

SIMPLE MODEL IN TROPICAL MALARIAL EPIDERMIC

¹ S.Sasikala, ²B.Elakkiya, ³S.Puvizhi

¹ Assistant Professor, ² UG Student, ³UG Student

¹Department of Mathematics,

¹Adhiyaman Arts and Science College For Women , Uthangarai, Krishnagiri(DT), Tamilnadu ,India

Abstract : A basic theoretical model is presented for the study of tropical malaria epidemics. A predator-prey type of formalism results in two pairs of partial differential equations which describe the latent and infectious states and two pairs of integro-differential equations which describe recovery and dying rates for humans or mosquitoes. The complete system of equations is solved numerically for a practical case, since coupled nonlinear boundary conditions destroy the linearity of the system.

IndexTerms - Predator Prey System , Incubation period, Epidemic

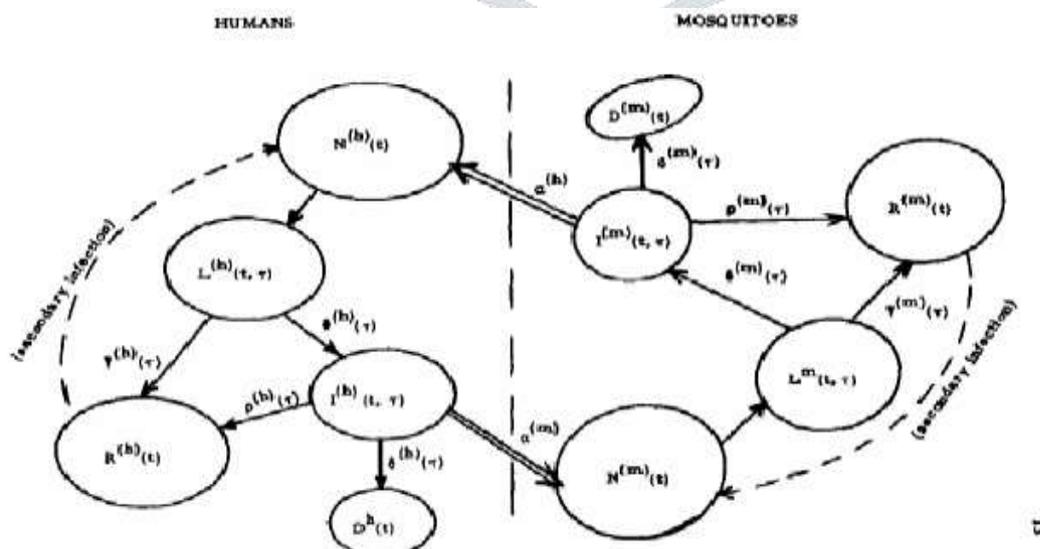
I. INTRODUCTION

In order to assist in field work as well as in theoretical study on tropical malaria epidemiology, a very simple model is considered. Mathematical models currently in use are of the deterministic, probabilistic, discrete, continuous or simulation type. In view of our experience that epidemic malaria appears to have reached a position of stability in tropical Africa, we have not only chosen a deterministic model, but have also employed a predator-prey type of formalism in which humans on the one hand and mosquitoes on the other act simultaneously as vectors (infectives) or susceptible relative to each other.

In Europe and North America and parts of Asia, malaria epidemics have been effectively controlled. Large areas of South America are undergoing some control processes. In the tropical belt of Africa, however, progress has been very slow. Obstacles to progress include inertia and conservatism; resistance of mosquitoes to insecticides resistance of malaria parasites to drugs; incapacity to mount an effective program; inaccessibility of people and of mosquitoes; and worst of all, lack.

