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A NONLINEAR MATHEMATICAL MODEL FOR MALARIA INCORPORATING VACCINATION PARAMETERS.

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ABSTRACT

Malaria is a life threatening illness that affect millions of people all over the world even though significant effort have been implemented with the use of Insecticide treated net, the disease remains chronic, however we formulated the model using the basic reproduction number and it was found that the basic reproduction number is less than 1, the disease free equilibrium and the Endemic Equilibrium of the disease were carried out. The dynamics of the model is also invested numerically using published data. Results suggest that the vaccination can be effective in wiping malaria, Specifically, it indicates that with vaccination, malaria eradication efforts could see a substantial boost, potentially leading to significant reductions in cases and deaths.

INTRODUCTION

Malaria, is a vector-borne disease caused by Plasmodium protozoans, and is transmitted through the bite of an infected female Anopheles mosquito. Malaria remains a significant global health issue, accounting for an estimated 247 million cases in 2021 [1], with the majority occurring in Africa, where it causes about 20% of child deaths. The disease poses a severe public health and socioeconomic burden in developing countries, contributing substantially to mortality and morbidity [2].

Malaria transmission is influenced by several factors, including the presence of infected mosquitoes, human susceptibility, and environmental conditions [3]. Asymptomatic carriers—individuals who harbor the malaria parasite without displaying symptoms—play a crucial role in the disease's spread by transmitting the parasite to mosquitoes, which then infect others. These carriers complicate control efforts, particularly in highly endemic regions [4,5]. The WHO estimates that 60 million people were asymptomatic carriers in 2021, forming a hidden reservoir that perpetuates malaria transmission.

The World Health Organization (WHO)'s 2023 World Malaria Report highlights that global malaria cases in 2022 exceeded pre-COVID-19 levels recorded in 2019. Approximately 249 million malaria cases were reported in 85 endemic countries in 2022, corresponding to an

incidence of 58 cases per 1000 population at risk. In comparison, 233 million cases were reported in 2019, with an incidence of 57 cases per 1000 people. Notably, the 2022 figures were 55% higher than the 2025 Global Technical Strategy for Malaria target of 26 cases per 1000 population at risk. Of the 249 million cases in 2022, 94% (approximately 233 million) occurred in the WHO African Region [1]. Additionally, malaria deaths were estimated at 619,000 in 2021 and 608,000 in 2022, reflecting a mortality rate of 14.3 deaths per 100,000 population at risk.

Environmental factors such as temperature, rainfall, and vegetation also significantly impact malaria transmission. Warm, humid conditions enhance mosquito activity and reproduction, while rainfall creates breeding sites, and vegetation provides shelter for mosquitoes and their hosts [6]. Climate change exacerbates malaria risks by expanding the geographic range of malaria-carrying mosquitoes and increasing breeding habitats due to extreme weather events such as floods and droughts, as emphasized in the WHO World Malaria Report.

Effective malaria control strategies include vector control, drug prophylaxis, as well as timely diagnosis and treatment. Vector control methods, such as insecticide-treated bed nets and residual indoor spraying, aim to reduce mosquito populations. The drug prophylaxis prevents malaria infections and is primarily recommended for travellers to endemic regions. Prompt and accurate diagnosis and treatment are essential to mitigate severe complications and fatalities.

Vaccination is a key strategy in combating Malaria, eith the RTS,S/AS01 vaccine showing promise in reducing cases and deaths.

Despite the success of existing interventions, efforts to eliminate malaria are hindered by the emergence of insecticide and drug resistance [7]. To complement traditional measures, the European Medicines Agency (EMA) approved the RTS, S/AS01 malaria vaccine, known as Mosquirix, targeting P. falciparum. This vaccine reduces severe malaria cases in infants aged 6 weeks to 17 months in high-malaria regions [8]. The WHO recommended the pilot implementation of the four-dose Mosquirix schedule in Ghana, Kenya, and Malawi, targeting children aged 1 year to 59 months. The schedule involved three initial doses administered four weeks apart, followed by a fourth dose 15–18 months later [9,10]. The efficacy of the vaccine is crucial for its role in reducing malaria transmission, morbidity, and mortality, making it a vital complementary tool in high-burden regions.

