Appendix A - Derivation of Discrete-time Evolutionary Model Parameters

Under the assumption that both natural mortality, μ, and average virulence, $\bar{v}$ are constant across all ages of infection, the quantities k and $\sigma(s)$ in equations 1 and 2 of the main text simplify to

$$k = \frac{\sum_{a=0}^{\infty} a\bar{\beta}(a) S\lambda^{-a}(1-\mu-\bar{v})^a}{\sum_{a=0}^{\infty} \lambda^{-a}(1-\mu-\bar{v})^a}, \quad \text{(A-1)}$$

$$\sigma(s) = \frac{\sum_{a=s}^{\infty} \bar{\beta}(a) S\lambda^{-a}(1-\mu-\bar{v})^a}{\lambda^{-s}(1-\mu-\bar{v})^s}, \quad \text{(A-2)}$$

where λ is the growth rate at the stable age distribution and $(1-\mu-\bar{v})^x$ gives the probability of an infection lasting to age x. These are the discrete-time analogues of expressions presented in the companion theory paper (Day et al., *submitted*). For the first analysis focusing on the evolutionary dynamics of transmission alone, we assume all genotype-specific virulences are zero, thus $\bar{v}$ is zero. For all analyses, μ is set to 0.005, which corresponds to a lifespan of 200 days (an underestimate for lab mice, but an over estimate for wild mice).

To predict the evolutionary trajectories in an endemic scenario, we need to define a situation where the number of infected hosts is not growing in size. Mathematically, this occurs when the leading eigenvalue of $\mathbf{L}$ is equal to 1 and there exists a unique value of the number of susceptible individuals, S^*, for which this occurs. This value is given by

$$S^* = \frac{1}{\sum_{a=0}^{n} \bar{\beta}(a)(1-\mu-\bar{v})^a}. \quad \text{(A-3)}$$

Appendix B - Supplementary Results

Figure B-1 shows the stable age distribution in the epidemic and endemic scenarios. In an expanding epidemic, most infections are very young, while in an endemic situation, older infections become more frequent.

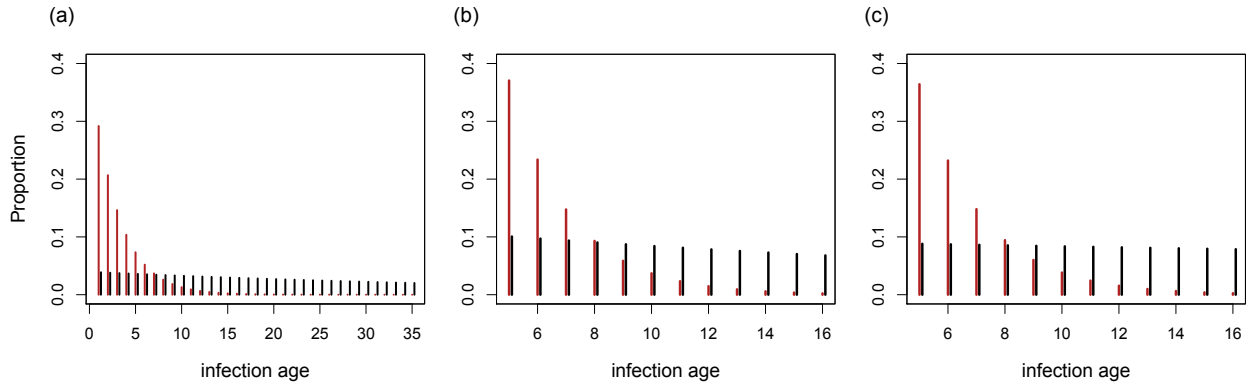

Figure B-1: Average stable age distributions, $q(s)$, in epidemic (red) and endemic (black scenarios). Shown are the average distributions across 10000 bootstrap replicates for infections in (a) C57 mice, (b) C57 mice, truncated data set, (c) MF1 mice.

Figure B-2 shows how evolutionary trajectories can be qualitatively altered by changing how host level measures are mapped to disease life history traits. We repeated all of the analyses in the main text, but with a different mapping of within-host parasite densities to transmission. In particular, we increased the linear coefficient of this mapping by an order of magnitude. This increases estimates of genetic variance and covariance, while leaving the qualitative patterns unaltered.

