha_d I_d+\eta_1)(Q_4+Q_5)}, \frac{\kappa_1 \alpha_m I_m Q_6}{(\alpha_d I_d + z_1)(\alpha_d I_d+\eta_1)(Q_4+Q_5)}, \\
\frac{\alpha_d I_d Q_6}{(\alpha_m I_m+\eta_2)(Q_4+Q_5)}, \frac{\kappa_2 \alpha_d I_d Q_6}{(\alpha_m I_m + z_2)(\alpha_m I_m+\eta_2)(Q_4+Q_5)}, \\
\frac{\alpha_d I_d \alpha_m I_m Q_3 Q_6}{\eta_3(Q_4+Q_5)}, \frac{\alpha_d I_d \alpha_m I_m \kappa_3 Q_3 Q_6}{z_3 \eta_3 (Q_4+Q_5)}, \frac{\Lambda_h Q_7}{(Q_4+Q_5)}, \\
\frac{\Lambda_m(\alpha_d I_d+\eta_1)(Q_4+Q_5)}{\alpha_{vm}\alpha_m I_m Q_1 Q_6 + \mu_m(\alpha_d I_d+\eta_1)(Q_4+Q_5)}, \\
\frac{\Lambda_m \alpha_{vm}\alpha_m I_m Q_1 Q_6}{\mu_m(\alpha_{vm}\alpha_m I_m Q_1 Q_6 + \mu_m(\alpha_d I_d+\eta_1)(Q_4+Q_5))}, \\
\frac{\Lambda_d(\alpha_m I_m+\eta_2)(Q_4+Q_5)}{\alpha_{vd}\alpha_d I_d Q_2 Q_6 + \mu_d(\alpha_m I_m+\eta_2)(Q_4+Q_5)}, \\
\frac{\Lambda_d \alpha_{vd}\alpha_d I_d Q_2 Q_6}{\mu_d(\alpha_{vd}\alpha_d I_d Q_2 Q_6 + \mu_d(\alpha_m I_m+\eta_2)(Q_4+Q_5))}
\end{array}\right) \quad (17)$$

Where

$$Q_1 = \left(\left(1+\frac{\kappa_1}{(\alpha_d I_d + z_1)}\right) + \frac{\alpha_d I_d}{\eta_3}\left(\frac{(\alpha_d I_d + \rho_1)(\alpha_m I_m + z_2)(\alpha_m I_m + \eta_2) + (\alpha_m I_m + \rho_2)(\alpha_d I_d + z_1)(\alpha_d I_d + \eta_1)}{(\alpha_d I_d + z_1)(\alpha_d I_d + \eta_1)(\alpha_m I_m + z_2)(\alpha_m I_m + \eta_2)} \right)\left(1+\frac{\kappa_3}{z_3}\right) \right) \quad (18)$$

$$Q_2 = \left(\left(1+\frac{\kappa_2}{(\alpha_m I_m + z_2)}\right) + \frac{\alpha_m I_m}{\eta_3}\left(\frac{(\alpha_d I_d + \rho_1)(\alpha_m I_m + z_2)(\alpha_m I_m + \eta_2) + (\alpha_m I_m + \rho_2)(\alpha_d I_d + z_1)(\alpha_d I_d + \eta_1)}{(\alpha_d I_d + z_1)(\alpha_d I_d + \eta_1)(\alpha_m I_m + z_2)(\alpha_m I_m + \eta_2)} \right)\left(1+\frac{\kappa_3}{z_3}\right) \right) \quad (19)$$

$$Q_3 = \left(\frac{(\alpha_d I_d + \rho_1)(\alpha_m I_m + z_2)(\alpha_m I_m + \eta_2) + (\alpha_m I_m + \rho_2)(\alpha_d I_d + z_1)(\alpha_d I_d + \eta_1)}{(\alpha_d I_d + z_1)(\alpha_d I_d + \eta_1)(\alpha_m I_m + z_2)(\alpha_m I_m + \eta_2)} \right) \quad (20)$$

$$Q_4 = z_3\eta_3\mu_h\left(\begin{array}{l} (\alpha_d I_d + \alpha_m I_m + \mu_h)(\alpha_d I_d + z_1)(\alpha_d I_d + \eta_1) \\ (\alpha_m I_m + z_2)(\alpha_m I_m + \eta_2) \end{array} \right) \quad (21)$$

