

APPENDIX A

The single season model that incorporates temperature related delay is formulated by the system

$$\begin{aligned}
 \dot{S}_V(t) &= \overbrace{b_V (S_V(t) + (1 - \rho_V)(E_V(t) + I_V(t)))}^{\text{birth}} \\
 &\quad - \underbrace{\alpha_V \beta_R \frac{I_R}{N_R} S_V}_{\text{disease transmission}} + \underbrace{\nu_V I_V}_{\text{infectivity loss}} - \underbrace{d_V S_V}_{\text{deaths}} \\
 \dot{E}_V(t) &= \underbrace{b_V \rho_V (E_V(t) + I_V(t))}_{\text{birth of infectives}} \\
 &\quad + \underbrace{\alpha_V \beta_R \frac{I_R}{N_R} S_V}_{\text{disease transmission}} - \underbrace{d_V E_V}_{\text{death}} - \underbrace{\kappa_V E_V(t - \tau)}_{\text{infected}} \\
 \dot{I}_V(t) &= \underbrace{\kappa_V E_V(t - \tau)}_{\text{infected}} - \underbrace{(d_V + \nu_V) I_V}_{\text{death and infectivity loss}} \\
 \dot{S}_R(t) &= \underbrace{-\alpha_R \beta_R \frac{I_V}{N_V} S_R}_{\text{disease transmission}} - \underbrace{d_R S_R(t)}_{\text{death}} + \underbrace{\nu_R R_R(t)}_{\text{loss of immunity}} \\
 \dot{I}_R(t) &= \underbrace{-\alpha_R \beta_R \frac{I_V}{N_V} S_R}_{\text{disease transmission}} - \underbrace{(d_R + \delta_R + \gamma_R) I_R(t)}_{\text{death, disease mortality, and recovery}}
 \end{aligned}$$

Parameters in the model are listed and defined in Table 2. As stated in the body of the text the basic reproduction number of the disease is quantity which one can use to develop policy decisions. The goal is to apply a control to the system that reduces the basic reproduction number to less than one forcing solutions to converge to a disease free equilibrium.

Computation of the basic reproduction number has been well established in the case of ordinary differential equations (Diekmann & Heesterbeek 2000, van den Driessche and Watmough 2002).

The basic reproduction number in the case of ordinary differential equations is the spectral radius of the matrix FV^{-1} where F - V is the matrix found by linearizing the differential equation around the disease free equilibrium. The matrix F is called an infection matrix and describes new infections and the matrix V is a transition matrix that describes how individuals transition from one stage to another. For ordinary differential equations the basic reproduction number is less than one exactly when all eigenvalues of F - V have negative real part (van den Driessche and Watmough 2002). Delay differential equations cannot be approximated by matrices because they are infinite dimensional models. However, we can extend the concept of analyzing the eigenvalues of the linearized model by calculating the roots of the characteristic polynomial and determining when these roots have negative real part less than one. One of the criteria that ensures that all roots of the characteristic polynomial of a linear delay differential equation is due to Stépán (Stépán 1989). The application of Stépán's criterion results in condition

$$R_0 = \frac{\kappa_V \alpha_R \alpha_V \beta_R^2}{(\kappa_V + d_V)(d_R + \delta_R + \gamma_R)(d_V + \nu_V)} \frac{N_V}{N_R} + \frac{b_V \rho_V (k_V + d_V + \nu_V)}{(\kappa_V + d_V)(d_V + \nu_V)} < 1$$

which is the same condition arrived at in (Wonham 2006) for the ordinary differential equation case.

Theorem: Assuming typical disease parameters, all roots of the characteristic polynomial of F - V , have negative real part provided that equation 2A, where N_V and N_R represent the total population densities for the vector population and the reservoir population respectively.

