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MODELLING THE PREVALENCE OF MALARIA IN WOMEN WITH PREGNANCY IN SELECTED LGAs OF TARABA STATES

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Abstract

African region experiences the highest proportion of malaria-related illnesses and deaths, especially those caused by the most lethal malaria parasite, Plasmodium falciparum. Year in year out, hundred millions of people are sick with malaria and between 1 and 3 million of deaths per year, the majority of these deaths are children between the age of 1 and 4 years and pregnant women. In pregnancy, malaria increases the risk of maternal anaemia, spontaneous abortions, stillbirths, premature deliveries, intra-uterine growth retardation and low birth weight babies, and these are all important causes of infant mortality. In this study a model using Mathematical modelling of malaria in women with pregnancy will be formulated. A total of 6793 samples of pregnant women with malaria was collected from six local government areas in the survey areas. These LGAs are: Ardo Kola 1180 (17.4%), Bali 1108 (16.3%), Donga 1082 (15.9%), Jalingo (18.2%), Kurmi 1127 (13.6%), Ibi 1059 (18.5%). It was discovered that Anopheles mosquito responsible for malaria parasites in human if put under control can reduce the rate of malaria infection among pregnant women in the study areas. Analysis of variance showed significant differences in mosquito genera in relation to study areas (P < 0.05).

KEY WORD
Mathematical Model, Infection, Pregnancy, Malaria and Prevention.

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INTRODUCTION

After tuberculosis, malaria is the second leading cause of mortality from infectious diseases. According to the Centers for Disease Control and Prevention (CDCP, 2015). Pregnant women lose some protection from malaria infection due to changes in their immune systems and the existence of a new organ (the placenta) with new locations for parasites to adhere. So, malaria in pregnancy is more severe due to the altered immune response in pregnancy. It can harm both mother and baby. It can cause anemia in the mother or even the death of the mother. Malaria can lead to preterm delivery, low-weight babies, growth restriction of the fetus inside, and death of the baby inside.

Malaria parasites have been with us since the dawn of time. They undoubtedly originated in African (along with mankind) and the fossils of mosquitoes dates up to 30 million years old, indicates that vector for malaria was present well before the earliest history. The minute intracellular organisms which infect the Red Blood Cell of man and cause malaria were seen as long ago as 1880 by a French

Army surgeon called Laveran. The way in which these parasites are transferred from one human being to another was discovered later in the 19th Century by two other workers, Ronald Ross, an officer in the Medical Service in Indian, and Giovanni Grassi, an Italian Doctor and Zoologist (Clegg & Clegg, 1980).

Malaria has since been labeled as the ultimate killer of all time. Among its victim was Alexander the Great (336 BC). The fall of the Greek and Roman civilizations has been attributed in part to the devastations of malaria. Today, it is confined to the hotter parts of the world on either side of the equator (Dowdeswell, 1984).

However, Malaria is an infectious disease that is caused by a parasite of the genus Plasmodium. It is spread by the bites of a specific species of mosquito from a genus Anopheles female mosquitoes. Of all the 123 species of Plasmodium we have, only four are definitely human (Egede and Paterne, 2021). Among these, Plasmodium falciparum is the one that is responsible for a large majority of deaths, while the other three species only cause mild forms of malaria that are not harmful: the ones that are not deleterious are Plasmodium vivax, Plasmodium ovale, and Plasmodium malariae. Malaria is one of the most prevalent vector-borne disease. Year in year out, hundred millions of people are vile with malaria and between 1 and 3 million of deaths

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occurred per year, the majority of these deaths are children between the age of 1 and 4 years and expectant women. 80% of these cases are found in sub-Saharan Africa. The disease has a recurrent decimal in places where control efforts were effective and has been appearing in places that are regarded as free from the disease despite decades of annihilation and control efforts of this epidemic (Faniran, Falade, Ogunsanwo, 2020). On a thoughtful note, it is a high time to have an insight knowledge of malaria and its mode of dynamic transmission as while as modeling for effective control and possible control since the Faniran, et el, (2020). Sensitivity Analysis of an Un- treated Liver-Stage Malaria. Journal of Computer Science & Computational Mathematics effort of all agencies is to have free malaria environment.

The World Health Organization (WHO, 2004) in her report rate Africa as having 90% of the world's encumbrance of malaria. The reports revealed that pregnant women and children in Africa are predominantly susceptible to the adverse consequences of malaria caused by the most lethal parasite, Plasmodium falciparum. The African Region was adjured by the World Health Organization (WHO) as experiencing the majority of the global burden of malaria-associated maternal illness and low birth weight. For instance, pregnant women in malaria-endemic areas do not always receive the necessary prevention and treatment they need, and this contributes to the extremely high numbers of maternal and infant deaths caused by malaria (WHO, 2017).

Kelechi, et el (2019) reported that Malaria has been a major public health problem in ninety-one countries world-wide with sub-Sahara Africa bearing 80% of the disease burden. At present, Malaria remains endemic in Nigeria where the parasitic disease is deleterious to children aged under 5 years and pregnant women compared to the rest of the population groups. In pregnancy, malaria increases the risk of maternal anemia, spontaneous abortions, stillbirths, premature deliveries, intra-uterine growth retardation and low birth weight babies, and these are all important causes of infant mortality. Ahmed, et el (2021) avert that Malaria infection has remains endemic in some countries including

Nigeria, which contributed the major percentage of cases (27%) to its global prevalence in the year 2016 (WHO, 2017). Complications like anaemia, abortion, stillbirth, low birth weight and preterm baby could arise from malaria infection during pregnancy. The World Health Organization (WHO)

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acclaims that all pregnant women living in malaria endemic regions of sub-Saharan Africa should always sleep under an Insecticide-Treated Net (ITN), and take monthly doses of intermittent preventive treatment in pregnancy (IPTP) but this has always results to low response from the population because of nonchalant attitudes (WHO, 2017).

According to available statistics, every year approximately 25 million African women become pregnant in malaria-endemic areas and are at risk of Plasmodium falciparum malaria infection during pregnancy (Kelechi et al 2019; WHO, 2004). Most women in the African Region reside in areas of comparatively stable malaria transmission where the principal effects of malaria infection during pregnancy are associated with malaria-related anemia in the mother and with the presence of parasites in the placenta. The resultant impairment of fetal nutrition contributes to low birth weight (LBW), which is a leading cause of poor infant survival and development in Africa (WHO, 2004).

The idea of evolving and consolidation the prevention and control of malaria during pregnancy is of paramount concern and it should be accorded the highest priority especially in a developing nation and in particular Nigeria. Malaria in Pregnancy (MIP) has been a major headache to the region of a tropical area where it cost huge amount of money to the government and the family (Egede and Paterne, 2021).

