A-25: A Mathematical model to describe heterogeneous transmission of malaria

L P Mutuwatta[1], K Mendis[1], A P K de Zoysa[2]
([1]*Malaria Research Unit, Dept. of Parasitology, Faculty of Medicine, Univ. of Colombo, Colombo 8*
[2]*Div. of Engineering Mathematics and Management of Technology, Faculty of Engineering Technology, Open Univ., Nawala, Nugegoda*)

The distribution of malaria within an endemic community is non-homogeneous and therefore clustered. This heterogeneity of transmission is partly attributable to unequal susceptibility of human-mosquito contact. Most mathematical models of malaria transmission to date, have however, assumed homogeneous transmission conditions within an area.

In this study a model for malaria transmission in an endemic area, based on heterogeneous transmission which account for differences in human-mosquito contact within this area, and differences in susceptibility among humans is presented.

Humans were grouped into heterogeneous patches on the following basis: (1) Physical patches comprising distinct geographical boundaries having different mosquito densities and (2) conceptual patches definable by one or more of any of the malaria susceptibility factors such as age, sex and house construction types. The model takes into consideration 2 categories of malaria-infected persons, (1) those having clinical symptoms and (2) those without clinical symptoms referred to as asymptomatic carriers.

A mathematical model of 2 first order coupled differential equations was developed to describe asymptomatic and symptomatic carriers. In the case of the physical patches we (1) developed the method of computing the transmission of malaria between patches due to infected mosquitoes flying across boundaries and (ii) modified the standard vectorial capacity equation used to quantify transmission in homogeneous situations, to include the heterogeneous case.

The model was based on interactions indicated in *Fig 1.*

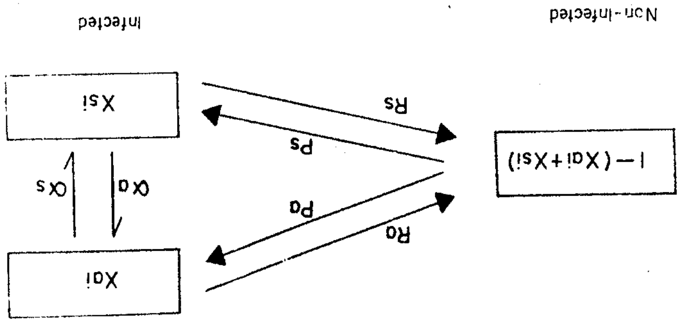

Fig. 1

The differential equations governing the diagram are

$dX_{ai}(t)/dt = H_{ai}(t) - (R_a+\alpha_a) X_{ai}(t) + \alpha_s x X_{si}(t)$
$dx_{si}(t)/dt = H_{si}(t) - (R_s+\alpha_s) X_{si}(t) + \alpha_a X_{ai}(t)$
where,

$H_{ai}(t)$ - Rate at which susceptible individuals contract the disease in patch "i" at time t. (Asymptomatics)

$H_{si}(t)$ - Rate at which susceptible individuals contract the disease in patch "i" at time t. (Symptomatics)

$X_{ai}(t), X_{si}(t)$ - Proportion of asymptomatic/symptomatic carriers in patch in the total population at time t.

R_a, R_s - Recovery rates for asymptomatics and symptomatics

α_a - Transfer rate from asymptomatics to symptomatics

α_s -- Transfer rate from symptomatics to asymtomatics

we can show that,

$H_{ai}(t) = Pa.g\,(C_{ii}(t-\Gamma)X_i(t-\Gamma)+\Sigma\, C_{ji}(t-\Gamma)X_j(t-\Gamma)).\,(1-X_i(t))$
$H_{si}(t)$ can be calculated using similar method.
where, $X_i(t) = X_{ai}(t) + X_{si}(t)$

Pa - The probability that an individual having the disease of being an asymptomatic carrier.

Γ - Time taken for extrinsic parasite cycle in mosquito.

g - Susceptibility parameter.

$C_{ji}(t-\Gamma)$ - Average number of bites being taken from the patch after the extrinsic cycle, given that the first bite was taken in the patch, named as vectorial capacity for transmission from patch j to patch i at time t.

The model was tested with actual malaria epidemiological data from southern Sri Lanka, for both geographical and conceptual patches. The malaria prevalence data generated by this model were found to be realistic.

We have developed a mathematical model which takes into account the heterogeneity of malaria transmission. The model has been developed in such a manner that field data can be used in it, to accurately predict the characteristics of transmission, and to make discerning predictions not possible using a homogeneous model.