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Coevolutionary stability of host-symbiont systems with mixed-mode transmission

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ABSTRACT

The coevolution of hosts and symbionts based on virulence and mode of transmission is a complex and diverse biological phenomenon. We introduced a conceptual model to study the stable coexistence and coevolution of an obligate symbiont (mutualist or parasite) with mixed-mode transmission and its host. Using an age-structured Leslie model for the host, we demonstrated how the obligate symbiont could modify the host's life history traits (survival and fecundity) and the long-term growth rate of the infected lineage. When the symbiont is vertically transmitted, we found that the host and its symbiont could maximize the infected lineage's evolutionary success (multi-level selection). Our model showed that symbionts' effect on host longevity and reproduction might differ, even be opposing, and their net effect might often be counterintuitive. The evolutionary stability of the ecologically stable coexistence was analyzed in the framework of coevolutionary dynamics. Moreover, we found conditions for the ecological and evolutionary stability of the resident host-symbiont pair, which does not allow invasion by rare mutants (each mutant dies out by ecological selection). We concluded that, within the context of our simplified model conditions, a host-symbiont system with mixed-mode transmission is evolutionarily stable unconditionally only if the host can maximize the Malthusian parameters of the infected and non-infected lineages using the same strategy. Finally, we performed a game-theoretical analysis of our selection situation and compared two stability definitions.

1. Introduction

The coevolution of hosts and symbionts (mutualists and parasites, including pathogens) is a complex and diverse biological phenomenon (Clayton et al., 2015; Gandon et al., 2008). The symbionts' virulence and modes of transmission are two factors that significantly influence these processes. *Virulence* is usually defined as the symbionts' ability to reduce infected hosts' life history traits (survival and reproductive success). In our interpretation, mutualists exhibit negative virulence since they increase (rather than decrease) infected hosts' survival and reproductive success. The modes of transmission of symbionts from one host individual to another are typified according to the genetic relatedness between the individuals. Transmission from parent to offspring (in a more general form, transmission between close genetic kins) is called *vertical transmission*. In contrast, we define *horizontal transmission* as the transfer of symbionts between genetically non-kin hosts. Most symbionts have a combination of vertical and horizontal transmission, which we call a mixed-mode transmission. A massive body of theoretical and empirical evidence unequivocally suggests that symbionts' virulence and mode of transmission are interrelated characteristics (Ebert, 2013; Ewald, 1987). Exclusive vertical transmission is frequently found only in mutualistic interactions (Bright and Bulgheresi, 2010). In this case, infected host populations outcompete non-infected ones; thus, the infection reaches fixation in host populations (Ewald, 1987). However, imperfect vertical transmission (when some offspring fail to inherit the symbiont) can prevent symbiont fixation (Afkhami and Rudgers, 2008). Contrarily, symbionts that transmit exclusively (or primarily) horizontally (like vector-borne and water-borne pathogens, mobile parasites, etc.) tend to be highly virulent, even lethal (Ebert, 2013; Ewald, 1987). The exclusively horizontal or exclusively vertical transmission systems are just the extremes of a continuum, while most real-life host-symbiont systems are characterized by mixed transmission. In this paper, we focus on such mixed-mode transmissions in host-symbiont systems. The symbionts' effect on the host's life history may also be quite complex in the sense

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that infections may increase or decrease host mortality, fecundity, or both. These effects may also markedly differ between different developmental stages of the host; for instance, in the case of COVID-19, mortality differs between young and adult individuals (Liu et al., 2020).

Our paper focuses on the evolutionarily stable coexistence of mixed (vertical and horizontal) transmission symbionts and their host. We only consider obligate (with no free-living stages) and host-specific (connected to a single host species) symbionts. Furthermore, we consider the aging of the hosts, i.e., hosts have different developmental stages (juvenile and adult stages) and a finite lifespan. We investigate how symbionts of different types can modify a host's life history and evolutionary success. The proposed conceptual model focuses on the host-symbiont interactions and the symbionts' effect on the infected host population's survival rate and fecundity. To ensure the ecological coexistence of the infected and the non-infected host populations, we consider density-dependent interactions, ecological competition, and horizontal infection between the populations. Moreover, we must also consider that the infected hosts can lose their symbionts, for instance, by stochastic loss or recovery from infection – often called 'clearing.' In our view, three mechanisms play a significant role in the coevolution of the hosts and their symbionts: 1) the nature of the host-symbiont interaction (how infection affects host mortality and fecundity), 2) vertical and horizontal transmission, and 3) ecological parameters (e.g., clearing of infected hosts and competitive abilities). These mechanisms may not evolve independently. For example, in the case of mutualism, vertical transmission and low clearing rates (often zero) benefit both species. Contrarily, in the case of parasitism, the hosts benefit from getting rid of their symbionts (recovering from infection) or avoiding infections (both horizontal and vertical). To focus exclusively on the demographics of the infected population as defined by the host-symbiont interactions, we apply the following *uniformity conditions* to the model: 1) the transmission mode (vertical and horizontal routes) is independent of the host phenotype, 2) the rate of clearing is also independent of the host phenotype, and 3) there is no difference in the competitive ability between different populations.

We look for an evolutionarily stable host-symbiont pair of phenotypes in the framework of a coevolutionary ecological model (Cressman and Garay, 2003a, 2003b) which does not allow any rare mutant to invade the resident system (Maynard Smith and Price, 1973). Moreover, optimization of individual (average) fitnesses does not necessarily imply evolutionary stability. For example, in the Prisoner's Dilemma game (Rapoport and Chammah, 1965; Axelrod and Hamilton, 1981), an individual's (player) fitness or payoff also depends on the opposite interacting player. Also, optimization of payoff does not mean the same for the involved players when there is a conflict of interest. However, we wanted to analyze if optimizing fitness or long-term growth rate (Murray, 1985; Nur, 1987) with respect to individual strategies that define life history traits has a role in evolutionary stability. In other words, in the case of mixed-mode transmission, whether the evolutionary stability is based on optimal life history traits. This is why we will first find the optimal strategies and use them to find the growth rates of the independent lineages (infected and non-infected). Note that we do not presume that the optimizing traits are uninvadable by mutants. Also, optimization is in terms of the independent growth rates of the lineages without considering the effects of competition within and between the lineages and clearing of infection. The individual (species) optimization criteria apply only to cases in which an individual's fitness is independent of (i.e., it is neither affected by nor affects) other interacting individuals (Cody, 1974; Riechert and Hammerstein, 1983). This is also why considering just the optimization within a lineage is not appropriate or sufficient for evolutionary stability in our perspective. Hence, we analyze the evolutionary stability of the optimizing traits (that maximize the fitness of the infected lineage of hosts) by coevolutionary dynamics, where the resident system gives the ecological dynamics. Following the Maynard Smith and Price setup (Maynard Smith and Price, 1973), we assume that the timescale of ecological dynamics (selection) is faster than the evolutionary timescale, and the mutants are introduced at the rest point of the ecological dynamics in very low densities (thus they are rare). The stability of the optimal (resident) traits is then analyzed in a different interpretation. Ecological dynamics gives selection, where mutants are introduced into the resident system as an additional dimension. Mutations occur sufficiently infrequently so that the population reaches its rest point before a new mutant emerges. We use the resident-mutant systems to check whether the mutant dies out, demonstrating uninvasibility. In other words, we check evolutionary stability in terms of the ecological selection dynamics and not just independent optimization of lineage fitnesses. Mathematically, we give the evolutionary stability condition by the local asymptotical stability of the coevolutionary dynamics combined with the uninvasibility of rare mutants into the stable resident system.

From the coevolutionary dynamics, we are interested in the conditions for the traits that optimize the infected lineage to be evolutionarily stable. We hypothesize that mixed-mode transmission would be crucial in coevolutionary stability because the two lineages are linked, so they cannot evolve independently. Furthermore, we are interested in the possible comparison between the Evolutionarily Stable Strategy (ESS) definition in game theory (Maynard Smith and Price, 1973) and the stability conditions of our coevolutionary dynamics. For this, we focus on the strict Nash equilibrium game solution, which claims that no player can increase its benefit at the ESS by unilaterally changing its strategy (phenotype).

2. Model and results

2.1. Preliminaries

The general framework of our selection situation belongs to the *multi-species group (multi-level) selection* models (Simon, 2014) since the host, together with its symbionts, form a well-defined 'group' (namely an infected individual). This group selection model has the following main features:

1) *Group formation process*: Groups can reproduce by means of host reproduction and vertical transmission. Horizontal transmission may change individuals of non-infected host lineages to infected ones; thus, new groups can appear. Finally, groups may dissolve due to the clearing of infection. We assume that the group formation dynamics is based on host-symbiont interactions. The horizontal infection and clearing are independent of the survival rate and fecundity of the infected populations. Note that the dynamics of the model is related to the standard epidemic models (Hethcote, 2000; Kermack and McKendrick, 1927; Tsay et al., 2020), focusing on horizontal transmission, which only connects infected and non-infected individuals. Even though some works studied epidemic models with vertical transmission (Inaba, 2006; Li et al., 2001) and mixed-mode transmission (Miao et al., 2018), our objectives cannot be met with such models.

2) *Group payoff*: The symbionts' and the hosts' fitnesses together determine the infected population's evolutionary success. Moreover, the evolutionary success (fitness) of the symbionts – since they are obligate – is given by the evolutionary success of the infected population. Thus, 'groups' have a well-defined payoff, i.e., the long-term growth rate of the infected population.

Since we focus on the fitnesses of different species, game theory is one of the inevitable methods that can be applied to the model (Ezoe, 2009; Noë and Hammerstein, 1995) to study the dynamics of the populations. However, the 'shared interest' (similar to group selection theory) makes the direct application of the evolutionary matrix game challenging (Ezoe, 2009; Maynard Smith and Price, 1973). The adaptive dynamics method (Dercole and Rinaldi, 2008; Dieckmann, 1997; Dieckmann and Law, 1996; Geritz et al., 1998; Genkai-Kato and Yamamura, 1999) can also be applied to this problem but cannot be generalized if the number of species and age classes are high. We recall a few relevant models on host-symbiont interactions without providing a

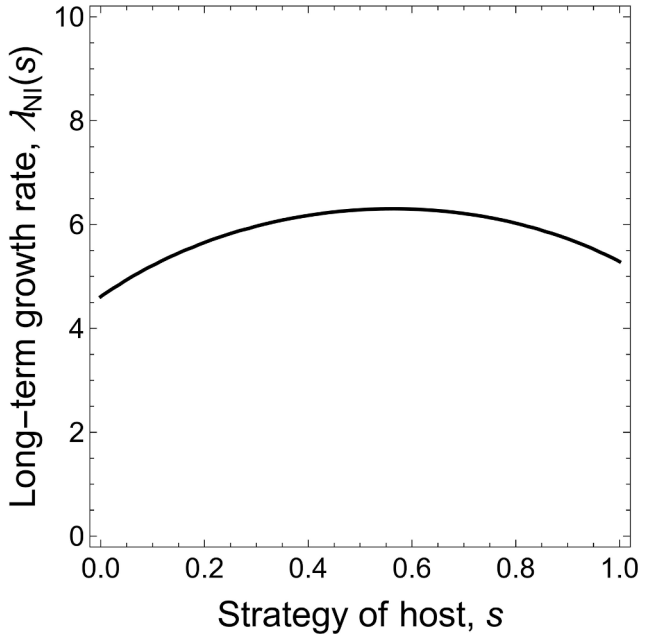

Fig. 1. Optimization of the long-term growth rate of the non-infected host population ($\lambda_{NI}(s)$) with respect to the host strategy (s). The maximum value is at $\bar{s} = 0.563$. Parameters are $\alpha_1 = 100$, $\omega_0 = 0.2$, and $\omega_1 = 0.3$.

comprehensive literature overview. Akçay (2015) and Friesen and Jones (2012) provide models on the evolutionary stability of mutualisms. Ferdy and Godelle (2005) investigated how symbionts' transmission mode (horizontal or vertical) and virulence should coevolve, and the basic structure of their ecological model is similar to ours. Some studies investigated how host demography affects host-symbiont coexistence using real-life examples (Afkhami and Rudgers, 2008; Bibian et al., 2016; Chung et al., 2015).

We consider that the infected host's life history parameters (survival rate and fecundity) at a time are determined by the symbiont and the host. Our starting point is the well-known Leslie demography model (Bibian et al., 2016; Caswell, 2001; Charlesworth, 1980); thus, the long-term growth rates of the different populations are given implicitly. The following are the reasons for using the Leslie matrices in the model:

1) Symbionts often change the host's life history traits, and we could study this biological phenomenon using Leslie matrices.

2) We could demonstrate the symbionts' effect on the host's life history traits and the host's growth rate.

3) Leslie model is an age-structured model that can capture vertical transmission, which connects generations.

4) We could introduce strategy-dependent survival rates and fecundities.

5) Leslie matrices also enable us to obtain new Malthusian growth rates for the non-infected and infected populations. The Malthusian growth rates can be modeled to depend on the life history traits.

