Rich dynamics in multi-strain models: non-linear dynamics and deterministic chaos in dengue fever epidemiology

Maíra Aguiar[1], Bob Kooi [2] & Nico Stollenwerk[1]

[1]Centro de Matemática e Aplicações Fundamentais da Universidade de Lisboa,

Avenida Prof. Gama Pinto 2, 1649-003 Lisboa, Portugal.

[2]Vrije Universiteit, Faculty of Earth and Life Sciences,

Department of Theoretical Biology, De Boelelaan 1087, NL 1081 HV Amsterdam, The Netherlands.

March 21, 2012

Abstract

Dengue fever is a viral mosquito-borne infection, a major international public health concern with more than 55% of the world population at risk of acquiring the infection. Two variants of the disease exist: dengue fever (DF), a non-fatal form of illness, and dengue hemorrhagic fever (DHF), which may evolve toward a severe form known as dengue shock syndrome (DSS). Epidemiological studies support the association of DHF with secondary dengue infection due to a process described as antibody-dependent enhancement (ADE), where the pre-existing antibodies to previous dengue infection cannot neutralize but rather enhance the new infection. Treatment of uncomplicated dengue cases is only supportive, and severe dengue cases require hospitalization and proactive treatment of hemorrhagic symptoms. A vaccine against dengue is not yet available, although several candidates of vaccines are at various stages of development.

Dengue epidemiology dynamics is well known to be particularly complex with large fluctuations of disease incidences and mathematical models describing the transmission of dengue viruses appeared in the literature as early as 1970. To capture differences in primary and secondary dengue infections, a two-strain SIR-type model for the host population has to be considered. Dengue models including multi-strain interactions via ADE, but without temporary cross-immunity, have shown already deterministic chaos when strong infectivity on secondary infection was assumed. The addition of the temporary cross-immunity peri- od in such models brings a new chaotic attractor in wider and unexpected parameter region.

In this talk we present different extensions of the classical single-strain SIR model motivated by modeling dengue fever epidemiology with its peculiar ADE phenomenology. We focus on a minimalistic model, where the notion of at least two different strains is needed to describe differences between primary (DF) and secondary dengue infections (DHF). The model, in its simplicity, has shown qualitatively very good results when comparing empirical DHF data and model simulation, offering a promising perspective on inference of parameter values from dengue case notifications. A model which can be fully parametrized on data referring to incidence of disease can become a predictive tool to guide the policies of prevention and control of the dengue virus transmission, including the implementation of vaccination programs when the candidate dengue fever vaccines will be available.