A stochastic multi-host model for West Nile Virus

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Enzootic West Nile virus (WNV) transmission demonstrates a great deal of temporal and spatial variability, and the ecological mechanisms determining when and where outbreaks will occur are not well understood. When introduced by a small number of infected individuals, the disease may die out before resulting in a major outbreak. With a deterministic ordinary differential equation model for WNV transmission, whether or not an outbreak occurs is dependent on whether the basic reproduction number R_0 is greater than one or less than one. In a stochastic model, early season extinction events can occur even when R_0 is greater than one. Here we present a Continuous-Time Markov Chain (CTMC) enzootic WNV transmission model with two avian hosts based on a corresponding deterministic host-vector model. We use multitype branching process theory to determine the probability of disease extinction in the population based on the type of hosts and/or vectors introducing the disease. We explore how the likelihood of a minor or major outbreak, along with the time to extinction, depends on the relative abundance of each species of host, the vector biting rates on each host species, and the ability of each host species to transmit WNV. We compare the disease dynamics for the deterministic and stochastic models and compare theoretical predictions for the probability of extinction to the results of stochastic simulations.