MODELLING THE EVOLUTIONARY DYNAMICS OF HOST RESISTANCE-RELATED TRAITS IN A SUSCEPTIBLE-INFECTED COMMUNITY WITH DENSITY-DEPENDENT MORTALITY

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ABSTRACT. This study explores the evolutionary dynamics of host resistance based on a susceptible-infected population model with density-dependent mortality. We assume that the resistant ability of susceptible host will adaptively evolve, a different type of host differs in its susceptibility to infection, but the resistance to a pathogen involves a cost such that a less susceptible host results in a lower birth rate. By using the methods of adaptive dynamics and critical function analysis, we find that the evolutionary outcome relies mainly on the trade-off relationship between host resistance and its fertility. Firstly, we show that if the trade-off curve is globally concave, then a continuously stable strategy is predicted. In contrast, if the trade-off curve is weakly convex in the vicinity of singular strategy, then evolutionary branching of host resistance is possible. Secondly, after evolutionary branching in the host resistance has occurred, we examine the coevolutionary dynamics of dimorphic susceptible hosts and find that for a type of concave-convex-concave trade-off curve, the finally evolutionary outcome may contain a relatively higher susceptible host and a relatively higher resistant host, which can continuously stably coexist on a long-term evolutionary timescale. If the convex region of trade-off curve is relatively wider, then the finally evolutionary outcome may contain a fully resistant host and a moderately resistant host. Thirdly, through numerical simulation, we find that for a type of sigmoidal trade-off curve, after branching due to the high cost in terms of the birth rate, always the branch with stronger resistance goes extinct, the eventually evolutionary outcome includes a monomorphic host with relatively weaker resistance.

1. Introduction. The host-pathogen interactions are ubiquitous in nature and hosts have evolved a diverse range of defence mechanisms in response to pathogens or parasites [2, 71, 11, 3, 45, 18, 12, 61, 63, 9, 55, 6, 10, 47, 4, 7, 70, 31, 73]. However,
the underlying demographic and evolutionary factors are not well understood. An understanding of the evolutionary dynamics of host resistance is clearly necessary both to illustrate the host-pathogen interaction mechanisms and to manage effectively disease in a variety of application environments. Therefore, it is significant to investigate the evolutionary mechanism of host resistance in the light of ecological feedbacks [2, 3, 18, 12, 9, 74, 68, 10, 6, 47, 4].

In nature, in order to avoid to be infected by a pathogen, the resistant ability of hosts may adaptively evolve, but this is usually costly to acquire. In general, the higher resistant host may pay a cost in its other life-history traits, such as fertility. The existence of these costs is supported by both theoretical arguments and empirical evidences [2, 71, 11, 3, 45, 18, 12, 14, 25, 17, 66, 32, 13, 54, 9, 10, 6, 69, 46, 33, 4]. In order to understand the evolutionary mechanism of host resistance, in the past few decades, many different modeling approaches have been developed, such as locus-based method, quantitative genetic method and adaptive dynamics approach [12, 14, 13, 10, 9, 6, 47, 4, 41]. In particular, the method of adaptive dynamics allows us to examine the evolutionary factors that lead to different levels of host resistance. Based on the technique of adaptive dynamics [56, 27, 34], a number of different mathematical models have been proposed in order to understand how the host resistance evolves [2, 3, 19, 18, 17, 12, 14, 67, 64, 65, 13, 58, 59, 9, 60, 10, 6, 47, 4, 41]. Antonovics and Thrall [3] and Bowers et al. [19] investigated an SI two-strain model. They assumed that the resistant host strain is less likely to become infected, but is more susceptible to crowding or has a lower birth rate. With the technique of analytical analysis and reciprocal invasion plot, they found that the evolution of host resistance depends mainly on the trade-off structure, highly susceptible strains can coexist with highly resistant strains. Boots and Haraguchi [14] proposed a multi-strain model to study the evolution of host resistance, where only the susceptible host includes the density-dependent growth rate. They assumed that different host strains differ in susceptibility to infection, with less susceptible host strains paying a cost leading to a lower intrinsic growth rate. Using the approach of adaptive dynamics and pairwise invasibility plot, they showed that the evolutionary outcome depends crucially on the shape of constraint function. With decelerating costly resistance, they found that evolutionary branching in the host resistance may occur and may lead to a dimorphic host with maximally resistant and no resistance. After branching in the host resistance occurs, based on an SIS (susceptible-infected-susceptible) model, Best et al. [4] showed that for sufficiently complex trade-off functions, the resulting invasion boundaries may form closed ‘oval’ areas of strategy coexistence. If there are no attracting singular strategies within this area, then the population may evolve out side of the coexistence region, leading to extinction of one host strain [42, 35, 44, 24, 62, 23, 40, 5, 1, 41]. This phenomenon is also called as ‘evolutionary murder’ [42, 35, 62, 23, 5, 4, 41].

