Transmission Dynamics of Eastern Equine Encephalitis Infection Rates: The Role of Avian Host Stage and Differential Mosquito Exposure

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ABSTRACT

The Eastern equine encephalitis virus (EEEV) is a neurological mosquito-borne disease that spans the northeastern coast of the United States and Canada. Prior studies have focused on how mosquitoes prefer to take blood meals from hatch-year avian hosts rather than adult avian hosts to determine the rate at which the virus is spread between the Black-Tailed Mosquito (*Culiseta melanura*) and select avian species. In these studies, it was found that mosquito blood meal preference correlated well with avian brooding seasons for certain avian species such as the European Starling (*Sturnus vulgaris*) and the American Robin (*Turdus migratorius*). In this study, a host stage-structured model is developed where the avian host group is split into two categories: adult avians and hatch-year avians. The system of ordinary differential equations (ODEs) used to create this model are analyzed to better understand the transmission dynamics of EEEV between the two host classes. The extent to which fluctuations occurred in transmission rates according to host/vector abundances, mosquito biting rate, and host stage was explored. By utilizing the model, it was found that when hatch-year avians are more exposed to the virus, a cyclic outbreak can be observed. Since hatch-year avians lack defensive mechanisms, unlike their adult counterpart, they are more readily exposed to the mosquito vector.

Keywords: Vector-Borne Disease, Host Stage Structure, Differential Equations, Heterogeneity

Author Summary

In this study, researchers developed a host stage-structured model to investigate how Eastern equine encephalitis virus (EEEV) transmission dynamics vary between adult and hatch-year avian hosts along the northeastern coast of North America. Previous research established that the primary vector, Black-Tailed Mosquito (Culiseta melanura), preferentially feeds on hatch-year (hatchling and fledgling) avians rather than adults, with blood meal patterns aligning with breeding seasons of species like European Starlings and American Robins. The authors constructed a system of ordinary differential equations to analyze transmission patterns between these two distinct host classes. Their model revealed that higher virus exposure in hatch-year

avians, which lack the defensive capabilities of adults, can trigger cyclic disease outbreaks. Key factors examined included host/vector populations, mosquito biting rates, and host life stage. The findings suggest that the increased vulnerability of hatch-year avians to mosquito feeding can be one of the factors that significantly influences EEEV transmission dynamics in the region.

1. INTRODUCTION

The Eastern equine encephalitis virus (EEEV), an arthropod-borne virus, was first introduced to the United States in 1938 and is currently considered one of the deadliest arboviral encephalitides affecting America (Banda, 2022). Showing an increased incidence across a larger population of humans and equine, EEEV is considered an emerging disease within the U.S. As one of the five major arboviral encephalitides endemic to the United States, EEEV causes an exceptionally deadly neurological disease most often found along the southeastern portion of the United States (Tsai, 1991). EEEV remains one of the most severe mosquito-borne pathogens in North America, with case fatality rates of 30-70% in humans and up to 90% in horses. Recent studies have significantly advanced our understanding of the complex interactions between EEEV, its mosquito vectors, and vertebrate hosts that drive transmission dynamics and disease outcomes.

EEEV is predominantly transmitted and retained within a mosquito-avian vector-host transmission cycle. Beyond the first vector-host transmission cycle, the bridge vector mosquito, different from the original vector, is thought to be responsible for the transmission of the virus between the avian reservoir hosts and a diverse set of vertebrate hosts such as humans, horses, and amphibians. Although there is a wide array of vertebrate hosts, only avian hosts can transmit EEEV to the mosquito bridge vector. This is because the viral concentration found within the bloodstream of most secondary hosts is insufficient to infect new mosquito vectors—they are called dead-end hosts (Centers for Disease Control and Prevention). However, most EEEV infections in avians are asymptomatic and can only cause mortality in some avian species (State of NJ Dept. of Ag., 2006).

During the mid-summer months, July and August, equine cases are found more often in unison with human cases scattered along the eastern coast of the United States. With these two hosts being the most well-known secondary hosts of EEEV, the virus-induced death rate (virulence) within both hosts is high, with human cases resulting in a mortality rate of about 30% (Banda, 2022) and equine cases resulting in a significantly higher mortality rate of about 90% (Young, 2021). Regarding human cases, up to 50% of cases result in neurological sequelae ranging from seizures to severe intellectual disability (Banda, 2022). Many individuals exhibit severe sequelae and require long-term hospice care, costing upwards of three million dollars, only to die two to three years after the initial onset of symptoms (Corrin, 2021).
Numerous studies have shown the prevalence of EEEV across the eastern coast of the United States, as well as within specific mosquito and avian species. Although the transmission of EEEV is highly dependent upon seasonality, prior studies were more focused on the length and intensity of viremia within avians and how large of a role it played in whether a mosquito was

inoculated with EEEV (Kessel, 1957). The interaction between mosquito vectors and avian reservoir hosts directly preceding human and equine EEEV cases has been widely observed to contain various dynamics that drive EEEV infection rates (Estep, 2013; Hassan, 2003; Heberlein-Larson, 2019; Molaei, 2016). Specifically, it has been suggested that most blood meals taken from avian reservoir hosts occur simultaneously with the brooding season of the avian target hosts.

Strong empirical evidence now supports the cyclic nature of EEEV transmission in North America. Long-term surveillance data from multiple states demonstrates clear 2–3-year periodicity in virus activity (Armstrong and Andreadis, 2022). In Connecticut, systematic monitoring over 24 years revealed that EEEV isolations from *Cs. melanu*ra are significantly correlated with mosquito abundance ($r = 0.69$, $p < 0.001$), with peak transmission occurring in July-August. This timing corresponds with a 60.1% detection rate of virus-positive mosquito pools and 75% of equine/human cases. Similar cyclic patterns have been documented in Massachusetts, where above-average populations of *Cs. melanura* in spring consistently predict subsequent EEEV activity. Quantitative analysis of vector abundance and infection rates demonstrates that early-season vector populations are a key determinant of outbreak potential (Burkett-Cadena et al., 2021).

Recent work has clarified the critical role of differential host exposure in maintaining EEEV transmission cycles. Studies comparing hatch-year and adult avian hosts show that juvenile birds experience 2.5-3.5 times higher infection rates than adults, creating an amplification effect that drives intense transmission (Mundis et al., 2022). This age-structured transmission is supported by both field observations and experimental data showing higher viral titers in young birds. The relationship between host diversity and disease risk is complex and depends on vector feeding preferences and host competence. Mathematical modeling demonstrates that when vectors prefer hosts with high transmission ability, increased host diversity can amplify transmission through a mechanism termed "diversity amplification" (Miller & Huppert, 2013). This occurs because vector preference concentrates bites on the most competent hosts even as their relative abundance decreases. Conversely, when vectors show no preference or prefer less competent hosts, the classic "dilution effect" emerges where increased diversity reduces transmission. Vector feeding patterns exhibit strong seasonal shifts that align with avian breeding cycles. Detailed blood meal analysis reveals that Cs. melanura takes 26.9% of blood meals from Northern Cardinals year-round, but this increases to over 40% during peak transmission periods in June (Mundis et al., 2022). This temporal synchronization of vector feeding with host breeding seasons provides a mechanistic explanation for observed transmission dynamics (Armstrong and Andreadis, 2022).