$$Q_5 = \gamma_h \left(\begin{array}{l} z_3\eta_3(\alpha_d I_d + \alpha_m I_m + \mu_h)(\alpha_d I_d + z_1)(\alpha_d I_d + \eta_1)(\alpha_m I_m + z_2) \\ (\alpha_m I_m + \eta_2) - \left(\begin{array}{l} \theta_1\kappa_1\alpha_m I_m z_3\eta_3(\alpha_m I_m + z_2)(\alpha_m I_m + \eta_2) \\ + \theta_2\kappa_2\alpha_d I_d z_3\eta_3(\alpha_d I_d + z_1)(\alpha_d I_d + \eta_1) \\ + \theta_3\kappa_3\alpha_d I_d\alpha_m I_m Q_3(\alpha_d I_d + z_1)(\alpha_d I_d + \eta_1) \\ (\alpha_m I_m + z_2)(\alpha_m I_m + \eta_2) \end{array} \right) \end{array} \right) \quad (22)$$

$$Q_6 = \Lambda_h z_3\eta_3(\gamma_h + \mu_h)(\alpha_d I_d + z_1)(\alpha_d I_d + \eta_1)(\alpha_m I_m + z_2)(\alpha_m I_m + \eta_2) \quad (23)$$

$$\begin{array}{l} Q_7 = \theta_1\kappa_1 z_3\eta_3\alpha_m I_m(\alpha_m I_m + z_2)(\alpha_m I_m + \eta_2) + \theta_2\kappa_2 z_3\eta_3\alpha_d I_d(\alpha_d I_d + z_1)(\alpha_d I_d + \eta_1) \\ + \theta_3\kappa_3\alpha_m I_m\alpha_d I_d(\alpha_d I_d + z_1)(\alpha_d I_d + \eta_1)(\alpha_m I_m + z_2)(\alpha_m I_m + \eta_2) \end{array} \quad (24)$$

and

$$\left. \begin{array}{l} z_1 = \delta_1 + \theta_1 + \mu_h \\ z_2 = \delta_2 + \theta_2 + \mu_h \\ z_3 = (\delta_3 + \theta_3 + \mu_h) \\ \eta_1 = \mu_h + \kappa_1 \\ \eta_2 = \mu_h + \kappa_2 \\ \eta_3 = (\kappa_3 + \mu_h) \\ \rho_1 = z_1 + \kappa_1 \\ \rho_2 = z_2 + \kappa_2 \end{array} \right\} \quad (25)$$

4.3 Local Stability of the Endemic Equilibrium (EE) Point

The Central Manifold Theorem [16] is applied in analyzing the local stability of the EE point.
The system equation (1) – (12) can be re-written in a dimensionless state variable as follows:

$$x_1 = S_h, x_2 = E_{hm}, x_3 = I_{hm}, x_4 = E_{hd}, x_5 = I_{hd}, x_6 = E_{md}, x_7 = I_{md}, x_8 = R_{hm}, \\ x_9 = S_m, x_{10} = I_m, x_{11} = S_d, x_{12} = I_d, \quad (26)$$

Using the vector notation, (1) – (12) can be re-written in the form

$$\frac{dX_t}{dt} = F(X_t) \quad (27)$$

where

$$\left.\begin{aligned} X_t &= (x_1, x_2, x_3, x_4, x_5, x_6, x_7, x_8, x_9, x_{10}, x_{11}, x_{12})^T \\ F &= (f_1, f_2, f_3, f_4, f_5, f_6, f_7, f_8, f_9, f_{10}, f_{11}, f_{12})^T \end{aligned}\right\} \quad (28)$$

so we now have

$$\frac{dx_1}{dt} = \Lambda_h + \gamma_h x_8 - (\alpha_d x_{12} + \alpha_m x_{10}) x_1 - \mu_h x_1 \quad (29)$$

$$\frac{dx_2}{dt} = \alpha_m x_{10} x_1 - (\alpha_d x_{12} + \kappa_1 + \mu_h) x_2 \quad (30)$$

$$\frac{dx_3}{dt} = \kappa_1 x_2 - (\alpha_d x_{12} + \delta_1 + \theta_1 + \mu_h) x_3 \quad (31)$$

$$\frac{dx_4}{dt} = \alpha_d x_{12} x_1 - (\alpha_m x_{10} + \kappa_2 + \mu_h) x_4 \quad (32)$$