Mathematical Modeling plays a pivotal role in understanding infectious disease dynamics and designing effective interventions. For malaria, models have been used to evaluate elimination strategies, assess delivery methods, and predict resistance spread, emphasizing the protective effects of multiple control measures [11]. Models integrating vaccine-induced immunity provide insights into the short- and long-term impacts of vaccines on transmission dynamics, including pre-erythrocytic and transmission-blocking vaccines [12,13]. These studies highlight the importance of vaccine-induced immunity, the duration of effectiveness, and combination strategies for optimal outcomes.

Advanced modeling approaches incorporate in-host dynamics, immune system interactions, and environmental factors to simulate real-world conditions. For instance, pre-erythrocytic vaccines reduce clinical severity, while combining vaccines amplifies transmission reduction and improves immune responses [14]. Broader vaccination models, such as those for measles, inform optimal vaccination coverage for disease control and herd immunity enhancement [17].

Malaria-specific models address complex transmission settings, showing how vaccines combined with vector control can push elimination thresholds [18]. Models, such as those based on the Garki Project, include immunity loss, booster mechanisms, and disease severity to simulate vaccination programs. These models predict interactions between transmission blocker immunity and loss of immunity, offering custom solutions for unstable transmission regions [19]. Optimal protocols for chemo-prevention during seasonal outbreaks further demonstrate the adaptability of modeling approaches [20]. Collectively, these efforts underscore the value of integrated strategies and ecological considerations in malaria control.

The primary objective of this paper is to analyze the dynamics of malaria transmission within a vaccinated population, focusing on the interraction between vaccination proportion and vaccine-induced immunity rate. Using a deterministic compartmental model, this study examines how different factors influence the spread and control of malaria in both human and mosquito populations. Inclusion of vaccination parameters, such as waning immunity and vaccine protection levels, allows for a detailed exploration of their impact on reducing disease prevalence. By assuming permanent immunity for recovered individuals and no disease-induced mortality in mosquitoes, the model establishes a framework for understanding fundamental transmission dynamics. The findings aim to provide critical insights into optimizing vaccination strategies and informing public health policies in regions with varying malaria endemicity.

The rest of the paper is organized as follows: Section 2 details the mathematical formulation of the model. In Section 3, we analyze the model, including the basic reproduction number and equilibria. Section 4 provides stability analyses. Section 6 presents numerical results, findings, and a discussion. Finally, conclusions are presented in Section 7.

MODEL FORMULATION

In this section, we formulate a deterministic compartmental model to describe the transmission dynamics of malaria. The model has five population classes for the host (human) population: susceptible individuals

$$\frac{ds_h}{ds} = \pi_h + \propto_h R_h - \beta_h S_h - (\tau_h + \mu_h) S_h$$

$$\frac{dE_h}{ds} = \beta_h S_h - (V_h + \mu_h) E_h$$

$$\frac{dI_h}{ds} = V_h E_h - \gamma I_h - (w_h + \mu_h + K\theta) I_h$$

$$\frac{dR_h}{ds} = K\theta I_h + \tau S_h - (\mu_m + \alpha_h) R_h$$

$$\frac{ds_m}{ds} = \pi_m - \beta_m S_m - (K\theta + \mu_m + \delta) S_m$$

$$\frac{dE_m}{ds} = \beta_m S_m - (V_m + \mu_m + \delta)E_m$$

$$\frac{dI_m}{ds} = V_m E_m - (\mu_m + \delta)I_m$$

To compute the disease free equilibrium for the model equation above for $(S_h, E_{h,} I_{h,} R_h)$

DFE $(\frac{\pi_h + \alpha_h R_h}{\tau_h + \mu_h + \beta_h}, 0,0, \frac{K\theta I_h + \tau S_h}{\mu_m + \alpha_h}, \frac{\pi_m}{\beta_m + K\theta + \mu_m + \delta)}, 0, 0)$

Basic Reproduction

The basic reproduction number is the number of secondary infection produce by a single infective in an entirely susceptible population.

