Evolutionarily Optimal Phage Life-History Traits: Burst Size *vs.* Lysis Time

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Abstract

A single dynamical equation for the virus to microbe ratio (VMR) shows that an optimal tradeoff occurs between a short lysis time and low burst size *vs.* a long lysis time and large burst size. The model predicts that interventions lowering phage adsorption by killing free virus and/or limiting their access to bacteria cause the evolution of an increased lysis time and higher burst size until the intervention either drives a virulent phage extinct or, for temperate phage, drives the phage from its lytic phase into its lysogenic phase. The model also predicts that an intervention that lowers bacterial growth, R, induces the prophages within it to switch to their lytic phase. An intervention that simultaneously lowers both viral accessibility to bacteria and bacterial growth rate may increase the net virus to bacterial ratio (VMR), a result reminiscent of the Volterra principle for predator-prey dynamics in ecology.

Introduction

Marine phage infect approximately 10^{23} bacteria every second, removing 20%–40% of the standing stock of marine bacteria each day (Suttle 2007). They exert top-down control of marine microbial abundance comparable to that of zooplankton grazing (Breitbart *et al.* 2018). Furthermore, marine phage represent 94% of the nucleic-acid-containing particles in the oceans (Breitbart *et al.* 2018). Hence, phage represent an enormous number of evolutionary agents whose phenotypes are shaped by natural selection.

What then are the phage phenotypes that natural selection is shaping? This article investigates the life-history aspect of a phage's phenotype—how long does a lytic phage wait until lysing and what is its burst size upon lysis. And if temperate, when does it lysogenize to join the genome of its bacterial host.

Moreover, phage may be subject to interventions intended to control them and perhaps drive them extinct. What then is the evolutionary impact on such phage of interventions that seek their control?

This article offers answers the questions just posed—it presents a model to predict how natural selection shapes phage life history and shows what the evolutionary impact on phage life history is from efforts to control them. The purpose of the model is to predict the evolutionarily optimal life history—that is, the optimal balance between reproducing early to benefit from geometric growth versus reproducing late to benefit from the time needed to produce a large burst size. In nature, phage may rarely possess the optimal life history for their present circumstances, but knowing the optimal life history in those circumstances reveals the direction toward which evolutionary change will occur.

The study of an evolutionary tradeoff between the benefits of early and late lysis time together with the prediction of an optimal life history enjoys a long history (Abedon 1989, Wang *et al.* 1996, Abedon

et al. 2001, Abedon *et al*. 2003, Bull *et al*. 2004, Bull 2006, Bull *et al*. 2006, Wang 2006, Heineman and Bull 2007, Bull *et al*. 2011, and Kannoly 2022). The models developed in the previous literature are generally based on a system of three delay-differential equations with interactions represented as mass action terms, that is, as quadratic terms such as $(N_1 N_2)$ to represent an interaction between species-1 and species-2, and also include an assumption of density dependence. The analysis of these equations generally features solving for the equilibrium abundance of uninfected bacteria, infected bacteria and free phage.

This article differs from the preceding literature in being based on a new model that is defined in discrete time and features viral colonization of bacteria as a Poisson process rather than as a product of viral and bacterial abundances (Roughgarden 2024). The model here pertains to a virus-bacteria system in the log phase, where both populations grow exponentially rather than exist at equilibrium in a stationary phase. The model's analysis rests on a single dynamical equation for the virus to microbe ratio (VMR) rather than a system of three coupled equations for uninfected bacteria, infected bacteria and free phage. Thus, the situation in which the optimal life history evolves is envisioned differently here as compared to the earlier literature—stationary phase versus log phase and the mathematical approach is different. Later, the Discussion section features a more detailed comparison of the differing intuition behind the prediction of an optimal life history found in earlier models compared to the present model.

The model in this paper has previously been used to predict the condition whereby a temperate phage switches from a lytic state to a lysogenic state and vice versa. It was also used to account for a set of eco-geographic rules pertaining to the relative frequency of lytic to lysogenic phage in nature. Here, the model is extended to the topic of an optimal phage life history.