$$\frac{dx_5}{dt} = \kappa_2 x_4 - (\alpha_m x_{10} + \delta_2 + \theta_2 + \mu_h) x_5 \quad (33)$$

$$\frac{dx_6}{dt} = \alpha_d x_{12} (x_2 + x_3) + \alpha_m x_{10} (x_4 + x_5) - (\kappa_3 + \mu_h) x_6 \quad (34)$$

$$\frac{dx_7}{dt} = \kappa_3 x_6 - (\delta_3 + \theta_3 + \mu_h) x_7 \quad (35)$$

$$\frac{dx_8}{dt} = \theta_1 x_3 + \theta_2 x_5 + \theta_3 x_7 - (\gamma_h + \mu_h) x_8 \quad (36)$$

$$\frac{dx_9}{dt} = \Lambda_m - \alpha_{vm} (x_2 + x_3 + x_6 + x_7) x_9 - \mu_m x_9 \quad (37)$$

$$\frac{dx_{10}}{dt} = \alpha_{vm} (x_2 + x_3 + x_6 + x_7) x_9 - \mu_m x_{10} \quad (38)$$

$$\frac{dx_{11}}{dt} = \Lambda_d - \alpha_{vd} (x_4 + x_5 + x_6 + x_7) x_{11} - \mu_m x_{11} \quad (39)$$

$$\frac{dx_{12}}{dt} = \alpha_{vd} (x_4 + x_5 + x_6 + x_7) x_{11} - \mu_m x_{12} \quad (40)$$

This method requires the evaluation of the Jacobian of the equations (29) - (40) disease free equilibrium (DFE) denoted by $J(\varepsilon_0)$.

$$J(\varepsilon_0)=$$

$$\begin{pmatrix}
-\mu_h & 0 & 0 & 0 & 0 & 0 & 0 & \gamma_h & 0 & -b_1 & 0 & -b_2 \\
0 & -\eta_1 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & b_1 & 0 & 0 \\
0 & \kappa_1 & -z_1 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\
0 & 0 & 0 & -\eta_2 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & b_2 \\
0 & 0 & 0 & \kappa_2 & -z_2 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\
0 & 0 & 0 & 0 & 0 & -\eta_3 & 0 & 0 & 0 & 0 & 0 & 0 \\
0 & 0 & 0 & 0 & 0 & \kappa_3 & -z_3 & 0 & 0 & 0 & 0 & 0 \\
0 & 0 & \theta_1 & 0 & \theta_2 & 0 & \theta_3 & -z_4 & 0 & 0 & 0 & 0 \\
0 & -b_3 & -b_3 & 0 & 0 & -b_3 & -b_3 & 0 & -\mu_m & 0 & 0 & 0 \\
0 & b_3 & b_3 & 0 & 0 & b_3 & b_3 & 0 & 0 & -\mu_m & 0 & 0 \\
0 & 0 & 0 & -b_4 & -b_4 & -b_4 & -b_4 & 0 & 0 & 0 & -\mu_d & 0 \\
0 & 0 & 0 & b_4 & b_4 & b_4 & b_4 & 0 & 0 & 0 & 0 & -\mu_d
\end{pmatrix} = 0 \quad (41)$$

Where

$$\left.\begin{aligned}
b_1 &= \frac{\alpha_m \Lambda_h}{\mu_h} \\
b_2 &= \frac{\alpha_d \Lambda_h}{\mu_h} \\
b_3 &= \frac{\alpha_{vm} \Lambda_m}{\mu_m} \\
b_4 &= \frac{\alpha_{vd} \Lambda_d}{\mu_d}
\end{aligned}\right\} \quad (42)$$

The right eigenvector denoted by

$$w = (w_1, w_2, w_3, w_4, w_5, w_6, w_7, w_8, w_9, w_{10}, w_{11}, w_{12})^T \quad (43)$$

are given as

$$[J(\varepsilon_0)][w] = [0] \quad (44)$$

Solving the equations we have;

$$w_1 = \frac{w_3(\kappa_1\theta_1\gamma_h - \eta_1 z_1 z_4),}{\kappa_1 z_4 \mu_h} + \frac{w_5(\kappa_2\theta_2\gamma_h - \eta_2 z_2 z_4),}{\kappa_2 z_4 \mu_h}, w_2 = \frac{z_1 w_3}{\kappa_1}, w_4 = \frac{z_3 w_5}{\kappa_2},$$

$$w_8 = \frac{\theta_1 w_3 + \theta_2 w_5}{z_4}, w_9 = -\frac{\eta_1 z_1 w_3}{\kappa_1 b_1} w_{10} = \frac{\eta_1 z_1 w_3}{\kappa_1 b_1}, w_{11} = -\frac{\eta_2 z_2 w_5}{\kappa_2 b_2}, \quad (45)$$

$$w_{12} = \frac{\eta_2 z_2 w_5}{\kappa_2 b_2}, w_3 > 0, w_5 > 0, w_6 = w_7 = 0.$$