To compute the basic reproduction number, we divide the system into the appearance of new infection which is the F matrix and the Transfer of Infection which is the V- Matrix, However, the basic reproduction number is computed as follows:

New infections (F):

F = $\begin{bmatrix} \lambda_h S_h \\ 0 \\ \lambda_m S_m \end{bmatrix}^T$ [λ_h S_h, 0, λ_m S_m, 0]^T

Transfers (V):

V= $\begin{bmatrix} (V_h + \mu_h)E_h \\ -V_h E_h + \gamma I_h + w_h + \mu_h + K\theta\,)I_h \\ (V_m + \mu_m + \varphi)E_m,, -V_m E_m + \mu_m + \varphi) \end{bmatrix}^T$

V = [(V_h + μ_h) E_h, -V_h E_h + γ I_h + (w_h + μ_h + Kθ) I_h, (V_m + μ_m + ψ) E_m, -V_m E_m + (μ_m + ψ) R_h]^T

Jacobian matrices (F and V):

F = ∂F/∂x | (DFE)

V = ∂V/∂x | (DFE)

Next-generation matrix: FV^(-1)

R0: spectral radius of FV^(-1)

Let's compute F and V:

$$F = \begin{bmatrix} 0 & \beta_h & 0 & 0 \\ 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & \beta_m \\ 0 & 0 & 0 & 0 \end{bmatrix}$$

F = [0 β_h 0 0; 0 0 0 0; 0 0 0 β_m; 0 0 0 0]

$$V = \begin{bmatrix} V_h + \mu_h, & 0 & 0 & 0 \\ -V_h\gamma + w_h + \mu_h + K\theta & 0 & 0 & 0 \\ 0 & 0 & V_m + \mu_m + \varphi\ 0, & 0,0,0, V_m(\mu_m + \varphi) \end{bmatrix}$$

V = [(V_h + μ_h) 0 0 0; -V_h γ + w_h + μ_h + Kθ 0 0; 0 0 (V_m + μ_m + ψ) 0; 0 0 -V_m (μ_m + ψ)]

R0 expression:

$$R_0 = \sqrt{\frac{\beta_h V_h}{(V_h+\mu_h)}}\left(\frac{\gamma+w_h+\mu_h+K\theta\times\beta_m V_m}{((V_m+\mu_m+\varphi)(\mu_m+\varphi)]}\right)$$

STABILITY OF THE DISEASE FREE EQUILIUBRIUM

$J(E_0) =$

$F_1 = \beta_h - (\tau_h + \mu_h) \quad 0 \quad 0 \quad 0 \quad \alpha_h \quad 0 \quad 0$

$F_2 = \beta_h \quad -(v_h + \mu_h) \quad 0 \quad 0 \quad 0 \quad 0 \quad 0$

$F_3 = 0 \quad v_h \quad$ y-$(w_h + \mu_h + k\theta)$ 0 0 0 0

$F_4 = 0 \quad 0 \quad k\theta \quad -(\mu_m + \alpha_h) \quad 0 \quad 0 \quad 0$

$F_5 = 0 \quad 0 \quad 0 \quad 0 \quad \beta_m - (k\theta + \mu_m + \delta) \quad 0 \quad 0$