Model for Population Dynamics of Phage and Bacteria

The phage/bacteria population-dynamic model used here is defined in discrete time with the time step being the viral lysis time period (Roughgarden 2024). A time step begins with the state variables, $N(t)$ and $V(t)$ for the number of bacteria and free virus particles (virions) in their environmental source pools at time t. Then the virus infect the uninfected bacteria with Poisson sampling such that some bacteria remain uninfected, some have only one infection, some have two infections *etc*. (Ellis and Delbrück 1939).

The Poisson distribution describing the infection process has density parameter, $\mu(t) \equiv a(v(t))\, v(t)$ where $v(t) \equiv V(t)/N(t)$ is the ratio of virus to bacteria in their source pools (the environmental virus to microbe ratio, VMR). The $a(v(t))$ is the adsorption function—it refers to the probability that a viral particle comes in contact with a bacterium, binds to surface molecules, and then is incorporated into the bacterial cell. adsorption is a function of $v(t)$ because the number binding sites on the surface of the bacterium is finite and the sites may become saturated. Thus, $a(v(t))$ includes information about the binding affinity of virus particles to receptors in the bacterial surface and also about the number of binding sites. Furthermore, $a(v(t))$ also includes information about the accessibility of the bacterium to virus particles. For a given ratio of virus to bacteria, $v(t)$, if the environment is such that virus are prevented from reaching the bacteria, then $a(v(t))$ is low compared to $a(v(t))$ in environments that allow ready access of the virus to the bacteria. Environments may differ in how viscous the media is, or for airborne virus particles, whether air filters are installed.

According to a Poisson density function, the fraction of uninfected bacteria that remain uninfected, $P_0(\mu(t))$, is $e^{-\mu(t)}$ and the fraction of bacteria colonized by m virus, $P_m(\mu(t))$, is $\frac{e^{-\mu(t)}\mu(t)^m}{m!}$ for $m \geq 0$ where $\mu(t) = a(v(t))\, v(t)$. The m indexes the number of virus per bacterium. The fraction of bacteria that are infected by one or more virus is $1 - P_0(\mu(t))$.

The uninfected bacteria population increases by a geometric factor of increase per time step, R. Necessarily, $R > 1$, for the bacteria to be able to increase in the absence of the virus. Accordingly, the uninfected bacteria resupply the bacterial source pool as

$$N(t+1) = R\, P_0(\mu(t))\, N(t) \tag{1}$$

where $P_0(\mu(t))$ is the Poisson probability that a bacterium is uninfected.

Meanwhile, the virus in the infected bacteria produce new virus particles as

$$V(t+1) = \Big(b(1)\, P_1(\mu(t)) + b(2) P_2(\mu(t)) + \dots \Big)\, N(t) \tag{2}$$

where $b(m)$ is the burst size from a bacterium infected with m virus particles (the multiplicity of infection, MOI) and $P_m(\mu(t))$ is the Poisson probability that a bacterium is infected by m virus particles.

The adsorption is taken as density-dependent and the burst size is assumed to depend linearly on the number of virus infecting a bacterium

$$a(v(t)) = a_o\,(1 - \frac{v(t)}{\kappa}) \tag{3}$$

$$b(m) = b_o\, m \tag{4}$$

where κ is the saturation density—the viral density at which all the binding sites per bacterium are occupied and a_o is the maximal probability of binding when all the binding sites are available, given the environmental conditions. The b_o is the burst per virus infecting the bacterium.

Identify $v(t+1)$ with $\frac{V(t+1)}{N(t+1)}$ and $v(t)$ with $\frac{V(t)}{N(t)}$. Then doing the sum yields

$$v(t+1) = \frac{b_o}{R}\, \frac{a_o\,(1 - \frac{v(t)}{\kappa})\, v(t)}{e^{-a_o\,(1-\frac{v(t)}{\kappa})}}\, v(t) \tag{5}$$

Equation 5 is a dynamical equation in one variable, $v(t)$.

In the limit, $v(t) \to 0$, the model in Eq. 5, upon suppressing the subscripts, reduces to

$$v(t+1) = \frac{a\, b}{R} v(t) \tag{6}$$

The virus population can infect the bacterial population if it can increase when rare, *ie.*, if $v(t) \approx 0$, then $v(t+1) > v(t)$. Inspection of Eq. 6 shows that if

$$a\, b > R \tag{7}$$

the virus can spread into a population of increasing bacteria. Alternatively, for a virulent virus, if $a\, b < R$, the virus goes extinct because the virus cannot keep up with bacterial population growth. But for a temperate virus, if $a\, b < R$, the virus switches to a prophage because its population grows faster as part of the bacterial genome than by bursting new virions each time step.