Statement of the Problem Malaria

Malaria in women with pregnancy has been a devastating menace in the tropical region and the SubSaharan Africa. The disease always leads to anemia, abortion, stillbirth and low birth weight. WHO and the government of this region has always been trying to see that the disease is minimize or eradicated (Egede and Paterne, 2021). For instance, in Africa, malaria's ill effects on pregnant women and children under 5 has been a burden in Nigeria including, Taraba States. The state has been losing huge amount of money to see that the disease is being eradicated. Although the serious impact of malaria infection during pregnancy has been known for a very long time now, coverage of pregnancies at risk for malaria infection according to World Health Organization (WHO, 2004) and national guidelines has been low in most malaria-endemic countries, especially in Taraba and Adamawa States. It is of paramount important to have a mathematical model that will monitor

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and forecast the prevalence of malaria in women with pregnancy (Kelechi, et al 2019; WHO, 2004).

Aim and Objectives of Study

The aim of this study is to model the prevalence of malaria in women with pregnancy in Taraba State with the following objectives:

i. To have a mathematical model for the occurrence of malaria in women with pregnancy; ii. To forecast the incidence and prevalence rate of malaria in women with pregnancy; iii. To determine the incidence rate of malaria in women with pregnancy.

Significance of the Study

This research work will be of benefit to the following among many others:

a. **Health sectors:** that is to know which drugs needed to purchase more to be distributed to various hospitals and clinics.
b. **Government:** it will enable them to know how the drugs are circulated and the endemic spread.
c. **Populace:** this will be of benefit to the people in the society to know the causes and prevention of these common diseases.

Literature Review

Malaria is a major public health problem and causes much distress and premature death in the poorer area of tropical Africa, Asia, and Latin America. In many endemic areas it is becoming increasingly difficult to control because the resistance of parasite to anti-malaria drugs and the failure of vector control measures.

According to the world health organization (WHO) estimated that in the Africa region, roughly one half of suspected malaria cases received parasitological confirmation, Laishram, et al. (2012), malaria is a transmission of dependent upon a vector (a bite resulted from female Anopheles mosquito) it is deposited by a parasite. Humphries, et al. (2011) discourses that malaria is extensively spread in many parts of the world in the tropical Countries and transmission occurs in many temperate regions like most other parasite diseases. A number of factors determine the epidemiology of malaria disease. This includes factors related to the vector, environment, climate and the host.

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According to World Health Organization (WHO) report "malaria occurs in 100 Countries with about 40% of the world's population at risk. Each year there are estimated to be 275 million clinical cases of malaria (90% of them in sub-Sahara Africa) resulting in 1.12 million deaths, mostly (75%) in children under 5 years of age. The prevalent is growing due to man-made conflict and climate associated disaster, causing the movement of non-immune population to malaria endemic area".

According to Goldman L, et al. (2008) stated that malaria is a mosquito borne infection disease caused by a eukaryotic protest of the genus plasmodium. It is widely spread in tropical and subtropical regions, including parts of the Africa and Asia. Urban and peri-urban malaria are now substantial problems in certain areas of difficult to manage in certain areas of multi-drug resistance where effective drugs are unavailable. Also it was observed that malaria transmission is influenced by inter-related factors such as temperature, humidity, rainfall pattern and behaviours of human population.

This parasite that is being deposited during the process when these mosquitoes feed is called plasmodium which is of four types:

i. Plasmodium viviax.
ii. Plasmodium malaria.
iii. Plasmodium falciparium.
iv. Plasmodium oval.

These deposits in human takes the following stages before symptoms are felt by the host (humans); from sporozoite to trophozoite to gametocycle. It takes up to 10-15 days after deposit for this parasite, to mature and start spreading through the blood. It is an endemic disease; the trend is that, out of every 10 reported cases, 7 are carriers.

Causes of Malaria

Malaria is caused by a parasite transported by infected mosquitoes. The parasite that most often causes malaria needs warm temperature to grow and thrive, so the disease is typical of temperature countries, malaria was once common in most of the Europe and North America but it was eradicated completely.

Symptoms of Malaria

A symptom can be define as the change in the body condition that indicates illness. Also the symptoms occur ten days to four weeks after been bitten and

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are similar to symptoms brought on by: Headache, Vomiting, Shivering, Body weakness, Muscles pain, Higher body temperature.

Prevention of Malaria

The disease can be prevented by taking anti-malaria drugs and by avoiding mosquito bites in areas where malaria infection is common, those infected with malaria can be treated with recommended drugs, which are most active when taken promptly in the course of the disease. However, the Federal government of Nigeria in conjunction with other agencies such as World Health Organization (WHO), United Nation (UN), and United Nation's Children's by immunization, distribution new medicated mosquito nets, anti-malaria drugs in support of treatment and control of malaria infections.

Women in pregnancy has been vulnerable to malaria infections which sometime cost their life. The control of malaria infection has now been further strengthen at eradication. For example, Egede and Paterne, (2021) use mathematical model to model the transmission of malaria. They use compartmental model which incorporates variables that were tested. A Lyapunov function was used and the result shows that this disease (malaria) free equilibrium point was globally asymptotically stable whenever the basic reproduction number is less than unity. The existence and uniqueness of endemic equilibrium were examined. The result of the model shows that, in order to reduce the spread of Malaria in the study area, the number of mosquito bites on human per unit of time, the vector population of mosquitoes, the probability of being infected for a human bitten by an infectious mosquito per unit of time and the probability of being infected for a mosquito per unit of time must be reduced by applying optimal control measures.

A study conducted by Kelechi et al (2019) on the malaria prevention among pregnant and #non pregnant women and the children under 5 years revealed that adequate knowledge of malaria prevention and control can help in reducing the growing burden of malaria among vulnerable groups, particularly pregnant women and children aged under 5 years living in malaria endemic settings. Their findings also revealed that socio-demographic factors such as marital and educational status greatly influence knowledge on malaria prevention and control measures.