Malaria infection is carried principally by female anopheles mosquitoes which generally breed locally, and have an average life span of about one month. When a susceptible mosquito bites an infectious person or an infectious mosquito bites a susceptible person, malaria parasites get transferred from the infectious to the susceptible. The rate of contact is as yet to be determined precisely, but a figure of 1% seems realistic. On contact, the susceptibles go through a latent period from which they may recover without showing any illness or symptoms or they may become infectious. Infectives also may recover (with or without treatment) or may die after a short period of time. The latent and infectious periods taken together constitute what is usually called the incubation period. For simplicity, those who have passed through part or all of the incubation period are assumed to be removed from circulation from the community, which is considered isolated or closed. These assumptions are justified by reports of observed isolation and immunity periods that last much longer than the incubation period.

II. BIOLOGICAL SYSTEM



Consider a population $N(t)$ of susceptibles in a community at a time $t > 0$. Let superscripts h and m denote properties of humans and of mosquitoes, respectively. (Except for cases of ambiguity, these superscripts will be suppressed throughout.)

Let a $\alpha^{(h)}$ ($0 < \alpha < 1$) probability that one infectious mosquito bites a human and $\alpha^{(m)}$ the probability that an infectious human is bitten by a

susceptible mosquito. We shall denote by τ the time spent in an infectious or latent state. Clearly this parameter does not depend on the observation time, t . On entering the incubation state let $\Phi(t)$ denote the probability of becoming infectious $\Psi(t)$ that of

recovery during the latent period τ_L . If $L(t, \tau)$ denotes the density of latent persons at time t who have spent a time τ in the incubation period, then the time change $\Delta(t)$ produces a flux out of this state into the recovery and infectious states given by

$$\frac{\partial L}{\partial t} + \frac{\partial L}{\partial \tau} = \frac{\Phi(\tau) + \psi(\tau)}{1 - \int_0^{\tau} [\Phi(\tau) + \psi(\tau)] d\tau} L(t, \tau), \tag{1}$$

2.1 MALARIA EPIDEMIC MODEL

Where $\Phi = \Phi(T)\Phi_0, \psi = \psi\psi_0$; (Φ_0, ψ_0 being normalizing constants satisfying $\Phi_0 + \psi_0 = \frac{1}{2}$), and

$$\int_0^{\tau_L} [\Phi(\tau) + \psi(\tau)] d\tau = 1 \tag{2}$$

In Similar manner the infectives satisfy

$$\frac{\partial I}{\partial t} + \frac{\partial I}{\partial \tau} = \frac{\rho(\tau) + \delta(\tau)}{1 - \int_0^{\tau} [\rho(\tau) + \delta(\tau)] d\tau} I(t, \tau), \tag{3}$$

Here $\rho(\tau)$ is proportional to the probability of recovery from the infectious state $\delta(\tau)$ is proportional to the probability of dying, and

$$\int_0^{T_1} [\rho(\tau) + \delta(\tau)] d\tau = 1 \tag{4}$$

T_1 being the infectious period. Equations (1) and (3) are the same as obtained by George Adler by a somewhat different formalism.

The rate of dying at time t is measured by the flux out of the infectious state from those who had become infective within the immediate prior T_1 period. Thus the $\delta(T)$ gives the rate of dying, the number of dead, $D(t)$, satisfies the equation

$$\frac{dD}{dt} = \int_0^{T_1} I(t, \tau) \delta(\tau) d\tau. \tag{5}$$

In a similar manner, the total recovery rate is the sum of the recovery rate from both the latent and the infectious state (Fig. 1), so that

$$\frac{dR}{dt} = \int_0^{\tau_L} L(t, \tau) \psi(\tau) d\tau + \int_0^{T_1} I(t, \tau) \rho(\tau) d\tau. \tag{6}$$

These equations are now solved subject to the boundary conditions at $T=0$ and $t=0$ for h and m . In the first case ($T=0$) we may choose $I(0,0)$ and $L(0,0)$ as we please, since for obvious reasons $I(0,T) \equiv 0$ and $L(0,T) \equiv 0$ whenever, $T > 0$. For $t > 0$ and $T = 0$, we make use of the Reed-Frost model (2) as follows.