Tradeoff Between Burst Size and Lysis Time

This section applies the phage-bacteria population-dynamic model of the previous section to the tradeoff between burst size and lysis time. Wang (2006) experimentally determined a functional relation between burst size and lysis time as

$$\begin{aligned} b &= \beta\,(l - \epsilon) \quad \text{for} \;\; l > \epsilon \\ &= 0 \quad \text{for} \;\; l \le \epsilon \end{aligned} \tag{8}$$

Table 1: Parameters

Name	Value	Notes
β	7.7	Wang 2006
ϵ	28	Wang 2006
R	1.035	$e^{2.04/60}$, Wang 2006
a	0.1	Schwartz 1976, Philipson 1983
L	100	(time step = minutes)

where l is the lysis time, ϵ is the eclipse, which is the time needed for the viral replication to commence, and β is the phage production rate (also called the phage maturation rate) once viral production has begun. The burst size increases linearly with the lysis time period after the eclipse has transpired.

To find the optimal lysis time period, a maximum time step, L, is stipulated that is longer than the largest feasible lysis time period. Then the model is iterated for the number of periods, l, that fit within L, given the eclipse. For example, suppose the eclipse is 0 and L is 100. If l is also 100, then only one iteration of the model takes place within L, whereas if l is 1, then 100 iterations fit within L, and if l is 25, then four iterations fit within L, and so forth. Thus, the v after the number of iterations that fit within L is

$$v_(t+L) = \left(\frac{a}{R}\,\beta\,(l-\epsilon)\right)^{\lfloor \frac{L}{l} \rfloor} v(t) \tag{9}$$

for l = (ϵ+1, ϵ+2 ... L) where $\lfloor \frac{L}{l} \rfloor$ indicates the integer part of $\frac{L}{l}$. The exponent in Eq. 9 is the number of iterations of Eq. 6 that fit into L. The optimal l, and corresponding b, is that with the highest viral production after L has elapsed.

Further analysis is aided by taking a continuous approximation in Eq. 9, as though a fractional iteration can fit into L,

$$v_(t+L) = \left(\frac{a}{R}\,\beta\,(l-\epsilon)\right)^{\frac{L}{l}} v(t) \tag{10}$$

for $l > \epsilon$. Solutions for the optimal lysis time from Eq. 10 can be rounded down to the nearest integer if needed. The expression in parentheses in Eq. 10 is the fitness over the period, L, as a function of l

$$W_L(l) = \left(\frac{a}{R}\,\beta\,(l-\epsilon)\right)^{\frac{L}{l}} \tag{11}$$

The optimal lysis time time, $\hat{l}$, is found by maximizing $W_L(l)$ with respect to l. The corresponding optimal burst size, $\hat{b}$, is found from Eq. 8, evaluated at $l = \hat{l}$.

Table 1 gives the parameters for an illustration. The β and ϵ, in units of min$^{-}1$ and phage/min, respectively, pertain to isogenic λ-phages with different lysis times from Wang (2006). The bacterial intrinsic rate of increase, R, from Wang (2006) for *Escherichia coli* K-12, is given as 2.04/hr—this converts to the value of R in the table in minutes. The adsorption parameter, a, is the product of the probability that a collision between a phage and a bacterial binding site results in a binding (10^{-4}, Philipson 1983) times the number of binding sites per bacterium (10^3, Schwartz 1976) leading to the value in the table. The adsorption parameter can vary considerably depending on environmental conditions affecting the accessibility of the bacteria to the virus and furthermore, the number of binding sites per bacterium varies with nutrient conditions (Schwartz 1976). The value used can be considered a nominal value.