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Malaria is highly endemic in Nigeria and poses a major challenge as it impedes human development. It is both a cause and consequence of underdevelopment and remains one of the leading causes of morbidity and mortality in the country (FMOH, 2005). It accounts for about 60% of all clinic attendance in the Country, with the most vulnerable groups being children under 5 years and pregnant women (FMOH, 2005). The Federal Ministry of Health, Abuja admits that Nigeria has lost over #132 billion to the treatment of malaria; and that a child will be sick as a result of malaria between two and four times in a year; 70 percent of pregnant women suffer from malaria which contributes to maternal anemia, low birth weight, still birth, abortion and other pregnancy-related complications and that malaria is responsible for 60 percent out-patient visits to health facilities, 30 percent childhood deaths, while 25 percent of deaths include children under one year and 11 percent maternal death (Joel, 2007; Lawal, 2012). It is reported that out of the 10 major killer diseases in the Country, malaria is the most deadly and costly (Chukwuocha, 2012). At least 50% of Nigerians suffer from one form of episode or the other making it the most significant health problem in the country (Molta, 2000; Chukwuocha, 2012). The high transmission rate and prevalence of malaria is a result of the diverse mosquitoes breeding sites, which include practically receptacle that holds water, such as tins, cans, old tyres tree holes, cisterns, open pools, drainage, stream and pond (Ingstad et al., 2012). The current malaria control strategy as designed by Roll Back Malaria Programme focuses on early diagnosis and prompt, effective treatment of the disease, prevention of malaria through use of insecticide-treated materials and other vector control measures including residual indoor spraying, larviciding and environmental management. The result of LSM trial in Africa shows that hand-application of larvicides can reduce transmission by 70-90% in settings where mosquito larval habitats are defined and can be an effective method of malaria control especially when combined with Long Lasting Insecticide Net (LLIN) (Ulrike and Steven, 2011). Part of the efforts being made is the official commemoration of April 25 every year, starting from 2008 as World Malaria Day (CDC, 2017).

The distribution of malaria in the World is determined by the distribution of the various species of anopheline mosquitoes in which the malaria parasite (Plasmodium) undergo the phase of sexual reproduction (Clegg and Clegg, 1980). The genus Anopheles, one of the three genera of subfamily

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Anophelinae that contains about 380 species, among which around 70 have been shown to be competent vectors of the human disease (Service, 2004).
In Africa, the two main vectors are a complex of species referred to as Anopheles gambiaesensu lato and Anopheles funestus which is also probably a complex of species (Godfray,2003; Awolola et al., 2005; Temu et al.,2007). The most important of which in Africa south of the Sahara are An. gambiae, An. arabiensis and An. funestus. Others of minor importance are An. nili; An. moucheti; An. hargeavesis and An. hancoki. What makes Anopheles gambiae (and to a lesser extent Anopheles funestus) efficient vectors is that they are relatively specialized on humans and Anopheles gambiae in particular which seems to have evolved to be being anthropophilic and endophagic species have more frequent contacts with humans and thus an extremely effective vector of malaria, especially in tropical Africa (Service, 1980; Godfray, 2013).
A number of studies have been carried out on anopheline mosquito species. Examples are studies of Wanji et al. (2003) on mount Cameroon and Okafor (1991) in human dwellings in the Obafemi Awolowo University, Ile – Ife, South West Nigeria. Okafor (1991) found An. gambiae, An. funestus and An. nili present in the campus and the neighboring village. Lamidi (2009), also in his study in Sahel region of Yobe state, Nigeria found Anopheles gambiae, Anopheles funestus and Anopheles arabiensis. Major studies are those of Awolola et al. (2005); Munhenga et al. 2014; Olayemi and Ande, (2008); Okwa et al., (2007) among others.

Methodology of the study

Introduction

A simple deterministic model, that requires data in the form of a single estimate of parasite prevalence as an input, is going to be considered for the purpose of comparison with other more complex models. The model will be designed to include key aspects of malaria transmission and integrated control. The model will be divided into four (4) compartments. This means the human body will be divided into SEIR: Susceptible (S), Exposed (E), Infection (I) and Recovered (R). However, of mosquito population, we will only establish two compartments: susceptible (S) and infectious (I). There is no recovered class for the vector as mosquitoes never recover or latent class (for simplicity of the model). The state will purposively be stratified into the government approved zones as Northern, Central and Southern Zones

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respectively for easy and convenience of the research. Simple random sampling will be used to select hospitals that data will be collected from each zone for the purpose of the research.

MODEL FOR
ESTABLISHMENT OF THE MODEL

$$\begin{cases} \frac{dS_h}{dt} = \alpha_h N_h - \frac{\sigma b S_h I_h}{N_h} + \gamma R_h - \mu_h S_h, \\ \frac{dL_h}{dt} = \frac{\sigma b S_h I_v}{N_h} - (\mu_h + \delta) L_h, \\ \frac{dL_h}{dt} = \delta L_h - (\eta + \mu_h + \lambda) I_h \\ \frac{dR_h}{dt} = \lambda I_h - (\mu_h + \gamma) R_h \\ \frac{dS_v}{dt} = \alpha_v N_v - \frac{\sigma c S_v I_h}{N_h} - \mu_v S_v \\ \frac{dl_v}{dt} = \frac{\sigma c S_v I_h}{N_h} - \mu_v l_v \end{cases} \quad (1)$$

Description of parameters and Variables **A. The considered parameters are**

α_h: Birth rate for humans

α_v: Birth rate for mosquitoes

σ: Number of bites of a mosquito to a human per unit of time (Biting Rate)

b: The probability of being infected for a human bitten by an infectious mosquito per unit of time

c: The probability of being infected for a mosquito biting an infectious human per unit of time

δ: Rate of progression from latent to infectious state for human incubation

λ: Rate of progression from infectious to recovered state for human convalescence

γ: Rate of progression from recovered to susceptible state for humans

μ_h: Human (natural) mortality rate (survivorship)

η: Human malaria induced death rate

μ_v:Mosquito mortality rate

B. The considered variables are:

N_h : Total population for human (host)

N_v: Total population for mosquito (vector)

S_h: Class (number) of susceptible humans

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L_h: Class (number) of latent humans
I_h: Class of number of infectious humans
R_h: Class (number) of recovered humans
S_v: Class (number) of susceptible mosquitoes
I_v: Class (number) of infectious mosquitoes

NOTE: All parameters of the model are assumed to be non-negative C. **Existence and Positivity of Solutions.**

We show that the system is epidemiologically and mathematically well posed in the feasible region Ω given by

$$\Omega = \{(S_h, I_h, R_h, S_v, I_v) \in \mathbb{R}^6_+ : 0 \le \mu_h \le \alpha_h, 0 \le \mu_v \le \alpha_v\} \quad (2)$$

Hypothesis 1. The system (1) always admits positive solutions for all positive initial conditions and biological region $\Omega \in \mathbb{R}^6_+$ is positively invariant and globally attractive for the same system.

