

1 Mathematical Appendix

1.1 Model Description

The population of *Aedes* vectors consists of uninfected (P_A) and infected (Q_A) eggs, and susceptible (S_A), incubating (E_A ; infected, but not yet infectious) and infectious (I_A) adult individuals. The size of the adult *Aedes* mosquito population is $N_A = S_A + E_A + I_A$. The population of adult *Culex* vectors consists of susceptible (S_C), incubating (E_C) and infectious (I_C) adult individuals. The size of adult *Culex* mosquito population is $N_C = S_C + E_C + I_C$. The aquatic population of *Culex* only has uninfected (P_C) eggs because we assume there is no vertical transmission of RVFV in *Culex*. The livestock populations consist of susceptible (S_L), incubating (E_L), infectious (I_L), and immune (R_L) individuals. The total livestock population size is $N_L = S_L + E_L + I_L + R_L$. The other host population serves as a sink, potentially diverting mosquito bites from competent hosts, and the total population size for these sink hosts is N_D . The resulting system of the ordinary differential equations is:

Vector 1 (*A*): *Aedes* mosquitoes with vertical transmission:

$$\frac{dP_A}{dt} = \frac{b_A K_A}{N_A} (N_A - q_A I_A) - \frac{b_A K_A}{N_A} P_A \quad (1)$$

$$\frac{dQ_A}{dt} = \frac{b_A K_A}{N_A} \left(\frac{q_A}{r_{LA}} I_A - Q_A \right) \quad (2)$$

$$\frac{dS_A}{dt} = \frac{b_A K_A}{N_A} P_A - \beta_{LA} S_A \frac{I_L}{N_L} - \frac{d_A N_A}{K_A} S_A \quad (3)$$

$$\frac{dE_A}{dt} = \beta_{LA} S_A \frac{I_L}{N_L} - \frac{d_A N_A}{K_A} E_A - \varepsilon_A E_A \quad (4)$$

$$\frac{dI_A}{dt} = \frac{b_A K_A}{N_A} Q_A + \varepsilon_A E_A - \frac{d_A N_A}{K_A} I_A \quad (5)$$

$$\frac{dN_A}{dt} = \frac{b_A K_A}{N_A} (P_A + Q_A) - \frac{d_A N_A}{K_A} N_A \quad (6)$$

Vector 2 (C): *Culex* mosquitoes:

$$\frac{dP_C}{dt} = \frac{b_C K_C}{N_C} N_C - \frac{b_C K_C}{N_C} P_C \quad (7)$$

$$\frac{dS_C}{dt} = \frac{b_C K_C}{N_C} P_C - \beta_{LC} S_C \frac{I_L}{N_L} - \frac{d_C N_C}{K_C} S_C \quad (8)$$

$$\frac{dE_C}{dt} = \beta_{LC} S_C \frac{I_C}{N_C} - \frac{d_C N_C}{K_C} E_C - \varepsilon_C E_C \quad (9)$$

$$\frac{dI_C}{dt} = \varepsilon_C E_C - \frac{d_C N_C}{K_C} I_C \quad (10)$$

$$\frac{dN_C}{dt} = \frac{b_C K_C}{N_C} P_C - \frac{d_C N_C}{K_C} N_C \quad (11)$$

Livestock host (L):

$$\frac{dS_L}{dt} = b_L N_L - \beta_{AL} S_L \frac{I_A}{N_A} - \beta_{CL} S_L \frac{I_C}{N_C} - \frac{d_L N_L}{K_L} S_L \quad (12)$$

$$\frac{dE_L}{dt} = \beta_{AL} S_L \frac{I_A}{N_A} + \beta_{CL} S_L \frac{I_C}{N_C} - \frac{d_L N_L}{K_L} E_L - \varepsilon_L E_L \quad (13)$$

$$\frac{dI_L}{dt} = \varepsilon_L E_L - (\mu_L + \gamma_L) I_L - \frac{d_L N_L}{K_L} I_L \quad (14)$$

$$\frac{dR_L}{dt} = \gamma_L I_L - \frac{d_L N_L}{K_L} R_L \quad (15)$$

$$\frac{dN_L}{dt} = b_L N_L - \frac{d_L N_L^2}{K_L} - \mu_L I_L \quad (16)$$

Dead-end host (D):

$$\frac{dN_D}{dt} = b_D N_D - \frac{d_D N_D^2}{K_D} \quad (17)$$

Table S1. Definitions for model parameters.

