Global analysis of malaria intra-host model

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ABSTRACT

Intra-host models of malaria describe the dynamics of the blood-stage of the parasite and their interaction with host-cells, in particular red blood cells (RBC) and immune effectors. During the past decade there has been considerable work on the mathematical modelling of *Plasmodium Falciparum* infection [1, 6, 5, 7, 10, 11, 13, 14, 18]. A review has been done by Molineaux and Dietz [15]. Usually the mathematical models are highly non linear, which makes the study of analytical solutions difficult. In this paper we focus on models originated from Anderson *et al.* [2] and on their global analysis. We give a global analysis of the dynamics of intra-host models of malaria. The disease free equilibrium is globally asymptotically stable if and only the basic reproduction number satisfies $\mathcal{R}_0 \leq 1$. We consider the case of models with and without the reaction of the immune system. When we ignore the immune system the models relate to classical models studied in [3]. We provide an analysis of the endemic equilibrium and we improve a condition of [3].

We also provide a intra-host model with k class of age for the parazited red blood cells and give an analysis of stability of the disease equilibrium and the endemic equilibrium. A global stability result, analogous to the precedent, is obtained. We explore the relation of our results with some classical within-host malaria models. We generalize the results obtained before. Once again the dynamics of the model is determined by $\mathcal{R}_0$.

Global results of stability for the DFE as well for the endemic equilibrium for high dimensional epidemic models are not so common[9, 8, 12, 19]. Our results generalize the results of [3]. As a by-product we obtain global stability results for $SE_1 \cdots E_k I$ models.

Key Words: Nonlinear dynamical systems, malaria models, global stability, *Plasmodium Falciparum*

AMS Classification: 34D23,34A34,92D30

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