Proof: The system (1) can be written in the form $(t) = f(x(t))$ where

$$x = (x_{1,2}, x_3, x_4, x_5, x_6) = (S_h, L_h, I_h, R_h, S_v, I_v) \quad (3)$$

and

$$f(x) = (f_1(x), f_2(x), f_3(x), f_4(x), f_5(x), f_6(x)) \quad (4)$$

Then, the system (1) becomes

$$\frac{dx_1}{dt} = \dot{x}_1 = \alpha_h(x_1 + x_2 + x_3 + x_4) - \frac{\sigma b x_1 x_6}{x_1 + x_2 + x_3 + x_4} + \gamma x_4 - \mu_h x_1$$

$$\frac{dx_2}{dt} = \dot{x}_2 = \frac{\sigma b x_1 x_6}{x_1 + x_2 + x_3 + x_4} - A x_2$$

$$\frac{dx_3}{dt} = \dot{x}_3 = \delta x_2 - B x_3$$

$$\frac{dx_4}{dt} = \dot{x}_4 = \lambda x_3 - C x_4$$

$$\frac{dx_5}{dt} = \dot{x}_5 = \alpha_v (x_5 + x_6) - \frac{\sigma c x_3 x_5}{x_1 + x_2 + x_3 + x_4} - \mu_v x_5,$$

$$\frac{dx_6}{dt} = \dot{x}_5 = \frac{\sigma c x_3 x_5}{x_1 + x_2 + x_3 + x_4} - \mu_v x_6$$

Where $A = \mu_h + \delta$, $B = \eta + \mu_h + \lambda$ *and* $C = \mu_h + \gamma$.

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As the second member of the system (1) is locally Lipschitzian, then it implies that a unique solution is applicable. It is clear that $\forall j$ = 1, … ,6, $f_j(x) \geq 0$ if $x \in \{0, +\infty\}^6$, hence the positivity of the solution. Added member to member, the first four equations of the system (1) and the last equations of the same system, we notice that the total population of human and vector satisfies the following equations:

$$\begin{cases} \dot{N_h} = \alpha_h N_h - \mu_h N_h - \eta I_h, \\ \dot{N_v} = \alpha_v N_v - \mu_v N_v \end{cases} \quad (6)$$

From the equation (6) we have $\dot{N_h} \leq \alpha_h N_h - \mu_h N_h \Rightarrow N_h \leq 0$ if $\alpha_h \leq \mu_h$. So $N_h(t) \leq N_h(0)exp[(\alpha_h - \mu_h)t]$. In the same vein, we have $\dot{N_v} \leq 0$ i $_v \leq \mu$, and $N_v(t) \leq N_v(0)exp[(\alpha_v - \mu_v)t]$. We conclude that the region Ω is positively invariant. Moreover, if $\alpha_h < \mu_h$ and $_v < \mu_v$, we see that the solution of the system (1) enter in Ω in finite time, i.e. $N_h(t)$ asymptotically approaches α_h and $N_v(t)$ approaches α_v asymptotically. Therefore, all solutions in $\mathbb{R}^6$, eventually enter Ω i.e. the biological region Ω is globally attractive for the same system. So the problem is then mathematically and epidemiologically well posed. Hence, every solution of the model (1) with initial conditions in Ω remains in Ω for all t > 0.

D. Basic Reproduction Number

In order to access the stability of disease equilibra, the computation of the basic reproduction number
R_0 as established by Watmough and Van den Driessche will be used for our case. We know that

$N_h = S_h + L_h + I_h + R_h$ with $\{ L_h{}^h, R^{,I}{}_h{}^h :: uninfected^{infected\ state}\ state$ (7) and

$N_v = S_v + I_h$ With $\{ {}_vI^v, :: uninfected^{infected\ state}\ state$ (8)

In the infection free state, we have $L_h = I_h = R_h = 0 \Rightarrow N_h = S_h$ and $I_v = 0 \Rightarrow N_v = S_v$. So for $(L_h, _h, I_v)$ and using the expressions for N_h, and N_v that we have just found above, we have the following linear system:

(9)

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$$\begin{cases} \frac{dL_h}{dt} = \sigma b I_v - (\mu_h + \delta) L_h, \\ \frac{dI_h}{dt} = \delta L_h - (\eta + \mu_h + \lambda) I_h, \\ \frac{dI_v}{dt} = \frac{\sigma c N_v I_v}{N_h} - \mu_v I_v \end{cases}$$

Let $X = (L_h, I_h, I_v)'$ where the prime denote the transpose. The infection subsystem linearized is then in the form:

$$\dot{X} = (T + \Sigma) \quad (10)$$

Where is the transmission matrix and Σ' is the transition matrix such that,

$$T = \begin{pmatrix} 0 & 0 & \sigma b \\ 0 & 0 & 0 \\ 0 & \frac{\sigma c N_v}{N_h} & 0 \end{pmatrix} \text{ and } \Sigma = \begin{pmatrix} -(\mu_h+\delta) & 0 & 0 \\ \delta & -(\eta+\mu_h+\lambda) & 0 \\ 0 & 0 & -\mu_v \end{pmatrix} \quad (11)$$

So, the next generation matrix $K = T\Sigma^{-1}$ where $\Sigma^{-1} = \frac{1}{|\Sigma|} . \Sigma^{Adj}$, thus $\Sigma^{adj} = [Com(\Sigma)]'$ and $Com(\Sigma)$ isthebmatrix of cofactors of Σ. thus,

$$K = \begin{vmatrix} 0 & 0 & \frac{\sigma b}{\mu_v} \\ 0 & 0 & 0 \\ \frac{\delta \sigma c N_v}{N_h(\mu_h+\delta)(\eta+\mu_h+\lambda)} & \frac{\sigma c N_v}{N_h(\eta+\mu_h+\lambda)} & 0 \end{vmatrix} \quad (12)$$

By computation the dominant eigenvalue of K which is the reproduction number basic, we have

$$R_0 = \rho(K) = \sigma \sqrt{\frac{\delta}{\mu_h+\delta} \frac{bcN_v}{\mu_v N_h(\eta+\mu_h+\lambda)}} \quad (13)$$

As det(K) = 0, we notice that the K found is the next generation matrix with large domain denoted K_L. So, from this K_L, we deduce K^* which is the next generation matrix (i.e. K^* is the reduction of K_L), knowing that $\rho(K_L) = \rho(K^*)$. We have

$$K^* = E'K_L E = -E'T\Sigma E \text{ with } E = \begin{pmatrix} 1 & 0 \\ 0 & 0 \\ 0 & 1 \end{pmatrix}$$

Thus,

$$K^* = \begin{pmatrix} 0 & \frac{\sigma b}{\mu_v} \\ \frac{\delta \sigma c N_v}{N_h(\mu_h+\delta)(\eta+\mu_h+\lambda)} & 0 \end{pmatrix} \quad (14)$$