The left eigenvalues denoted by

$$v = (v_1, v_2, v_3, v_4, v_5, v_6, v_7, v_8, v_9, v_{10}, v_{11}, v_{12}, v_{13}, v_{14})^T \quad (46)$$

are given below as

$$[J(\varepsilon_0)]^T[v]=[0] \tag{47}$$

Solving the equations we have;

$$v_2=\frac{\mu_m v_{10}}{b_1}, v_3=\frac{\eta_1\mu_m v_{10}}{b_1(z_1+\kappa_1)}, v_4=\frac{\mu_d v_{12}}{b_2}, v_5=\frac{\eta_2\mu_d v_{12}}{b_2(z_2+\kappa_2)},$$
$$v_7=\frac{\eta_2 v_6}{(z_2+\kappa_2)}, v_6>0, v_{10}>0, v_{12}>0, v_1=v_8=v_9=v_{11}=0. \tag{48}$$

Consider $R_0=1$ (assuming that $R_{0d}<R_{0m}$) and choose $\alpha_m=\alpha_m^*$ as the bifurcation parameter. Solving for $\alpha_m=\alpha_m^*$ from $R_0=1$ gives

$$\alpha_m=\alpha_m^*=\frac{\eta_1 z_1\mu_h\mu_m^2}{\Lambda_h\Lambda_m\alpha_{vm}(z_1+\kappa_1)} \tag{49}$$

The following theorem is used to compute whether or not there exists a backward bifurcation $R_0=1$ in the system (29) - (40) [17].

Theorem 1: Consider the following general system of ordinary differential equations with a parameter ϕ such that

$$\frac{dX}{dt}=f(x,\phi):\mathbb{R}^n\times\mathbb{R}\to\mathbb{R}^n and f\in\mathbb{C}^2(\mathbb{R}^n\times\mathbb{R})$$

where 0 is an equilibrium point of the system $\left(i.e. f(0,\phi)\equiv 0 \text{ for all } \phi\right)$ and

i. $Q=D_x f(0,0)=(\frac{\partial f_i}{\partial x_j}(0,0))$ is the linearization matrix of the system around the equilibrium point 0 with ϕ evaluated at 0;
ii. Zero is a simple eigenvalue of Q and all other eigenvalues of Q have negative real parts;
iii. Matrix Q has a right eigenvector w and a left eigenvector v corresponding to the zero eigenvalue.

Let f_k be the kth component of f and

$$a=\sum_{k,i,j=1}^{n} v_k w_i w_j\frac{\partial^2 f_k}{\partial x_i\partial x_j}(0,0) \tag{50}$$

$$b=\sum_{k,i,j=1}^{n} v_k w_i\frac{\partial^2 f_k}{\partial x_j\partial\phi^*}(0,0) \tag{51}$$

then the dynamics of the system around the equilibrium point 0 is totally determined by the sign of a and b. Particularly.

i. $a>0$, $b>0$. When $\phi<0$ with $|\phi|\ll 1$; 0 is locally asymptotically stable; and there exists a positive unstable equilibrium; when $0<\phi\ll 1$; 0 is unstable and there exists a negative and locally asymptotically stable equilibrium.
ii. $a<0$ $b<0$. When $\phi<0$ with $|\phi|\ll 1$; 0 is unstable; when $0<\phi\ll 1$; 0 is locally asymptotically stable; and there exists a positive unstable equilibrium.
iii. $a>0$ $b<0$. When $\phi<0$ with $|\phi|\ll 1$, 0 is unstable, and there exists a locally asymptotically stable negative equilibrium; when $0<|\phi|\ll 1$; 0 is stable; and a positive unstable equilibrium appears.
iv. $a<0$, $b>0$. When ϕ changes from negative to positive, 0 changes its stability from stable to unstable. Correspondingly a negative unstable equilibrium becomes a positive and locally asymptotically stable.