We utilize our formerly published *Kin Demographic Selection Model* (Garay et al., 2016; Garay et al., 2018a, 2018b) based on the Leslie matrix for a single species. The main idea behind the previous model is that the evolutionarily best phenotype maximizes its phenotypic (fitness) long-term growth rate (see, e.g., Rózsa and Garay, 2023). We assumed age-structured Leslie models where two phenotypes A and B can be described by their population vectors (containing the number of individuals at n different age-classes) $\boldsymbol{X}(t), \boldsymbol{Y}(t) \in \mathbb{R}^n$, respectively, and populations of A and B are governed by the corresponding Leslie matrices: $\boldsymbol{L}_A, \boldsymbol{L}_B \in \mathbb{R}^{n\times n}$. The discrete dynamics for phenotype A is $\boldsymbol{X}(t+1) = \boldsymbol{L}_A\boldsymbol{X}(t)$, and similarly for phenotype B. The structure of the Leslie matrices corresponding to the model in this paper is described in subsection 2.2. Population vector $\boldsymbol{X}(t)$ asymptotically tends to the equilibrium age-structure distribution represented by the leading eigenvalue of the Leslie matrix. The corresponding leading eigenvalue λ_A (the dominant eigenvalue of $\boldsymbol{L}_A$) defines the long-term growth rate of the population. If $\lambda_A, \lambda_B > 1$, both populations grow and if $\lambda_A > \lambda_B$, the relative frequency of phenotype B tends to zero. According to the original Darwinian view, if we introduce some degree of density-dependent selection to keep the total density of these two phenotypes at the carrying capacity K (Garay et al., 2016), by selection, the total density of the system reduces to K proportionally, i.e.,

$$\boldsymbol{X}(t+1) = \frac{K}{\|\boldsymbol{L}_A\boldsymbol{X}(t)\| + \|\boldsymbol{L}_B\boldsymbol{Y}(t)\|}\boldsymbol{L}_A\boldsymbol{X}(t) \tag{1}$$

$$\boldsymbol{Y}(t+1) = \frac{K}{\|\boldsymbol{L}_A\boldsymbol{X}(t)\| + \|\boldsymbol{L}_B\boldsymbol{Y}(t)\|}\boldsymbol{L}_B\boldsymbol{Y}(t) \tag{2}$$

where $\|\boldsymbol{X}(t)\| = \sum_i X_i(t)$ denotes the sum of elements of the vector.

While we considered phenotypes of the same species in the former model as stated above, in this work, we generalize it for the interactions between an obligate symbiont and its host. This results in the formation of two populations, i.e., non-infected and infected. The populations considered in the *Kin Demographic Selection Model* (Garay et al., 2016; Garay et al., 2018a, 2018b) were independent. While in the present model, the infected and the non-infected populations are not independent since the infected individuals can be cleared (getting rid of symbionts), and the non-infected individuals may get infected through horizontal transmission. In the following subsection, we utilize the Leslie matrix (Caswell, 2001; Metcalf and Pavard, 2007) and introduce the strategy-dependent life history models to analyze the effects of the symbionts on the hosts.

2.2. Strategy-dependent life history model

We first introduce a generalized model to consider the infected and non-infected lineages separately. We consider that the infected host's life history parameters (survival rate and fecundity) at a time are determined by the symbiont and the host together. We demonstrate how the symbionts can modify their hosts' survival rate and fecundity; for instance, parasites and pathogens decrease their hosts' fecundity or survival rate, or both, while mutualists increase that.

2.2.1. Life history model of the non-infected host

For simplicity, we assume that the host's lifespan is only three years. In the first year, juvenile hosts do not reproduce. $\alpha_1, \alpha_2 > 1$ denote the average fecundities (asexual reproduction) of the host during the second and third years, respectively. Further, $0 < \omega_0 < 1$ and $0 < \omega_1 < 1$ denote the average survival rates from juvenile to one-year-old host and one-year-old to two-year-old host, respectively. The 3-year-old hosts die after reproduction. Using these notations, the standard Leslie model for the non-infected host population is

$$\boldsymbol{L}_{NI} := \begin{pmatrix} 0 & \alpha_1 & \alpha_2 \\ \omega_0 & 0 & 0 \\ 0 & \omega_1 & 0 \end{pmatrix}. \tag{3}$$

The long-term growth rate of the non-infected population is given by the leading eigenvalue (λ_{NI}), which is the unique, dominant, real, and positive solution of the following characteristic polynomial of the matrix $\boldsymbol{L}_{NI}$:

$$P(\boldsymbol{L}_{NI}) = \lambda_{NI}^3 - \alpha_1\omega_0\lambda_{NI} - \alpha_2\omega_0\omega_1 = 0. \tag{4}$$

Our model considers a trade-off between host fecundities and survival rates. Let $s \in [0,1]$ denote the host's resource allocation strategy. Introducing strategy-dependent fecundity functions $\alpha_1(s)$, $\alpha_2(s) \gg 1$, which decrease with increasing s, and strategy-dependent survival rates $\omega_0(s), \omega_1(s) : [0,1] \to (0,1)$, which increase with increasing s, we get the

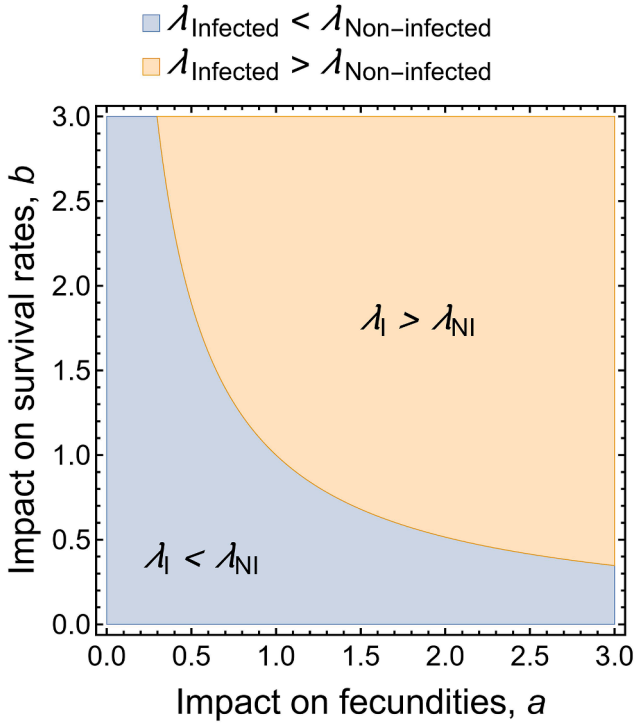

Fig. 2. The plot denotes the parameter pairs a (impact on fecundities) and b (impact on survival rates) when the long-term growth rate of the infected population is higher than that of the non-infected population and vice versa. Parameters are $\alpha_1 = 100, \omega_0 = 0.2$, $\omega_1 = 0.3$, and we assumed age class independent effect on fecundities and survival rates.

following strategy-dependent Leslie matrix for the non-infected population:

$$\boldsymbol{L}_{\mathrm{NI}}(s) := \begin{pmatrix} 0 & \alpha_1(s) & \alpha_2(s) \\ \omega_0(s) & 0 & 0 \\ 0 & \omega_1(s) & 0 \end{pmatrix}. \tag{5}$$

Example 1. *Consider the simplest trade-off in the form of linear functions* $\alpha_i(s) = \alpha_1 - 75s$ *for* $i = 1, 2$, $\omega_0(s) = \omega_0 + 0.75s$ *and* $\omega_1(s) = \omega_1 + 0.65s$, *we have,*

$$\boldsymbol{L}_{\mathrm{NI}}(s) := \begin{pmatrix} 0 & \alpha_1 - 75s & \alpha_1 - 75s \\ \omega_0 + 0.75s & 0 & 0 \\ 0 & \omega_1 + 0.65s & 0 \end{pmatrix}. \tag{6}$$

For simplicity, throughout this paper, we fix the weights of this trade-off (i.e., 0.75, 0.65, and 75), where $0 < \omega_0 + 0.75s < 1$ and $0 < \omega_1 + 0.65s < 1$ for $s \in [0, 1]$. Now we look for $0 < \bar{s} < 1$ which maximizes $\lambda_{\mathrm{NI}}(s)$ when $\alpha_1 = 100, \omega_0 = 0.2, \omega_1 = 0.3$ (see Fig. 1). The corresponding characteristic polynomial is

$$\begin{aligned} P(\boldsymbol{L}_{\mathrm{NI}}(s)) = {} & \lambda_{\mathrm{NI}}^3 - (100 - 75s)(0.2 + 0.75s)\lambda_{\mathrm{NI}} \\ & - (100 - 75s)(0.2 + 0.75s)(0.3 + 0.65s) = 0. \end{aligned} \tag{7}$$

2.2.2. Life history model of the infected host

Now we consider the symbiont-infected host population. The obligate symbionts can modify the hosts' fecundity and survival. This modification strategy is denoted by $\sigma \in [0, 1]$. For some value of σ, the symbionts' effect on the fecundity of their host is given by a function $f_i(\sigma)$, where the index denotes different cohorts (age classes or developmental stages). Similarly, the function $g_i(\sigma)$ gives the symbionts' effect on their host's survival rate. In the case when hosts have no alternative strategies (for fixed s), we get the following general model for the infected host lineage with vertically transmitted symbionts:

$$\boldsymbol{L}_{\mathrm{I}} := \begin{pmatrix} 0 & f_1(\sigma)\alpha_1 & f_2(\sigma)\alpha_2 \\ g_1(\sigma)\omega_0 & 0 & 0 \\ 0 & g_2(\sigma)\omega_1 & 0 \end{pmatrix}. \tag{8}$$

Note that a trade-off can be considered in this model when the functions f and g increase or decrease with respect to $\sigma \in [0, 1]$.

Special case: Consider the case when the functions f and g are constants, i.e., let $a_1, a_2 \in \mathbb{R}_+$ and $b_0, b_1 \in \mathbb{R}_+$ such that $f_1(\sigma) = a_1$, $f_2(\sigma) = a_2$, $g_1(\sigma) = b_0$ and $g_2(\sigma) = b_1$ for each $\sigma \in [0, 1]$. Assume $\alpha_1 = \alpha_2$. We get the following life history model for the infected hosts:

$$\boldsymbol{L}_{\mathrm{I}} = \begin{pmatrix} 0 & a_1\alpha_1 & a_2\alpha_1 \\ b_0\omega_0 & 0 & 0 \\ 0 & b_1\omega_1 & 0 \end{pmatrix}. \tag{9}$$

For the consistency of this model, we need $0 < b_j\omega_j < 1$ for $j = 0, 1$, since $b_j\omega_j$ is the survival rate of the j-th infected host age class. The following are the possible biological interpretations of positive parameters a_i and b_j:

1. If the symbiont is purely parasitic, i.e., decreases both survival and reproduction of its host species, we have $0 < a_i < 1$ and $0 < b_j < 1$.
2. If the symbiont is purely mutualistic, i.e., increases both host survival and fecundity, we have $a_i > 1$ and $\omega_j < b_j\omega_j < 1$.
3. Mixed case, i.e., when the infection increases host survival but reduces its fecundity or vice versa.

For simplicity, we assume that the vertical transmission is perfect. Let us now focus on the Leslie matrix $\boldsymbol{L}_{\mathrm{I}}$ with fixed parameters. Here the long-term growth rate of the infected host population (λ_{I}) is given by the unique and dominant solution of the following characteristic polynomial of $\boldsymbol{L}_{\mathrm{I}}$ in Eq. (9):

$$P(\boldsymbol{L}_{\mathrm{I}}) = \lambda_{\mathrm{I}}^3 - a_1\alpha_1\omega_0 b_0\lambda_{\mathrm{I}} - a_2\alpha_1 b_0\omega_0 b_1\omega_1 = 0. \tag{10}$$

After simple rearrangement, we obtain the following equation for the eigenvalues,

$$\frac{a_1\alpha_1\omega_0 b_0}{\lambda_{\mathrm{I}}^2} + \frac{a_2\alpha_1\omega_0 b_0\omega_1 b_1}{\lambda_{\mathrm{I}}^3} = 1. \tag{11}$$

Eq. (11) shows that the long-term growth rate is a strictly increasing function of parameters a_1, a_2, b_0, b_1. An obvious consequence of these monotonicities is that the symbionts can increase their own evolutionary success by increasing their host's fecundity and survival parameters.

Example 2. *To demonstrate the possible effects of a symbiont species on its host species, we consider the following numerical example for the infected host population. Let us assume that the non-infected population has the following demographic parameters:* $\alpha_1 = \alpha_2 = 100$, $\omega_0 = 0.2$, *and* $\omega_1 = 0.3$. *The corresponding long-term growth rate of the non-infected population (i.e., the dominant eigenvalue of the Leslie matrix in Eq. (3) is* $\lambda_{\mathrm{NI}} = 4.615$. *Consider the following Leslie matrix for the infected lineage:*

$$\boldsymbol{L}_{\mathrm{I}} = \begin{pmatrix} 0 & 100a & 100a \\ 0.2b & 0 & 0 \\ 0 & 0.3b & 0 \end{pmatrix} \tag{12}$$

where, for simplicity, we assume that the effects on fecundities and survival rates are age-class independent, i.e., $a_1 = a_2 = a$ and $b_0 = b_1 = b$. Fig. 2 shows the curve of function $b(a)$ based on Eq. (11) that satisfies $\lambda_{\mathrm{I}} = \lambda_{\mathrm{NI}}$. Over this curve, where $\lambda_{\mathrm{I}} > \lambda_{\mathrm{NI}}$, the infected population dominates the non-infected population.