In addition, the interaction between host and pathogen is commonly a coevolutionary process. Both pathogen and host may adaptively evolve. Based on an SIS model, Restif and Koella [64] investigated the coevolutionary dynamics of host-pathogen interactions. They assumed that the transmission rate is determined by the traits of both host and pathogen and showed that the resistance reaches its maximum at an intermediate pathogen replication rate. Best et al. [6] also explored a coevolutionary model of a host-parasite system. They took the ecological feedbacks into consideration and found that evolutionary branching in the host resistance leads to parasites increasing their virulence, and small changes in the host resistance will
drive large changes in the parasite virulence. However, the evolutionary branching in one species does not induce branching in the other. Particularly, Boots et al. [15] showed that in a broad range of realistic infection scenarios, if there are costs to both infectivity in the parasite and resistance in the host, then epidemiological feedbacks may generate diversity, but this is often of extreme types. Dieckmann et al. [28] introduced a model of resistance evolution with density-dependent mortality of infecteds and susceptibles, and also compared this to the equivalent system without density-dependent mortality.

However, in the previous studies the invasion analysis is conducted in a simply way by looking at the growth rate of the invading strain, rather than rigorously proving the result of ‘invasion implies substitution’. But this analysis is necessary for studying the evolutionary dynamics of host resistance step by step. Moreover, in some of the previous studies, the trade-off function between host resistance and its intrinsic growth rate was assumed to be a specific form, and some of which were not a saturation function. But more realistically, the trade-off relationship may be a monotonically increasing function and eventually converges to a saturated state. In addition, previous studies did not robustly look at what happens after branching, they showed some results through numerical simulation, lack of theoretical analysis. After the branching has occurred in the host resistance, it is still unknown whether or not the coexistence of dimorphic hosts can be maintained over evolutionary timescale and how does the finally evolutionary outcome depend on the shape and strength of trade-off relationship between host resistance and its birth rate.

In this article, we assume that both susceptible hosts and infected hosts are subject to density-dependent mortality and a less susceptible host strain will pay a cost resulting in a lower birth rate. The trade-off relationship between host resistance and its fertility is assumed to be a monotonically increasing function and eventually converges to a saturated state. Based on an SI (susceptible-infected) model with density-dependent mortality, we will rigorously analyze the evolutionary invasion process of host resistance step by step. In particular, both strictly mathematical proofs and numerical simulations are presented for each step of evolutionary invasion analysis. Specifically, the purpose of this study is aim to examine the following three questions. Firstly, under what demographic and evolutionary conditions a host population will change from monomorphism to dimorphism from the perspective of resistance. Using the method of critical function analysis [36, 39, 8, 75], we will identify the general properties of trade-off function that can induce the evolutionary branching in the host resistance and explore how will the shape and strength of trade-off relationship influence the evolutionary outcome. Besides, we will perform the bifurcation analysis of evolutionary dynamics and discuss the impact of demographic parameters on the evolutionary behaviour of host resistance. Secondly, under what demographic and evolutionary conditions the dimorphic susceptible host can continuously stably coexist on a long-term evolutionary timescale. Thirdly, whether the coevolution of dimorphic susceptible hosts will lead to the extinction of one strain. How complex a trade-off function must be in order for previously evolved dimorphism to be subject to evolutionary loss. Our main methods are based on the theory of adaptive dynamics and critical function analysis [56, 27, 48, 34, 25, 53, 26, 16, 43, 36, 39, 8, 75, 47, 4, 41]. By using these approaches, we will clarify the interplay between ecological feedback and evolutionary feedback in the evolution of host resistance. Meanwhile, we will illustrate how the
shape and strength of trade-off function are important in determining the level of resistance that evolves [10].

The rest of the paper is organized as follows. In the next section, we will present the population dynamics, evolutionary dynamics and critical function analysis. Afterwards, we summarize the demographic and evolutionary conditions that allow for a continuously stable strategy and evolutionary branching in the host resistance and discuss the influence of demographic parameters on the evolutionary outcome. After branching, we further study the coevolutionary dynamics of dimorphic susceptible hosts. Except for the strictly theoretical proof, numerical simulation results are also presented respectively to illustrate the feasibility of our main results. A brief discussion is given at the end of this paper.