Let $I^*(t)$ denote the total number of infectives at time $t \neq 0$. Then

$$I^*(t) = \int_0^{T_1} I(t, \tau) d\tau \tag{7}$$

Similarly the total number of latent members at time t is

$$L^*(t) = \int_0^{\tau_L} L(t, \tau) d\tau \tag{8}$$

Now since $\alpha^{(h)}$ is the probability of contact of a human with an infectious mosquito, the probability of escaping any infection from $I^*(m)(t)$ mosquitoes at time t becomes

$$(1 - \alpha^{(h)})^{I^*(m)(t)}.$$

Thus probability of adequate contact is $1 - (1 - \alpha^{(h)})^{I^*(m)(t)}$, hence we obtain the Reed-Frost formula for the density of newly latent persons, $L^{(h)}(t, 0)$:

$$L^{(h)}(t, 0) = N^{(h)}(t) \left[1 - (1 - \alpha^{(h)})^{I^*(m)(t)} \right]. \tag{9}$$

The density of newly latent mosquitoes, $L^{(m)}(t, 0)$, satisfies the same equation with superscripts h and m interchanged. Here

$$N(t) = N(0) - Z^*(t) - L^*(t) - D(t) - R(t). \tag{10}$$

The boundary condition (9) complicates the solution of Eqns. (I), (3), (5) and (6) by its nonlinearity. Consequently, it is difficult to proceed to an analytical solution of these equations, which describe our epidemic model.

In addition to (9) we require the corresponding boundary condition for the newly infectious category $I(t,0)$. This reads

$$I(t, 0) = \int_0^T L(t, T)\Phi(T)dT \quad (t > 0). \tag{11}$$

It is a matter of interest that Eq. (9) can be simplified in two cases: αI^* large or small. For $\alpha I^* \rightarrow \infty$

$$L^{(h)}(t, 0) \rightarrow N^{(h)}(t) \left(1 - e^{-\alpha^{(h)} I^{*(m)}}\right). \tag{12}$$

$$\text{and for } \alpha I^* \rightarrow 0 \quad L^{(h)}(t, 0) \rightarrow \alpha N^{(h)}(t) I^{*(m)}(t) \tag{13}$$

Unfortunately, neither of these can be used for all values of t . A matching procedure may be worth attempting.

