

Transmission patterns that reduce population size without increasing disease prevalence: masting and chronic wasting disease in white-tailed deer

Article for *Theoretical Ecology*

Virginia Kanzinger¹ and Karen C. Abbott^{1,2}

¹Department of Biology, Case Western Reserve University
10900 Euclid Avenue, Cleveland, OH 44106 USA

²Corresponding author: kcabbott@case.edu

Online Resource 1

In this supplement, we explain the basis for the parameter values used to generate results shown in the main text (Table 2, Figures 2-3). Wherever possible, these values were based on published accounts. However, we lacked concrete estimates for many of the model's parameters and some choices were necessarily arbitrary. It is for this reason that we carefully studied the effect of each parameter on equilibrium model behavior (see Results and main text Table 1). This is important for understanding how our results would change if we used different estimates, and as reassurance that our conclusions are not undermined by our lack of precise parameter estimates.

In the baseline simulation, q was set to 0.4, consistent with Habib et al. (2011) and Storm et al. (2013)'s findings that CWD transmission is intermediate between density ($q = 0$) to frequency ($q = 1$) dependence. We assigned the parameter f a value of 0.04 month^{-1} , which is roughly $\frac{1}{24}$ and therefore represents one deer birth per year for every two deer (Green et al. 2017). Because the Hanley et al. (2022) model that we used as a baseline does not include density-dependent demography, the population dynamics are very sensitive to the balance between the intrinsic birth and death rates. For realistic death rates, the birth rate must remain near this $f = 0.04 \text{ month}^{-1}$ estimate to avoid unbounded population growth or decline (Table 1). For the death rates, we set $\mu_S = \frac{1}{36} \approx 0.0278 \text{ month}^{-1}$ which represents an average lifespan of 3 years. This is within a realistic range for areas with deer hunting (Brinkman et al. 2004). We assigned μ_E , μ_I , and μ_D the same value, but since the non-CWD death rates of infected and diseased deer are split into removed (w) and *in situ* (d) deaths, we arbitrarily assumed 20% of these deer killed would be removed. Therefore, $\mu_{Iw} = \mu_{Dw} = 0.2\mu_S \approx 0.0056 \text{ month}^{-1}$ and $\mu_{Id} = \mu_{Dd} = \mu_S - \mu_{Iw} \approx 0.0222 \text{ month}^{-1}$. We assumed that infected deer would be less infectious than fully diseased deer, so we used a value of 0.001 month^{-1} for γ_D and $0.00075 \text{ month}^{-1}$ for γ_I , i.e. pre-symptomatic infected deer transmit CWD at 75% of the efficacy of diseased deer. We assigned σ a value of 1×10^{-5}

month⁻¹, or 1% the transmission rate of diseased deer. We set $\omega = \frac{1}{8} = 0.125$ month⁻¹ to reflect the eight-month average period of exposure before a deer becomes infectious (Plummer et al. 2017, Belsare and Stewart 2020). Because of the average 23-month period between becoming infectious and the onset of symptomatic disease, ε was assigned a value of $\frac{1}{23} \approx 0.0435$ month⁻¹ (Johnson et al. 2011, Belsare and Stewart 2020). Since the amount of time a deer is diseased before dying from CWD is typically less than a year (Williams and Miller 2002), α was assigned a value of $\frac{1}{7} \approx 0.1429$ month⁻¹. Because the units on the environmental reservoir are arbitrary, we set $\phi_x = 1$ month⁻¹ and adjusted the other shedding rates to be relative to this. Therefore, we set $\phi_I = 0.8$ month⁻¹, or 80% of ϕ_x , and $\phi_D = 0.9$ month⁻¹, or 90% of ϕ_x . We assumed that living deer shed prions at roughly 10% of the rate of dead deer. Therefore, θ_I was set to 0.08 month⁻¹, and θ_D was set to 0.1 month⁻¹. Finally, η was set to 0.1 month⁻¹.

The original model from Hanley et al. (2022) also included a parameter, which they called D but is unrelated to our state variable D , to represent prions entering the environment from other mechanisms, but we omitted this process ($D = 0$) due to the lack of a known mechanism through which it would occur.