Symbol	Description	Definition	Reference
b_A	Birth rate of <i>Aedes</i> vectors	$= d_A$	
b_C	Birth rate of <i>Culex</i> vectors	$= d_C$	
b_L	Birth rate of livestock	$= d_L$	
b_D	Birth rate of dead-end hosts	$= d_D$	
K_A	Carrying capacity for <i>Aedes</i> vectors	$(\frac{Aedes\ females}{CO_2\ trap-night})_{time+1} \times GPA \times (N_L + N_D)$	

K_C	Carrying capacity for <i>Culex</i> vectors	$(\frac{Culex\ females}{CO_2\ trap-night})_{time+1} \times GP_C \times (N_L + N_D)$	
K_L	Carrying capacity for livestock	$= N_L$ (from data)	(see text & Table S2)
K_D	Carrying capacity for dead-end hosts	$= N_D$ (from data)	(see text & Table S2)
$1/d_A$	Life span of <i>Aedes</i> vectors	10 days	[1]
$1/d_C$	Life span of <i>Culex</i> vectors	10 days	[2, 3]
$1/d_L$	Life span of livestock	5 years	
$1/d_D$	Life span of dead-end hosts	1 year	[4, 5]
q_A	Probability of vertical transmission	0.001	[6, 7]
β_{LA}	Transmission rate from livestock to <i>Aedes</i>	$\frac{r_{LA}}{GP_A} \times f_L$	
β_{LC}	Transmission rate from livestock to <i>Culex</i>	$\frac{r_{LC}}{GP_C} \times f_L$	
β_{AL}	Transmission rate from <i>Aedes</i> to livestock	$\beta_{LA} \frac{N_A}{N_L}$	
β_{CL}	Transmission rate from <i>Culex</i> to livestock	$\beta_{LC} \frac{N_C}{N_L}$	
r_{LA}	Probability of transmission from livestock to <i>Aedes</i> per bite	0.005	[8]
r_{LC}	Probability of transmission from livestock to <i>Culex</i> per bite	0.09	[8]
GP_A	Gonotrophic period for <i>Aedes</i> in days	$2 + (-0.066 + 0.018T)^{-1}$	[9]
GP_C	Gonotrophic period for <i>Culex</i> in days	$2 + (-0.066 + 0.018T)^{-1}$	[9]

f_L	Probability of mosquito feeding on livestock	$\frac{N_L}{N_L + N_D}$	
$1/\varepsilon_A$	Extrinsic incubation period of RVFV in <i>Aedes</i>	$(-0.1038 + 0.0071T)^{-1}$	[10, 11]; but see methods
$1/\varepsilon_C$	Extrinsic incubation period of RVFV in <i>Culex</i>	$(-0.1038 + 0.0071T)^{-1}$	[10, 11]; but see methods
$1/\varepsilon_L$	Intrinsic incubation period of RVFV in livestock	1 day	[12]
T	Temperature (°C)	10-year mean daily temperatures, 2002–2011	TOPS [13]
$1/\gamma_L$	Infectious period of livestock	4 days	[14]
$1/\mu_L$	Excess disease-related mortality of livestock	$-\log(1 - 0.25) \times \gamma_L$	[14]

Table S2. Data-based definitions for state variables for each grid cell.^a

Symbol	Description	Definition	Source
N_A	Number of <i>Aedes</i> vectors	$\left(\frac{Aedes\ females}{CO_2\ trap-night}\right)_{time} \times GPA \times (N_L + N_D)$	CO ₂ trap records from mosquito control agencies linked to land use classes defined in the National Land Cover Data Set 2006
N_C	Number of <i>Culex</i> vectors	$\left(\frac{Culex\ females}{CO_2\ trap-night}\right)_{time} \times GPC \times (N_L + N_D)$	CO ₂ trap records from mosquito control agencies linked to land use classes defined in the National Land Cover Data Set 2006
N_L	Number of livestock	Direct tabulation from spatial data	California Water Resources Control Board
N_D	Number of dead-end hosts	$\left(\frac{Birds}{Survey\ route}\right) \times \left(\frac{25}{50\pi 0.2}\right)$	USGS Breeding Bird Survey

^a See the methods section for further explanation.

1.2 Computation of \mathcal{R}_0

\mathcal{R}_0 is computed according to the next-generation matrices method described by van den Driessche and Watmough [15], and the details are summarized here for completeness. For vertical transmission, the next-generation matrices (F_V and V_V) are as below:

$$F_V = \begin{bmatrix} 0 & \frac{b_A K_A}{N_A} \frac{q_A}{r_{LA}} \\ 0 & 0 \end{bmatrix} \quad (18)$$

$$V_V = \begin{bmatrix} \frac{b_A K_A}{N_A} & 0 \\ -\frac{b_A K_A}{N_A} & \frac{d_A N_A}{K_A} \end{bmatrix} \quad (19)$$