It has been suggested that the development of infectious circulating viremias within hatch-year avians is more rapid than in adult avians (McLean, 1995). However, the effect of the difference in concentration at which mosquitoes take blood meals from the hatch-year avians versus adult avians on the intensity of EEEV transmission has not been thoroughly explored. Vector feeding patterns exhibit strong seasonal shifts that align with avian breeding cycles. In a

previous study, a mathematical model was created to explore this difference in concentration of blood meals and test whether feeding on hatch-year avians has any influence on the dynamics of EEEV (Unnasch, 2006). This model allowed for proper exploration into how the development of avian enzootics of EEEV was impacted by preferential feeding upon hatch-year avians.
Within this paper, a host stage-structured transmission model of EEEV that focuses on the enzootic interaction between the mosquito vector, the Black-Tailed Mosquito (*Culiseta melanura*), and specific avian reservoir hosts, European Starlings (*Sturnus vulgaris*) and American Robins (*Turdus migratorius*), is evaluated. This transmission model explores the relationship between the timing and intensity of each outbreak and the magnitude at which hatch-year and adult avians are exposed to the virus. In particular, an analysis of the effect of avian reservoir host age on the magnitude of EEEV outbreaks within both vector and reservoir host populations are completed. Our findings suggest that the cyclic nature of EEEV transmission is an inherent property of the host-vector system, driven by biological parameters rather than purely environmental factors. This understanding has important implications for predicting and potentially controlling EEEV outbreaks, as it identifies key biological parameters that could be targeted for intervention strategies.

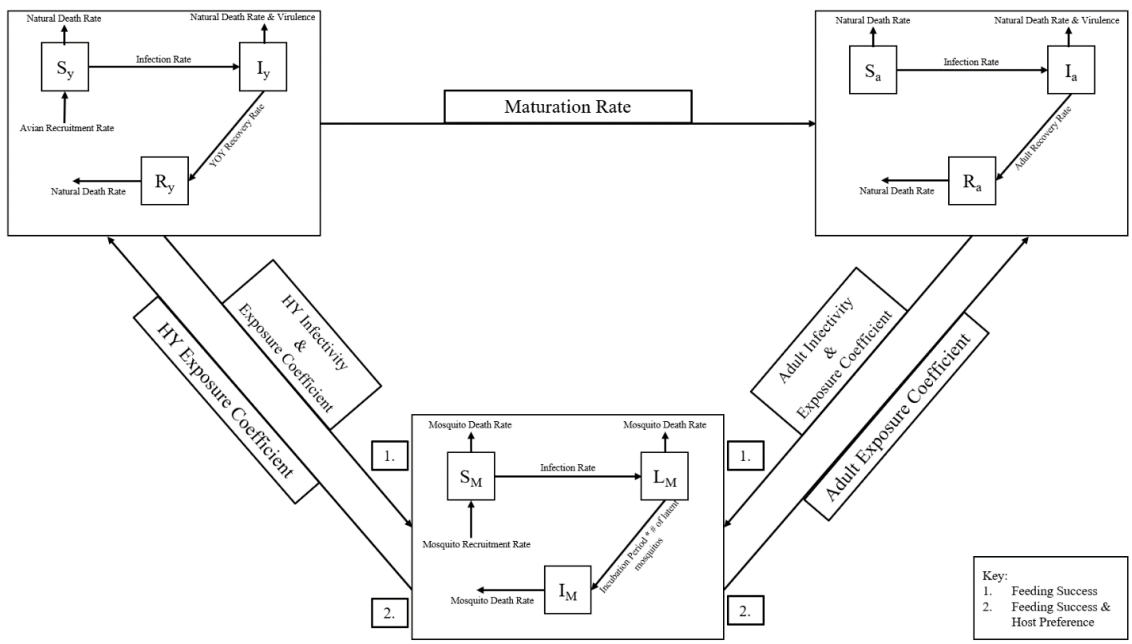


Fig 1. Eastern Equine Encephalitis virus host stage-structured model flow chart. The large box in the top left represents the hatch-year (y) avian class, the large box in the top right represents the adult avian (a) class, and the large box at the bottom represents the mosquito (M) class. The classes are connected by arrows which indicate their interaction with each other with respect to the direction the arrow.

2. MODEL DEVELOPMENT

In the model, the host avian class is split into hatch-year avians (y) and adult avians (a) to better understand host age-specific transmission dynamics where each avian class contain 3

separate stages, susceptible (S), infected (I), and recovered (R) (Fig 1.). For the rest of this study, the term 'young host' is the same as the term 'hatch-year avian', the term 'adult host' is the same as the term 'adult avian', and the term 'vector' is the same as the term 'mosquito'. Both avian classes have a recovered stage where they are classified as non-competent hosts, implying that they are no longer able to receive or transmit the virus. For this model it is assumed that once an individual from either avian class reaches the recovered stage, they remain recovered for life. This is assumed as both avian species considered for this research project remain recovered for the same timespan as their average lifespan (Kessel 1957; Morneau 2000).

The young host class matures into the adult host class at rate m_Y from the susceptible and recovered stages, but not the infected stage. It is assumed that young hosts must recover and make it into the recovered class before they can mature. Natural mortality rates for both hosts in each stage are given by μ_y and μ_a respectively. It should be noted that the carrying capacity term, $(1 - \frac{S_y}{c})$, keeps logistic growth of the avian population within the model while simultaneously keeping the population bounded, where c denotes the numerical carrying capacity.

Through the development of the vector transmission dynamics within this model, it was determined that the mosquito class has a different stage structure when compared to both avian classes, the mosquito class moves between a susceptible, latent, and infected stage. It is assumed that all mosquitoes are recruited into the susceptible class, S_M, and that a vector must move from the latent stage, L_M, into the infected, I_M. before they are considered infectious. This is because an extrinsic incubation period must pass before infection can take place. Additionally, once a mosquito has made it to the infectious stage, it is assumed that it remains infectious for life. For this model it is also assumed that there is a constant birth rate, ψ_M, within the mosquito population along with a constant mosquito death rate, μ_M, throughout the duration of the model.

It was observed that the relative number of mosquito bites on each avian species is determined by the number of female mosquitoes present and the abundance of avian hosts within the model (Molaei 2016). To get a value for the mosquito biting rate, α, the product of the two parameters is taken. However, the value for this parameter is simplified with this model whereas the realistic transmission of EEEV occurs between a variety of different host and vector species.

Mosquito bites are distributed among both the young and adult host classes where the exposure coefficient of the hosts to mosquito bites is given by $1 - \alpha$ and α respectively. If $\alpha = 0.5$ then each avian class is bitten in proportion to the abundance of their respective population and all avians receive an equal number of bites. Higher α values correlate with increased exposure within the adult host class whereas lower α values correlate with increased exposure within the young host class.