$F_6 = 0 \quad 0 \quad 0 \quad 0 \quad \beta_m \quad (V_m + \mu_m + \delta)E_m$

$F_7 = 0 \quad 0 \quad 0 \quad 0 \quad 0 \quad V_m \quad (\mu_m + \delta)I_m$

ENDEMIC EQUILIBRIUM

Equations:*

$$\Lambda_h + \propto_h R_h - \lambda_h S_h - (\tau_h + \mu_h) S_h$$

$\Lambda_h + \alpha_h R_h - \lambda_h S_h - (\tau_h + \mu_h) S_h = 0$

$\lambda_h S_h - (V_h + \mu_h) E_h = 0$

$V_h E_h - \gamma I_h - (w_h + \mu_h + K\theta) I_h = 0$

$K\theta I_h + \tau_h S_h - (\mu_m + \alpha_h) R_h = 0$

$\Lambda_m - \lambda_m S_m - (K\theta I + \mu_m + \psi) S_m = 0$

$\lambda_m S_m - (V_m + \mu_m + \psi) E_m = 0$

$V_m E_m - (\mu_m + \psi) I_m = 0$

Solving:

Let's express some compartments in terms of others:

$E_h = \lambda_h S_h / (V_h + \mu_h)$

$I_h = V_h E_h / (\gamma + w_h + \mu_h + K\theta) = V_h \lambda_h S_h / ((V_h + \mu_h)(\gamma + w_h + \mu_h + K\theta))$

$I = I_h$ (for simplicity)

$\lambda_h = \beta_h I_m$

$\lambda_m = \beta_m I_h$

Substituting and solving for S_h, S_m, I_h, I_m:

$S_h = \Lambda_h / (\lambda_h + \tau_h + \mu_h)$

$S_m = \Lambda_m / (\lambda_m + \mu_m + \psi)$

Using $\lambda_h = \beta_h I_m$ and $\lambda_m = \beta_m I_h$:

$I_h = (V_h \beta_h I_m S_h) / ((V_h + \mu_h)(\gamma + w_h + \mu_h + K\theta))$

$I_m = (V_m \beta_m I_h S_m) / ((V_m + \mu_m + \psi)(\mu_m + \psi))$

Solving these equations leads to:

$I_h = \sqrt{(\Lambda_h \Lambda_m \beta_h \beta_m V_h V_m / (...))}$ (non-zero if R0 > 1)

Endemic Equilibrium (EE):

$(S_h, E_h, I_h, R_h, S_m, E_m, I_m, R_m) \neq$ (DFE values)

The EE exists if R0 > 1.

Parameter values of the model

parameter	value	
π_h	0.07	Recruitment rate of susceptible humans
α_h	0.000017	Loss of immunity by recovered human population
R_h	0.89	Recovered Humans
β_h	0.24	Transmission rate of infected mosquitoes to human
S_h		Susceptible Humans
τ_h	0.008	Vaccination Rate
μ_h	0.00004643	Natural death rate
v_h	0.0007	Incubation Period
w_h	0.006	Disease Induced death rate
β_m	0.0067	Transmission from infected Humans to susceptible mosquitoes
v_m	0.0065	Incubation period of Mosquitoes
δ	0.0004	Death rate due to Insectide spray
γ	0.05	Infected Malaria due to Congenital