Now we give different numerical examples to demonstrate the symbiont's effect on the long-term growth rate of the infected population. Assume $\alpha_1 = \alpha_2 = 100$, $\omega_0 = 0.2$, and $\omega_1 = 0.3$; thus, the long-term growth rate of the non-infected population is $\lambda_{\mathrm{NI}} = 4.615$.

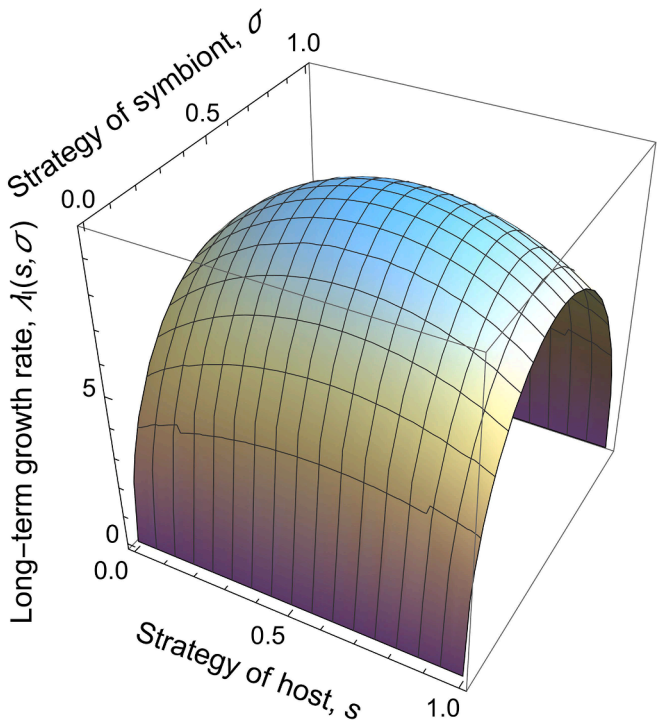

Fig. 3. Long-term growth rate of the infected population based on different host and symbiont strategies with maximum value 9.647 at $(s^*, \sigma^*) = (0.544, 0.492)$.

1. Purely mutualistic: the symbionts increase the fecundities and survival rates of the hosts. For instance, if $a = 2.5, b = 1.5$, then $\lambda_I = 8.877$.
2. Purely parasitic: the symbionts decrease the fecundities and survival rates of the hosts. For instance, if $a = 0.5, b = 0.5$, then $\lambda_I = 2.308$. Our former model (Garay et al., 2016) predicted the extinction of parasitic symbionts in the absence of horizontal infections.
3. Mixed strategy: the symbionts increase host survival but decrease host reproduction or vice versa. This type of symbionts can either increase or decrease the long-term growth rate of the infected population. For instance, when the symbiont increases host reproduction but decreases host survival, i.e., $a = 2.5, b = 0.5$, $\lambda_I = 5.073$; the infected population has a higher growth rate ($\lambda_{NI} < \lambda_I$). Contrarily, when the symbiont decreases host reproduction but increases host survival, i.e., $a = 0.5, b = 1.5$, $\lambda_I = 4.081$; the growth rate of the non-infected population is higher.

2.2.3. Life history model of the infected host population with host and symbiont strategies

Let us now focus on the hosts' and their symbionts' common effect on the survival and fecundity of the vertically infected host population. As we have already considered, the host has a trade-off between fecundity and survival ($s \in [0, 1]$), and the symbionts can modify infected hosts' fecundities and survival rates ($\sigma \in [0, 1]$). Assuming perfect vertical transmission of symbionts, the generalized Leslie matrix corresponding to the model is

$$\boldsymbol{L}_I(s, \sigma) := \begin{pmatrix} 0 & f_1(\sigma)\alpha_1(s) & f_2(\sigma)\alpha_2(s) \\ g_1(\sigma)\omega_0(s) & 0 & 0 \\ 0 & g_2(\sigma)\omega_1(s) & 0 \end{pmatrix}. \tag{13}$$

Example 3. *Consider two trade-offs in the Leslie matrix of the above infected population*:

1. Host trade-off between reproduction and survival (as in Example 1): let $\alpha_i(s) = \alpha_1 - 75s$, $\omega_0(s) = \omega_0 + 0.75s$, and $\omega_1(s) = \omega_1 + 0.65s$.
2. Trade-off between the symbionts' effects on host survival and fecundity: let $f_1(\sigma) = f_2(\sigma) = 10\sigma$ and $g_1(\sigma) = g_2(\sigma) = 1 - \sigma$.

Now the Leslie matrix of the infected population is

$$\boldsymbol{L}_I(s, \sigma) := \begin{pmatrix} 0 & 10\sigma(\alpha_1 - 75s) & 10\sigma(\alpha_1 - 75s) \\ (1-\sigma)(\omega_0 + 0.75s) & 0 & 0 \\ 0 & (1-\sigma)(\omega_1 + 0.65s) & 0 \end{pmatrix}. \tag{14}$$

The long-term growth of the infected population and its optimization with respect to different values of s and σ are given in Fig. 3. We can observe that the host and the symbiont can together optimize the fitness (long-term growth rate) of the infected lineage, with both species having the possibility of increasing their fitness by the association. In other words, altering the life history traits of the host can impact the evolutionary success of the host as well as the symbiont.

2.3. Competitive selection dynamics of the resident system

Based on the discrete, strategy-dependent, and age-structured model of vertical transmission in infected and non-infected populations (or lineages), we can derive the "ecological" dynamics. We introduce selection dynamics for the resident system with interacting infected and non-infected populations. Infected and non-infected populations interact in three ways: 1) by horizontal transmission (when a non-infected individual becomes infected) (Ebert, 2013), 2) by clearing (when an infected individual becomes non-infected), and 3) by competition between individuals of the two populations. Implementing the interactions in the structured model results in high-dimensional systems with limited analytical tractability (Castelletti and Barbarossa, 2020; Tian et al., 2018). To avoid these difficulties, we assume continuous-time population dynamics with the Malthusian growth rates derived from the structured model. The dynamics becomes two-dimensional by considering the dynamics of the two populations' total densities. This simplification allows us to connect the dynamics of a structured population and the process of population regulation in a simple way, even though the higher-dimensional model would yield more accurate predictions. When the matrix dimension is high, it is also hard to use the standard invasibility plot method of adaptive dynamics theory (Dercole and Rinaldi, 2008).

First, let us show how we introduce the Malthusian growth rate into the dynamical system. In the discrete model, consider the non-infected and the infected populations with λ_{NI} and λ_I respectively as the long-term growth rates. We assume that the interconnection between these populations is uniform, i.e., density-dependent competition, horizontal infection, and clearing are independent of the host's age and phenotype. We can use the well-known asymptotic behavior of the Leslie model (Caswell, 2001), i.e., for each fixed Leslie matrix (independently of the initial state of the population), the population reaches an equilibrium vector (stable age structure of the Leslie matrix) after enough time. In this case, the whole population's growth rate at the stable age distribution (asymptotic growth rate) is the Leslie matrix's unique leading eigenvalue, and the equilibrium vector is the corresponding eigenvector. The discrete dynamics of the non-infected population is governed by the following equation: $\boldsymbol{x}_{NI}(t+1) = \boldsymbol{L}_{NI}\boldsymbol{x}_{NI}(t)$, where $\boldsymbol{x}_{NI}(t)$ is the population vector of the non-infected population at time t and $\boldsymbol{L}_{NI}$ is the Leslie matrix corresponding to the non-infected population. Based on the asymptotic behavior of the Leslie model, the long-term growth rate of the non-infected population, denoted by λ_{NI} (the leading eigenvalue of $\boldsymbol{L}_{NI}$), gives the population's asymptotic growth rate. Similarly, we have the long-term growth rate of the infected population (λ_I). We invoke the known fact that the logarithm of the growth rate from a Leslie matrix (Caswell, 2001; Nur, 1987) can be interpreted as the Malthusian parameter (m) of the corresponding continuous-time dynamics ($m = \ln\lambda$). Based on this, we can consider $\ln(\lambda_{NI})$ and $\ln(\lambda_I)$ respectively as the

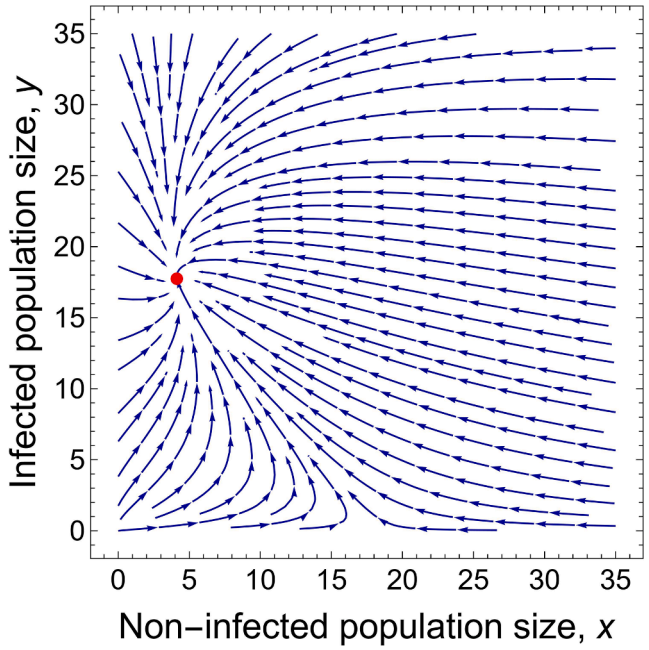

Fig. 4. Phase portrait showing the trajectory of the non-infected (x) and the infected (y) population densities for $\lambda_{\mathrm{NI}} = 6.303$ (from $\boldsymbol{L}_{\mathrm{NI}}(s)$ in Eq. (6) for $s^* = 0.544$), $\lambda_{\mathrm{I}} = 9.647$ (from $\boldsymbol{L}_{\mathrm{I}}(s,\sigma)$ in Eq. (14) for $s^* = 0.544$ and $\sigma^* = 0.492$), $\beta = 0.15$, $\gamma = 0.1$, and $c_r = 0.7$. The phase diagram has a stable node (red point) at $(x^*, y^*) = (4.131, 17.732)$.

Malthusian growth rates of the non-infected and the infected populations. Note that the Malthusian growth rates for the dynamics are obtained when the host strategy is s^* and the symbiont strategy is σ^*, i.e., the strategy pair that maximizes the long-term growth rate of the infected lineage.

We denote $x, y \in \mathbb{R}_+$ as the total population size of the non-infected and infected populations, respectively, i.e., the total size of the population at the stable asymptotic state of the respective Leslie matrices. Further, we denote the horizontal transmission rate by $\beta \in (0,1)$. For simplicity, we assume that the horizontal transmission rate does not depend on the individual's age. Furthermore, at the state when the population densities of the non-infected and infected populations are x and y respectively, horizontal transmission produces βxy infected individuals. We follow the basic SIR models for modeling horizontal transmission; thus, the transmission of infection is proportional to the densities of the "infected" and that of the "susceptible (non-infected)" individuals (Hethcote, 2000). However, we cannot use the SIR-type models directly since, in our model, we have both vertical and horizontal transmissions, and both are independent events. The vertical one occurs along a lineage of descendants, while the horizontal one is realized across lineages during the non-reproductive period. Further, in our model, there is no acquired immunity or resistance, i.e., an individual can be cleared and then horizontally re-infected several times. Let $c_r \in (0,1)$ denote the clearing rate, i.e., the rate at which an infected host loses its symbiont and becomes non-infected. We also consider density-dependent competition between infected and non-infected populations for food or other resources, and we assume that both populations are equally effective in the context of this competition. Denote the density-dependent competition rate by $\gamma \in (0,1)$. For the sake of simplicity, we apply the *uniformity conditions* to the new model, i.e., the density-dependent competition, the horizontal transmission, and the clearing are all independent of the host's age and phenotype. Based on these assumptions, we get the following simplified dynamical system:

$$\dot{x} = x(\ln\lambda_{\mathrm{NI}}(s^*) - \gamma x - \gamma y) - \beta xy + c_r y \tag{15}$$

$$\dot{y} = y(\ln\lambda_{\mathrm{I}}(s^*, \sigma^*) - \gamma x - \gamma y) + \beta xy - c_r y. \tag{16}$$

This set of differential equations is implicitly given since the Malthusian growth rates $\ln(\lambda_{\mathrm{NI}})$ and $\ln(\lambda_{\mathrm{I}})$ are implicitly given by the eigenvalues of the Leslie matrices of the two populations. However, our model is well-defined since there exist unique, positive, and dominant eigenvalues for both Leslie matrices (Caswell, 2001; Varga et al., 2020).

Observe that features of three model families constitute our model; these features handle the evolution and the effects of the interaction between the host and its symbiont: 1) The symbiont can change the life history parameters of the host; thus, it can change the Malthusian growth rates of the lineages. In other words, the effect of the symbiont determines one fundamental ecological parameter of the host. The age-structured and strategy-dependent Leslie model thus gives the Malthusian growth rates of the lineages for the ecological dynamics. 2) Density-dependent competition between lineages, selection between lineages, and extinction and coexistence of the lineages are modeled similar to the Lotka-Volterra framework. 3) The connection between the infected and non-infected lineages is given by the horizontal infection and clearing of infection, which are modeled like in the basic epidemic models (Susceptible-Infected-Susceptible, SIS).