Figure 1 shows the fitness of a lytic phage after a period of 100 minutes as a function of the lysis time, l, based on the parameters in Table 1. The curve for $W_{100}(l)$ has a maximum at $\hat{l}$ = 45.7. For

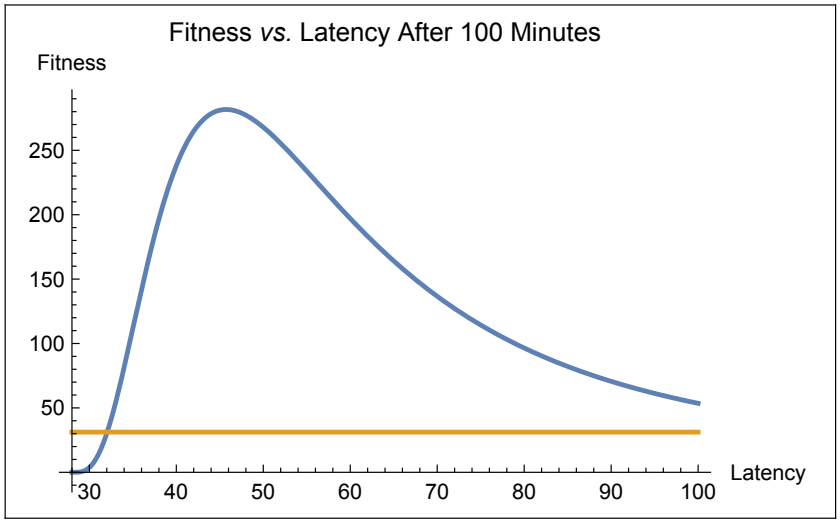

Figure 1: *Fitness of lytic phage after 100 minutes, W_{100}, as a function of the lysis time, l, is shown as a humped-shaped curve starting from the eclipse period of 28 minutes. The optimal lysis time occurs at $\hat{l}$ = 45.7 which yields a maximum fitness, $\widehat{W_{100}}$, of 281.7. Fitness after 100 minutes as a prophage incorporated into bacterial genome, w_{100} is shown as horizontal line. The fitness of a lytic phage exceeds that of a prophage provided the lysis time, l, exceeds the critical lysis time, l_c, of 32.0. If the lysis time of the phage is between 28 and 32.0, the phage cannot coexist with the bacteria unless it becomes a prophage.*

comparison, the fitness over the same time interval of a prophage that has incorporated into the bacterial chromosome and reproduces with the bacteria is shown as a horizontal line. The prophage fitness, w_L, is

$$w_L = R^L \tag{12}$$

For 100 minutes, w_{100} is 31.2 based on R in Table1. The critical lysis time, l_c, at which being lytic becomes a better strategy than being a prophage is found by setting

$$W_l(l) = R^L \tag{13}$$

and solving for l, which works out to be 32.0 using the parameters in Table 1. If l is greater than 32.0, then the lytic phase has a higher fitness than the lysogenic phase. If l is between ϵ and l_c, *i.e.* between 28 and 32.0 minutes, then the phage cannot coexist with the bacteria in its lytic phase—the bacteria population grows faster than the viral population, leaving it behind, so to speak. Instead, the phage must lysogenize—incorporate into the bacterial genome to acquire the population growth rate of the bacteria.

To find the optimal lysis time, differentiate W_L with respect to l. Then the quantity, Q, independent of L, is identified

$$Q(l) = \frac{1}{(l-e)} - \frac{\log\left(\frac{a}{R}\,\beta\,(l-e)\right)}{l} \tag{14}$$

The optimal lysis time, $\hat{l}$ is the root of $Q(l) = 0$. Using the NSolve[] function in Mathematica with the parameters from Table 1 returns the value,

$$\hat{l} = 45.7 \tag{15}$$

independent of L. The corresponding optimal burst size from Eq. 8 is

$$\hat{b} = 136.5 \tag{16}$$

and the corresponding maximal fitness from Eq. 11 is

$$\widehat{W_{100}} = 281.7 \tag{17}$$

Wang (2006) measured the fitness of 11 strains of λ phage whose latencies varied from 28.3 to 63.0 minutes. The study found that the strain whose lysis time was 51.0 minutes had the highest fitness, a value quite close to that predicted in the model here, 45.7, based on the parameters in Table 1. The burst size for the strain with the highest fitness was 170.0, also fairly close to the value predicted here, 136.5. This initial degree of agreement between theory and experiment is likely coincidental because the nominal value of the adsorption parameter, a, in Table 1 was conjectured and not experimentally determined. Instead, if a is lowered to 0.054, then $\hat{l}$ works out to be 50.9 and $\hat{b}$ to 176.6, almost exactly the same as Wang(2006) found experimentally. Thus, lowering a from the nominal value of 0.100 to 0.054, while keeping the other parameters from Table 1 the same, brings the predicted optimal lysis time and burst size into close agreement with the experimental results. The next section considers further implications of variation in a.