Susceptible hosts, S_y and S_a respectively, are able to move into the infectious class, I_y and I_a respectively, once bitten by an infectious mosquito vector, I_M, dependent on their

exposure to the virus. Although it has been observed that EEEV has the ability to be transmitted vertically within the avian population (Scott 1998), vertical transmission is ignored within the model and the principal method of transmission is observed to occur between the mosquito vector and the avian host during the viral amplification season (Komar 2003; McLean 1995).Transmission of the virus from infectious mosquito vectors to susceptible hosts is partially determined by the proportion of susceptible hosts to the total population of avians N_B, $\frac{S_y}{N_B}$ and $\frac{S_a}{N_B}$. The class-dependent virulence is given by ν_y and ν_a and the class-dependent recovery rate, is given by γ_y and γ_a. To analyze the independent effect of differential avian class exposure to the virus, it is assumed that infectivity and recovery rate baseline values of each avian class is equal.

Mosquitoes within the susceptible stage can move into the latent stage, L_M, after successfully biting an infectious host. Transmission of the virus from infectious avian hosts to susceptible mosquito vectors is partially determined by the proportion of susceptible mosquitoes to the total population of mosquitoes (N_M), $\frac{S_M}{N_M}$. Susceptible mosquitoes take *a* bites per day, with respect to host class, where only a fraction of the bites taken are from infectious hosts, $\frac{I_y}{N_B}$ and $\frac{I_a}{N_B}$. The probability that avian-mosquito transmission will successfully occur per bite, also known as avian infectivity, is given by δ. Latent mosquitoes move into the infectious stage at a rate k, where $\frac{1}{k}$ is the extrinsic incubation period of the virus that must pass before a mosquito can be considered fully infectious and transmit the virus. Although it has been observed that EEEV can affect the reproductive fitness of *Culiseta melanura* (Buckner 2016), due to their short life span, it is assumed that infectious mosquitoes do not have a virulence, never recover from the virus, and can only exit the infectious stage through natural death.

The system of ordinary differential equations (ODEs) created for the model are given below, the complete list of parameters and parameter values can be found in *Table 1*:

$$\frac{dS_y}{dt} = \psi_B(S_a + R_a)\left(1 - \frac{S_y+R_y+S_a+R_a}{c}\right) - a(1-\alpha)I_M\left(\frac{S_y}{N_B}\right) - (m_y + \mu_y)S_y \tag{1A}$$

$$\frac{dI_y}{dt} = a(1-\alpha)I_M\left(\frac{S_y}{N_B}\right) - (\gamma_y + \mu_y + \nu_y)I_y \tag{1B}$$

$$\frac{dR_y}{dt} = \gamma_y I_y - (m_y + \mu_y)R_y \tag{1C}$$

$$\frac{dS_a}{dt} = m_y S_y - a\alpha I_M\left(\frac{S_a}{N_B}\right) - \mu_a S_a \tag{1D}$$

$$\frac{dI_a}{dt} = a\alpha I_M\left(\frac{S_a}{N_B}\right) - (\gamma_a + \mu_a + \nu_a)I_a \tag{1E}$$

$$\frac{dR_a}{dt} = m_y R_y + \gamma_a I_a - \mu_a R_a \tag{1F}$$

$$\frac{dS_M}{dt} = \psi_M - a\left(\frac{S_M}{N_M}\right)\delta\left((1-\alpha)I_y + \alpha I_a\right) - \mu_M S_M \tag{1G}$$

$$\frac{dL_M}{dt} = a\left(\frac{S_M}{N_M}\right)\delta\left((1-\alpha)I_y + \alpha I_a\right) - (k+\mu_M)L_M \tag{1H}$$

$$\frac{dI_M}{dt} = kL_M - \mu_M I_M \tag{1I}$$

We assume that all the parameters within the model are always positive. Susceptible young hosts (S_y) are produced at a rate of ψ_B, where it is assumed that a majority of female avians are capable of laying 2 clutches of eggs per year with a mean clutch size of 5 (Kessel 1957; Morneau 2000). To bound the growth of the avian population, a carrying capacity c is used, where it is assumed that the carrying capacity of the avian population will remain constant.

Table 1: List of parameters for the *Eastern Equine Encephalitis virus* stage-structured model.

Parameter	Description	Value	Reference
ψ_B	Birth rate of hatch-year avians	$0.05\ \frac{birds\ day^{-1}}{birds}$	(Kessel 1957; Morneau 2000)
a	Mosquito biting rate	$2.5\ day^{-1}$	(Molaei 2016)
α	Exposure coefficient	$0 \leq \alpha \leq 0.5$	Varied
γ_y	Hatch-year avian loss of infectivity/ recovery rate	$\frac{1}{3} day^{-1}$	(Komar 2003)
γ_a	Adult avian loss of infectivity/ recovery rate	$\frac{1}{3} day^{-1}$	(Komar 2003)
μ_y	Hatch-year avian death rate	$0.002\ day^{-1}$	(Kessel 1957; Morneau 2000)
μ_a	Adult avian death rate	$\frac{1}{547} day^{-1}$	(Kessel 1957; Morneau 2000)
μ_M	Mosquito death rate	$0.1\ day^{-1}$	(Buckner 2016)
ν_y	Hatch-year avian disease-induced death rate/ virulence	$0.5\ day^{-1}$	
ν_a	Adult avian disease-induced death rate/ virulence	$0.5\ day^{-1}$	
ψ_M	Birth rate of mosquitoes	$3{,}000\ mosquitoes\ day^{-1}$	(Kessel 1957; Morneau 2000)
δ	Infectivity of avians	0.2	(Komar 2003)
k	Virus extrinsic incubation period	$\frac{1}{3} day^{-1}$	
m_y	Maturation rate of hatch-year avians	$0.04\ day^{-1}$	(Royal Society for the Protection of Birds)
N_B	Total population of avians	$Varies$	
N_M	Total population of mosquitoes	$Varies$	
c	Carrying capacity of the avian population	$Varies$	

3. NUMERICAL & SENSITIVITY ANALYSIS

3.1 Numerical Analysis of Cyclic Behavior

For the equations within the model, the basic reproduction number, $\mathcal{R}_0$, was derived utilizing the next generation matrix approach (Heffernan 2005; Van Den Driessche 2017; Vitek 2009). By using this method, the only stages that must be considered are the four infected classes $M = \left(I_y, I_a, L_M, I_M\right)^T$ since the creation and removal of infection within the model only occurs due to these classes. When evaluated at the Disease-free equilibrium (DFE), $I_y = I_a = L_M = I_M = 0$,

$$S_y = \frac{c\,(\psi_B - m_Y - \mu_Y)}{\psi_B},\ S_a = \frac{c\,m_Y\,(\psi_B - m_Y - \mu_Y)}{\mu_A\,\psi_B},\ S_M = \frac{\psi_M}{\mu_M} \qquad \text{(2A, B, C)}$$

By utilizing the next generation matrix approach, the basic reproductive number $\mathcal{R}_0$ is given and defined as

$$\mathcal{R}_0 = \frac{a\sqrt{k}\sqrt{\delta}\sqrt{(m_Y + \mu_A)\left((-1+\alpha)^2\mu_A(\gamma_A + \mu_A + \nu_A) + m_Y\ \alpha^2\,(\gamma_Y + \mu_Y + \nu_Y)\right)}}{(m_Y + \mu_A)\sqrt{\mu_M}\sqrt{k+\mu_M}\sqrt{\gamma_A + \mu_A + \nu_A}\sqrt{\gamma_Y + \mu_Y + \nu_Y}}. \qquad (3)$$

If $\mathcal{R}_0 < 1$, then the DFE is locally asymptotically stable, which means that there is an absence of all infection whereas, if $\mathcal{R}_0 > 1$, then the DFE is unstable.