Since K^* is a 2x2 matrix, we have

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$$R_0 = \rho(K^*) = \frac{1}{2}\left[tr(K^*) + \sqrt{tr(K^*)^2 - 4\det(K^*)}\right] \qquad (15)$$

$$= \sigma\sqrt{\frac{\delta}{\mu+\delta}\,\frac{bcN_v}{\mu_v N(\eta+\mu_h+\lambda)}}$$

Stability Analysis of Disease Equilibria

There are two types equilibra, which are obtained by solving the system (1), for $\dot{S_h} = \dot{L_h} = \dot{I_h} = \dot{R_h} = \dot{S_v} = \dot{I_v} = 0$. In particular the disease-free equilibrium point (DFE), E_0, which is obtained by adding the condition $\dot{L_h} = \dot{I_h} = \dot{R_h} = \dot{I_v} = 0$. With these conditions, the resolution of the system (1) then gives

$$E_0 = \left(\frac{\alpha_h N_h}{\mu h}; 0; 0; \frac{\alpha_v N_v}{\mu v}; 0\right) \qquad (16)$$

And the endemic equilibrium "EE" point, is obtained with the condition $\dot{S_h} \neq 0$; $L_h \neq 0$; $I_h \neq 0$; $R_h \neq 0$; $S_v \neq 0$; $I_v \neq 0$. implicitily,we have

$$E_1^* = (S_h^*; {}^*h;\ I_h^*; R_h^*\ ;\ S_v^*; I_v^*;\ ) \qquad (17)$$

Stability of DFE

Theorem 2: The disease-free equilibrium, E_0,(DFE) of Equation (1), given by Equation (16), is locally asymptotically stable if $R_0 < 1$, and unstable $R_0 > 1$.

Proof. Let (M) be the jacobian of Equation (1) at point $M = (S_h, L_h, R_h, S_v, I_v$

$$J(M) = \begin{bmatrix} \frac{\sigma b I_v}{N_h} - \mu_h & 0 & 0 & \gamma & 0 & -\frac{\sigma b S_h}{N_h} \\ \frac{\sigma b I_v}{N_h} & -(\mu+\delta) & 0 & 0 & 0 & \frac{\sigma b S_h}{N_h} \\ 0 & \delta & -(\eta+\mu_h+\lambda) & 0 & 0 & 0 \\ 0 & \lambda & -(\mu+\gamma) & 0 & 0 & 0 \\ 0 & 0 & -\frac{\sigma c S_v}{N_h} & 0 & -\frac{\sigma c I_h}{N_h} - \mu_v & 0 \\ 0 & 0 & \frac{\sigma c S_v}{N_h} & 0 & \frac{\sigma c I_h}{N_h} & -\mu_v \end{bmatrix} \qquad (18)$$

The Jacobian matrix in equation (1) at a point E_0 then becomes

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$$J(E_0) = \begin{bmatrix} -\mu_h & 0 & 0 & \gamma & 0 & -\frac{\sigma b \delta_h}{\mu_h} \\ 0 & -(\mu_h + \delta & 0 & 0 & 0 & \frac{\sigma b \delta_h}{\mu_h} \\ 0 & \delta & -(\eta + \mu_h + \lambda) & 0 & 0 & 0 \\ 0 & 0 & \lambda & -(\mu + \gamma) & 0 & 0 \\ 0 & 0 & -\frac{\sigma c \alpha_v N_v}{\mu_v N_h} & 0 & -\mu_v & 0 \\ 0 & 0 & \frac{\sigma c \alpha_v N_v}{\mu_v N_h} & 0 & 0 & -\mu_v \end{bmatrix} \quad (19)$$

Consider (λ^*) the characteristic polynomial of $J(E_0)$, we then have
$|(E_0) - \lambda^* I_6| = P(\lambda^*)$

$$P(\lambda^*) = \begin{bmatrix} -\mu_h - \lambda^* & 0 & 0 & \gamma & 0 & -\frac{\sigma b \alpha_h}{\mu_h} \\ 0 & -(\mu_h + \delta - \lambda^* & 0 & 0 & 0 & \frac{\sigma b \alpha_h}{\mu_h} \\ 0 & \delta & -(\eta + \mu_h + \lambda) - \lambda^* & 0 & 0 & 0 \\ 0 & 0 & \lambda & -(\mu + \gamma) - \lambda^* & 0 & 0 \\ 0 & 0 & -\frac{\sigma c \alpha_v N_v}{\mu_v N_h} & 0 & -\mu_v - \lambda^* & 0 \\ 0 & 0 & \frac{\sigma c \alpha_v N_v}{\mu_v N_h} & 0 & 0 & -\mu_v - \lambda^* \end{bmatrix} \quad (20)$$

By expanding, we have

$$(\lambda^*) = \lambda^{*6} + (A + B + C + \mu_h + 2\mu_v)\lambda^{*5} + [\mu(2\mu_h + \mu_v) + (\mu + 2\mu_v)(A + B + C) + AB + AC + BC]\lambda^{*4} + [\mu_h\mu_v^2 + \mu(2\mu_h + \mu_v)(A + B + C) + (\mu_h + 2\mu_v)(AB + AC + BC) - D]\lambda^{*3} + [z]\lambda^{*2} + [\mu_h\mu_v^2(AB + AC + BC) + \mu(2\mu_h + \mu_v)ABC - (\mu_h\mu_v + C\mu_h + C\mu_v)D]\lambda^* + ABC\mu_h\mu_v - CD\mu_h\mu_v$$

Where A= $\mu_h + \delta, B = \mu_h + \eta + \lambda, C = \mu_h + \gamma$ and $D = \frac{bc\sigma^2\delta\alpha_h\alpha_v N_v}{\mu_h\mu_v N_h}$.

With Descartes rule of signs (13), if $_0 < 1$, all the coefficients of $P(\lambda^*)$ are strictly positive then $P(\lambda^*)$ does not have a positive roots. So, (E_0) has all its eigenvalues with strictly negative real part, hence E_0 is locally asymptotically stable by the Poincarre-Lyapunov theorem (13). Otherwise, with the same rule, if $R_0 > 1$, there is a variation of coefficients of (λ^*), then $P(\lambda^*)$ has at least one positive root.

So (E_0) hass at least one eigenvalues with a strictly positive real part, hence then E_0 is unstable by the Poincarre-Lyapunov theorem.

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Theorem 3: The Disease Free Equilibrium point (DFE) of the model, denoted E_0, is globally asymptotically stable if $R_o < 1$ and unstable if $R_o > 1$.