Varying Viral Adsorption

Figure 2 shows the impact of varying adsorption on phage evolution. Top left: As a decreases from the nominal value of 0.10, the peaks of the curves for the lytic phase progressively become lower and shift to the right. Top right: As a decreases from 0.10, the optimal lysis time increases. Bottom right: As a decreases from 0.10, the optimal burst size also increases, reflecting the increasingly longer lysis time. Bottom left: As a decreases from 0.10, the optimal lytic fitness decreases and intersects the horizontal line representing the prophage fitness at $a = 0.033$, at which point the phage lysogenizes, switching from its lyric phase to being a prophage.

Many interventions to control phages, and viruses more generally, involve techniques such as air or water filters, or controlling humidity that lower the adsorption of phage by bacteria (*cf.* Sobsey *et al.* 2008, Clokie and Kropinski 2009, Wommack *et al.* 2009, Moriyama *et al.* 2020, Curtius *et al.* 2021, Van Charante *et al.* 2021, Beltrán *et al.* 2023). Overall, the model predicts that such interventions lowering a cause the evolution of an increased lysis time and correspondingly higher burst size until the intervention is sufficient either to drive a virulent phage extinct, or for temperate phage, to drive the phage from its lytic phase into its lysogenic phase.

Varying Bacterial Growth

The bacterial growth rate, represented by the bacterial geometric factor, R, is the other bacterial parameter, in addition to a, that can influence the phage's optimal lysis time. The equation for the optimal lysis, $\hat{l}$, Eq. 14 has the quantity, R, in the second term and hence $\hat{l}$ is a function of R in addition to the other parameters. Indeed, (a/R) could be treated as a lumped parameter in Eqs. 11 and 14. This section focusses specifically on the role of R.

Figure 3 shows the impact of varying bacterial growth, R, on phage evolution. Top left: Fitness of the lytic phase *vs.* lysis time for several values of the bacterial geometric growth factor, R. As R increases from 1.0, the peaks of the curves for the lytic phase progressively become lower and shift slightly to the right. Top right: Optimal lysis time *vs.* the bacterial geometric growth factor, R. As R increases from 1.0, the optimal lysis time slightly increases (notice the scale on the vertical axis). Bottom right: Optimal burst size *vs.* the bacterial geometric growth factor, R. As R increases from 1.0, the optimal burst size also slightly increases, reflecting the increasingly longer lysis time. Bottom left: Optimal fitness of lytic