To understand the cyclic outbreak patterns observed in nature, we focused our numerical analysis on the exposure coefficient (α), which quantifies the relative mosquito biting preference between young and adult hosts. This parameter is crucial because it directly controls the primary transmission mechanism between vectors and hosts. When α decreases, mosquitoes show increased preference for biting young hosts, potentially driving the cyclical patterns seen in field data. Our analysis revealed that while the system maintains only two equilibria (disease-free and endemic), the stability of these states depends significantly on α. Using a base case of $\alpha = 0.5$, (equal exposure between age groups), we demonstrated that the endemic equilibrium remains stable at lower α values, suggesting that preferential feeding on young birds may help maintain persistent transmission cycles.

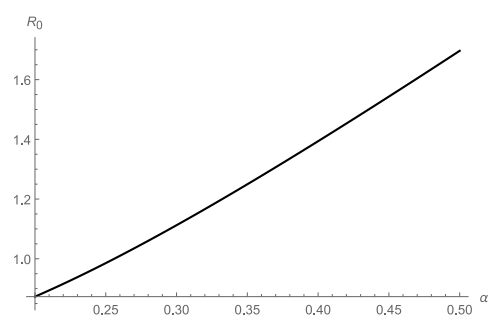


Fig 2. R_0 as a function of α. $R_0 > 1$ when $\alpha \approx 0.26$, which is an increased exposure to young avian.

In order to determine when cycles can occur, standard Jacobian analysis on the original model was used, where the sign of the largest eigenvalue is determined. Two results are of particular interest. First, in order to determine when cycles occur, the eigenvalues of the Jacobian

were evaluated for their imaginary part. The largest was found and is plotted as a function of α in Figure 3. Even though there are two equilibria, only one was shown to have imaginary part, and it was always the endemic equilibrium.

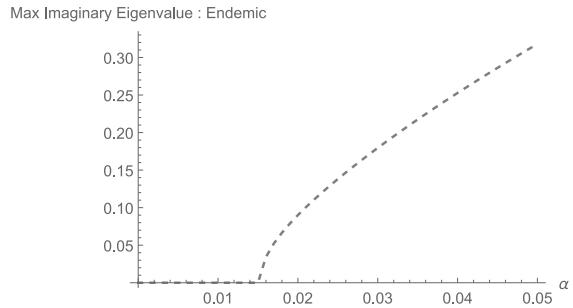


Fig 3. The max eigenvalue imaginary part of the endemic equilibrium. Cycles occur when α is small but are not sustained except for a small window of α.

Cyclic behavior can occur when α is small, but in order to determine the nature of those cycles and if dampening is occurring the max real part of the largest eigenvalue was found. As seen in Figure 4 for the DFE and the endemic equilibrium, the sign of the max eigenvalue can be used to determine the stability.

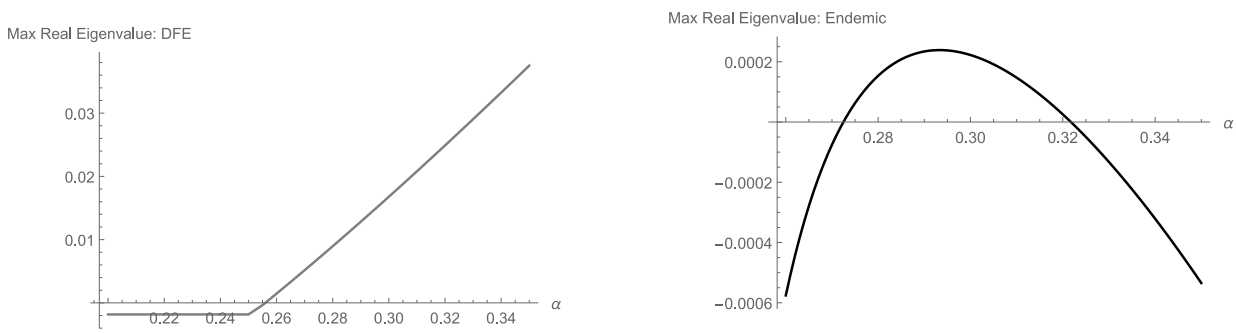


Fig 4. The max eigenvalue real part of the disease-free (left) and endemic (right) equilibrium. For the left plot, the disease-free equilibrium will never become stable again as R_0 is an increasing function in α. For the endemic, it can be seen that there is a small window where cycles are sustained and not dampened out.

From the left side of Figure 4, the DFE follows the typical pattern that R_0 dictates, it is unstable when α is large enough and will never be stable again. This is again due to R_0 being an increasing function in α. From the right side of Figure 4, there is a small range of values for α where the endemic is not stable, and as seen in the results, this is where cycles are sustained and match what is seen in nature. This range of values are when the exposure coefficient is much higher for young avian as opposed to adult avian, further solidifying the hypothesis that the young are the driving force of the infection.

3.2 Sensitivity Analysis

A comprehensive sensitivity analysis was conducted to identify and quantify the relative influence of other model parameters on peak infection levels across three key populations: hatch-

year avians (I_Y), adult avians (I_a), and mosquitoes (I_M). By systematically varying individual parameters while holding others constant, we assessed how each parameter impacts disease transmission dynamics. This analysis reveals distinct patterns of parameter influence, providing crucial insights into the most significant drivers of EEE transmission and potential control points. The results, visualized through tornado plots, demonstrate varying degrees of sensitivity across the different populations, with some parameters showing consistent importance across all groups while others exhibit population-specific effects. Figure 5 shows these results.