Proof. Consider then the following Lyapunov candidate function for E_0.

$$V = \frac{1}{2}\left(S_h - \frac{\alpha_h N_h}{\mu_h}\right)^2 + \frac{1}{2}L_h^2 + \frac{1}{2}I_h^2 + \frac{1}{2}\left(S_v - \frac{\alpha_v N_v}{\mu_v}\right)^2 + \frac{1}{2}I^2 \qquad (22)$$

Its first derivative gives us

$$\begin{aligned}\dot{V} = {} & 2\alpha_h N_h S_h + \gamma S_h R_h + \frac{\sigma b \alpha_h S_h I_v}{\mu_h} + \frac{\sigma b S_h L_h I_h}{N_h} + \delta L_h I_h + \lambda I_h R_h + 2\alpha_v N_v S_v + \frac{\sigma c \alpha_v N_v S_v I_h}{\mu_v N_h} \\ & + \frac{\sigma c S_v I_v I_h}{N_h} - \left(\frac{\sigma b S_h^2 I_v}{N_h} + \mu S_h^2 + \frac{\alpha_h^2 N_h^2}{\mu_h} + \frac{\gamma \alpha_h N_h R_h}{\mu_h}\right) \\ & - \left[(\mu_h + \delta)L_h^2 + (\eta + \lambda + \mu_h)I_h^2 + (\gamma + \mu_h)R_h^2 + \frac{\sigma c S_v^2 I_h}{N_h} + \mu_v S_v^2 + \frac{\alpha_v^2 N_v^2}{\mu_v}\right. \\ & \left. + \mu_v I_v^2 \right. \qquad (23)\end{aligned}$$

]

We notice that if $_o < 1$, the Lyapunov candidate function V thus defined is in the strict sense in the whole domain of Ω if $R_o < 1$ and unstable if $R_o > 1$.

Existence and Uniqueness of Endemic Equilibrium (EE): Endemic Equilibrium "EE" exists if and only if $_o > 1$.

Proof: Let us recall the endemic equilibrium point, E_1, found previously was determined implicity due to the complexity of this system. With the notions of the equilibrium point, the system (1) becomes:

$$\begin{cases} 0 = \alpha_h N_h - \frac{\sigma b S^* I_v^*}{N_h} + \gamma R_h^* - \mu_h S_h^*, \\ 0 = \frac{\sigma b S_h^* I_v^*}{N_h} - (\mu_h + \delta) L_h^*, \\ 0 = \delta L^* - (\quad + \quad + \lambda) I^* \\ \quad {}_h \quad \eta \quad \mu_h \quad {}_h, \\ 0 = \lambda I_h^* - (\mu_h + \gamma) R_h^* \gamma, \\ 0 = \alpha_v N_v - \frac{\sigma c S_v^* I_h^*}{N_h} - \mu_v S_v^*, \\ 0 = \frac{\sigma c S_v^* I_h^*}{N_h} - \mu_v I_v^*. \end{cases} \qquad (24)$$

From this system, we deduce that

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$$\begin{cases} S_h^* = \frac{N_h(\alpha_h N_h + \gamma R_h^*)}{\sigma b I_v^* + \mu_h N_h}, \\ L_h^* = \frac{\sigma b S_h^* I_v^*}{N_h(\mu_h + \delta)}, \\ I_h^* = \frac{\delta}{\eta + \mu + \lambda} L_h^*, \\ R_h^* = \frac{\lambda}{\mu_h + \gamma} I_h^*, \\ S_v^* = \frac{\alpha_v N_v N_h}{\sigma c I_h^* + \mu_v N_v}, \\ I_v^* = \frac{\sigma c S_v^* I_h^*}{N_h \mu_v}. \end{cases} \quad (25)$$

By making substitutions, we notice that the EE satisfies the following polynomial function:

$$(I_h^*) = I_h^*(\psi_1 I_h^* \psi_2) = 0 \quad (26)$$

Where

$$\psi_1 = \sigma^2 bc\delta\gamma\lambda\alpha_v N_v - AB(\sigma^2 bc\alpha_v N_v + \sigma c\mu_h\mu_v N_h),$$

$$\psi_2 = N_h C(\sigma^2 bc\delta\alpha_v\alpha_h N_v - AB\mu_h\mu_v^2 N_h) \quad (27)$$

From equation (26), we have $I^* = 0$ which is the solution of DFE, or $\psi_1 I^* + \psi_2 = 0$, hence the uniqueness of endemic equilibrium whenever $R_0 > 1$, otherwise, no endemic equilibrium.

Stability of EE

The endemic equilibrium point (EE), noted E_1, is globally asymptotically stable if $R_0 > 1$.

Proof. The proof of this theorem is based on the lyapunov-lasalle's invariance principle. Consider then the following lyapunov candidate function for E_1:

$$V = \frac{1}{2}(S_h - S_h^*)^2 + \frac{1}{2}(L_h - L_h^*)^2 + \frac{1}{2}(I_h - I_h^*)^2 + \frac{1}{2}(R_h - R_h^*)^2 + \frac{1}{2}(S_v - S_v^*)^2 + \frac{1}{2}(I_v - I_v^*)^2 \quad (28)$$

By deriving this function once, we have,

$$\begin{aligned} \dot{V} = (S_h - S_h^*)\dot{S}_h + (L_h - L_h^*)\dot{L}_h + (I_h - I_h^*)\dot{I}_h + (R_h - R_h^*)\dot{R}_h + (S_v - S_v^*)\dot{S}_v + (I_v - I_v^*)\dot{I}_v \\ = \left[S_h(\alpha_h N_h + R_h) + S_h^*\left(\frac{\sigma b S_h I_v}{N_h} + \mu_h I_h\right) + \frac{\sigma b S_h I_v L_h}{N_h} + (\mu_h + \delta)L_h L_h^* + \delta L_h I_h \right. \\ + (\eta + \mu + \lambda)I_h I_h^* + \lambda I_h R_h + (\mu_h + \gamma)R_h R_h^* + \alpha_v N_v S_v + \frac{\sigma c S_v I_h S_v^*}{N_h} + \mu_v S_v S_v^* \\ \left. + \frac{\sigma c S_v I_h I_v}{N_h} + \mu_v I_v I_v^*\right] \\ - \left[S_h\left(\frac{\sigma b S_h I_v}{N_h} + \mu_h s_h\right) + S_h^*(\alpha_h N_h + \gamma R_h) + (\mu_h + \gamma R_h) + (\mu + \delta)L_h^2 + \frac{\sigma b S_h I_v L_h^*}{N_h}\right. \\ + (\eta + \mu_h + \lambda)I_h^2 + \delta L_h I_h^* + (\mu_h + \gamma)R_h^2 + \lambda I_h R_h^* + \frac{\sigma c S_v^2 I_h}{N_h} + \mu(S_v^2 + I_v^2) \\ \left. + \alpha_v N_v S_v^* + \frac{\sigma c S_v I_h I_v^*}{N_h}\right] \quad (29) \end{aligned}$$

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Consequently, the largest compact invariant set in $\{(S_h, L_h, R_h, S_v, I_v) \in \Omega: V \leq 0\}$ is the EE, E_1.