2. Model description. We use the method of adaptive dynamics to analyze the evolutionary invasion process of host resistance step by step. Firstly, we will develop a population dynamics for an evolving susceptible host. Then based on this population model, the invasion fitness of mutant hosts and evolutionary model of host resistance will be derived. Finally, we use the method of critical function analysis to identify the evolutionarily singular strategy and its stability [53, 36, 75, 76, 77].

2.1. Population dynamics. We consider a pathogen (a microparasite) that can cause lifelong infection of its host, and assume that the host population may develop resistance against this pathogen (i.e., the host population is able to defend against getting infected), but only at some cost [10]. Specifically, we assume that different host strains differ in how much they are resistant to the disease. A higher resistant host strain implies a lower rate of transmission the disease and thus a smaller value of transmission rate $\beta$ (full resistance is achieved when $\beta = 0$). Moreover, a higher resistant host strain is assumed to pay a cost in its other life-history trait, such as fertility, namely, a higher resistant host will result in a lower birth rate $b$ such that $\frac{db}{d\beta} > 0$, and eventually converges to a saturated state. In other words, there is a trade-off relationship between the transmission rate $\beta$ and the birth rate of susceptible hosts $b$.

In addition, it is assumed that both the susceptible host population and infected host population are subject to density-dependent mortality $m(N)$, which is given by a linear function of total population density $N = S + I$, i.e.,

$$m(N) = m_0 + m_1 N,$$

where $m_0$ is the natural death rate of hosts, and $m_1$ is a constant representing the strength of density-dependence. We also assume that infected individuals neither reproduce nor recover, which is a reasonable assumption for most invertebrate pathogens. In this way we focus on one possible route to disease resistance, that is, avoidance of infection by reduced susceptibility to the disease. Therefore, the population dynamics of a lifelong infection we have is given by

$$\begin{cases}
\frac{dS}{dt} = b(\beta)S - \beta SI - m(N)S, \\
\frac{dI}{dt} = \beta SI - \alpha I - m(N)I,
\end{cases}$$

where $\frac{db}{d\beta} > 0$, $N = S + I$, $m(N) = m_0 + m_1 N$. 

and $S$ and $I$ denotes respectively the population density of susceptible hosts and population density of infected hosts. $\alpha$ is the pathogen-induced mortality rate, also called the virulence. All of the parameters in model (1) are positive. The model is most applicable to invertebrate diseases and plant diseases [14].

Biologically, a convex trade-off curve $b(\beta)$ means that decreasing $\beta$ implies less and less decrease in $b(\beta)$, that is to say, the cost increases slower than the benefit. In this case, we say there is a decelerating cost. In contrast, a concave trade-off curve $b(\beta)$ means that decreasing $\beta$ implies more and more decrease in $b(\beta)$, in other words, the cost increases faster than the benefit. In this case, we say there is an accelerating cost [39, 10, 76, 77].

For model (1), the condition for initial spread of a pathogen arriving into this healthy population is then

\[ \beta b(\beta) > m_0 \beta + (\alpha + b(\beta))m_1, \]  

(2)

that is, the basic reproduction number

\[ R_0 = \frac{\beta(b(\beta) - m_0)}{m_1(\alpha + b(\beta))} > 1. \]

When condition (2) is satisfied, setting the right-hand side of model (1) to zero, we obtain an endemic equilibrium $(S^*(\beta), I^*(\beta))$, where

\[ \begin{cases} 
S^*(\beta) = (\beta(\alpha + m_0) + m_1(\alpha + b(\beta))) / \beta^2, \\
I^*(\beta) = (\beta(b(\beta) - m_0) - m_1(\alpha + b(\beta))) / \beta^2.
\end{cases} \]  

(3)

By using the method of Lyapunov function, we obtain the following result about the globally asymptotical stability of $(S^*(\beta), I^*(\beta))$.

**Proposition 1.** If condition (2) holds, then the endemic equilibrium $(S^*(\beta), I^*(\beta))$ of model (1) is globally asymptotically stable in $\mathbb{R}_+^2 = \{S > 0, I > 0\}$.