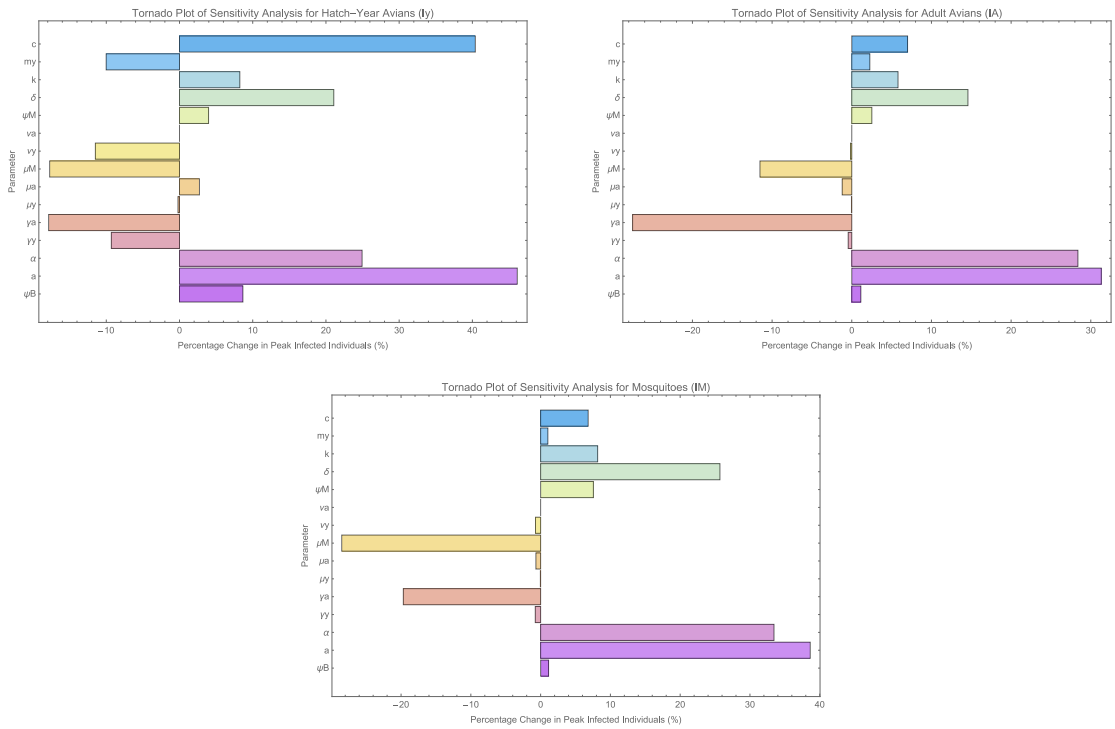


Fig 5. Tornado plots illustrating parameter sensitivity analysis for Eastern Equine Encephalitis transmission. Each bar represents the percentage change in peak infected individuals when the corresponding parameter is increased by 10%. **Top left:** Sensitivity analysis for hatch-year (young) avians (I_Y). **Top right:** Sensitivity analysis for after-hatch-year (adult) avians (I_A). **Bottom:** Sensitivity analysis for mosquito population (I_M). Parameters are denoted as follows: carrying capacity (c), avian maturation rate (m_y), virus extrinsic incubation period (k), avian infectivity (δ), mosquito birth rate (ψ_M), adult avian virulence (ν_a), hatch-year virulence (ν_y), mosquito death rate (μ_M), adult avian natural death rate (μ_a), hatch-year natural death rate (μ_y), adult recovery rate (γ_a), hatch-year recovery rate (γ_y), exposure coefficient (α), mosquito biting rate (a), and avian birth rate (ψ_B).

3.2.1 Parameter Impact Across Populations

The mosquito biting rate (a) and avian exposure coefficient (α) emerge as the dominant drivers of infection dynamics across all populations, with 30-45% increases in peak infections. This strong sensitivity reflects the fundamental role these parameters play in disease transmission - they directly control the frequency and success rate of virus transmission events between mosquitoes and avians. The biting rate represents how often mosquitoes seek and successfully feed on avian hosts, while the exposure coefficient captures the probability of successful virus transmission during these encounters. Their consistent importance across both hatch-year and

adult avians, as well as mosquitoes, demonstrates that they are the core transmission mechanism that drives EEE spread, rather than population-specific factors like mortality or recovery rates. This suggests that interventions targeting mosquito feeding behavior (through repellents or habitat modification) and virus transmission efficiency (through host immunity) could be particularly effective in controlling outbreaks.

3.2.2 Hatch-Year Avian Population (I_Y)

The hatch-year avian population exhibits the highest sensitivity to mosquito biting rate (a), showing approximately a 45% increase in peak infections. Trailing not too far behind is the carrying capacity (c) showing approximately a 40% increase on infection levels, a much higher significance when compared to the other two infectious classes, which highlights the clear role of dynamics within the young host population. Lastly, the avian exposure coefficient (α) shows a strong positive influence on infection, at a similar level compared to the other infectious classes (approximately 25%). Negative sensitivities, on the other hand, are observed in response to mosquito death rate (μ_M) and adult recovery rate (γ_a), with both parameters leading to roughly 20% decreases in peak infected individuals.

3.2.3 Adult Avian Population (I_a)

The adult avian population demonstrates significant positive sensitivity to both the exposure coefficient (α) and biting rate (a), with approximately 30% increases in peak infections when these parameters are elevated. A moderate positive response is observed with avian infectivity (δ), showing about a 15% increase in infection levels. The population exhibits clear negative sensitivity to adult recovery rates, about a 30% decrease, indicating that accelerated recovery could potentially reduce peak infection levels by moving individuals more quickly through infectious life stages. Notably, adult avians show reduced sensitivity to mosquito-related parameters, such as biting rate and mosquito death rate, compared to their hatch-year counterparts, suggesting that established avians may have different risk factors in the transmission cycle than hatch-years.

3.2.4 Mosquito Population (I_M)

The mosquito population exhibits sensitivity patterns that parallel those observed in avian populations, with the biting rate (a) and exposure coefficient (α) remaining the most influential parameters at 35% and 40% respectively. Avian infectivity (δ) shows a moderate positive effect on mosquito infection levels at around 27%, highlighting the interconnected nature of host-vector dynamics. The negative sensitivity to mosquito death rate and adult recovery rate, at 30% and 20% respectively, is similar to that of the host classes. This suggests that while the intrinsic mosquito population dynamics may serve as natural limiting factors in disease transmission, their negative impact is less pronounced than the cross-species interaction parameters.

The analysis reveals that while all three populations share similar sensitivity patterns to key parameters, the magnitude of these sensitivities varies. The hatch-year avian population (I_y)

generally shows the highest sensitivity to parameter changes, followed by mosquitoes (I_M), while the adult avian population (I_A) demonstrates more moderate responses to parameter variations.

Overall, the sensitivity analysis demonstrates that EEE transmission dynamics are most significantly influenced by fundamental biological parameters related to avian hosts. The consistent sensitivity patterns across young avians, adult avians, and mosquito populations suggest that targeted interventions focusing on these key parameters could yield the most effective results in disease control. This understanding of parameter sensitivity serves as a crucial foundation for identifying optimal intervention points in the EEE transmission cycle.

4. NUMERICAL DATA ANALYSIS & FEATURE IMPORTANCE

Aiming to validate and quantify these associations, machine learning techniques were employed to extend the results of Section 3 regarding the relationship between parameter values and cyclic behavior. Machine learning techniques can offer more information about parameter interactions and their relative significance in determining system behavior, even if the prior analytical approach was able to identify crucial parameter ranges and stability requirements. The seven most important parameters found in the present model—mosquito biting rate (a), exposure coefficient (α), avian infectivity (δ), virus extrinsic incubation period (k), mosquito death rate (μ_m), avian recovery rate (γ_A), and carrying capacity (c). To create a comprehensive dataset for analysis, these parameters were uniformly sampled across their biologically relevant ranges, generating 10,000 distinct parameter combinations. Equilibrium points were determined and used to evaluate the stability properties of each parameter combination.

