An epidemiological model for West Nile virus: invasion analysis and control applications

Marjorie J. Wonham1,2,3*, Tomás de-Camino-Beck1 and Mark A. Lewis1,2

1Department of Biological Sciences, and 2Department of Mathematical and Statistical Sciences, University of Alberta, Edmonton, Alberta T6G 2G1, Canada
3Great Lakes Institute for Environmental Research, University of Windsor, Windsor, Ontario N9B 3P4, Canada

Infectious diseases present ecological and public health challenges that can be addressed with mathematical models. Certain pathogens, however, including the emerging West Nile virus (WN) in North America, exhibit a complex seasonal ecology that is not readily analysed with standard epidemiological methods. We develop a single-season susceptible–infectious–removed (SIR) model of WN cross-infection between birds and mosquitoes, incorporating specific features unique to WN ecology. We obtain the disease reproduction number, \( R_0 \), and show that mosquito control decreases, but bird control increases, the chance of an outbreak. We provide a simple new analytical and graphical method for determining, from standard public health indicators, necessary mosquito control levels. We extend this method to a seasonally variable mosquito population and outline a multi-year model framework. The model’s numerical simulations predict disease levels that are consistent with independent data.

**Keywords:** arbovirus; emerging infectious disease; outbreak threshold; public health; reproduction number

1. INTRODUCTION

Emerging infectious diseases are a growing agent of global change that present compelling challenges in public health, agriculture and wildlife management (Blower & McLean 1991; Binder et al. 1999; Keeling et al. 2001). Arthropod-borne diseases including West Nile virus (WN) provide unique opportunities to explore the ecological links between host and vector species. Translating this ecology into a dynamic model allows the evaluation of different control strategies (Anderson & May 1991). At the same time, however, a biologically realistic model of seasonal host–vector cross-infection is necessarily complicated and not necessarily amenable to classical analysis. As we show here, the application of new graphical methods can simplify the calculation of threshold parameters controlling disease outbreak.

We focus on the emerging WN epidemic in North America, which has been exceptionally well documented at both host and vector levels. The virus is widespread in Africa, the Middle East and western Asia, with occasional European outbreaks introduced by migrating birds (Hayes 1988; Rappole et al. 2000). In North America, the first recorded epidemic was initially detected in New York state in 1999 and spread rapidly across the continent causing unprecedented bird, horse and human mortality attributed to a highly virulent emerging virus strain (Anderson et al. 1999; Petersen & Roehrig 2001). Control strategies focus primarily on the eradication of vector mosquitoes (New York City 2003). We develop the simplest possible biologically relevant ordinary differential equations model for WN transmission, obtain the disease basic reproduction number \( R_0 \) (Anderson & May 1991), determine outbreak criteria and graphically relate virus detection and control metrics.

2. MODEL DESCRIPTION

Like many arboviruses, WN persists in natural transmission cycles between vectors (mosquitoes) and reservoir hosts (birds). Mammals are secondary hosts generally considered unimportant to disease persistence in the wild (Hayes 1988). We therefore focused only on cross-infection between birds and mosquitoes. Understanding this simplified system has clear implications for disease management in mammalian hosts, including humans.

To account for time-scales specific to WN, we extended the classical SIR differential-equation model for malaria transmission (Anderson & May 1991; Thomas & Urena 2001) to an eight-compartment model describing WN cross-infection in one season (figure 1). The dimensional equations for this dynamic system (equations (2.1)) describe susceptible (\( S_B \)), infectious (\( I_B \)) and dead (\( X_B \)) birds, where the total live bird population is \( N_B = (S_B + I_B + R_B) \), and larval (\( L_M \)), susceptible (\( S_M \)), exposed (\( E_M \)) and infectious (\( I_M \)) female mosquitoes, where the total female mosquito population is \( N_M = (L_M + S_M + E_M + I_M) \) (figure 1) (all parameters are defined in table 1):

\[ \frac{dS_B}{dt} = -abIM_S_NB \]  
\[ \frac{dI_B}{dt} = abIM_{S_B} - \mu I_B - gI_{B3} \]  
\[ \frac{dR_B}{dt} = gI_{B3} \]  
\[ \frac{dX_B}{dt} = \mu I_{B3} \]  

*Author for correspondence (mwonham@ualberta.ca).