With this parameterization, the evolutionary predictions for the truncated C57 data set, in the epidemic case, are altered. Unlike in the main text, selection for increasing transmission rate can overcome selection for lower virulence, because the genetic variance in transmission rates has been increased. The predictions for the endemic case are, here, unchanged presumably since the strength of selection for increasing transmission remains too low to overcome the strength of selection for lower virulence. The other two data sets show quantitative changes in predictions (e.g., responses to selection for higher transmission rates are now stronger in the epidemic cases since, again, genetic variance has been increased), but hasn't qualitatively altered evolutionary trajectories. Changing the mapping of within-host densities to transmission in these cases also increases the magnitude of the covariances between transmission at different ages. Consequently, the evolutionary predictions are still constrained by negative covariances (i.e., trade-off) between transmission rates, and the qualitative patterns are unchanged.

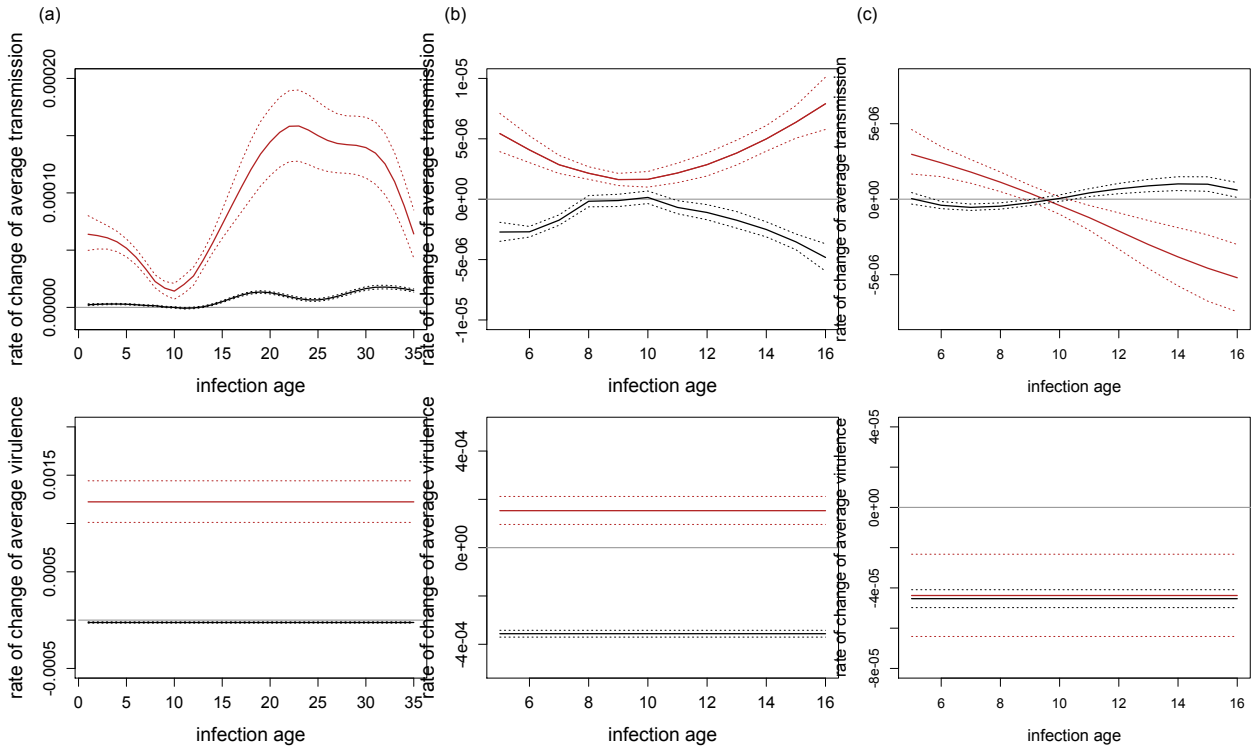

Figure B-2: Evolutionary predictions for transmission rate (top panel) and virulence (bottom panel) when the relative cost of virulence is lower. As before, (a) C57 mice, (b) C57 mice, truncated data set, (c) MF1 mice. Red lines are predictions for epidemic conditions, black lines for endemic. Solid lines denote mean predictions and dotted lines denote confidence intervals. Changing how within-host parasite densities map to transmission rates qualitatively alters the evolutionary trajectories in (b) but not (a) or (c).