

Mathematical modeling of disease transmission of West Nile Virus: A review

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ABSTRACT

West Nile virus is a globally spreading virus infecting birds and to some extent human population as well. Many mathematical models have been proposed and studied to predict the disease dynamics of the virus. Different models incorporate different factors leading to the epidemic and thus modelled by using different transmission terms. In this paper, we give an overview of the mainly the differential equations approach and emphasize on what the predictions are.

1. Introduction

West Nile virus (WNV), a member of the family Flaviviridae (genus Flavivirus) [9], was first isolated in 1937 in the West Nile district of Uganda [19]. WNV has now spread globally, with the first case in the Western hemisphere being identified in New York City in 1999 [18]. Main mode of WNV transmission is via various species of mosquitoes. It mainly infects birds, and it is also known to infect humans, horses, dogs, cats, bats, chipmunks, skunks, squirrels, domestic rabbits, crocodiles and alligators [3, 5, 10, 11, 17, 23]. In the USA, the disease is of serious public-health importance, with more than 30,000 cases and hundreds of deaths reported in 48 States since 1999 [24].

WNV is maintained in nature in a mosquito-bird-mosquito cycle [6, 7], but the disease can be passed on to humans as a zoonotic disease when an infected mosquito changes hosts to bite people, who are dead-end hosts. The principal vectors are mosquitoes in the genera Culex, Aedes, Anopheles and Ochlerotatus, but other genera are also known to be infected in the wild.

2. Literature review

Several mathematical models have been developed and studied to explain a variety of features on the transmission of WNV disease. In [22], the authors used a core model that summarized the biological assumptions common to several of these models to compare the different R_0 obtained for each model. Some models include the exposed class in the vector population to account for the viral incubation time in the mosquitoes [14, 21]. In particular, in [14], simulation models were used to compare the two viruses by considering the impact of bird mortality on the transmission dynamics of arboviruses in south Florida. Transmission models without disease-induced mortality (SLEv) were compared with models including disease-induced mortality (WNV). The most important factor in both the models in the likelihood of epizootics was mosquito population size; the mosquito mortality rate was also important. The additional avian mortality altered the factors most important in the size and timing of epizootics, although it did not always directly affect the outcome of the simulations. In some cases, low-level

transmission occurred prior to the epizootic peak. When disease-induced avian mortality was included in the simulations, appreciable numbers of dead birds occurred prior to high levels of infection in mosquitoes. This has implications for the use of dead birds as a surveillance tool monitoring the spread and transmission of WNV.

In [21], the authors developed a single-season susceptible-infectious-removed (SIR) model of WNV cross-infection between birds and mosquitoes and incorporated specific features unique to WN ecology. They obtained the disease reproduction number, R_0 , and showed that mosquito control decreases, but bird control increases, the chance of an outbreak. They provided a simple new analytical and graphical method for determining, from standard public health indicators, necessary mosquito control levels. They also extended this method to incorporate seasonal fluctuations of mosquito population and presented a multi-year model framework. Disease levels that are consistent with independent data were predicted from the model's numerical simulations.

There are other models that assumed vertical transmission in the vector population [7, 20]. For instance, in [7], the authors formulated and analyzed a mathematical model for the transmission of WNV infection between mosquito and avian population. They found the Basic Reproductive Number \tilde{R}_0 in terms of certain parameters. \tilde{R}_0 is the threshold condition that determines the transmission of WNV infection. In particular, if $\tilde{R}_0 \leq 1$ the disease fades out, and for $\tilde{R}_0 > 1$ the disease remains endemic. Using experimental and field data, they estimated \tilde{R}_0 for several species of birds. Using numerical simulations of the temporal course of the infected bird proportion, they showed that the damped oscillations approach the endemic value.

Some models incorporated the aquatic life stage of the mosquitoes (eggs, larval and pupal stages) [21]. In case of the avian population, most of the models took into consideration a recovered class [3, 7, 14, 20, 21]. Spatial diffusion of WNV was modelled in [12, 13, 15, 16], and seasonal effects on new outbreaks starting from an endemic situation were studied in [6]. Most of the above models considered only one species of

birds and one species of mosquitoes except that in [4] the authors divided the susceptible birds into two groups: the crow family birds and the remaining birds under consideration to show that the non-crow family birds susceptible to WNV are one of the key factors responsible for the endemicity of the virus in the region of study.

In a recent study [2], the authors developed a mathematical model for transmission of WNV that incorporated resident and migratory host avian populations and a mosquito vector population. They used the model to investigate the interplay of WNV in both resident and migratory bird hosts. They found that yearly seasonal outbreaks depend primarily on the number of susceptible migrant birds entering the local population each season. In a recent study [1], instead of incorporating either multiple host species or multiple host life stages, the authors incorporated both between-host and within-host heterogeneity. They modeled two avian host species each with juvenile and adult stages. They studied the comparison of vector feeding preferences

for host species and for host stages, and explored the interaction of the two mechanisms.

3. Conclusion

Mathematical models applied to West Nile virus are either using Ordinary Differential Equations to understand the temporal dynamics or Partial Differential Equations to understand the spatial effects. The models incorporate different life stages and correspondingly different kinetics. Regardless of the model, they take into consideration a limited number of species of mosquito and avian population. An interesting question could be how the transmission of the disease is affected by the species that is taken into consideration. It would be worthwhile exploring if a certain species lead to epidemics faster than others. Increased research on the factors that affect the disease transmission and the interaction between host and vector would help in predicting the dynamics and in proposing the control measures.

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