Upon analytical investigation, the population size of the infected individuals at the positive equilibrium, according to Eq. (16) is

$$y^* = \frac{\ln\lambda_{\mathrm{I}} - (\gamma - \beta)x^* - c_r}{\gamma}. \tag{17}$$

The equilibrium population size x^* of the non-infected population is the solution of the following equation:

$$\beta^2 x^2 + [\gamma(\ln\lambda_{\mathrm{I}} - \ln\lambda_{\mathrm{NI}}) + \beta(\ln\lambda_{\mathrm{I}} - 2c_r)]x + c_r(c_r - \ln\lambda_{\mathrm{I}}) = 0. \tag{18}$$

The sufficient conditions for the existence of the positive fixed point of the resident system (15)–(16) are $\ln\lambda_{\mathrm{I}} > c_r$ and $\beta > \gamma$. In other words, the interior equilibrium exists if the Malthusian growth rate of the infected population is larger than the clearing rate and the rate of horizontal transmission is larger than the rate of competition. Also, this unique interior fixed point is locally asymptotically stable if $\gamma < \beta < 3\gamma$, and γ is small (see Appendix A for proof). The locally asymptotically stable rest point (x^*, y^*) of the resident system (15)–(16) is also globally asymptotically stable (using Lyapunov stability criterion, see Appendix A for proof). Thus, the ecological coexistence of both populations as well as the coexistence of hosts and symbionts (in the form of infected individuals), is guaranteed under the conditions. Fig. 4 shows the local dynamics of the resident system around (x^*, y^*).

2.4. Evolutionary stability of the obligate symbiont and the host

We face a coevolutionary problem since the system with the obligate symbiont and the host is susceptible to invasion by mutant phenotypes. Following the primary idea by Maynard Smith and Price (1973), we consider the stable resident ecological system to be evolutionarily stable if rare mutants cannot invade the system. This leads us to the question of conditions for the existence of such an evolutionarily stable ecological state that is resistant to invasion by mutants. For this, we apply the N-species evolutionary stability concept (Cressman et al., 2020; Cressman and Garay, 2003a, 2003b; Garay, 2007). This concept belongs to the general theory of coevolution (combining the effects of ecology and evolution) based on fitness and a finite number of phenotypes (but for the sake of convenience, we use a continuous strategy set). We assume mutations (heritable changes in strategies or characters) are rare enough, and there is enough time for ecological selection (or ecological dynamics) to eliminate the least fit types and for the system to reach a stable state. Thus, each mutant appears in the ecologically stable state of the resident system. We need to consider only the case when there is a single mutant type in each population because the population reaches its stable rest point before the next mutant arises. Also, we assume that the

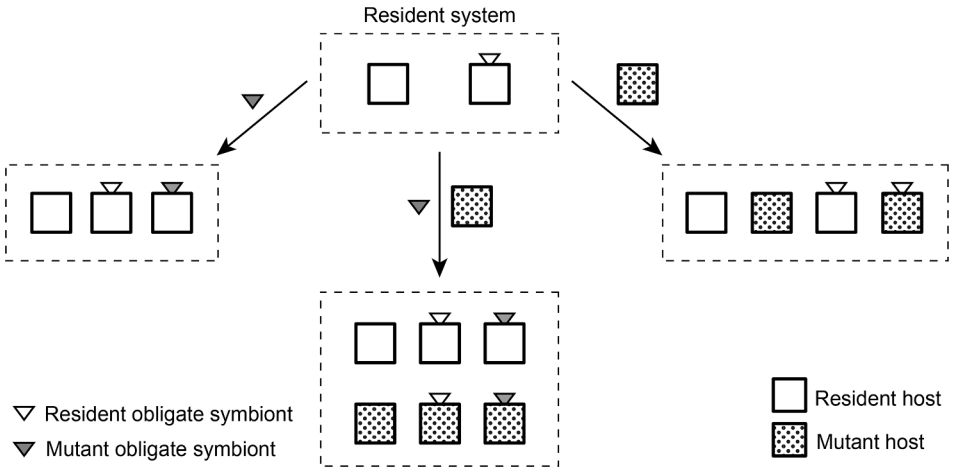

Fig. 5. Schematic of mutants introduced into the resident system and the resulting mutant systems with infected and non-infected populations.

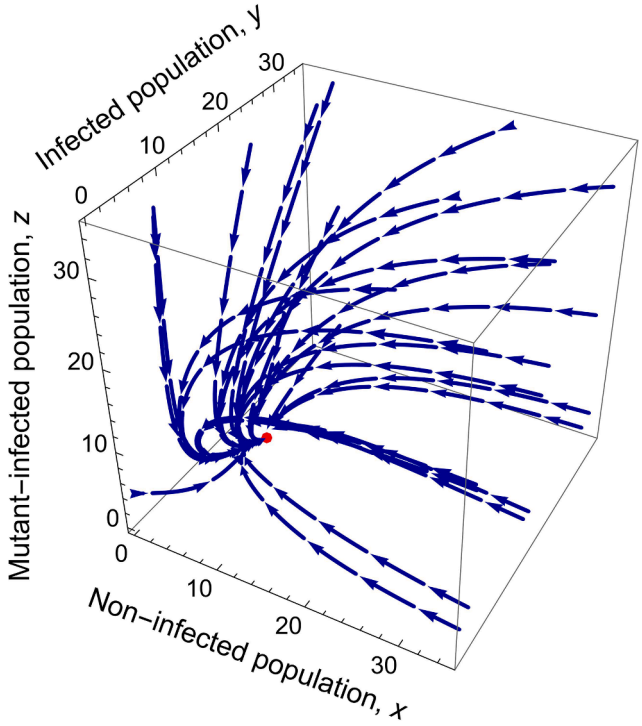

Fig. 6. Phase portrait showing the trajectory of the non-infected (x), infected (y), and mutant-infected (z) population densities for $\lambda_{\mathrm{NI}} = 6.303$, $\lambda_{\mathrm{I}} = 9.647$, $\lambda_{\mathrm{I}}^{\mathrm{M}} = 3.547$, $\beta = 0.15$, $\gamma = 0.1$, and $c_r = 0.7$. The phase diagram has a stable node (red point) at $(x^*, y^*, 0) = (4.131, 17.732, 0)$ that does not allow invasion by the mutant phenotype of the symbiont. Observe that the trajectories go to the resident plane. On the resident plane, the fixed point is the same as in Fig. 4.

time scale of mutation (evolutionary timescale) is much slower than the ecological time scale. Furthermore, mutations increase the dimension of the system since new types appear. To preserve analytical tractability, we set up a conceptual and qualitative model explaining the behavior of the considered symbiotic systems without allowing quantitative validation.

We also implement an often-used simplifying assumption that one host has only one symbiont type at a time. In other words, different symbiont types cannot coexist with the same host because they tend to displace each other (Ferdy and Godelle, 2005; Gandon et al., 2001). We are interested in when a rare mutant dies out, and the conditions for evolutionary stability when the possible mutant host is defined by its allocation strategy ($s \in [0,1]$) and the possible mutant symbiont is defined by its impact strategy ($\sigma \in [0,1]$). According to our assumption that mutations are rare enough, we can consider a single mutant, which appears in the ecologically stable state (x^*, y^*) of the resident system. Recall that the stable ecological state (x^*, y^*) of the resident ecosystem is obtained when the host strategy is s^* and the symbiont strategy is σ^*. We may call the resident equilibrium densities $(x^*(s^*, \sigma^*), y^*(s^*, \sigma^*))$. Thus, we have two cases: 1) when a mutant arises in the symbiont (when σ appears, $\sigma \neq \sigma^*$), and 2) when a mutant arises in the host (when s appears, $s \neq s^*$). Finally, since we use the coevolutionary dynamics, we can also consider the extremely rare situation when mutation arises in both host and symbiont species (when both s and σ appear simultaneously). The Malthusian growth rates of the mutant-infected populations will change in each case. However, we assume new populations with mutants have identical ecological parameters (competitive abilities, clearing rate, and transmission rate) as their resident counterparts. The resident strategy pair (s^*, σ^*) that optimizes the life history traits of the infected lineage is evolutionarily stable if coevolutionary dynamics pushes all other possible invading mutants into extinction. We get the required condition for evolutionary stability based on the conditions for the mutant to go extinct. Fig. 5 shows the formation of new mutant systems with the introduction of mutant hosts and symbionts.

2.4.1. *Host-symbiont coevolutionary dynamics with mutant symbiont*

We first consider the case when a rare mutant arises in the symbiont. For the evolutionary stability of the resident system, we need the mutant to die out by ecological dynamics. Let z denote density of the rare infected mutant population (mutant symbiont strategy, $\sigma \neq \sigma^*$) with long-term growth rate $\lambda_{\mathrm{I}}^{\mathrm{M}} := \lambda_{\mathrm{I}}(s^*, \sigma)$. x and y are as in the resident system (15)–(16). The coevolutionary dynamics of the system with the mutant phenotype of the symbiont is as follows:

$$\dot{x} = x(\ln\lambda_{\mathrm{NI}}(s^*) - \gamma x - \gamma y - \gamma z) - \beta xy - \beta xz + c_r y + c_r z \tag{19}$$

$$\dot{y} = y(\ln\lambda_{\mathrm{I}}(s^*, \sigma^*) - \gamma x - \gamma y - \gamma z) + \beta xy - c_r y \tag{20}$$

$$\dot{z} = z\left(\ln\lambda_{\mathrm{I}}^{\mathrm{M}}(s^*, \sigma) - \gamma x - \gamma y - \gamma z\right) + \beta xz - c_r z. \tag{21}$$

$(x^*(s^*, \sigma^*), y^*(s^*, \sigma^*), 0)$ is an equilibrium of the system (19)–(21). Sufficient conditions for the given mutant phenotype of the symbiont to die out (mutant cannot invade the stable resident system) are $\gamma < \beta < 2\gamma$ and $\lambda_{\mathrm{I}}^{\mathrm{M}}(s^*, \sigma) < \lambda_{\mathrm{I}}(s^*, \sigma^*)$ (see Appendix B for proof). In mathematical terms, $(x^*, y^*, 0)$ is a locally asymptotically stable (l. a. s.) equilibrium of the coevolutionary dynamics (19)–(21) for the above conditions. Note that we only require local stability because the mutants are introduced in small (rare) densities. The condition $\lambda_{\mathrm{I}}^{\mathrm{M}}(s^*, \sigma) < \lambda_{\mathrm{I}}(s^*, \sigma^*)$ is always

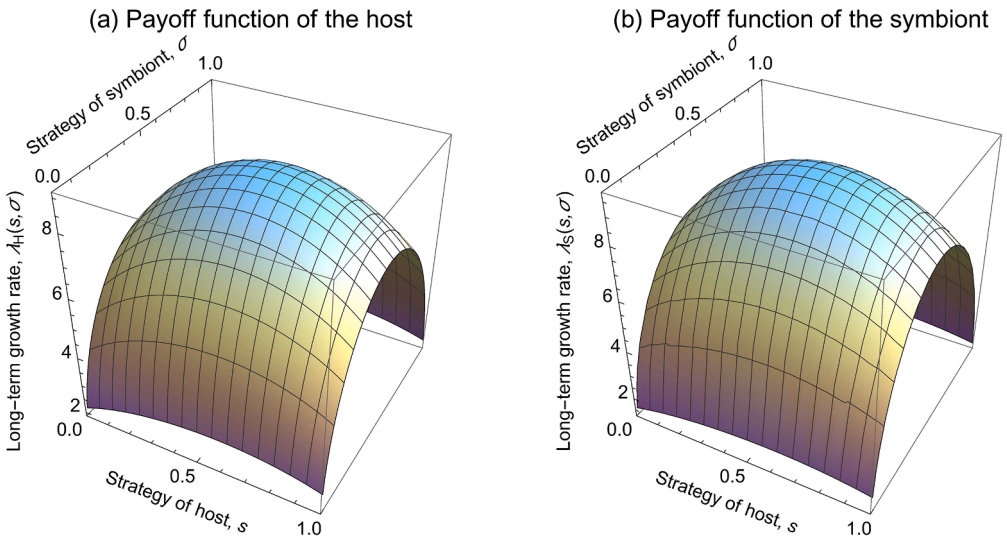

Fig.7. a) The payoff function of the host and **b)** the payoff function of the symbiont for different strategy pairs (s,σ). Observe that the payoff functions $\lambda_{\mathrm{H}}(s,\sigma)$ and $\lambda_{\mathrm{S}}(s,\sigma)$ are continuous and strictly concave-downward functions with a maximum at a single point. Analyzing the plots, the best response function of host $\delta_{\mathrm{H}}(\sigma)$ maps to a singleton set with element $s^* = 0.544$ and the best response function of symbiont $\delta_S(s)$ maps to a singleton set with element $\sigma^* = 0.492$. Therefore, the strict Nash equilibrium is $(s^*,\sigma^*) = (0.544, 0.492)$.