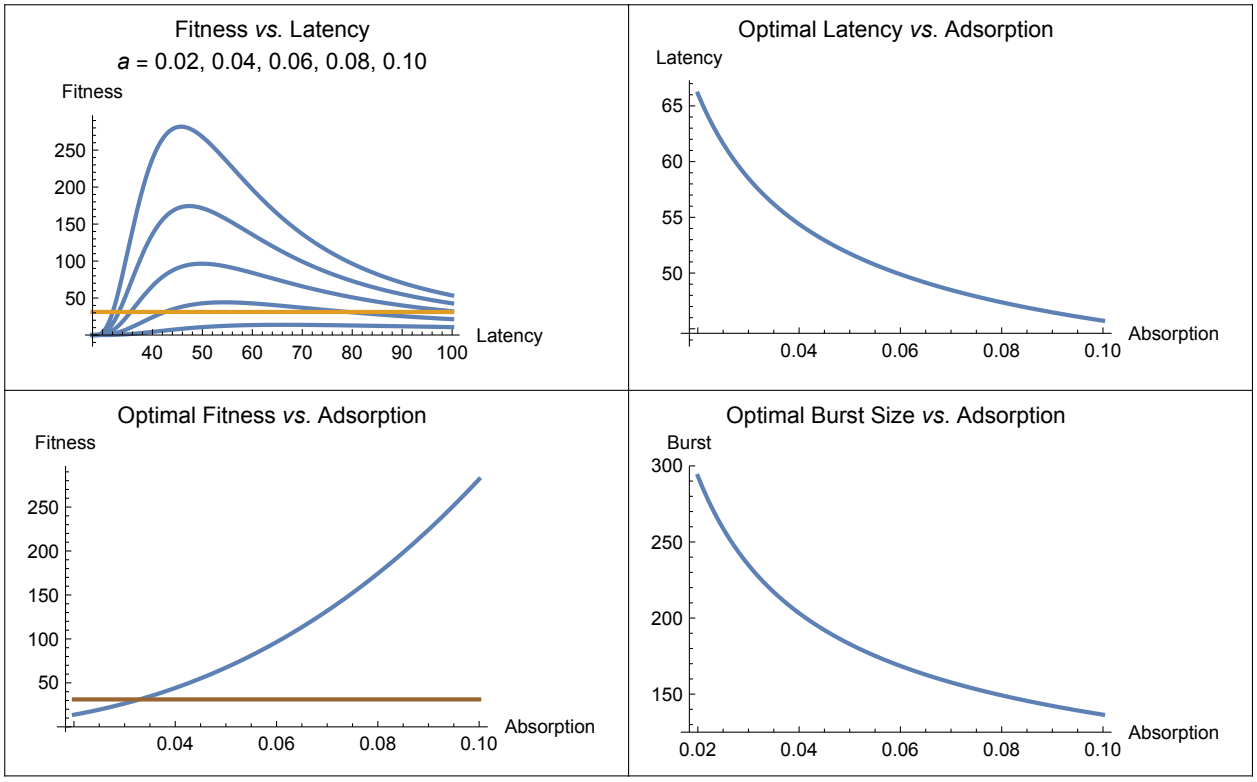

Figure 2: *Impact of varying adsorption on phage evolution. Top left: Fitness of the lytic phase* vs. *lysis time for several values of the adsorption coefficient,* a*. The top curve is for* $a = 0.10$ *and is identical to that shown in Figure 1. The curves below the top are successively for* $a = 0.08$*, 0.06, 0.04, and 0.02. The horizontal line is the fitness of the lysogenized phage incorporated into the bacterial genome as a prophage. As* a *decreases, the peaks of the curves for the lytic phase progressively become lower and shift to the right. Top right: Optimal lysis time* vs. *the adsorption parameter,* a*. As* a *decreases from 0.10, the optimal lysis time increases. Bottom right: Optimal burst size* vs. *the adsorption parameter,* a*. As* a *decreases from 0.10, the optimal burst size also increases, reflecting the increasingly longer lysis time. Bottom left: Optimal fitness of lytic phase* vs. *the adsorption parameter,* a*. The horizontal line is the fitness of the lysogenized phage incorporated into the bacterial genome as a prophage. As* a *decreases from 0.10, the optimal lytic fitness decreases and intersects the horizontal line at* $a = 0.033$*, at which point the phage lysogenizes, switching from its lyric phase to being a prophage.*

phase *vs.* the bacterial geometric growth factor, R. The exponential curve is the fitness of the prophage incorporated into the bacterial genome. As R increases from 1.0, the optimal lytic fitness decreases and intersects the exponential curve, at which point the phage lysogenizes, switching from its lyric phase to being a prophage.

Figure 3 shows that varying R has rather little impact on the optimal lysis time, optimal burst size, or optimal fitness. However, varying R has a large impact on the fitness of the lysogenic phase lodged within the bacterial chromosome. As the bacterial R increases, the curve for the fitness of the lysogenic phase quickly crosses the curve for the optimal fitness of the lytic phase, indicating a switch from the lytic to lysogeny.

A consequence of the switch depicted in the bottom left of Figure 3 is that an intervention that lowers bacterial growth induces the prophages within it to switch to their lytic phase. Conversely, high bacterial growth, as in the microbializaton environment on coral reefs and the gut environment of vertebrates, promotes the occurrence of lysogeny (Silveira *et al.* 2021).