The dataset's initial analysis showed a natural class imbalance, with 28% of parameter combinations producing sustained cycles and 72% of parameter combinations producing non-cyclic behavior. For most parameters, especially $a, \alpha, k,$ and δ, parameter distribution analysis using Mann-Whitney U tests substantial variations between cyclic and non-cyclic instances ($p < 0.001$) were observed. Particularly, Figure 6's correlation matrix revealed no collinearity between the parameters, indicating that each one influences system behavior independently.

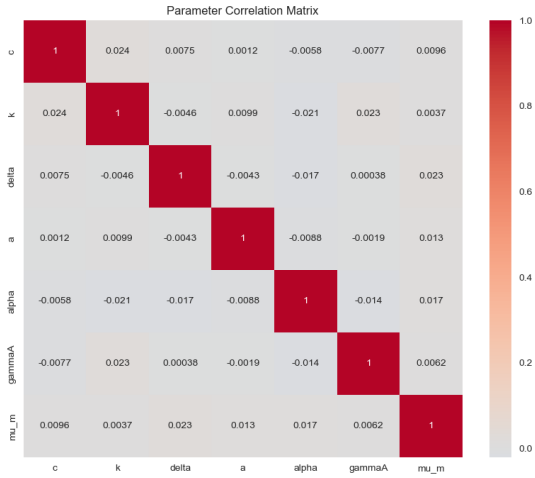


Fig 6. Pairwise correlations between model parameters are displayed in this parameter correlation matrix. The mostly low correlation values ($\forall\ |r| < 0.025$) show that there is little collinearity between the parameters, indicating that each one influences system behavior independently. This autonomy improves the interpretability of the feature importance analyses.

4.1 Machine Learning Methodology

Due to their interpretability and ability to capture non-linear associations and parameter interactions, three tree-based machine learning algorithms were employed: Random Forest, XGBoost, and LightGBM. Since tree-based algorithms can easily handle parameter interactions and offer reliable feature importance estimates, they are especially well-suited for this type of research. Optuna (Akiba 2019) was used to construct a Bayesian hyperparameter optimization function, which effectively explores the hyperparameter space through trial-and-error learning, to guarantee optimal model performance. By using 6-fold stratified cross-validation, model reliability significantly improved while retaining class distribution and guaranteeing consistent performance across various data subsets.

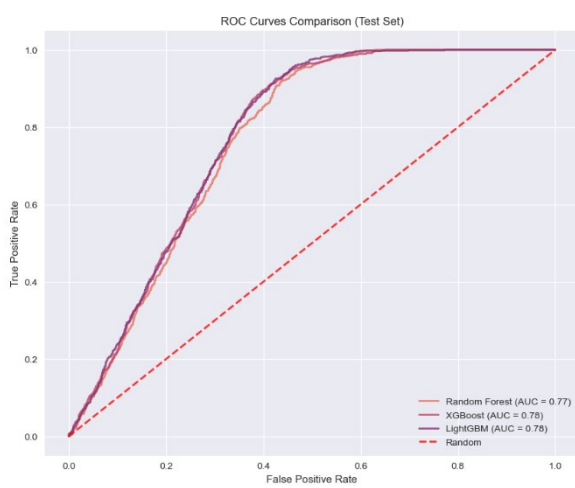


Fig 7. ROC curves that evaluate how well the model performs on test data. With comparable performance, all three models exhibit strong discriminative ability (AUC scores: LightGBM=0.78, XGBoost=0.78, Random Forest=0.77).

The almost matching curves provide better validity of prior findings by indicating strong and consistent prediction capability across various modeling methodologies.

The process of optimizing hyperparameters uncovered interesting trends among the models. The most important parameter for the Random Forest was bootstrap sampling, followed by the tree depth control parameters (maximum depth and minimum samples per leaf). LightGBM demonstrated comparable importance for feature subsampling (colsample_bytree) and maximum depth, but XGBoost's leading hyperparameters were subsample ratio and maximum depth. These trends imply that having a variety of tree architectures and managing model complexity were crucial elements in reaching peak performance. As shown in Figure 7, all models produced robust and reliable results. LightGBM and XGBoost performed almost identically (ROC-AUC of 0.77-0.79 across runs), whereas Random Forest came in second (ROC-AUC of 0.76-0.77 between runs). Despite having diverse architectures and ideal hyperparameter settings, the performance across these three modeling approaches is similar, which implies that the current model findings represent true underlying patterns in the data rather than artifacts unique to any one model.

4.2 Feature Importance Analysis

Using SHAP (SHapley Additive exPlanations) values, which offer model-agnostic feature importance measurements based on game theory principles, the contribution of each parameter to cyclic behavior was measured (Lundberg 2017, Lundberg 2020). By calculating the contribution of each parameter to prediction away from the expected baseline, SHAP values provide both local and global feature importance in interpreting a model's predictions.

Three different levels of parameter influence were identified by the SHAP analysis:

1. **Primary Drivers:** In all models, the two most important factors were the exposure coefficient (α) and the mosquito biting rate (a). In the ridge plots seen in Figure 7, both parameters had wide, asymmetric SHAP value distributions, suggesting significant non-linear impacts on cycle formation. While the exposure coefficient displayed a more intricate distribution pattern that reflected its function in mediating host-vector interactions, the mosquito biting rate showed exceptionally strong positive SHAP values, indicating that higher biting rates consistently increase the probability of cyclic behavior.
2. **Secondary Drivers:** The virus extrinsic incubation period (k) and avian infectivity (δ) clearly established a second level of importance. According to their ridge plots in Figure 7, which show clear bimodal distributions centered around zero, these parameters function as threshold modulators, becoming significant inside particular ranges but less significant outside of them. This behavior is consistent with the analytical conclusions of the current model concerning the prerequisites for the emergence of cycles.
3. **Tertiary Drivers:** Near zero, the carrying capacity (c), avian recovery rate (γ_A), and mosquito death rate (μ_m) displayed more concentrated SHAP distributions, suggesting more subtle impacts on system dynamics. Among the tertiary drivers, μ_m had the widest

distribution, indicating that it has the most impact, especially when combined with primary drivers.

The robustness of these important rankings is strongly supported by the fact that these patterns are consistent across all three modeling approaches, even though their underlying structures differ. Additionally, the ridge plots seen in Figure 8 show intricate patterns of interaction, especially between primary and secondary drivers, which contribute to the explanation of the system's non-linear cycle development.

