1073-92-260      **Helen J. Wearing\*** (`hwearing@unm.edu`). *Deconstructing dengue dynamics: modeling a multi-strain disease.*

The dengue virus is one of the most important mosquito-borne pathogens that infects humans. In regions where all four dengue serotypes co-circulate, human incidence data exhibit seasonal cycles of varying amplitude in which the dominant serotype may change from one epidemic to the next. The precise mechanisms underlying these temporal patterns have been the subject of much debate. To understand how alternative hypotheses concerning dengue infection and transmission may explain observed multi-annual cycles in disease incidence, we developed a differential equation model that incorporates both ecological and immunological mechanisms. We demonstrate that, contrary to perceived wisdom, dynamics generated solely by antibody-dependent enhancement are not consistent with serotype-specific notification data in important ways. To generate epidemics with the characteristic signatures observed in data, we find that a combination of seasonal variation in vector demography and, crucially, a short-lived period of cross-immunity is sufficient. We also show how understanding the persistence and eradication of dengue serotypes critically depends on the alternative assumed mechanisms. (Received August 03, 2011)

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