Therefore, by Lyapunov- La-salle's Invariance principle, it follows that every solution in Ω approaches E_1 for $R_0 > 1$ as t ∞. So the EE, E_1, is globally asymptotically stable. The epidemiological implication of this result is that malaria will persist and invade population whenever $R_0 > 1$.

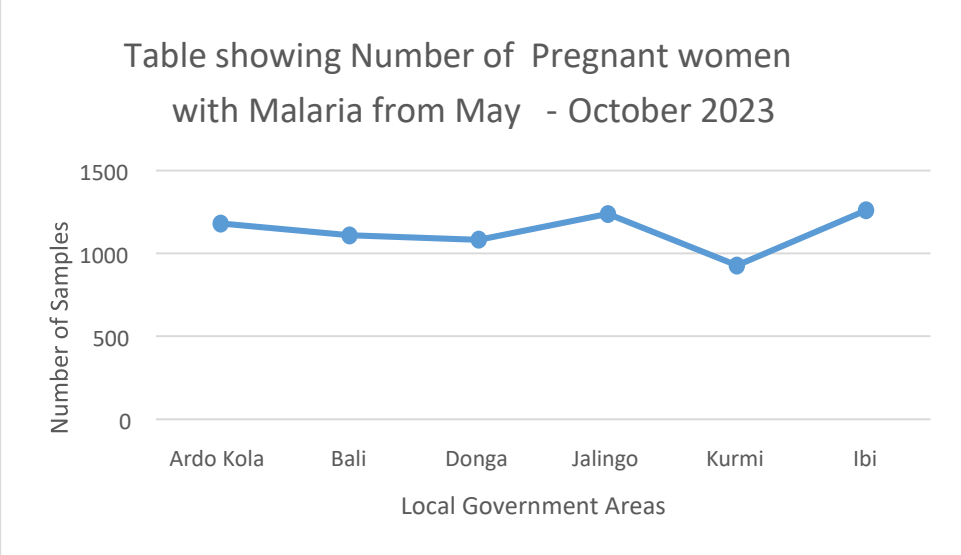
RESULT, DATA ANALYSIS

4.1 Data Presentation Table 1: Distribution of Pregnant women with malaria in relation to the study areas in Taraba State.

Table 1: **Showing number and percentage of pregnant women with malaria from May – October 2023**

Ardo - Kola	Bali	Donga	Jalingo	Kurmi	Ibi	Total
No. (%)	No. (%)	No (%)	No. (%)	No. (%)	No. (%)	No. (%)
1180 (17.4)	1108 (16.3)	1082 (15.9)	1237 (18.2)	927 (13.6)	1259 (18.5)	6793 (100)

Figure 1: Number of Pregnant women with malaria from May – October 2023



The HBI, the proportion of a vector species that fed in human blood was indicated thus:

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HBI = Number of Anopheles mosquito with Human blood / Total number of the mosquito species with blood

Determination of Man biting Rates:

This is Bites per person per night, month, season or year. The above pyrethrum spray catch index was determined by dividing the total number of freshly fed mosquitoes by the total number of occupants who spent the night multiplied by HBI. Since the collection was done on a centain number of days per month, the average number of bites per night was standardised to the average number of days in a month (30.5) or a year 365 to arrive at the Man-Biting Rate (WHO, 2013).

I.e Human Biting Rate = Freshly fed Anopheles X Proportion Fed on humans (HBI) / Number of occupants who spent the night in the rooms used for collection **4.2 Results**

The results of the research are that a model will be developed for the prevention of malaria in women with pregnancy. This will greatly reduce the huge amount of money always been used for the cure of malaria in women with pregnancy. The results will also reduce or eradicate stillbirth, abortion, aneamia and low birth weight. The prediction of the incidence rate will inform policies maker, especially, the stakeholders in Health sector to take proactive measures in perverting the disease before it becomes wild.

A total of 6,793 Indoor- Resting mosquitoes belonging to six genera, Anopheles 2,186 (50.0%), Culex 1,987 (45.5%), Aedes 15 (0.3%), Mansonia 127 (3.0%), Sabethes 36 (0.8%) and Toxorhynchites 19 (0.4%) were collected. Abundance of the Indoor - Resting mosquitoes in relation to study areas showed that Ibi LGA had the highest abundance of pregnant women with malaria with 1,259 (18.5%), followed by Jalingo 1237 (18.2%), Ardo-Kola 1180 (17.4%), Bali 1,108 (16.3%), Donga 1082 (15.9%) and Kurmi 927 (13.6%). Anopheles was the most abundant species in Ardo Kola 1319 (60.3%) of the entire Anopheles collected in the areas, whereas Culex was most abundant in Donga 999 (50.5%). In all the study areas Aedes was low in abundance 15 (0.3%) with Donga recording 9(60.0%), Bali 6(40.0%) and Ardo Kola had none. Analysis of variance showed significant differences in mosquito genera in relation to study areas ($P < 0.05$).

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Simulation and interpretation

In this section, we will analyze the model (1) numerically. In particular, we will be interested in the numerically analysis of the infected human population with malaria. To so this, we collect a reasonable set of data for the parameters of the model. Most of these are obtained from models developed in the literature and other parameters assumed.

In what follows, we will use the below parameters:

α_h: The human birth rate is 38.377 per year per 1000 inhabitants

α_v: The vector birth rate is 130 adult female mosquitoes per year per 1000 female mosquitoes σ : 20.425 bites per man per might (average bites per man per day inside and outside the home) [Assumed].

b: The probability of being infected for a human bitten by an infectious mosquito per unit of time is 0.0181.

c. The probability of being infected for a mosquito biting an infectious human per unit of time is 0.11 per day.

δ : Rate of progression from infectious state for humans is 0.1 [*As-sumed*].

λ : Rate of progression from infectious to recovered state for human is 0.0022 per day .

γ : Rate of progression from recovered to susceptible state for human 5.5 x 10^{-4}.

μ_h: Human (natural) mortality rate is 7.766 per year per 1000 inhabitants.

η: Human malaria-induced death rate is 32%.

μ_v: Mosquito mortality rate 0.003.

