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Supplementary Figures

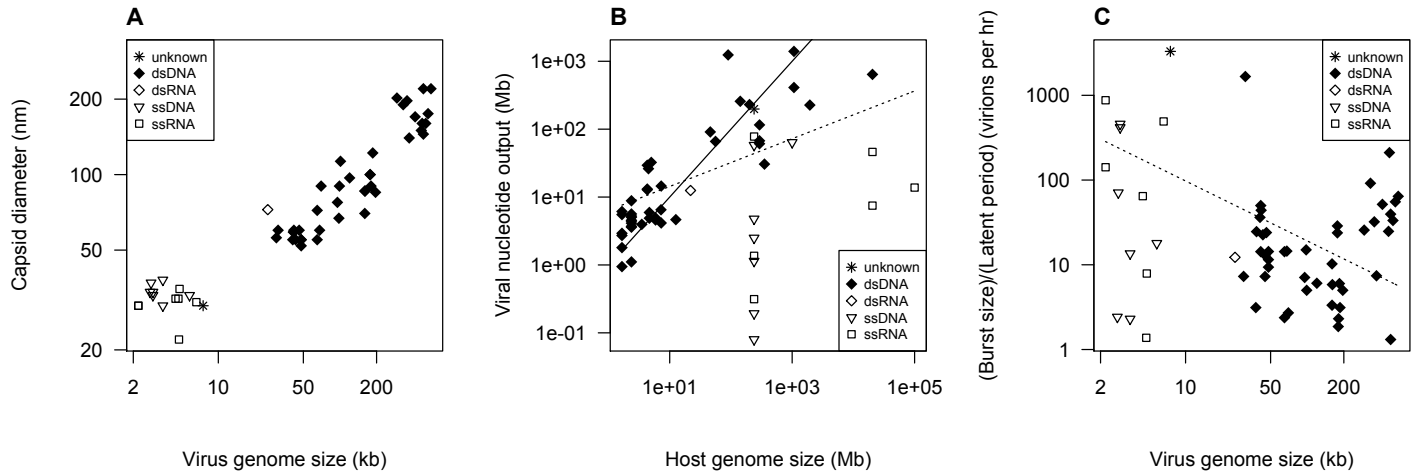


Figure S1. Supplementary data plots. (A) Virus capsid diameter vs. virus genome size, for all strains in the dataset with both measurements. Because these traits are well correlated, we use genome size as the sole metric of virus size in the analyses. (B) Viral nucleotide output (burst size multiplied by viral genome size) vs. host genome size. The solid line is the 1:1 line and the dashed line is the fitted line to all of the data from a mixed model ($R^2 = 0.54$, $F_{1,5} = 16$, $p = 0.01$). (C) Virion production rate (approximated as burst size divided by latent period) vs. virus genome size. The dashed line shows the fitted relationship from a mixed model, $p = 0.004$, $R^2 = 0.19$.

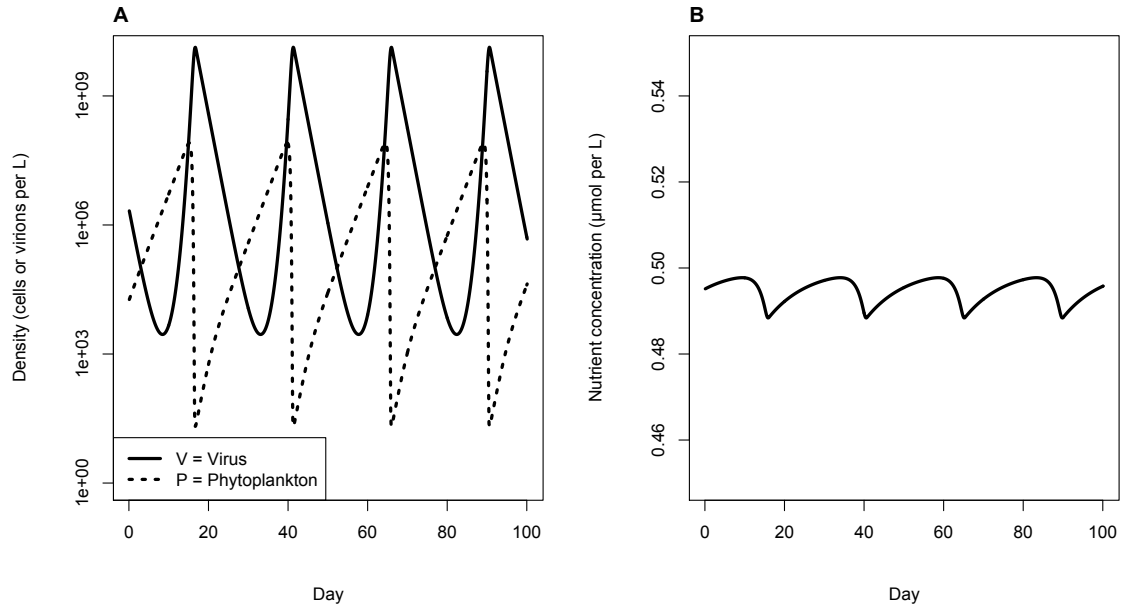


Figure S2. Example model dynamics. (A) Virus and phytoplankton host density. (B) Nutrient concentration. Model parameters are burst size $b_i = 1000$ (virions per cell), latent period $L_i = 16$ hrs, host growth rate $\mu_{\max} = 1$ (d^{-1}), host mortality rate $d_p = 0.3$ (d^{-1}), viral decay rate $d_v = 0.2$ (d^{-1}), virion production rate constant $\rho_m = 480$ virions cell^{-1} , other parameters assigned the values in Table 1.