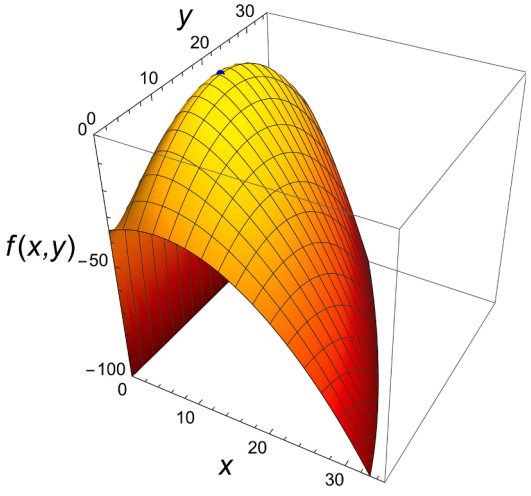

Fig. A1. The time derivative of the Lyapunov function, $\dot{V}(x,y) = f(x,y)$ attains maximum value at $(x^*,y^*) = (4.131, 17.732)$ (blue point) for $\lambda_{\mathrm{NI}} = 6.303$, $\lambda_{\mathrm{I}} = 9.647$, $\beta = 0.15$, $\gamma = 0.1$, and $c_r = 0.7$. Since $\dot{V}(x^*,y^*) = 0$, $\dot{V}(x,y) < 0$ for all $(x,y) \neq (x^*,y^*)$.

true as $\lambda_{\mathrm{I}}(s^*,\sigma^*)$ is the maximum possible value of λ_{I} for any strategy pairs. Fig. 6 shows the local dynamics of the system (19)–(21) around $(x^*,y^*,0)$.

2.4.2. *Host-symbiont coevolutionary dynamics with mutant host*

Now consider the case when a rare mutant arises in the host. Let x denote the density of the non-infected population of resident hosts (strategy s^*) and x_{M} denote the density of the non-infected population of mutant hosts (strategy $s \neq s^*$). We have only one resident symbiont with strategy σ^*, which forms two types of infected populations. Let y denote the density of the infected population with the resident host and $\widehat{z}$ denote the density of the infected population with the mutant host (strategy $s \neq s^*$). The long-term growth rates of the infected and non-infected population with the mutant host are $\widehat{\lambda_{\mathrm{I}}^{\mathrm{M}}} := \lambda_{\mathrm{I}}(s,\sigma^*)$ and $\lambda_{\mathrm{NI}}^{\mathrm{M}} := \lambda_{\mathrm{NI}}(s)$, respectively. When a non-infected (resident or mutant) host encounters any infected populations (either of the two), they get infected. The coevolutionary dynamics of the system with the free-living mutant host and infected population with the mutant host added to the resident system is as follows:

$$\dot{x} = x(\ln\lambda_{\mathrm{NI}}(s^*) - \gamma x - \gamma y - \gamma\widehat{z} - \gamma x_{\mathrm{M}}) - \beta xy - \beta x\widehat{z} + c_r y \tag{22}$$

$$\dot{x}_{\mathrm{M}} = x_{\mathrm{M}}\left(\ln\lambda_{\mathrm{NI}}^{\mathrm{M}}(s) - \gamma x - \gamma y - \gamma\widehat{z} - \gamma x_{\mathrm{M}}\right) - \beta x_{\mathrm{M}} y - \beta x_{\mathrm{M}}\widehat{z} + c_r\widehat{z} \tag{23}$$

$$\dot{y} = y(\ln\lambda_{\mathrm{I}}(s^*,\sigma^*) - \gamma x - \gamma y - \gamma\widehat{z} - \gamma x_{\mathrm{M}}) + \beta xy + \beta x\widehat{z} - c_r y \tag{24}$$

$$\dot{\widehat{z}} = \widehat{z}\left(\ln\widehat{\lambda_{\mathrm{I}}^{\mathrm{M}}}(s,\sigma^*) - \gamma x - \gamma y - \gamma\widehat{z} - \gamma x_{\mathrm{M}}\right) + \beta x_{\mathrm{M}} y + \beta x_{\mathrm{M}}\widehat{z} - c_r\widehat{z}. \tag{25}$$

For the evolutionary stability of the resident system, we need the local stability of the equilibrium $(x^*,0,y^*,0)$ of (22)–(25). Sufficient conditions for a given mutant phenotype of the host to die out, or in other words, for $(x^*,0,y^*,0)$ to be l. a. s. are $\lambda_{\mathrm{NI}}^{\mathrm{M}}(s) < \lambda_{\mathrm{NI}}(s^*)\exp\left(c_r\frac{y^*}{x^*}\right)$ and $\widehat{\lambda_{\mathrm{I}}^{\mathrm{M}}}(s,\sigma^*) < \lambda_{\mathrm{I}}(s^*,\sigma^*)\exp(\beta x^*)$ (see Appendix C for proof).

Since (s^*,σ^*) maximizes the long-term growth rate of the infected population, the inequality $\widehat{\lambda_{\mathrm{I}}^{\mathrm{M}}}(s,\sigma^*) < \lambda_{\mathrm{I}}(s^*,\sigma^*)\exp(\beta x^*)$ is always true. However, $\lambda_{\mathrm{NI}}^{\mathrm{M}}(s) < \lambda_{\mathrm{NI}}(s^*)\exp\left(c_r\frac{y^*}{x^*}\right)$ is not always true because the long-term growth rate of the non-infected population is maximized at $\bar{s}$, not at s^* (see Example 1). Thus, the evolutionary stability of the ecologically stable resident rest point in the coevolutionary dynamics of the mutant system happens unconditionally only if $s^* = \bar{s}$, i.e., if the host can maximize the growth rates of the two lineages using the same strategy. An additional example of Leslie matrices for the non-infected and infected populations where this happens is shown in Appendix E. Counterexamples for $s^* \neq \bar{s}$ have already been mentioned in Example 1 (Eq. (6)) and Example 3 (Eq. (14)).

2.4.3. *Host-symbiont coevolutionary dynamics with both mutant host and mutant symbiont*

Mutations are infrequent; thus, the possibility of independent mutations in the host and symbiont strategies simultaneously is extremely rare. However, if the densities of hosts and symbionts in the resident system are either extremely high, or both species coexist for a very long time, then there is a possibility (extremely rare) for two independent mutations in the hosts and symbionts simultaneously. The Evolutionarily Stable Strategy (ESS) definition in game theory (Maynard Smith

and Price, 1973) is based on the assumption that a single mutation is more probable to occur, i.e., either (s, σ^*) or (s^*, σ) only. However, in biology, the basic assumption of the Nash equilibrium (only one player changes its strategy) does not necessarily hold, and there is no biological reason to neglect the rare cases when mutations happen in both species at the same time. Below we consider the case when mutant phenotypes arise simultaneously in both hosts and symbionts. x, x_M, y, z and $\widehat{z}$ are defined as in systems (19)–(21) and (22)–(25). Let $\widetilde{z}$ be the infected population with mutant host and mutant symbiont, having long-term growth rate $\widetilde{\lambda_I^M} := \lambda_I(s, \sigma)$. Consequently, we get the following six-dimensional coevolutionary dynamics:

$$\dot{x} = x(\ln\lambda_{NI}(s^*) - \gamma(x + y + z + x_M + \widehat{z} + \widetilde{z})) - \beta x(y + z + \widehat{z} + \widetilde{z}) + c_r(y + z) \tag{26}$$

$$\dot{x}_M = x_M\left(\ln\lambda_{NI}^M(s) - \gamma(x + y + z + x_M + \widehat{z} + \widetilde{z})\right) - \beta x_M(y + z + \widehat{z} + \widetilde{z}) + c_r(\widehat{z} + \widetilde{z}) \tag{27}$$

$$\dot{y} = y(\ln\lambda_I(s^*, \sigma^*) - \gamma(x + y + z + x_M + \widehat{z} + \widetilde{z})) + \beta xy + \beta x\widehat{z} - c_r y \tag{28}$$

$$\dot{z} = z\left(\ln\lambda_I^M(s^*, \sigma) - \gamma(x + y + z + x_M + \widehat{z} + \widetilde{z})\right) + \beta xz + \beta x\widetilde{z} - c_r z \tag{29}$$

$$\dot{\widehat{z}} = \widehat{z}\left(\ln\widehat{\lambda_I^M}(s, \sigma^*) - \gamma(x + y + z + x_M + \widehat{z} + \widetilde{z})\right) + \beta x_M y + \beta x_M\widehat{z} - c_r\widehat{z} \tag{30}$$

$$\dot{\widetilde{z}} = \widetilde{z}\left(\ln\widetilde{\lambda_I^M}(s, \sigma) - \gamma(x + y + z + x_M + \widehat{z} + \widetilde{z})\right) + \beta x_M z + \beta x_M\widetilde{z} - c_r\widetilde{z}. \tag{31}$$

The equilibrium $(x^*, 0, y^*, 0, 0, 0)$ of the system (26)–(31) with mutations in both host and symbiont is stable if (see Appendix D for proof):

1) $\lambda_I^M(s^*, \sigma) < \lambda_I(s^*, \sigma^*)$,
2) $\widehat{\lambda_I^M}(s, \sigma^*) < \lambda_I(s^*, \sigma^*)\exp(\beta x^*)$
3) $\lambda_{NI}^M(s) < \lambda_{NI}(s^*)\exp\left(c_r\frac{y^*}{x^*}\right)$, and
4) $\widetilde{\lambda_I^M}(s, \sigma) < \lambda_I(s^*, \sigma^*)\exp(\beta x^*)$.

Similar to the explanation in 2.4.2, the inequalities $\lambda_I^M(s^*, \sigma) < \lambda_I(s^*, \sigma^*)$, $\widehat{\lambda_I^M}(s, \sigma^*) < \lambda_I(s^*, \sigma^*)\exp(\beta x^*)$, and $\widetilde{\lambda_I^M}(s, \sigma) < \lambda_I(s^*, \sigma^*)\exp(\beta x^*)$ of the above conditions are always true as λ_I is maximized at (s^*, σ^*). However, $\lambda_{NI}^M(s) < \lambda_{NI}(s^*)\exp\left(c_r\frac{y^*}{x^*}\right)$ is not always true.

Conclusively, from the stability analysis of the mutant systems in (19)–(21), (22)–(25), and (26)–(31), the host-symbiont system is evolutionarily stable unconditionally only if the host can maximize the growth rates of the infected and non-infected lineages using the same strategy. We can also observe that the long-term growth rates (fitnesses) of the populations govern the conditions for the stability of the resident equilibrium. This leads us to question whether our model can be interpreted from the game theory perspective. In the following section, we introduce plausible fitness definitions for both species (host and symbiont) and compare the results of our coevolutionary analysis to that of ESS.

2.5. Game-theoretic approach

From the evolutionary game theory perspective, there exists a conflict in our selection situation since the host and the symbiont together determine the infected population's long-term growth rate. We now try to compare the Evolutionarily Stable Strategy (ESS) and the linear stability of the coevolutionary dynamics in our model. From a biological point of view, the strict Nash equilibrium (strict Nash implies ESS) means that neither mutant symbionts nor mutant hosts can invade the system (Maynard Smith and Price, 1973). For this, we need to define the fitness functions of the players. This problem is intuitively clear for the obligate and vertically transmitted symbionts since their evolutionary success can be given by that of the infected populations. However, the same is not apparent for the hosts as they are involved in both infected and non-infected populations. Clearing and horizontal transmission create difficulty since the number of infected and non-infected descendants are dynamically determined in each population. However, we try to provide a reasonable fitness function for the host. Remember that the concept of Nash equilibrium is based on only one player changing its strategy, which means that the mutation (infrequent) occurs only in one of the two species at a time. The original verbal definition of the ESS with a frequency-dependent interaction scheme is the following for a single species. If the overwhelming part of the population uses this strategy (or phenotype), then a rare mutant cannot invade the population (Maynard Smith and Price, 1973).

We start by formally defining the strict Nash equilibrium for an asymmetric game. Consider two players (Host and Symbiont) with strategy sets $s \in [0, 1]$ and $\sigma \in [0, 1]$ and payoff functions $\lambda_H(s, \sigma)$ and $\lambda_S(s, \sigma)$, respectively. Host's resource allocation strategy is $s \in [0, 1]$. The host has a trade-off between reproduction and survival. Symbiont's strategy is $\sigma \in [0, 1]$, and it is indicative of its effect on the survival and fecundity of the host.