III. SOLUTIONS OF EQUATIONS

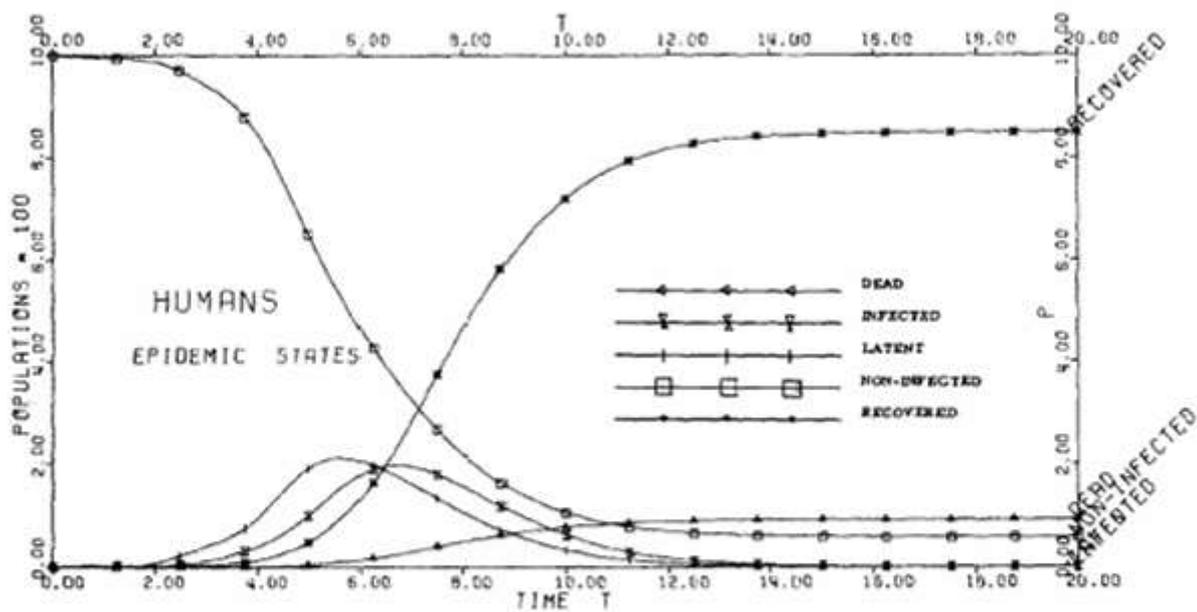


FIG. 3. Mathematical model of epidemics of malaria in Nigeria. (a) Epidemic states: humans, (b) epidemic states: mosquitoes. $\delta^{(h)} = 0.05$ (or $\rho^{(h)} = 0.45$); $\delta^{(m)} = 0.495$ (or $\rho^{(m)} = 0.005$); $\Phi = 0.98$ (or $\Psi = 0.02$); $\tau_I = 2$, $\tau_L = 1$; $\alpha = 0.01$.



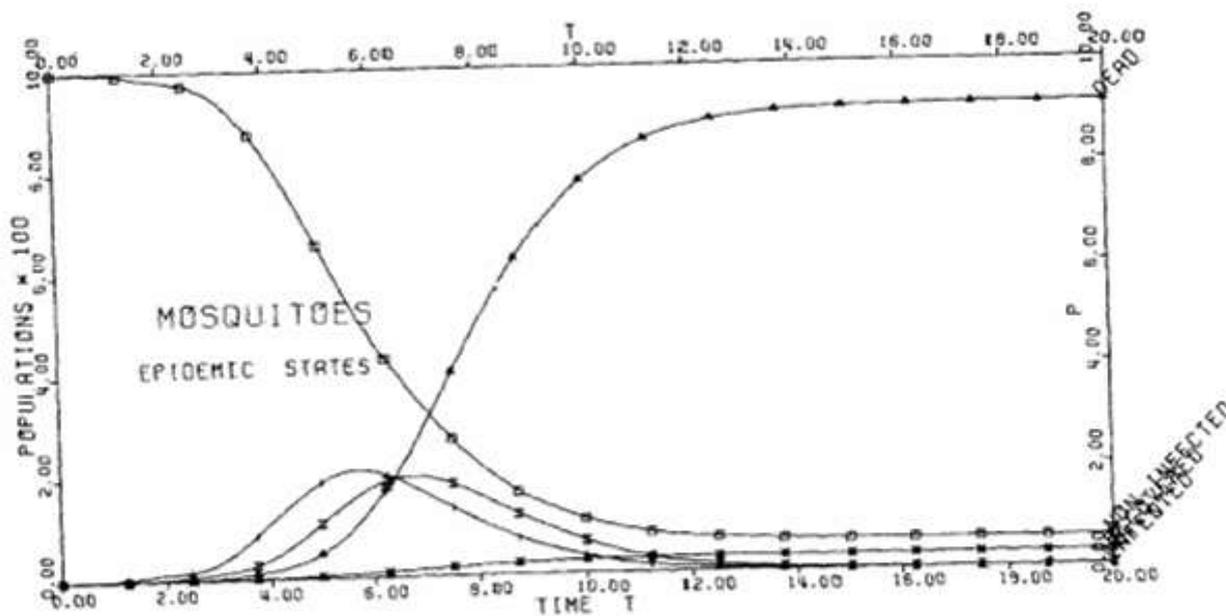


FIG. 3(continued). Part (b).