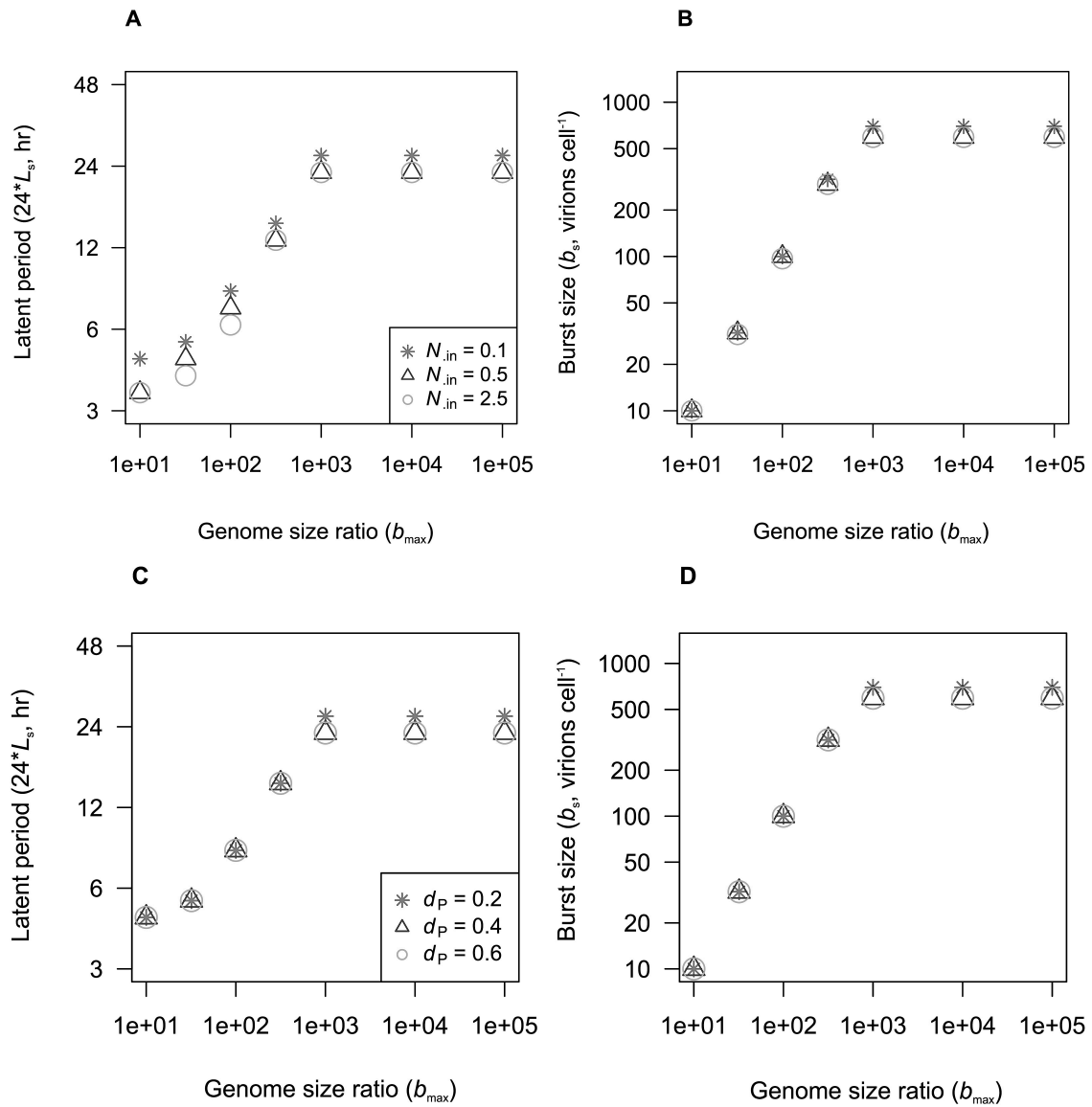


Figure S3. Model results when varying the concentration of nutrients entering the system (N_{in} , panels A-B) and host mortality rate (d_p , panels C-D). This figure is analogous to Fig. 1C-D, but with viral decay rate d_v held at 0.7 (d^{-1}) and virion production rate constant ρ_m held at 20 . Host maximum growth rate $\mu_{max} = 1$ (d^{-1}), and other parameters are assigned the values in Table 1.