After so many computations we have

$$a = w_{10}\alpha_m \begin{pmatrix} v_2 w_1 \\ + w_4 (v_6 - v_4) \\ + w_5 (v_6 - v_5) \end{pmatrix} + w_{12}\alpha_d \begin{pmatrix} v_4 w_1 \\ + w_2 (v_6 - v_2) \\ + w_3 (v_6 - v_3) \end{pmatrix} + (w_2 + w_3) \begin{pmatrix} v_{10} w_9 \alpha_{vm} \\ + v_{12} w_{11} \alpha_{vd} \end{pmatrix} > 0 \tag{52}$$

and

$$b = v_2 w_{10} \frac{\partial^2 f_2}{\partial x_{10} \partial \alpha_m^*} = \frac{v_2 w_{10} \Lambda_h}{\mu_h} > 0 \tag{53}$$

It is observed that $a > 0$ and $b > 0$ the result satisfies the theorem above. Hence, it is locally asymptotically stable.

4.4 Global Stability of Endemic Equilibrium Points

Theorem 2: The endemic equilibrium ε_E of the system is globally asymptotically stable wherever $R_0 > 1$.

Proof: We construct a common quadratic Lyapunov function [18]

$$V(S_h, E_{hm}, I_{hm}, E_{hd}, I_{hd}, E_{md}, I_{md}, R_h, S_m, I_m, S_d, I_d) = \frac{1}{2}\begin{bmatrix} (S_h - S_h^*) + (E_{hm} - E_{hm}^*) + (I_{hm} - I_{hm}^*) + (E_{hd} - E_{hd}^*) \\ + (I_{hd} - I_{hd}^*) + (E_{md} - E_{md}^*) + (I_{md} - I_{md}^*) + (R_h - R_h^*) \end{bmatrix}^2 + \frac{1}{2}\left[(S_m - S_m^*) + (I_m - I_m^*)\right]^2 + \frac{1}{2}\left[(S_d - S_d^*) + (I_d - I_d^*)\right]^2 \tag{54}$$

Differentiating

$$\frac{dV}{dt} = \begin{bmatrix} (S_h - S_h^*) + (E_{hm} - E_{hm}^*) + (I_{hm} - I_{hm}^*) + (E_{hd} - E_{hd}^*) \\ + (I_{hd} - I_{hd}^*) + (E_{md} - E_{md}^*) + (I_{md} - I_{md}^*) + (R_h - R_h^*) \end{bmatrix} \frac{d}{dt}(S_h + E_{hm} + I_{hm} + E_{hd} + I_{hd} + E_{md} + I_{md} + R_h) + \left[(S_m - S_m^*) + (I_m - I_m^*)\right]\frac{d}{dt}(S_m + I_m) + \left[(S_d - S_d^*) + (I_d - I_d^*)\right]\frac{d}{dt}(S_d + I_d) \tag{55}$$

$$\frac{dV}{dt} = \begin{bmatrix} (S_h - S_h^*) + (E_{hm} - E_{hm}^*) + (I_{hm} - I_{hm}^*) + (E_{hd} - E_{hd}^*) \\ + (I_{hd} - I_{hd}^*) + (E_{md} - E_{md}^*) + (I_{md} - I_{md}^*) + (R_h - R_h^*) \end{bmatrix} \begin{pmatrix} \Lambda_h - \mu_h (S_h + E_{hm} + I_{hm} + E_{hd} + I_{hd} + E_{md} + I_{md} + R_h) \\ - (\delta_1 I_{hm} + \delta_2 I_{hd} + \delta_3 I_{md}) \end{pmatrix} + \left[(S_m - S_m^*) + (I_m - I_m^*)\right](\Lambda_m - \mu_m (S_m + I_m)) + \left[(S_d - S_d^*) + (I_d - I_d^*)\right](\Lambda_d - \mu_d (S_d + I_d)) \tag{56}$$

Assuming

$$\left.\begin{aligned} \Lambda_h &= \mu_h (S_h^* + E_{hm}^* + I_{hm}^* + E_{hd}^* + I_{hd}^* + E_{md}^* + I_{md}^* + R_h^*) \\ &+ (\delta_1 I_{hm}^* + \delta_2 I_{hd}^* + \delta_3 I_{md}^*) \\ \Lambda_m &= \mu_m (S_m^* + I_m^*) \\ \Lambda_d &= \mu_d (S_d^* + I_d^*) \end{aligned}\right\} \tag{57}$$