Average payoff function of symbiont: Since the symbiont is obligate, its evolutionary success (fitness) is the same as that of the infected population in our model. Thus, its payoff is the long-term growth of the infected population, i.e.,

$$\lambda_S(s, \sigma) = \lambda_I(s, \sigma). \tag{32}$$

Average payoff function of host: Using $\lambda_I(s^*, \sigma^*)$ and $\lambda_{NI}(s^*)$ as the long-term growth rates of each population in the resident system, we can calculate x^* and y^* (densities at the locally asymptotically stable rest point of the resident dynamics (15)–(16)). Since mutations are rare, there is enough time for the dynamics (15)–(16) to reach its stable rest point (x^*, y^*). Note that the payoffs are not independent. Due to the mixed transmission mode, each host's lineage will contain infected and non-infected descendants due to clearing and horizontal transmission. Hence, each host individual can alter between infected and non-infected stages throughout its life. Thus, the host's average payoff must consider the long-term growth rates of the infected and the non-infected populations. The resident system's rest point determines the ratio of the infected and non-infected individuals at the endpoint of evolution; therefore, we use this ratio to weigh the long-term growth rates of the infected and non-infected populations. Thus, at the resident equilibrium, a host is non-infected or infected with probability $\frac{x^*}{x^*+y^*}$ or $\frac{y^*}{x^*+y^*}$, respectively. We define the host's payoff as

$$\lambda_H(s, \sigma) := \frac{x^*(s^*, \sigma^*)}{x^*(s^*, \sigma^*) + y^*(s^*, \sigma^*)}\lambda_{NI}(s) + \frac{y^*(s^*, \sigma^*)}{x^*(s^*, \sigma^*) + y^*(s^*, \sigma^*)}\lambda_I(s, \sigma). \tag{33}$$

where $\lambda_{NI}(s)$ and $\lambda_I(s, \sigma)$ are the long-term growth rates of the non-infected and infected populations respectively, i.e., the dominant eigenvalue of the Leslie matrices $\boldsymbol{L}_{NI}(s)$ in Eq. (6) and $\boldsymbol{L}_I(s, \sigma)$ in Eq. (14). If all hosts are infected at the stable rest point of the resident dynamics, i.e., $x^* = 0$, (say when $c_r = 0$ and β is large enough), then the payoff functions of both players are the same and equals $\lambda_I(s, \sigma)$. If majority of the hosts are non-infected (e.g., $c_r \approx 1$), then the host payoff is nearer to $\lambda_{NI}(s)$.

The host's best response function $\delta_H(\sigma)$ provides the best strategies (which maximize the payoff function) that the host must choose when the symbiont plays a given strategy σ. In other words, $\delta_H(\sigma)$ is a set represented as

$$\delta_H(\sigma) = \{s \in [0, 1] \,|\, \lambda_H(s, \sigma) > \lambda_H(s', \sigma) \forall s' \in [0, 1], s \neq s'\}.$$

Similarly,

$$\delta_S(s) = \{\sigma \in [0, 1] \,|\, \lambda_S(s, \sigma) \rangle \lambda_S(s, \sigma')) \forall \sigma' \in [0, 1], \sigma \neq \sigma'\}.$$

A strict Nash equilibrium is a strategy pair (s^*, σ^*) such that $s^* \in \delta_H(\sigma^*)$ and $\sigma^* \in \delta_S(s^*)$, where s^* and σ^* are the best strategies of the host and the symbiont respectively (see Fig. 7a and 7b). Equivalently in our model, a strategy pair (s^*, σ^*) is an ESS (strict Nash equilibrium) if for all $s \neq s^*$ and $\sigma \neq \sigma^*$, we have $\lambda_S(s^*, \sigma) < \lambda_S(s^*, \sigma^*)$ and $\lambda_H(s, \sigma^*) < \lambda_H(s^*, \sigma^*)$. Based on this, we arrive at the following inequalities:

1. $\lambda_I^M(s^*, \sigma) < \lambda_I(s^*, \sigma^*)$,

2. $\frac{x^*}{x^*+y^*}\lambda_{NI}^M(s) + \frac{y^*}{x^*+y^*}\widehat{\lambda_I^M}(s, \sigma^*) < \frac{x^*}{x^*+y^*}\lambda_{NI}(s^*) + \frac{y^*}{x^*+y^*}\lambda_I(s^*, \sigma^*)$.

Thus, in our model, game-theoretic analysis gives coarser conditions compared to the following conditions for evolutionary stability from our coevolutionary dynamical model:

$\lambda_I^M(s^*, \sigma) < \lambda_I(s^*, \sigma^*)$,

$\lambda_{NI}^M(s) < \lambda_{NI}(s^*)\exp\left(c_r\frac{y^*}{x^*}\right)$ and $\widehat{\lambda_I^M}(s, \sigma^*) < \lambda_I(s^*, \sigma^*)\exp(\beta x^*)$.

Note that the above conditions are for cases with only one mutant at a time. Also, the definition of strict Nash equilibrium of the above game is strictly based on our uniform simplifying assumptions (i.e., clearing, horizontal transmission, and competition between the infected and non-infected resident/mutant populations are independent of the strategies). We observed that the game-theoretical method allows relaxed conditions compared to that obtained via analysis of the coevolutionary dynamics. However, this conjecture needs more studies in more general selection situations when our uniformity conditions are not satisfied.

3. Discussion, interpretation, and biological examples

In this manuscript, we introduced a combination of the Leslie demography model (vertical transmission) and competitive selection dynamics (horizontal transmission with clearing) to explore the coevolution of obligate symbionts and hosts. We observed that the obligate symbionts could increase their evolutionary success by altering the life history traits of the host. The hosts and the symbionts can together optimize the fitness of the infected lineage (multi-level selection). In other words, changing the host's life history parameters can impact the coevolution of the host and the symbiont as a unit or group. The analysis of the ecological dynamics of the infected and the non-infected populations (dynamical systems) provided the conditions that guaranteed the coexistence of the populations. An unusual feature of the coevolutionary model was that the appearance of two mutants (mutant host and mutant symbiont) in the coevolutionary system increased its dimensionality to six. Then, we applied a game-theoretical approach to the same model as an alternative method. From a purely methodological point of view, we observed that the game-theoretical approach yields coarser results than the analysis of coevolutionary dynamics for two reasons. First, the strict Nash definition allows only one mutant phenotype at a time, either in the host or symbiont. Second, coevolutionary dynamics performs better even if it is limited to one mutant type, as we were able to obtain more stringent and precise conditions for the uninvasibility of mutants.

From a biological point of view, our model yields both trivial and non-trivial connotations. Evolutionary theory predicts that uniparentally and vertically transmitted parasites must be harmless to their hosts (Fine, 1975; Yamamura, 1993; Lipsitch et al., 1995). Thus, obligate symbiosis with vertical transmission will likely end up as mutualism. Accordingly, a symbiont species may not develop or maintain a parasitic way of life (i.e., may not decrease host fitness) in a uniparental system unless capable of horizontal transmission (Garay et al., 2016). This means parasites that utilize only the parent-offspring (vertical) transmission routes may not survive because the non-infected lineages outcompete the infected ones since it has a better long-term growth rate. Presuming that the bodily contacts between parents and their offspring are usually more direct and more long-lasting than between other conspecifics – thus more proper for symbiont transmission – this means that mutualism is supposed to be an archaic form of symbiosis. Parasitism is likely a derived way of life that can emerge only after the symbiont has evolved the more advanced ways of horizontal transmission. Alternatively, the parasitic way of life may evolve from a sapronotic life strategy (Kuris et al., 2014).

We observed that the evolutionary success of an obligate symbiont and its host depends on at least three factors; 1) the symbiont's effect on the host's life history, 2) the ecological parameters, and 3) the mode of transmission. The connection between obligate symbionts' effects on hosts' life history and their transmission mode is well explored in both theoretical and empirical studies (Bibian et al., 2016; Brown and Akçay, 2019; Chung et al., 2015; Clayton et al., 2015; Ebert, 2013; Ewald, 1987; Gandon et al., 2008; Rudgers et al., 2012). In the standard models, these effects are on host survival and fecundity (Ferdy and Godelle, 2005). Further, the trade-offs between host survival and fecundity have been shown theoretically to determine the persistence of symbioses (Bibian et al., 2016; Chung et al., 2015; Rudgers et al., 2012; Yule et al., 2013). Note that the symbionts' effects on the hosts' life history can be more complex, particularly in hosts having a long and complex life cycle with different developmental stages. During the coevolutionary process, the symbiont and host strategies can modify the infected hosts' life history parameters. To get an insight, we strictly focused on how the two partners' strategies modify the infected population's life history traits. For this purpose, we applied simplifying assumptions. Hence, our conceptual model was strictly based on uniformity conditions (i.e., clearing, transmission mode, and competitive ability are independent of host and symbiont strategies). These assumptions ensure the following advantages:

1. They radically decrease the dimension of the system (Hancock et al., 2011; Chung et al., 2015; Yule et al., 2013). For instance, if the host has three developmental stages (say, with different horizontal transmission rates), we get a six-dimensional resident system. Further, if obligate mutant symbionts and mutant hosts are introduced, we have nine and twelve-dimensional coevolutionary dynamics, respectively.
2. This gives an insight into cases when the host has several developmental stages, and the symbiont can manipulate the survival and fecundity of the different stages in different ways. This is one of the main novelties of our proposed conceptual model.
3. They separate the density-dependent phenomena (like competition and horizontal transmission) from the host-symbiont interaction within the host body.

Our model also provides a close insight into the complexity of the concept of virulence. Classical textbook wisdom says that virulence is the infection-induced reduction of host survival or reproductive success, or both (Anderson and May 1978). The idea that symbionts may affect host lifespan and fecundity differently is not new (Brown and Akçay, 2019). However, our model theoretically shows that symbionts' effect on host longevity and reproduction may be different, even opposing, and their net effects may often be counterintuitive. To exemplify the potential complexity of host-symbiont interactions, we list eight categories based on the infections' effects on host longevity and reproductive success below, with biological examples:

1. **Survival-reducers:** The Japanese subgroup of Human T-cell lymphotropic virus type 1 (HTLV-I) can serve as an example of this category. It is often transmitted from mother to child through breastfeeding and is frequently associated with a highly lethal disease, the adult T-cell leukemia. However, since the onset of the disease is about sixty years (Murphy et al., 1989), we can reasonably

assume that it reduces only host longevity without affecting its reproductive success.

2. **Fecundity-reducers:** Cytoplasmic incompatibility induced by *Wolbachia* infections in insects (Sinkins, 2004) nicely exemplify this category. Note that reduced host fecundity may either result from pathogenic effects or as a damage limitation strategy of the host (Hurd, 2001).
3. **Survival-and-fecundity-reducers:** Several well-known parasites and pathogens reduce host longevity and reproductive success in parallel. For example, *Plasmodium falciparum* is a unicellular protozoan causing malaria in humans. Being one of the deadliest pathogens of our species, it dramatically reduces the survival and reproduction chances of infected people (WHO, 2022).
4. **Survival-increasers:** Infection of *Temnothorax nylanderi* ant workers with Cestode (*Anomotaenia brevis*) larvae increases the host lifespan multiple-fold. The direct reproductive success of worker ants is zero, regardless of whether they are infected (Hartke et al., 2022).
5. **Fecundity-increasers:** *Wolbachia* infections increase male fertility in the beetle *Tribolium confusum* (Wade and Chang, 1995). Another intracellular parasitic bacterium, the so-called Cytophaga-Like Organism (CLO), increases female fertility without influencing the mortality of the infected host, the predatory mite *Metaseiulus occidentalis* (Weeks and Stouthamer, 2004).
6. **Survival-and-fecundity-increasers:** Several well-known mutualists belong to this category. For example, consider the so-called zooxanthellae, which are photosynthetic dinoflagellates (Eukaryota: Myzozoa) living in corals' bodies (Animalia: Cnidaria: Anthozoa). They increase the host's survival and reproduction by providing nutrients (sugar, glycerol, and amino acids) to their host (Muscatine and Porter, 1977).
7. **Survival-increaser-and-fecundity-reducer:** The larva of several helminths (like Cestodes, Trematodes, and Acanthocephalans) destruct host gonads (a phenomenon called 'parasitic castration') apparently to increase host body size ('parasitic gigantism') and also survival (Berec and Maxin, 2012). Fungal endophytes decrease fecundity and increase survival for the grass *Poa alsodes* (Chung et al., 2015). Larva of the rat tapeworm *Hymenolepis diminuta* also increases the survival of the intermediate host (the mealworm beetle *Tenebrio molitor*) at the expense of reducing its fecundity (Hurd et al., 2001).
8. **Survival-reducer-and-fecundity-increaser:** Fungal endophytes increase fecundity in the grass *Agrostis hyemalis* at the expense of reducing survival (Yule et al., 2013). *Toxoplasma gondii*, a widespread human infection, may cause flu-like illness and various neuropsychiatric symptoms. On the other hand, these infections make patients sexually more attractive. Since they have more sexual partners, their reproductive success may increase (Borráz-León et al., 2022).

In our study, we fixed the infection rate (β) and the clearance rate (c_r). This has two significant consequences. First, the transmission is a mixture of horizontal and vertical transmission routes. Therefore, the infected and non-infected lineages cannot be separated from each other. Second, these conditions enabled us to focus on the evolution of the Malthusian growth rate. As we have already emphasized, symbionts can exert a multifaceted effect on the host's life history parameters. This means that the symbionts can grossly alter the hosts' death and reproduction, in line with biological examples. In principle, the Leslie matrix defining the growth of the infected lineage can almost freely differ from the Leslie matrix of the non-infected lineage. Therefore, the hosts face two significantly different optimization problems to optimize the growth rates of the two lineages simultaneously. We found that in the case of mixed transmission, the host-symbiont system is evolutionarily stable unconditionally only if the host can maximize the Malthusian parameters of these two lineages using the same strategy. We believe this is because mixed transmission links the two lineages, so they cannot evolve independently. Of course, this statement is valid only in the context of our simplified model conditions. Real-life host species may often evolve facultative strategies that manifest when infected with a particular parasite. However, exploring the consequences of such facultative strategy sets exceeds the scope of this paper and requires another study.