**Proof.** For simplicity, we use $(S^*, I^*)$ instead of $(S^*(\beta), I^*(\beta))$. Consider the following Lyapunov function

\[ V_1 = \left( S - S^* - S^* \ln \frac{S}{S^*} \right) + \left( I - I^* - I^* \ln \frac{I}{I^*} \right). \]  

(4)

It is clear that $V_1 \geq 0$ and the equality holds only for $(S, I) = (S^*, I^*)$ in $\mathbb{R}_+^2 = \{S > 0, I > 0\}$. Its time derivative along solutions of model (1) becomes

\[ \frac{dV_1}{dt} \bigg|_{(1)} = (S - S^*) \frac{1}{S} \frac{dS}{dt} + (I - I^*) \frac{1}{I} \frac{dI}{dt} = -m_1((S - S^*) + (I - I^*))^2. \]  

(5)

It can be seen that $dV_1/dt \leq 0$ in $\mathbb{R}_+^2$ and $dV_1/dt = 0$ if and only if $(S, I) = (S^*, I^*)$. The globally asymptotical stability of $(S^*(\beta), I^*(\beta))$ follows from Lyapunov-LaSalle’s invariance principle.

Next, based on model (1) and endemic equilibrium $(S^*(\beta), I^*(\beta))$, we derive the evolutionary dynamics of host resistance.

**2.2. Invasion fitness of mutant host and trait substitution.** We assume that only the host resistance (a type of phenotypic trait of susceptible hosts) can adaptively evolve, but the mutation in the host resistance is very small and the mutant host is rare. Before a mutant susceptible host appears, the resident host has
reach to an endemic equilibrium \((S^*(\beta), I^*(\beta))\). Therefore, the mutant host encounters resident population that is at the infected equilibrium state \((S^*(\beta), I^*(\beta))\) [27, 48, 34, 29].

When a mutant host with a slightly different resistance \(\beta_m\) enters into the resident population at a low density, the invasion fitness for mutant hosts [56] is given by

\[
f(\beta_m, \beta) = b(\beta_m) - \beta_m I^*(\beta) - m_0 - m_1(S^*(\beta) + I^*(\beta)). \tag{6}
\]

If \(f(\beta_m, \beta) > 0\), the population density of mutant hosts will increase, in other words, the mutant host can invade. Furthermore, we find that a successful invasion of mutant host will cause a trait substitution [23, 37, 38, 57, 20]. In the following, by using the method of Lyapunov function we will rigorously prove the result of ‘invasion implies trait substitution’.

**Proposition 2.** If the mutation in the host resistance is small, the mutant host is rare and the transmission rate \(\beta\) is far from an evolutionarily singular strategy, then a successful invasion of mutant host will cause a trait substitution.

**Proof.** Firstly, we extend the resident population model (1) by considering the presence of a mutant susceptible host population \(S_m\). When the mutant susceptible hosts with a slightly different resistance ability \(\beta_m\) enter into the resident populations at a low density, the resident-mutant population dynamics is given by

\[
\begin{aligned}
    \frac{dI}{dt} &= \beta SI + \beta_m S_m I - \alpha I - (m_0 + m_1(S + S_m + I))I, \\
    \frac{dS}{dt} &= b(\beta)S - \beta SI - (m_0 + m_1(S + S_m + I))S, \\
    \frac{dS_m}{dt} &= b(\beta_m)S_m - \beta_m S_m I - (m_0 + m_1(S + S_m + I))S_m,
\end{aligned} \tag{7}
\]

where \(S_m\) denotes the population density of mutant susceptible hosts at time \(t\). One boundary equilibrium of the resident-mutant model (7) is \((I^*(\beta_m), 0, S_m^*(\beta_m))\).

Next, by using the method of Lyapunov function, we show that if \(|\beta_m - \beta|\) is sufficiently small, and \(\beta_m\) is not in a neighbourhood of the singularity, and \(f(\beta_m, \beta) > 0\), then the boundary equilibrium \((I^*(\beta_m), 0, S_m^*(\beta_m))\) is globally asymptotically stable in \(R^3_+ = \{I > 0, S \geq 0, S_m > 0\}\), which means that the successful invasion by a mutant host implies trait substitution. For simplicity, we use \(I^*\) and \(S_m^*\) instead of \(I^*(\beta_m)\) and \(S_m^*(\beta_m)\). Consider the following Lyapunov function

\[
V_2 = \left(I - I^* - I^* \ln \frac{I}{I^*}\right) + S + \left(S_m - S_m^* - S_m^* \ln \frac{S_m}{S_m^*}\right). \tag{8}
\]