The data of confirmed cases used, are obtained from the ministry of public Health and the fight against HIV/AIDS for the period. As given in the literature, we parameters and use minimize function with noise in python for obtaining parameter values corresponding to the data in study. Initial conditions of state are S_h = 498901; L_h =374176; I_h823; R_h = 560; S_v =3582; I_v = 66 for the following.

Using the parameters derived from the fitted model above and taking

N_v = 1000 [*Assumed*] ;

N_h = 11890781, the basic reproduction number as mentioned in section (4) is 0.8092009797722537.

According to this value and to the section (5), we conclude that the average of an individual infected produces less than one new infected individual during their infection period, hence the disease- free equilibrium, E_0 , (DFE) of Equation (1), given by equation (16), is locally asymptotically stable.

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When we assume N_v = 10000 [assumed], using the same parameters and let fix N_h = 11890781 [14] than, the value of basic reproduction is 2.5589181809201627. That implies that each infected individual produces an average of more than one; the infection and disease persist and invade the human population. It implies that the infection is greater than recovery rate.

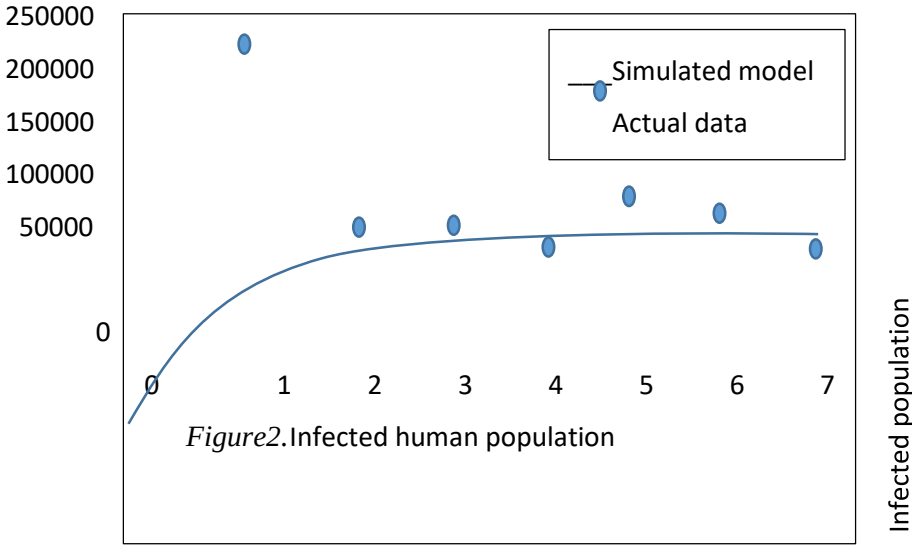

*Figure2.*Infected human population

Summary

Mosquitoes constitute a very important component in the epidemiology of some parasitic and viral diseases of humans. The most common occurrence of these diseases is malaria caused by Plasmodium species. The prevalence of infection in any region is determined by vectorial capacity of indigenous Anopheles species which includes Anopheles density in relation to man, longevity, Man Biting and Infective Biting Rates. Anopheles mosquito responsible for malaria parasites in human if put under control can reduce the rate of malaria infection among pregnant women in the study areas.

The study determined the abundance of mosquito species and behavior, density of Anopheles so as to identify main malaria vectors in Taraba state, Nigeria. Indoor mosquitoes in major riverine communities of Ardo Kola, Bali, Jalingo, Kurmi, Ibi and Donga areas were collected using Pyrethrum-Spray Catch (PSC) between May and October, 2023. According to Lamidi et al (2019) Mosquito species were sorted out morphologically and Anopheles species preserved over silica gel in eppendorf tubes for further analysis, biochemical and molecular. Anopheles gambiae complex was further analysed to identify molecular species using PCR-Restriction

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Length Fragment Polymorphism assay. Enzyme-linked Immuno-Sorbent Assay (ELISA) was used to detect Plasmodium sporozoite protein and Human Blood antigen in fed Anopheles species to determine Man-Biting Rate/Infective Biting Rate and degree of anthropophily. Relative frequencies (percentage) were used for the presentation of data in tables. Excel window 2010 was used to prepare graph (line charts). Analysis of Variance (ANOVA) was used to analyze the followings: Anopheline/Culicine abundance in selected areas and months/seasons; between Indoor-Resting Densities, Mean Indoor-Resting Densities, Coefficient of Indoor Resting Habits and Man-Biting Rates of Anopheles species and the six selected areas. Student t test was however used to analyse the parameters, their averages in wet and dry seasons to determine significant variation using SPSS.

The study showed that the study area have diverse mosquito species resting indoor. Mosquito species were most abundant in Ibi community. This was followed by those in Jalingo, Bali, Ardo kola, Donga and Kurmi. The most abundant mosquito genera collected indoor **Malaria fevers:** is a common diseases cause by mosquito bite. Also as a serious acute and chronic relapsing infection in humans characterized by periodic paroxysm of chills and fever anemia, malaria fever causes found in apes, birds, monkey, rats, and various species of the protozoa. Among the symptoms are headache, vomiting, body weakness etc. it prevents and control taking anti-malaria drugs such as quinine, fensider, and vaccinate children by immunization and used the roll back malaria net.

CONCLUSION

The study showed that the study area have diverse mosquito species resting indoor. Mosquito species were most abundant in Mayo-renewo community (Ardo Kola). This was followed by those in Bali and Donga. The most abundant mosquito genera collected indoor **Malaria fevers:** is a common diseases cause by mosquito bite. Also as a serious acute and chronic relapsing infection in humans characterized by periodic paroxysm of chills and fever anemia, malaria fever causes found in apes, birds, monkey, rats, and various species of the protozoa. Among the symptoms are headache, vomiting, body weakness etc. it prevents and control taking anti-malaria drugs such as quinine, fensider, and vaccinate children by immunization and used the roll back malaria net.

RECOMMENDATION

From the findings in this research work it is therefore recommended that:

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i. The hospital should always base their prescription of anti-malaria on the result of recent scientific findings that shows more potent, efficacious and effective drugs. This will improve success towards curbing the menace.

ii. As far as this findings, I urge the government to create more awareness of these diseases especially (malaria) how dangerous the diseases are and introduced new ways to prevent and controlled. iii. The use of vaccine to immunize against the diseases so as there is reduction on the number of patient affected.

iv. Stricter health policies on the use of dispensing of antimicrobials should be reappraising in the counting in general. This will help to reduce abuse of drugs on these ailments.

v. Personal hygiene and environmental sanitation should be encouraged. These calls for the judicious use of the technical knowhow.

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