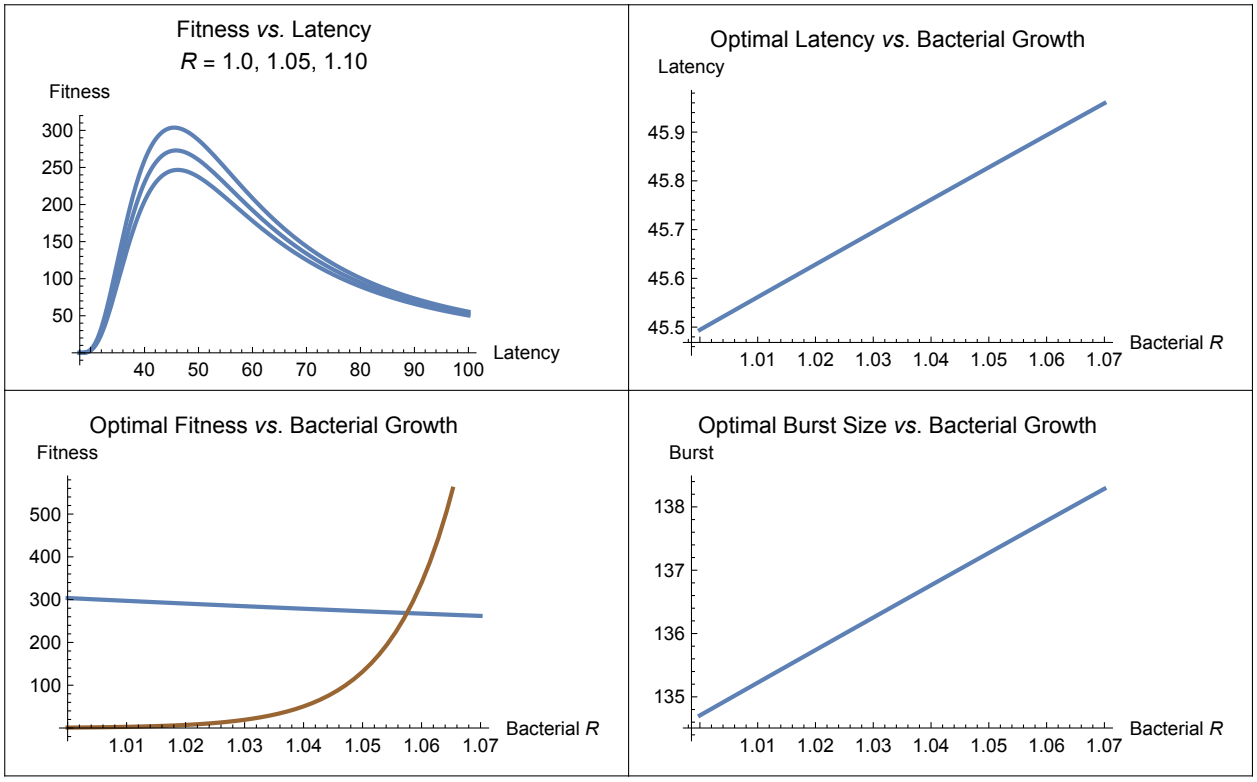

Figure 3: *Impact of varying bacterial growth on phage evolution. Top left: Fitness of the lytic phase* vs. *lysis time for several values of the bacterial geometric growth factor,* R*. The top curve is for* $R = 1.0$ *The curves below the top are successively for* $R =$ *1.05 and 1.10. As* R *increases from 1.0, the peaks of the curves for the lytic phase progressively become lower and shift slightly to the right. Top right: Optimal lysis time* vs. *the bacterial geometric growth factor,* R*. As* R *increases from 1.0, the optimal lysis time increases. Bottom right: Optimal burst size* vs. *the bacterial geometric growth factor,* R*. As* R *increases from 1.0, the optimal burst size also increases, reflecting the increasingly longer lysis time. Bottom left: Optimal fitness of lytic phase* vs. *the bacterial geometric growth factor,* R*. The exponential curve is the fitness of the lysogenized phage incorporated into the bacterial genome as a prophage. As* R *increases from 1.0, the optimal lytic fitness decreases and intersects the exponential curve at about* $R = 1.055$*, at which point the phage lysogenizes, switching from its lyric phase to being a prophage.*

Discussion

This article provides a mathematical model for the evolutionarily optimal tradeoff between lysis time and burst size. Experimental evidence from two studies demonstrates that such an optimal exists. Wang (2006) demonstrated the optimal tradeoff with measurements on strains of λ phage infecting *E. coli*. Kannoly *et al*. 2022) also measured strains of λ phage infecting *E. coli*. The value of the optimal lysis time differed between these studies because the environmental conditions in the experiments differed. In Wang's (2006) study the optimal lysis time was 51 minutes, and in the Kannoly *et al*. (2022) study the optimal lysis time was about 80 minutes. Given the demonstrated reality of an optimal lysis time that depends on environmental conditions, the issue is how to explain it.