We believe that complexities in the life history of an organism contribute to its fitness in a controlled way and hence can be the starting point for theoretical analysis of evolutionary changes. We used a theoretical approach to understanding ecosystems, starting from the simplest models and building on this instead of describing the more complicated systems. We aimed to develop a model that enables us to handle the complexity of host-symbiont interactions. For this purpose, we proposed a generalized model where we considered infected and non-infected lineages that competed. Additionally, we assumed uniform interaction patterns between the two interacting species, and relaxing the uniformity conditions could be an interesting extension of this work. One of the novelties of this general model is that horizontal infection and clearing of infection connect the infected and non-infected lineages with adequate tractability even after the introduction of mutant populations. The strategy-independent (constant) transmission is just an initial step, and the transmission depending on the host or symbiont traits, could be an immediate extension of this work. This opens future avenues to build more complex models with other features like evolving horizontal transmission, clearing, or competitive abilities. In this sense, we incorporate different aspects of ecology to study resistance to mutant invasion and evolutionary stability.

CRediT authorship contribution statement

Nandakishor Krishnan: Methodology, Formal analysis, Visualization, Writing – original draft, Writing – review & editing. **Lajos Rózsa:** Conceptualization, Writing – original draft. **András Szilágyi:** Methodology. **József Garay:** Conceptualization, Methodology, Writing – original draft, Supervision.

Declaration of Competing Interest

The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

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Appendices.

A Stability of the resident system

We conduct the stability analysis of the equilibrium points corresponding to the set of differential equations (15)–(16) in the main text. The equilibrium population size of the infected population is

$$y^* = \frac{\ln\lambda_I - (\gamma-\beta)x^* - c_r}{\gamma}.$$

The equilibrium population size x^* of the non-infected population is the solution of the following equation:

$$\beta^2 x^2 + (\gamma(\ln\lambda_I - \ln\lambda_{NI}) + \beta(\ln\lambda_I - 2c_r))x + c_r(c_r - \ln\lambda_I) = 0.$$

The roots are positive real if $\ln\lambda_I > c_r$. This relation also guarantees that there is one positive x^*. Also, y^* is positive if $\beta > \gamma$. Hence, the sufficient conditions for the existence of unique positive rest points of (15)–(16) are $\ln\lambda_I > c_r$ and $\beta > \gamma$.

Theorem 1. *The rest point $(x^*, y^*) \in \mathbb{R}^2_+$ of the resident system (15)–(16) is locally asymptotically stable for $\ln\lambda_I > c_r$, $\gamma < \beta < 3\gamma$, and small γ.*

Proof: Consider the fixed point of the dynamics (15)–(16) in the positive quadrant, i.e., $(x^*, y^*) \in \mathbb{R}^2_+$. The Jacobian matrix at this fixed point is

$$J^*_{(x^*,y^*)} = \begin{pmatrix} \ln\lambda_{NI} - 2\gamma x^* - (\beta+\gamma)y^* & c_r - (\beta+\gamma)x^* \\ (\beta-\gamma)y^* & \ln\lambda_I - (\gamma-\beta)x^* - 2\gamma y^* - c_r \end{pmatrix}.$$

The local stability of the rest point (x^*, y^*) is implied by the following two inequalities: $\mathrm{tr}J^*_{(x^*,y^*)} < 0$ and $\det J^*_{(x^*,y^*)} > 0$. The trace is negative if $\ln\lambda_{NI} + \ln\lambda_I - c_r - (3\gamma-\beta)x^* - (3\gamma+\beta)y^* < 0$. If the competition between the two populations is low, i.e., γ is small, and $\beta < 3\gamma$, the negativity is possible. Note that small γ would imply a large equilibrium density y^* (in Eq. (17)), and relatively large x^*, as x^* is a monotonically decreasing function of γ (solving Eq. (18)). Small γ, thereby, also help to satisfy the positivity condition of the determinant by making J^*_{11}, J^*_{12}, and J^*_{22} negative, while J^*_{21} is positive because of $\beta > \gamma$. This implies a $\begin{pmatrix} - & - \\ + & - \end{pmatrix}$ sign pattern resulting in a positive determinant. Hence, small γ makes the local asymptotic stability of (x^*, y^*) probable, but for a given set of parameters (for example, see Fig. 4). However, since the dominant eigenvalues also affect the equilibrium population sizes in a very complex way, only the calculation of the eigenvalues of the Jacobian matrix answers the question of stability with better precision. To sum up, the following conditions make the existence and local stability of the positive equilibrium (x^*, y^*) possible:

$\ln\lambda_I > c_r$, $\gamma < \beta < 3\gamma$, and small γ

In other words, (x^*, y^*) is a stable (locally asymptotically) node for the above conditions.

Global stability of the resident system

Theorem 2. *The locally asymptotically stable rest point $(x^*, y^*) \in \mathbb{R}^2_+$ of the resident system (15)–(16) is also globally asymptotically stable.*

Proof: Let (x^*, y^*) be the unique interior equilibrium of the dynamical system (15)–(16). The conditions for the existence of the locally asymptotically stable unique interior equilibrium (as mentioned before) of the resident system are:

1) $\ln\lambda_I > c_r$,
2) $\gamma < \beta < 3\gamma$, and
3) Small γ.

We now use the Lyapunov direct method to conduct global stability analysis. Consider the following Lyapunov function:

$$V(x,y) = \left(x - x^* \ln\frac{x}{x^*} - x^*\right) + \left(y - y^* \ln\frac{y}{y^*} - y^*\right).$$

The candidate Lyapunov function is radially unbounded as the function is increasing for $x > x^*$, $y > y^*$.

Also, $V(x^*, y^*) = 0$ and $V(x,y) > 0$ for $(x,y) \neq (x^*, y^*)$. Time derivative of the Lyapunov function is

$$\dot{V}(x,y) = \frac{x - x^*}{x}\dot{x} + \frac{y - y^*}{y}\dot{y}.$$

For asymptotic stability, we need to prove that $\dot{V}(x,y) < 0$ for $(x,y) \neq (x^*, y^*)$. Let $\dot{V}(x,y) = f(x,y)$, hence $f(x^*, y^*) = 0$.

$$f(x,y) = \frac{x - x^*}{x}\dot{x} + \frac{y - y^*}{y}\dot{y}$$

$$f(x,y) = (x - x^*)\left(\ln(\lambda_{NI}) - \gamma y - \gamma x - \beta y + \frac{c_r y}{x}\right) + (y - y^*)(\ln(\lambda_I) - c_r - \gamma y - \gamma x + \beta x)$$

Differentiating $f(x,y)$ w.r.t x and y:

$$f_x(x,y) = \ln(\lambda_{NI}) - 2\gamma y - 2\gamma x + \gamma x^* + \gamma y^* - \beta y^* + \frac{c_r x^* y}{x^2}$$

$$f_y(x,y) = \ln(\lambda_I) - 2\gamma y - 2\gamma x + \gamma x^* + \beta x^* + \gamma y^* - \frac{c_r x^*}{x}$$

$f_x(x^*,y^*) = \ln(\lambda_{NI}) - \gamma x^* - \gamma y^* - \beta y^* + \frac{c_r y^*}{x^*} = 0$ (From Eq. (15))

$f_y(x^*,y^*) = \ln(\lambda_I) - \gamma x^* + \beta x^* - \gamma y^* - c_r = 0$ (From Eq. (16))

(x^*,y^*) is the unique interior equilibrium point of the dynamics (15)–(16) and is also the unique critical point of $f(x,y)$ for $x>0$ and $y>0$. The Hessian matrix corresponding to $f(x,y)$ at (x^*,y^*) is

$$H_f(x^*,y^*) = \begin{pmatrix} f_{xx}(x^*,y^*) & f_{xy}(x^*,y^*) \\ f_{yx}(x^*,y^*) & f_{yy}(x^*,y^*) \end{pmatrix} = \begin{pmatrix} -2\gamma - \frac{2y^* c_r}{(x^*)^2} & -2\gamma + \frac{c_r}{x^*} \\ -2\gamma + \frac{c_r}{x^*} & -2\gamma \end{pmatrix}.$$

We see that $H_f(x^*,y^*)$ is negative definite (all eigenvalues are negative) if $c_r < 4\gamma(x^*+y^*)$. Since x^*&y^* are large (due to small γ), this is possible. Therefore, the unique critical point (x^*,y^*) is a maximum point of $f(x,y)$ (see Fig. A1).

Thus, for any $(x,y) \neq (x^*,y^*)$, $f(x,y) < f(x^*,y^*)$. Since $f(x^*,y^*) = 0$, we can conclude,

$$f(x,y)<0 \Rightarrow \dot{V}(x,y)<0.$$

Therefore, by Lyapunov stability criterion, (x^*,y^*) is globally asymptotically stable.

B Stability analysis of host-symbiont coevolutionary dynamics with mutant symbiont

Consider the coevolutionary dynamics of the system (19)–(21) with the mutant phenotype of the symbiont, where z denotes the infected population with mutant symbiont (strategy $\sigma \neq \sigma^*$) with long-term growth rate $\lambda_I^M := \lambda_I(s^*,\sigma)$, and x and y are as in the resident system.

Theorem 3. *If for a given rare infected mutant population with mutant symbiont, we have $\lambda_I^M(s^*,\sigma) < \lambda_I(s^*,\sigma^*)$, then this mutant phenotype cannot invade the resident system.*

Proof: For the condition when mutants die out in this case, i.e., $(x^*,y^*,0)$ is locally asymptotically stable, we investigate the Jacobian matrix of the dynamics (19)–(21) at $(x^*,y^*,0)$, which reads as,

$$J_{(x^*,y^*,0)} = \begin{pmatrix} \ln\lambda_{NI} - 2\gamma x^* - (\beta+\gamma)y^* & c_r - (\beta+\gamma)x^* & c_r - (\beta+\gamma)x^* \\ (\beta-\gamma)y^* & \ln\lambda_I - (\gamma-\beta)x^* - 2\gamma y^* - c_r & -\gamma y^* \\ 0 & 0 & \ln(\lambda_I^M) - \gamma y^* - (\gamma-\beta)x^* - c_r \end{pmatrix}.$$

Recall from the stability analysis of the resident system (15)–(16), we have $\ln\lambda_I > c_r$ and $3\gamma > \beta > \gamma$, for the existence of (x^*,y^*). According to the Routh Hurwitz criterion (the necessary and sufficient conditions for the linear stability of the system), the conditions for the local asymptotic stability of the equilibrium point are:

1) $\mathrm{tr}\, J_{(x^*,y^*,0)} < 0$,
2) $\det J_{(x^*,y^*,0)} < 0$,
3) $W = \det\begin{pmatrix} J_{11} & J_{12} \\ J_{21} & J_{22} \end{pmatrix} + \det\begin{pmatrix} J_{11} & J_{13} \\ 0 & J_{33} \end{pmatrix} + \det\begin{pmatrix} J_{22} & J_{23} \\ 0 & J_{33} \end{pmatrix} > 0$, and
4) $\mathrm{tr}\, J_{(x^*,y^*,0)} * W < \det J_{(x^*,y^*,0)}$.

The trace is negative if $\ln\lambda_{NI} + \ln\lambda_I + \ln\lambda_I^M - 2c_r - (4\gamma - 2\beta)x^* - (4\gamma+\beta)y^* < 0$. Small γ (large equilibrium densities x^*&y^*) and $\beta < 2\gamma$ make the negativity possible. The conditions $\ln\lambda_I > c_r$, $\gamma < \beta < 3\gamma$, small γ make the $\det\begin{pmatrix} J_{11} & J_{12} \\ J_{21} & J_{22} \end{pmatrix}$ positive as stated in the stability analysis of the resident system. Therefore, $\det J_{(x^*,y^*,0)} < 0$ if $J_{33} < 0$, i.e.,

$$\ln(\lambda_I^M(s^*,\sigma)) - \gamma y^* - (\gamma-\beta)x^* - c_r < 0.$$

Also, $W = \det\begin{pmatrix} J_{11} & J_{12} \\ J_{21} & J_{22} \end{pmatrix} + \det\begin{pmatrix} J_{11} & J_{13} \\ 0 & J_{33} \end{pmatrix} + \det\begin{pmatrix} J_{22} & J_{23} \\ 0 & J_{33} \end{pmatrix} > 0$ if $J_{33} < 0$.

$\mathrm{tr}\, J_{(x^*,y^*,0)} < 0$, $\det J_{(x^*,y^*,0)} < 0$, $W > 0$ and $\mathrm{tr}\, J_{(x^*,y^*,0)} * W < \det J_{(x^*,y^*,0)}$ for $\gamma < \beta < 2\gamma$, large x^*, large y^* and $\ln\lambda_I^M - \gamma y^* - (\gamma-\beta)x^* - c_r < 0$. Sufficient conditions for a given mutant symbiont to die out are small γ, $\gamma < \beta < 2\gamma$, $\ln\lambda_I^M(s^*,\sigma) - \gamma y^* - (\gamma-\beta)x^* - c_r < 0$ (or equivalently $\lambda_I^M(s^*,\sigma) < \lambda_I(s^*,\sigma^*)$, see below).