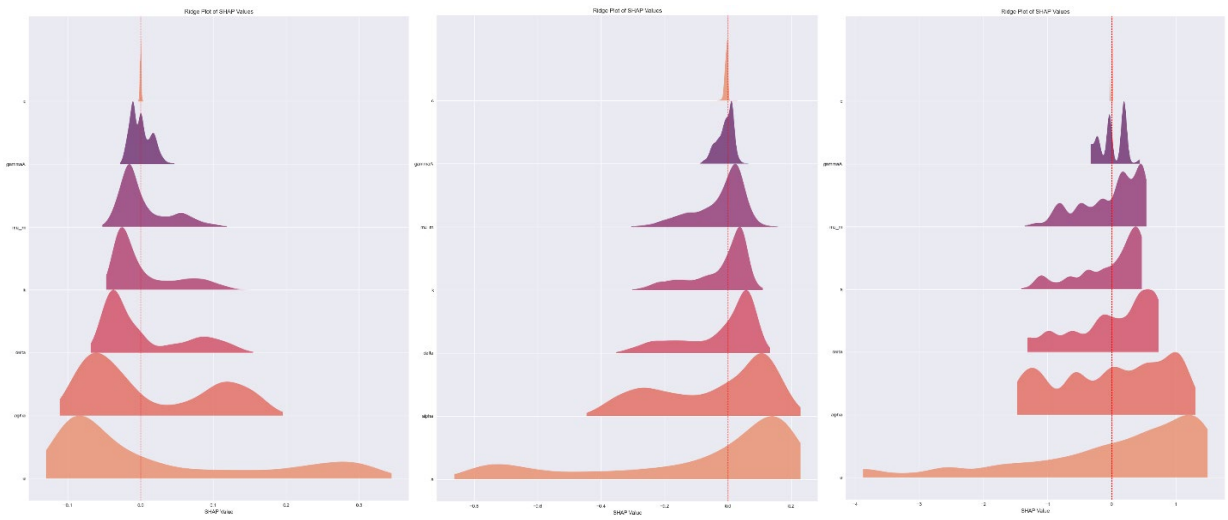


Fig 8. SHAP value distributions for model parameters for the Random Forest (left), XGBoost (middle), and LightGBM (right) models are displayed as ridge plots. The vertical red line at zero indicates baseline impact, and the x-axis shows SHAP values. The frequency of SHAP values is indicated by the breadth of each distribution, and the directional influence on cyclic behavior is shown by the position with respect to zero. Observe how the models all exhibit the same hierarchical impact pattern, with the exposure coefficient (α) and mosquito biting rate (a) displaying the biggest effects and the widest distributions.

4.3 Biological Implications

The machine learning analyses provide quantitative evidence that vector-host interaction parameters (a and α), serve as the primary control points for EEEV transmission dynamics. Reducing effective contact rates between mosquitoes and avians should be the primary goal of control measures, as indicated by the major influence of vector-host interaction parameters (a and α), which is consistent with ecological theory. Considering that these factors demonstrated the highest predictive power for cycle development across all modeling methodologies, this is especially pertinent.

The discovery of threshold effects in secondary drivers, namely in viral development parameters (k and δ), implies that, under the right circumstances, little adjustments to these values might result in notable changes in system behavior. This discovery has major implications for comprehending how environmental elements that impact viral growth may impact epidemic

trends, since even slight modifications to these parameters could cause the system to surpass crucial thresholds.

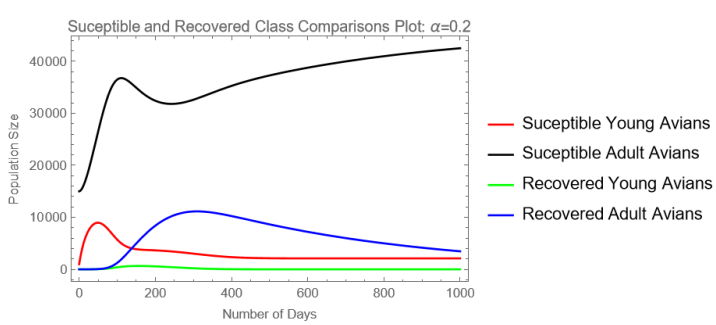
The minimal impact of population-level factors, especially carrying capacity, suggests that interaction rates may have a greater influence on system dynamics than absolute population sizes. This implies that control measures that only aim to reduce the population may be less successful than those that also target vector-host interactions or the effectiveness of viral transmission.

The analytical work done in this study is enhanced and expanded by these data-driven insights, which offer a quantitative foundation for comprehending parameter relevance and interaction effects. These results direct our attention to the parameter combinations that are most likely to result in biologically meaningful dynamics and aid in the explanation of the mechanisms underlying the cyclic patterns seen in natural EEEV transmission systems when proceeding to look at particular simulation scenarios.

5. MODEL SIMULATIONS & RESULTS

The host stage-structured EEEV model was simulated and analyzed in Mathematica to better understand the impact class-dependent differences found in host exposure to vectors has on the ecological mechanism structuring the enzootic transmission of EEEV. All model simulations were started on January 1st, which was classified as day 1, with 15,000 susceptible adult hosts, 1,000 susceptible young hosts, 1,499 susceptible mosquitoes, and 1 infectious mosquito. All parameter values remain static throughout the duration of the model as seen within *Table 1*, unless otherwise stated. The number of infectious mosquitoes and avians were tracked at the peak of each outbreak seen within the simulations to properly understand the transmission of EEEV. The proportionality in population size between host stages, both adult and young, is also tracked throughout the duration of the model.

To start, the relationship between the timing and intensity of each individual disease outbreak and the extent to which adult hosts are exposed to the virus is explored. The exposure coefficient for the adult host class was varied ($0 < \alpha \leq .5$) and the exposure coefficient for the young host class was $1 - \alpha$. The baseline would be $\alpha = 0.5$ as that would be when there is no preference given to young or adult. Using the numerical analysis, we consider three different values for α: $0.2, 0.3,$ and 0.5. Each of these was chosen based on the analysis from section 3.



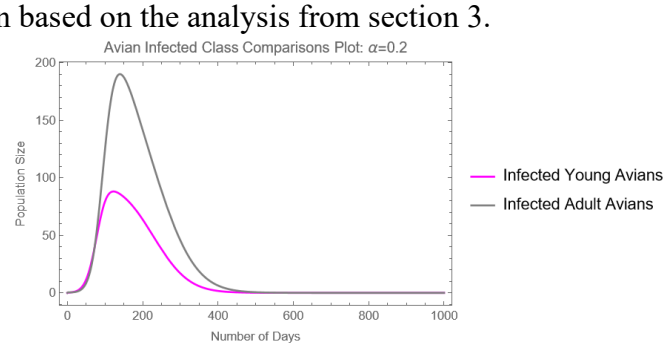


Fig 8. EEEV model simulations with $\alpha = 0.2$, young hosts are more exposed to the virus than their adult counterpart, but not enough to sustain the outbreak. Top-left plot shows susceptible and recovered stages, top-left plots show infectious stages.

As seen in Figure 8, when $\alpha = 0.2$ the outbreak would die out in a little over a year. In this case $R_0 < 1$. This with too much preference given to young, the disease is unable to persist, leading to eradication.

When the exposure coefficient is raised to $\alpha = 0.3$, we expect a cyclic outbreak from the numerical analysis. That can be seen in the left plot in Figure 9. There is a cyclic outbreak pattern and peak infection rates occur around day 1,000. These cycles tend to last around 100 days which seems to match with nature cycles of around 2-3 years.