By making use of the method of characteristics, Eqns. (1) and (3) can be integrated. For the characteristics are (in both cases)

$$\begin{aligned} dT &= dr, \text{ or} \\ T &= t_0 + T \end{aligned} \tag{14}$$

Thus for $t > T$,

$$L(t, T) = L(t - T, 0) \left\{ 1 - \int_0^T [\Phi(\xi) + \Psi(\xi)] d\xi \right\} \tag{15}$$

$$\text{And } I(t, T) = I(t - T, 0) \left\{ 1 - \int_0^T [\rho(\xi) + \delta(\xi)] d\xi \right\} \tag{16}$$

We observe immediately that from Eqns. (2) and (4)

$$L(t, T_L) \equiv 0, \quad I(t, T_I) \equiv 0, \tag{17}$$

Which verify the conditions of maximum latent period T_L and maximum infectious period T_I . Also,

$$L(t, T) = L(t - h, T - h) - L(t - T, 0)\Psi, \tag{18}$$

which is particularly useful for computational purposes. Hence, it is easy to show that

$$L(t, kh) \left[1 - \int_0^{(k-1)h} (\Phi + \Psi) d\Psi \right] = L(t - h, (k - 1)h) \left[1 - \int_0^{kh} (\Phi + \Psi) d\Psi \right]$$

Thus $L(t, T)$ is a decreasing function along the characteristics for all $T < T_L$ and $L(t, T)$ vanishes for $T \geq T_L$.

3.1. NUMERICAL METHODS

In Figs. 2 and 3 we show plots of solutions of Eqns. (1), (3), (5) and (6). Since $I(t, T)$ and $L(t, T)$ behave very much like density functions, we have plotted $I^*(t)$ (curves marked **INFECTED**) and $L^*(t)$ (curves marked **LATENT**). Other curves shown represent the dead, non-infected and recovered as marked. $I^*(t)$ and $L^*(t)$ are, respectively, the total numbers of infected and latent populations at observation time t ; $I^*(0)$ is set equal to 1 for mosquitoes and 0 for humans. The total initial population $N(0)$ is chosen as 1000 for humans or mosquitoes, and the probability α of adequate contact is fixed at 0.01. The rate of transfer from one epidemic state to the next is assumed constant. The input transfer rates are

$$\text{Fig. 2: } \Phi = 0.49; \delta^{(h)} = 0.1; \delta^{(m)} = 0.99;$$

$$\text{Fig. 3: } \Phi = 0.98; \delta^{(h)} = 0.05; \delta^{(m)} = 0.495;$$

The other parameters ρ and ψ are determined from Eqns. (2) and (4), which depend on the infectious period t_1 and latent period T_L , respectively. The infection period T_1 , is chosen as unity for Fig. 2, while the latent period T_L . Is chosen as unity for Fig.3, the incubation period being 3 units for both cases. Figures 2 and 3 illustrate the complete epidemic history for $0 < t < 20$ units. The infectious curves show excellent qualitative agreement with previous results [1]. For the first time (as far as we are aware), we have the prediction for the dead, the recovered and the non-infected for a single epidemic. In addition, by having the history simultaneously for both humans and mosquitoes, a good measurement of the interaction is predictable.

We observe a small peak in each of the incubation curves during the initial incubation period. This is followed several incubation times later by a large peak at the height of the epidemics. As expected, $L^*(t)$ attains its maximum before $L(t)$, both quantities vanishing as $t \rightarrow \infty$. It may be remarked that the positions of these peaks depend also on the ratio T_L/T_1 as well as the relative rate of recovery of the humans with respect to that of the mosquitoes. Indeed, it appears that with nearly equal rate of recovery for both, the position of the peaks would recede to infinity. This might be one possible explanation for the apparent stability of the tropical malaria epidemics.

We note also that if the recovered do not develop sufficient immunity, and are not removed from circulation, secondary peaks will appear, for each incubation curve, some time after the maximum infection period.

IV. CONCLUSION

It is evident that our model should be very suitable not only for determining the relevant parameters of tropical malaria epidemics but also for general epidemiology and ecological systems. For example, it will be easy to predict the peak of an epidemic as soon as it is known that the epidemic has begun. Many variants of our model are easily derivable for example, it may be decided to leave latent persons in circulation. Generalizations to include normal birth and death rates, super- or multiple infections, geographical spread, etc., are also readily deduced.

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