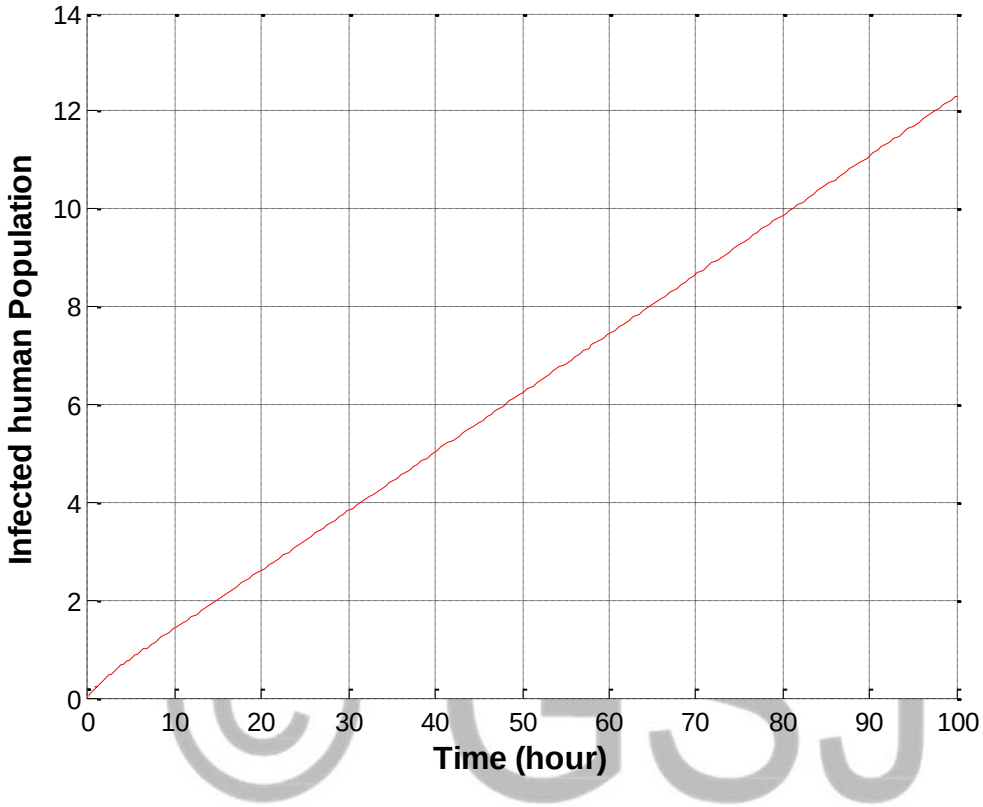

FIG 1 Shows the graph of Infected Population in a disease free population

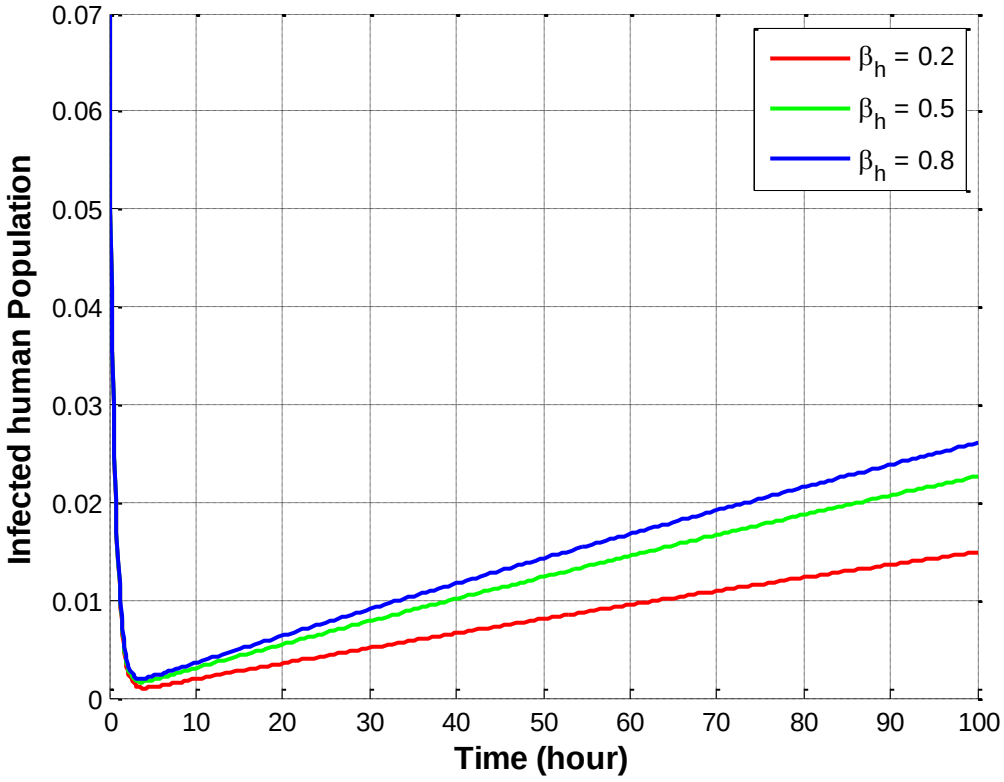

Fig 2 shows the graph of the transmission rate of infected mosquitoes to human at different varying parameters.

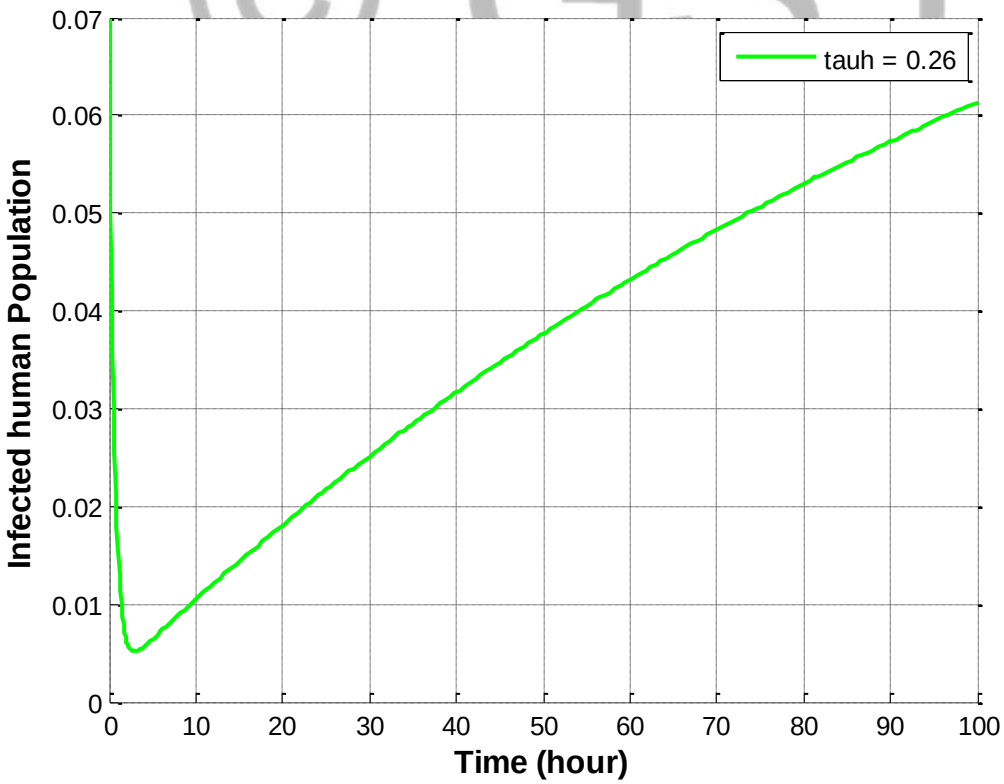

Figure 3 shows the graph of the vaccination parameter.

CONCLUSION

The dynamics of malaria transmission within a vaccinated population, focusing on the interraction between vaccination proportion and vaccine-induced immunity rate. this study examines how different factors influence the spread and control of malaria in both human and mosquito populations, Stability analysis shows the malaria free equilibrium is locally and Asymtotically stable when the malaria control is less than one. The existence of the endemic equilibrium was shown and the condition for local and global stability were obtained. Results suggest that the vaccination can be effective in wiping malaria,

Specifically, it indicates that with vaccination, malaria eradication efforts could see a substantial boost, potentially leading to significant reductions in cases and deaths.

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