This article explains the optimal lysis time by finding the optimal tradeoff between rapid reproduction with a short lysis time at the cost of a low burst size *vs*. slow reproduction with a long lysis time with the benefit of a large burst size. The optimal tradeoff between these two considerations is derived using a single dynamical equation in discrete time for the virus to microbe ratio (VMR) during the log phase of

phage/bacteria population growth (Roughgarden 2024).

Previous models for the optimal tradeoff use three delay-differential equations for the dynamics of uninfected bacteria, infected bacteria and free phage, respectively, in the stationary phase of virus-bacterial population growth (*eg*. Bull 2006, Bull *et al*. 2006). The three-equation system is an extension of the original two delay differential equations introduced by Campbell (1961). The original Campbell model is critiqued in detail in Roughgarden (2024, incl. Supplementary Material) and that critique carries over to the three-equation extension as well.

In the present context however, the relevant distinction between the one-equation analysis in this paper and the three-equation analysis in previous papers pertains to the intuition behind what is optimal about the lysis time *vs*. burst size tradeoff. The Eq. 4 in Bull (2006) gives a formula for the optimal lysis time (called, L). When the phage is at population-dynamic equilibrium (called $\hat{\lambda} = 0$), Bull's Eq. 4 predicts that the optimal lysis time varies inversely with the parameter called d, the death rate of the bacterial cells. The intuition is that a high bacterial death rate implies an infecting phage has a short time to make virions and hence needs a short lysis time. Thus, the tradeoff in Bull's (2006) model is between the time needed to produce a burst and the time available within a bacterial cell to do it. This explanation for the optimal tradeoff is conceptually different from that offered by this paper's model that focusses on the tradeoff between rapid reproduction with low burst *vs*. slow reproduction with high burst.

Grounds for choosing between predictions from this paper's single-equation model and the previous three-equation model, in addition to the former's relative simplicity and better tractability, perhaps rest on which environmental situation is more common—lag phase growth or stationary growth of the phage-bacteria pair. The three-equation model, as with the earlier two-equation model, is directed to experimental situations such as a chemostat where a stationary phase can be realized. But in nature, it is hard to imagine phage and bacteria in equilibrium. In nature the populations are invariably either recovering from or being decimated by environmental events such as storms *etc*. Natural populations of phage and bacteria are likely continually in a bust-boom regime where a log-phase model is preferable to a stationary-phase model.

This paper also offers predictions about the evolutionary impact on phage of interventions to control them. The model predicts that interventions lowering phage adsorption, a, cause the evolution of an increased lysis time and correspondingly higher burst size until the intervention is sufficient either to drive a virulent phage extinct, or for temperate phage, to drive the phage from its lytic phase into its lysogenic phase. The model also predicts that an intervention that lowers bacterial growth, R, induces the prophages within it to switch to their lytic phase. Conversely, high bacterial growth promotes the occurrence of lysogeny.

Interventions that affect both a and R simultaneously, keeping the ratio (a/R) approximately constant, can produce effects reminiscent of the so-called Volterra principle in ecology (*e.g*. Boyce *et al*. 2025). By this principle, an insecticide that impacts both an insect predator, such as a wasp, and also it's prey, such as an herbivorous caterpillar pest, has the net effect of increasing the number of the pests and lowering the number of wasps. The impact of the insecticide on the caterpillars is more than offset by the removal of the caterpillar's predator leading, paradoxically, to a net increase in the very pest the insecticide was intended to control. This principle is readily derived from the classic Lotka-Volterra predator-prey equations (*cf*. Roughgarden 1998). Here, a somewhat similar principle emerges for an intervention that simultaneously lowers both viral accessibility to bacteria, a, and bacterial growth rate R. Introducing a disinfectant that directly impacts the phage, a, may also lower the bacterial R which will induce prophage within the bacteria to lyse, thereby increasing the net virus to bacterial ratio (VMR).

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