Dengue Transmission in Time and Space: Models and Methods

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ABSTRACT

Dengue fever transmission has not been successfully modeled spatially. The reason for this shortcoming is mainly due to the difficulty of tracing the temporal-spatial patterns of the four different but related dengue serotypes, which are responsible for dengue and its more virulent form, dengue hemorrhagic fever. In addition, two incubation processes [intrinsic (3 to 5 days) and extrinsic (10 to 14 days)] allow for considerable change in host population patterns over these time periods. Movement patterns of the most common vector, the mosquito *Aedes aegypti*, are only generally known. For example, no one has traced, minute by minute, the movement pattern of the vector in a non-laboratory setting. Unavailable are answers to important questions such as the following: Exactly what role do climatic variables play in the existence of and the biting behavior of the mosquitoes? What thresholds of mosquito and human population density enable the transmission process to begin and continue? What combinations of secondary infections are the most likely to spawn the transmission of dengue hemorrhagic fever? How are the number of susceptibles to be enumerated when so many of those immune to a particular serotype displayed no disease symptoms in the past?

In this study, data on risk factors (entomology) and serology were collected from 1998 in Iquitos, Peru, and for the last two years in Kamphaeng Phet, Thailand, to help better understand the spatial aspects of dengue transmission and aid in the control of the disease.[1] In several earlier papers, we described and tested hypotheses on the spatial manifestation of the disease.[2] In this paper, we explore our data using a variety of spatial statistics and attempt to model the space-time characteristics of the disease. The exploratory techniques, including k-function and local statistics analysis and also the software system *STARS*[3] (space-time analysis of regional systems), help trace the spatial patterns over time. The models include a four-stage Markov stochastic process and a metapopulation model. We trust that the results presented at this conference will shed new light on the dengue transmission process. In addition, by demonstrating these techniques of analysis we lay the groundwork for further work on the time-space characteristics of the transmission of dengue and other vector-borne diseases.

Footnotes

* The names of the additional contributing authors will be included in the final paper.

[1] National Institutes of Health (principal investigator: T.W. Scott, UC Davis, dengue fever; investigators, A. Getis, A.C. Morrison, J. Aldstadt), Peru: 1998-2003, Thailand: 2003-2008.

[2] Getis, A., A.C. Morrison, K. Gray, and T.W. Scott, 2003, “Characteristics of the Spatial Pattern of the Dengue Vector, *Aedes Aegypti*, in Iquitos, Peru,” *American Journal of Tropical Medicine and Hygiene,* 69(5), 494-505.

Morrison A.C., H. Astete, F. Chapilliquen, C. Ramirez-Prada, G. Diaz, A. Getis, K. Gray, T.W. Scott, 2004. “Evaluation of a sampling methodology for rapid assessment of Aedes aegypti infestation levels in Iquitos, Peru.” *Journal of Medical Entomology,* 41(3), 502-10.

[3] Rey, S. *STARS*, available as an open source program on the internet. http://stars-py.sourceforge.net/