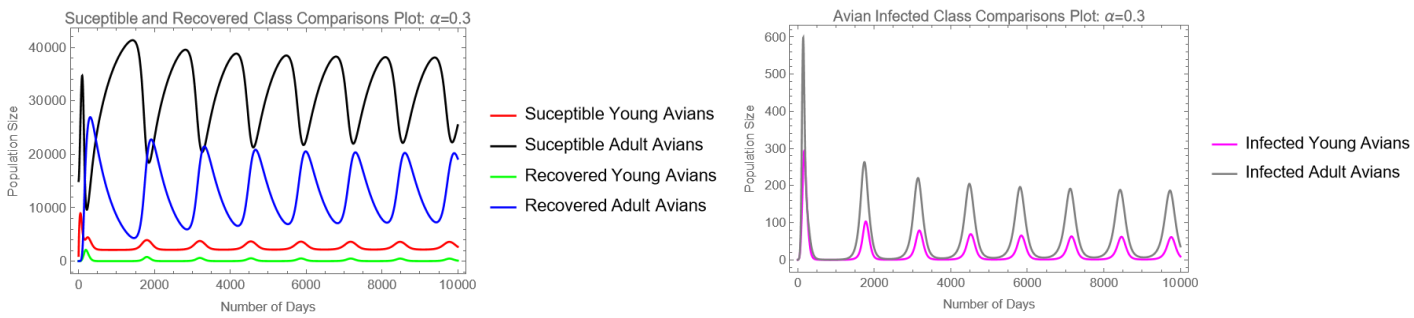


Fig 9. EEEV model simulations with $\alpha = 0.3$, young hosts are more exposed to the virus than their adult counterpart. Top-left plot shows susceptible and recovered stages, top-left plots show infectious stages.

When we look at the baseline exposure rate, $\alpha = 0.5$, where there is equal exposure between young and adults, we can see that an outbreak occurs and is sustained, but we lose the cyclic nature of the outbreak as is seen in nature. Everything settles down to the stable endemic equilibrium.

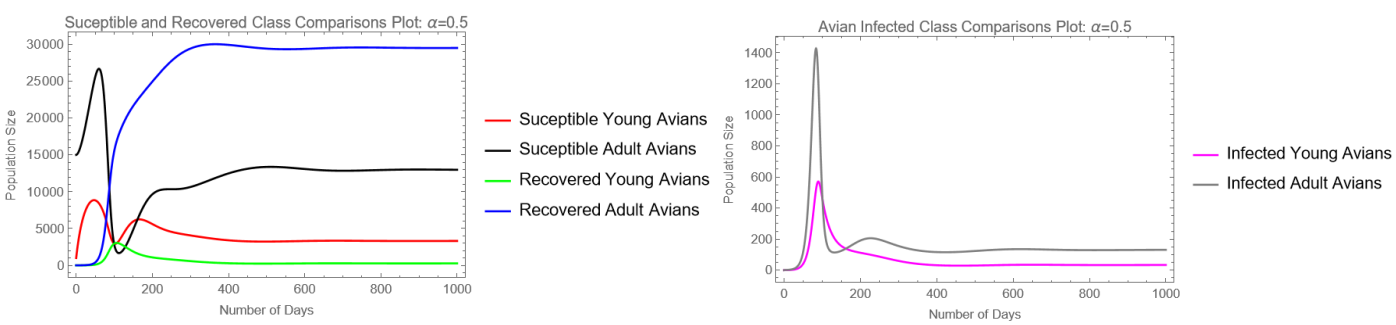


Fig 10. EEEV model simulations with $\alpha = 0.5$, equal exposure to the virus across both hosts. Top-left plot shows susceptible and recovered stages, top-left plots show infectious stages.

6. DISCUSSION

Our study reveals the critical importance of age structure in EEEV transmission dynamics, particularly highlighting the amplifying role of hatch-year avians. The model successfully reproduced biologically observed 2–3-year cyclic outbreak patterns without requiring seasonal forcing, demonstrating that host age structure alone can drive these dynamics. This finding aligns with field observations in European Starlings and American Robins (Estep, 2013), providing strong validation for our modeling approach.

Young birds emerge as key amplifiers in EEEV transmission due to their heightened exposure and immunological vulnerability during nesting seasons. The model shows that increased exposure in young hosts drives cyclic outbreaks, while equal exposure levels in adults and young would lead to a sustained outbreak level. This distinction underscores the importance of age-specific parameters in accurately modeling EEEV transmission and suggests that traditional approaches that ignore age structure may miss crucial aspects of disease dynamics.

The temporal alignment between model predictions and observed outbreak patterns provides strong evidence for the role of host age structure in driving EEEV transmission cycles. Our findings demonstrate that the inherent biological differences between young and adult hosts - including immune response, behavior, and exposure patterns - are sufficient to explain observed outbreak patterns without invoking external forcing mechanisms. This insight fundamentally changes our understanding of EEEV ecology and transmission dynamics.

These results extend beyond previous studies that focused primarily on viral biology and vector competence (Hassan, 2003; Komar, 1999; McLean, 1995; Molaei, 2016) by demonstrating how host age structure influences outbreak patterns. The model's success in capturing real-world patterns suggests that age-structured approaches should be considered in studies of other vector-borne diseases where host age may influence transmission dynamics.

7. CONCLUSION & FUTURE WORK

Our research demonstrates the fundamental importance of age-structured exposure in EEEV transmission dynamics. Machine learning analyses identified vector-host interaction parameters - specifically exposure coefficient (α) and mosquito biting rate (a) - as primary drivers of transmission, suggesting that intervention strategies should prioritize reducing effective contact rates rather than simply targeting population reduction. The model's ability to reproduce biologically observed 2–3-year outbreak cycles validate the critical role of hatch-year avians in maintaining EEEV transmission.

Key findings reveal that threshold effects in viral development parameters could lead to significant changes in transmission patterns from small environmental alterations. This insight, combined with our understanding of age-specific exposure rates, provides clear direction for control strategies. Particularly, the model suggests that interventions focused on protecting young birds during vulnerable periods could effectively disrupt transmission cycles. The identification of these threshold effects also highlights the potential sensitivity of EEEV

transmission to environmental changes, raising important considerations for climate change impacts.

The success of our age-structured approach in capturing EEEV dynamics suggests broader applications for studying vector-borne diseases. By focusing on the mechanistic understanding of how host-vector interactions drive disease patterns, this work provides a foundation for developing targeted, effective control strategies. The framework developed here could be particularly valuable for diseases where host age significantly influences transmission dynamics.

Future research directions should expand the model in several key ways. Incorporating avian migration patterns and seasonal variations will enhance predictive accuracy by capturing the temporal dynamics of host populations. Implementation of data fitting algorithms using mosquito pooling and avian infection rates will refine parameter estimates and model validation. The addition of spatial components will enable analysis of regional transmission variations, while climate change scenarios will help predict shifting patterns in EEEV transmission. Finally, including additional host species will provide insights into community-level impacts, particularly how interspecies interactions affect transmission dynamics. These expansions will create a more comprehensive framework for understanding and predicting EEEV outbreaks across different spatiotemporal scales.

Integration of these elements will enhance the model's predictive power and provide more comprehensive guidance for public health interventions. Particularly important is the need to understand how climate change might affect the threshold effects identified in our analysis, as this could have significant implications for future outbreak patterns and control strategies.

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