Let $x_j = \frac{X_j}{N_j}$, $j = A, C, L$ and $X = S, E, I, K$. Then the next-generation matrices of the horizontal transmission (F_H and V_H) are:

$$F_H = \begin{bmatrix} 0 & 0 & 0 & \beta_{LASA} & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & \beta_{ALS_L} & 0 & 0 & 0 & \beta_{CLS_L} \\ 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & \beta_{LCS_C} & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 \end{bmatrix} \quad (20)$$

$$V_H = \begin{bmatrix} d_A/k_A + \varepsilon_A & 0 & 0 & \beta_{LASA} & 0 & 0 \\ -\varepsilon_A & d_A/k_A & 0 & 0 & 0 & 0 \\ 0 & 0 & d_L/k_L + \varepsilon_L & 0 & 0 & 0 \\ 0 & 0 & -\varepsilon_L & d_L/k_L + \mu_L + \gamma_L & 0 & 0 \\ 0 & 0 & 0 & 0 & d_C/k_C + \varepsilon_C & 0 \\ 0 & 0 & 0 & 0 & -\varepsilon_C & d_C/k_C \end{bmatrix} \quad (21)$$

\mathcal{R}_0 can be calculated as:

$$\mathcal{R}_0 = \rho(F_V V_V^{-1}) + \rho(F_H V_H^{-1}), \quad (22)$$

where $\rho(\text{matrix})$ represents the maximum eigenvalue of the matrix.

At disease-free equilibrium (DFE), $s_A = 1, s_C = 1, s_L = 1$. And $k_A = \frac{K_A}{N_A}, k_C = \frac{K_C}{N_C}, k_L = \frac{K_L}{N_L}$ were computed from vector and livestock data as in Tables S1 and S2.

1.3 Computation of \mathcal{E}_0

\mathcal{E}_0 was computed according to the method described by Hosack et al. [16]. \mathcal{E}_0 was generated from the Hermitian parts of the next-generation matrices used for the \mathcal{R}_0 computation as follows:

$$\begin{aligned} \mathcal{E}_0 &= \rho(H(F_V)H(V_V)^{-1}) + \rho(H(F_H)H(V_H)^{-1}) \\ &= \rho\left(\frac{F_V + F_V^t}{2} \cdot \left(\frac{V_V + V_V^t}{2}\right)^{-1}\right) + \rho\left(\frac{F_H + F_H^t}{2} \cdot \left(\frac{V_H + V_H^t}{2}\right)^{-1}\right), \end{aligned} \quad (23)$$

where $\rho(\text{matrix})$ represents the maximum eigenvalue of the matrix.

At the disease-free equilibrium (DFE), $s_A = 1, s_C = 1, s_L = 1$. And $k_A = \frac{K_A}{N_A}, k_C = \frac{K_C}{N_C}, k_L = \frac{K_L}{N_L}$ were computed from vector and livestock data as in Tables S1 and S2.

1.4 Sensitivity analysis for \mathcal{R}_0 and \mathcal{E}_0

The following Table S3 shows the detailed results of the sensitivity analysis.

Table S3. Ranges of parameters and their partial rank correlation coefficient (PRCC) and p -values in relation to \mathcal{R}_0 and \mathcal{E}_0 .

Symbol	Range	To \mathcal{R}_0		To \mathcal{E}_0	
		PRCC	p -value	PRCC	p -value
$d_A(= b_A)$	$[\frac{1}{21}, \frac{1}{7}]$	-4.7826	< 0.0001***	-3.4486	0.0007**
$d_C(= b_C)$	$[\frac{1}{21}, \frac{1}{7}]$	-1.2888	0.1990	-3.7628	0.0002**
$d_L(= b_L)$	$[\frac{1}{10 \times 365}, \frac{1}{1 \times 365}]$	0.3857	0.7002	-0.1829	0.8550
$d_D(= b_D)$	$[\frac{1}{3.0 \times 365}, \frac{1}{0.5 \times 365}]$	1.0375	0.3007	1.3555	0.1768
N_A	(0, 1000]	-5.1767	< 0.0001***	5.8943	< 0.0001***
K_A	(0, 1000]	8.4685	< 0.0001***	6.9289	< 0.0001***
N_C	(0, 1000]	-5.5447	< 0.0001***	7.3618	< 0.0001***
K_C	(0, 1000]	5.1922	< 0.0001***	6.8351	< 0.0001***
$N_L(= K_L)$	[144, 25130]	-0.6223	0.5345	-0.6508	0.5160
$N_D(= K_D)$	[21, 262]	-1.0991	0.2731	-0.7998	0.4248
q_A	[0.001, 0.008]	0.2612	0.7942	1.3173	0.1893
r_{LA}	[0.001, 0.70]	8.7827	< 0.0001***	11.9349	< 0.0001***
r_{LC}	[0.001, 0.70]	6.8898	< 0.0001***	11.9748	< 0.0001***
ε_L	$[\frac{1}{6}, 1]$	-0.8097	0.4191	-7.5587	< 0.0001***
γ_L	$[\frac{1}{5}, 1]$	-4.0321	0.0001**	-3.6577	0.0003**
μ_L	[0.025, 0.1]	-0.9156	0.3610	-0.2306	0.8179
T	[6.97°C, 31.79°C]	16.2418	< 0.0001***	2.6719	0.0082*
*: significant at 0.01 level **: significant at 0.001 level ***: significant at 0.0001 level					

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