

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

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In the Hanley et al. (2022) model, and our extension of it, disease plays an integral role in governing deer population dynamics. In the absence of disease, the model collapses to a simple exponential growth model. That is, if $E = I = D = P = 0$ so all deer are susceptible ($S = N$),

$$\frac{dN}{dt} = (f - \mu_S)N \quad . \quad (\text{OR2.1})$$

This model is neither interesting nor particularly realistic, but it is useful to consider in comparison to the way the model behaves with disease present. Specifically, we assert in the main text that the changes in equilibrium mean population size with masting are due to disease dynamics, but how do we know they were not caused simply by temporal variability in the demographic rates, independent of disease? In this Online Resource, we answer that question.

Let $r_i = f_i - \mu_{Si}$ for any particular scenario, i . That is, in simulations without masting ($i=0$), the population grows at per capita rate $r_0 = f_0 - \mu_{S0}$ where the 0 subscript here indicates the default parameter values shown in Table 1. If we add masting but only allow it to impact the frequency dependence parameter q , populations will still grow at a constant rate r_0 in the absence of disease because without disease, q does not affect population dynamics. When masting impacts fecundity, we'll use the subscript f^+ to indicate the parameter values in masting years and f^- to indicate values in non-masting-years. Now, the population grows at rate $r_{f^+} = f_{f^+} - \mu_{S0}$ during masting years and at $r_{f^-} = f_{f^-} - \mu_{S0}$ during non-masting years. Recall that in masting

simulations, we computed the non-mast-year value of f such that the time-average value of f would remain at f_0 as in the no-masting simulations. So, by this definition, $48 f_0 = 36 f_{f^-} + 12 f_{f^+}$, recalling that we measure rates in units of month^{-1} and that masting occurs on a 4-year cycle. Furthermore, because masting only affects fecundity in this scenario, μ_{S0} remains the same throughout and so we also have $48 r_0 = 36 r_{f^-} + 12 r_{f^+}$. By the same logic, if masting affects death rates instead of fecundity, $48 r_0 = 36 r_{\mu^-} + 12 r_{\mu^+}$.

Over any 4-year period, a population that is not experiencing masting effects will grow by a factor of $\exp(48 r_0)$ (from equation (OS2.1)). A population with time-varying fecundity due to masting will grow by a factor of $\exp(36 r_{f^-})$ for the three non-mast years, then by an additional factor of $\exp(12 r_{f^+})$ in the mast year, for a total growth factor of $\exp(36 r_{f^-}) * \exp(12 r_{f^+}) = \exp(36 r_{f^-} + 12 r_{f^+})$. Due to the relationships between r_0 , r_{f^-} , and r_{f^+} given in the previous paragraph, $\exp(36 r_{f^-} + 12 r_{f^+}) = \exp(48 r_0)$. Likewise, a population with time-varying death rates due to masting would grow by a factor of $\exp(36 r_{\mu^-}) * \exp(12 r_{\mu^+}) = \exp(36 r_{\mu^-} + 12 r_{\mu^+}) = \exp(48 r_0)$ over any 4-year period.

In sum, because we set parameter values to preserve long-term average rates when we added variation due to masting, the deer population experiences the same total amount of population growth over a 4-year masting cycle regardless of whether masting effects are present and, if they are, which parameters are affected. For this reason, we can confidently say that changes in deer population size with masting are due to the effects of masting on disease dynamics, and not due to a disease-independent nonlinear averaging effect of temporal variability per se.