Reinterpreting the stability condition,

$$\ln\lambda_I^M(s^*,\sigma) - \gamma y^*(s^*,\sigma^*) - (\gamma-\beta)x^*(s^*,\sigma^*) - c_r < 0,$$

where $\lambda_I^M(s^*,\sigma)$ is the dominant eigenvalue of the Leslie matrix corresponding to the infected lineage at (s^*,σ). Moreover $(x^*(s^*,\sigma^*), y^*(s^*,\sigma^*))$ is the rest point of the resident two-dimensional ecological dynamics (15)–(16). From the rest point of the resident ecosystem (15)–(16), we have,

$$y^* = \frac{\ln\lambda_I(s^*,\sigma^*) - (\gamma-\beta)x^*(s^*,\sigma^*) - c_r}{\gamma}.$$

Thus, for the evolutionary stability, we need,

$$\ln\lambda_I^M(s^*,\sigma) - \gamma\frac{\ln\lambda_I(s^*,\sigma^*) - (\gamma-\beta)x^*(s^*,\sigma^*) - c_r}{\gamma} - (\gamma-\beta)x^*(s^*,\sigma^*) - c_r < 0.$$

After some elementary simplification we get,

$\ln\lambda_{\mathrm{I}}^{\mathrm{M}}(s^*,\sigma) - \ln\lambda_{\mathrm{I}}(s^*,\sigma^*) < 0.$

Since the function ln is strictly monotone, the resident system with strategy pair (s^*,σ^*) is evolutionary stable (resistant against invasion of mutant symbiont strategy σ) if

$\lambda_{\mathrm{I}}^{\mathrm{M}}(s^*,\sigma) < \lambda_{\mathrm{I}}(s^*,\sigma^*).$

C Stability analysis of host-symbiont coevolutionary dynamics with mutant host

Consider the coevolutionary dynamics (22)–(25) with mutant hosts.

Theorem 4. *If for a given rare infected mutant population with mutant host, $\lambda_{NI}^{M}(s) < \lambda_{NI}(s^*)exp\left(c_r\frac{y^*}{x^*}\right)$ and $\widehat{\lambda_I^M}(s,\sigma^*) < \lambda_I(s^*,\sigma^*)exp(\beta x^*)$, then this mutant cannot invade the stable resident system. In mathematical terms, $(x^*,0,y^*,0)$ is a l.a.s. fixed point of the coevolutionary dynamics (22)–(25) under the conditions.*

Proof: We investigate the Jacobian matrix of dynamics (22)–(25) at $(x^*,0,y^*,0)$, which reads as,

$$\widehat{J}_{(x^*,0,y^*,0)} = \begin{pmatrix} \ln\lambda_{\mathrm{NI}} - 2\gamma x^* - (\beta+\gamma)y^* & -\gamma x^* & c_r - (\beta+\gamma)x^* & -(\beta+\gamma)x^* \\ 0 & \ln\lambda_{\mathrm{NI}}^{\mathrm{M}} - (\beta+\gamma)y^* - \gamma x^* & 0 & c_r \\ (\beta-\gamma)y^* & -\gamma y^* & \ln\lambda_{\mathrm{I}} - (\gamma-\beta)x^* - 2\gamma y^* - c_r & -\gamma y^* + \beta x^* \\ 0 & \beta y^* & 0 & \ln\widehat{\lambda_{\mathrm{I}}^{\mathrm{M}}} - \gamma y^* - \gamma x^* - c_r \end{pmatrix}.$$

The eigenvalues of $\widehat{J}_{(x^*,0,y^*,0)}$ are:

$$\frac{1}{2}\left(\widehat{J}_{11}+\widehat{J}_{33} - \sqrt{\widehat{J}_{11}^2 + 4\widehat{J}_{13}\widehat{J}_{31} - 2\widehat{J}_{11}\widehat{J}_{33} + \widehat{J}_{33}^2}\right),$$

$$\frac{1}{2}\left(\widehat{J}_{11}+\widehat{J}_{33} + \sqrt{\widehat{J}_{11}^2 + 4\widehat{J}_{13}\widehat{J}_{31} - 2\widehat{J}_{11}\widehat{J}_{33} + \widehat{J}_{33}^2}\right),$$

$$\frac{1}{2}\left(\widehat{J}_{22}+\widehat{J}_{44} - \sqrt{\widehat{J}_{22}^2 + 4\widehat{J}_{24}\widehat{J}_{42} - 2\widehat{J}_{22}\widehat{J}_{44} + \widehat{J}_{44}^2}\right),$$

$$\frac{1}{2}\left(\widehat{J}_{22}+\widehat{J}_{44} + \sqrt{\widehat{J}_{22}^2 + 4\widehat{J}_{24}\widehat{J}_{42} - 2\widehat{J}_{22}\widehat{J}_{44} + \widehat{J}_{44}^2}\right)$$

All the eigenvalues are negative if $\widehat{J}_{11},\widehat{J}_{22}$, $\widehat{J}_{33}$, and $\widehat{J}_{44}$ are negative and the following inequalities $\widehat{J}_{13}\widehat{J}_{31} < \widehat{J}_{11}\widehat{J}_{33}$, and $\widehat{J}_{24}\widehat{J}_{42} < \widehat{J}_{22}\widehat{J}_{44}$ hold. From proof of Theorem 1, we can observe that $\ln\lambda_{\mathrm{NI}} - 2\gamma x^* - (\beta+\gamma)y^* < 0$ and $\ln\lambda_{\mathrm{I}} - (\gamma-\beta)x^* - 2\gamma y^* - c_r < 0$ are required for the stability of the resident system (15)–(16). Since the mutant is introduced to the stable resident system, it follows that $\widehat{J}_{11},\widehat{J}_{33} < 0$ and $\widehat{J}_{13}\widehat{J}_{31} < \widehat{J}_{11}\widehat{J}_{33}$ (see elements of $J^*_{(x^*,y^*)}$ in proof of Theorem 1 and compare it with elements of $\widehat{J}_{(x^*,0,y^*,0)}$). Also, for sufficiently small $\gamma(\text{large}\,x^*,y^*)$, as in the resident system, $\widehat{J}_{24}\widehat{J}_{42} < \widehat{J}_{22}\widehat{J}_{44}$. Finally, the required conditions for all the eigenvalues to be negative are $\widehat{J}_{22} < 0$ and $\widehat{J}_{44} < 0$.

$$\widehat{J}_{22} < 0 \Rightarrow \ln\lambda_{\mathrm{NI}}^{\mathrm{M}} < (\beta+\gamma)y^* + \gamma x^* = \ln\lambda_{\mathrm{NI}} + c_r\frac{y^*}{x^*}$$

$$\Rightarrow \frac{\lambda_{\mathrm{NI}}^{\mathrm{M}}}{\lambda_{\mathrm{NI}}} < \exp\left(c_r\frac{y^*}{x^*}\right)$$

$$\widehat{J}_{44} < 0 \Rightarrow \ln\widehat{\lambda_{\mathrm{I}}^{\mathrm{M}}} < \gamma y^* + \gamma x^* + c_r = \ln\lambda_{\mathrm{I}} + \beta x^*$$

$$\Rightarrow \frac{\widehat{\lambda_{\mathrm{I}}^{\mathrm{M}}}}{\lambda_{\mathrm{I}}} < \exp(\beta x^*)$$

The rest point $(x^*,0,y^*,0)$ is locally asymptotically stable if $\lambda_{\mathrm{NI}}^{\mathrm{M}}(s) < \lambda_{\mathrm{NI}}(s^*)\exp\left(c_r\frac{y^*}{x^*}\right)$ and $\widehat{\lambda_{\mathrm{I}}^{\mathrm{M}}}(s,\sigma^*) < \lambda_{\mathrm{I}}(s^*,\sigma^*)\exp(\beta x^*)$.

D Stability analysis of host-symbiont coevolutionary dynamics with mutant host and mutant symbiont

Consider the six-dimensional coevolutionary dynamics (26)–(31) for the case when mutant phenotypes are introduced in both hosts and symbionts.

Theorem 5. *The rest point $(x^*,0,y^*,0,0,0)$ of the system (26)–(31) with both mutant hosts and mutant symbionts is stable if $\widetilde{\lambda_I^M}(s,\sigma) < \lambda_I(s^*,\sigma^*)exp(\beta x^*)$, $\lambda_{NI}^{M}(s) < \lambda_{NI}(s^*)exp\left(c_r\frac{y^*}{x^*}\right)$, $\widehat{\lambda_I^M}(s,\sigma^*) < \lambda_I(s^*,\sigma^*)exp(\beta x^*)$, and $\lambda_I^M(s^*,\sigma) < \lambda_I(s^*,\sigma^*)$.*

Proof: We investigate the Jacobian matrix of system (26)–(31) at $(x^*,0,y^*,0,0,0)$,

$$\begin{pmatrix} \ln\lambda_{\mathrm{NI}} - 2\gamma x^* - (\beta+\gamma)y^* & -\gamma x^* & c_r - (\beta+\gamma)x^* & c_r - (\beta+\gamma)x^* & -(\beta+\gamma)x^* & -(\beta+\gamma)x^* \\ 0 & \ln\left(\lambda_{\mathrm{NI}}^{\mathrm{M}}\right) - (\beta+\gamma)y^* - \gamma x^* & 0 & 0 & c_r & c_r \\ (\beta-\gamma)y^* & -\gamma y^* & \ln\lambda_{\mathrm{I}} - (\gamma-\beta)x^* - 2\gamma y^* - c_r & -\gamma y^* & -\gamma y^* + \beta x^* & -\gamma y^* \\ 0 & 0 & 0 & \ln\left(\lambda_{\mathrm{I}}^{\mathrm{M}}\right) - (\gamma-\beta)x^* - \gamma y^* - c_r & 0 & \beta x^* \\ 0 & \beta y^* & 0 & 0 & \ln\left(\widehat{\lambda_{\mathrm{I}}^{\mathrm{M}}}\right) - \gamma y^* - \gamma x^* - c_r & 0 \\ 0 & 0 & 0 & 0 & 0 & \ln\left(\widetilde{\lambda_{\mathrm{I}}^{\mathrm{M}}}\right) - \gamma y^* - \gamma x^* - c_r \end{pmatrix}.$$

The corresponding characteristic polynomial is (if μ is an eigenvalue of the above Jacobian matrix)

$$\left(\ln\widetilde{\lambda_{\mathrm{I}}^{\mathrm{M}}} - \gamma(y^* + x^*) - c_r - \mu\right) * \left(\ln\lambda_{\mathrm{I}}^{\mathrm{M}} - \gamma(y^* + x^*) + \beta x^* - c_r - \mu\right) * \det\left(\widehat{J}_{(x^*,0,y^*,0)} - \mu I\right) = 0.$$

The eigenvalues are negative and hence the system with both mutant hosts and mutant symbionts is stable at $(x^*, 0, y^*, 0, 0, 0)$ under the following conditions:

$\widetilde{\lambda_{\mathrm{I}}^{\mathrm{M}}}(s,\sigma) < \lambda_{\mathrm{I}}(s^*,\sigma^*)\exp(\beta x^*)$, $\lambda_{\mathrm{I}}^{\mathrm{M}}(s^*,\sigma) < \lambda_{\mathrm{I}}(s^*,\sigma^*)$, $\lambda_{\mathrm{NI}}^{\mathrm{M}}(s) < \lambda_{\mathrm{NI}}(s^*)\exp\left(c_r\frac{y^*}{x^*}\right)$, and $\widehat{\lambda_{\mathrm{I}}^{\mathrm{M}}}(s,\sigma^*) < \lambda_{\mathrm{I}}(s^*,\sigma^*)\exp(\beta x^*)$.

E Additional Leslie matrix

Recall that the dominant eigenvalue of the following Leslie matrix corresponding to the non-infected population is maximized at $\bar{s} = 0.563$.

$$\boldsymbol{L}_{\mathrm{NI}}(s) := \begin{pmatrix} 0 & 100 - 75s & 100 - 75s \\ 0.2 + 0.75s & 0 & 0 \\ 0 & 0.3 + 0.65s & 0 \end{pmatrix}$$

The following is an example Leslie matrix corresponding to the infected population where s^* (which maximizes the long-term growth of the infected population) is equal to $\bar{s}$:

$$\boldsymbol{L}_{\mathrm{I}}(s,\sigma) := \begin{pmatrix} 0 & 5\sigma(100 - 75s) & 5\sigma(100 - 75s) \\ \frac{10}{1+\sigma}(0.2 + 0.75s) & 0 & 0 \\ 0 & \frac{10}{1+\sigma}(0.3 + 0.65s) & 0 \end{pmatrix}.$$

The dominant eigenvalue of the above Leslie matrix $\boldsymbol{L}_{\mathrm{I}}(s,\sigma)$ is maximized at $s^* = \bar{s} = 0.563$ and $\sigma^* = 1.0$. In this case, the evolutionary stability of the ecologically stable resident rest point in the coevolutionary dynamics of the mutant systems happens unconditionally. For counterexamples of $s^* \neq \bar{s}$, see Example 1 (Eq. 6) and Example 3 (Eq. 14).

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