We have

$$\frac{dV}{dt}=\begin{bmatrix}\left(S_h-S_h^*\right)+\left(E_{hm}-E_{hm}^*\right)+\left(I_{hm}-I_{hm}^*\right)+\left(E_{hd}-E_{hd}^*\right)\\+\left(I_{hd}-I_{hd}^*\right)+\left(E_{md}-E_{md}^*\right)+\left(I_{md}-I_{md}^*\right)+\left(R_h-R_h^*\right)\end{bmatrix}$$

$$\begin{pmatrix}-\mu_h\begin{pmatrix}\left(S_h-S_h^*\right)+\left(E_{hm}-E_{hm}^*\right)+\left(I_{hm}-I_{hm}^*\right)+\left(E_{hd}-E_{hd}^*\right)\\+\left(I_{hd}-I_{hd}^*\right)+\left(E_{md}-E_{md}^*\right)+\left(I_{md}-I_{md}^*\right)+\left(R_h-R_h^*\right)\end{pmatrix}\\-\left(\delta_1\left(I_{hm}-I_{hm}^*\right)+\delta_2\left(I_{hd}-I_{hd}^*\right)+\delta_3\left(I_{md}-I_{md}^*\right)\right)\end{pmatrix} \quad (58)$$

$$-\mu_m\left[\left(S_m-S_m^*\right)+\left(I_m-I_m^*\right)\right]\left(\left(S_m-S_m^*\right)+\left(I_m-I_m^*\right)\right)$$

$$-\mu_d\left[\left(S_d-S_d^*\right)+\left(I_d-I_d^*\right)\right]\left(\left(S_d-S_d^*\right)+\left(I_d-I_d^*\right)\right)$$

Let

$$\begin{aligned}&T_1=S_h-S_h^*,T_2=E_{hm}-E_{hm}^*,T_3=I_{hm}-I_{hm}^*,T_4=E_{hd}-E_{hd}^*,T_5=I_{hd}-I_{hd}^*\\&T_6=E_{md}-E_{md}^*,T_7=I_{md}-I_{md}^*,T_8=R_h-R_h^*,T_9=S_m-S_m^*,T_{10}=I_m-I_m^*,\\&T_{11}=S_d-S_d^*,T_{12}=I_d-I_d^*,T_{13}=T_1+T_2+T_3+T_4+T_5+T_6+T_7+T_8,\\&T_{14}=T_9+T_{10},T_{15}=T_{11}+T_{12}\end{aligned} \quad (59)$$

So

$$\frac{dV}{dt}=-\left(\mu_hT_{13}^2+T_{13}\left(\delta_1T_3+\delta_2T_5+\delta_3T_7\right)+\mu_mT_{14}^2+\mu_dT_{15}^2\right) \quad (60)$$

It can be seen that $\frac{dV}{dt}\le 0$ and $\frac{dV}{dt}=0$ if and only if

$$\begin{aligned}&S_h=S_h^*,E_{hm}=E_{hm}^*,I_{hm}=I_{hm}^*,E_{hd}=E_{hd}^*,I_{hd}=I_{hd}^*E_{md}=E_{md}^*,\\&I_{md}=I_{md}^*,R_h=R_h^*,S_m=S_m^*,I_m=I_m^*,S_d=S_d^*,I_d=I_d^*\end{aligned} \quad (61)$$

From LaSalle's invariant Principle all solutions in (1) – (12) approaches ε_E as $t\to\infty$ if $R_0>1$. The endemic equilibrium ε_E is therefore globally asymptotically stable in Γ whenever $R_0>1$.

V. DISCUSSION AND CONCLUSION

In this work, a model to evaluate malaria and dengue fever co-infection is proposed using system of non-linear ordinary differential equations. We compute the reproduction number using the next generation matrix and established the Disease Free and Endemic Equilibrium points. Applying the central Manifold theorem we prove that the Endemic point is locally stable and we prove using the quadratic Lyapunov function that the endemic equilibrium is globally stable. It shows that when protective precaution are taken, the disease transmission will not cause much death. Also, future analysis can be carried out to consider sensitivity analysis and optimal control, age structure, impact of hygiene, climate etc can be considered in extending the model.

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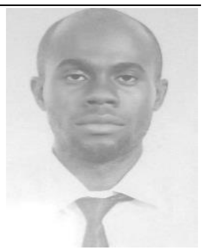

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