We can see that \(V_2 \geq 0\) and the equality holds only for \((I, S, S_m) = (I^*, 0, S_m^*)\). Its time derivative along solutions of model (7) becomes

\[
\frac{dV_2}{dt} = (I - I^*) \frac{dI}{dt} + \frac{dS}{dt} + (S_m - S_m^*) \frac{1}{S_m} \frac{dS_m}{dt}
\]

\[
= (I - I^*) \left(\beta S + \beta_m S_m - \alpha - (m_0 + m_1(S + S_m + I))\right)
+ S(\beta(\beta_m - \beta)I - (m_0 + m_1(S + S_m + I)))
+ (S_m - S_m^*)(b(\beta_m) - \beta_m I - (m_0 + m_1(S + S_m + I)))
= (I - I^*) \left(-m_1(I - I^*) + \beta S - m_1 S + \beta_m(S_m - S_m^*) - m_1(S_m - S_m^*)\right)
+ S(b(\beta) - \beta I^* - m_0 - m_1(S_m^* + I^*)) \tag{9}
\]
Gradient directions of such an evolutionary change is determined by the sign of selection and replacement, the resistance of susceptible hosts will gradually evolve. The evolutionary dynamics of host resistance.

2.3. Evolutionary dynamics of host resistance. Through successive invasion and replacement, the resistance of susceptible hosts will gradually evolve. The direction of such an evolutionary change is determined by the sign of selection gradient $g(\beta)$, which is given by

$$g(\beta) = \frac{\partial f(\beta_m, \beta)}{\partial \beta_m} \bigg|_{\beta_m = \beta} = b'(\beta) - I^*(\beta),$$

(10)

where $b'(\beta)$ denotes the derivative of $b(\beta_m)$ with respect to $\beta_m$ evaluated at $\beta_m = \beta$.

By the results of Dieckmann and Law [27], if the mutation process is homogeneous and the mutation is small and rare, then the step by step evolution of host resistance can be approximated by the following equation

$$\frac{d\beta}{d\tau} = \frac{1}{2} \mu S^*(\beta) \sigma^2 g(\beta),$$

(11)

where time $\tau$ spans the evolutionary timescale and $\mu$ is the probability that a birth event in the susceptible host is a mutant, $S^*(\beta)$ is the equilibrium population density of susceptible hosts, $\sigma^2$ is the variance of phenotypic effect of mutation, and $g(\beta)$ is the selection gradient described as in (10). The product $\frac{1}{2} \mu S^*(\beta) \sigma^2$ as a whole serves to scale the speed of evolutionary change [26, 23]. Equation (11) tells us how the expected value of host resistance $\beta$ will change [76, 77]. Due to the uncertainty of the trade-off relationship $b(\beta)$, we next use the method of critical function analysis to identify the ‘evolutionarily singular strategy’ and determine its stability.

2.4. Critical function analysis. A strategy $\beta^*$ at which the selection gradient equals to zero is called an ‘evolutionarily singular strategy’ [30, 21, 34, 26, 22]. From (10), we can see that a singular strategy $\beta^*$ should satisfy

$$b'(\beta^*) = I^*(\beta^*).$$

(12)

Because the trade-off function $b(\beta)$ is uncertain, the singular strategy $\beta^*$ cannot be solved analytically. Therefore, we use the method of critical function analysis to identify the singular strategy and determine its stability [53, 36, 75, 76, 77].

Firstly, a critical function $b_{crit}(\beta)$ is a continuously differentiable function such that its slope is equal to the critical slope at all values of $(\beta, b(\beta))$ [53, 36, 75, 76, 77]. Thus, every strategy $\beta$ on a critical function curve might be a singular strategy.

From (3) and (12), we can see that the critical function is a solution of the following ordinary differential equation

$$b_{crit}'(\beta) = (\beta (b_{crit}(\beta) - m_0) - m_1 (\alpha + b_{crit}(\beta)))/\beta^2,$$

(13)

where a subscript is added to distinguish it from the trade-off function. Taking the derivative again with respect to $\beta$ on both sides of the equation (13), we further obtain the curvature of this critical function, which is given by
\[ b_{\text{crit}}''(\beta) = \frac{m_1(\alpha + m_0) + m_2(\alpha + b_{\text{crit}}(\beta))}{\beta^4}, \tag{14} \]

which is always positive, thus the curve of critical function is always convex. Generally speaking, given an arbitrary trade-off function, if the trade-off curve is tangential to a critical function curve, then the point of tangency is an evolutionarily singular strategy \([53, 36, 75, 76, 77]\).

Secondly, an evolutionarily singular strategy \(\beta^*\) is convergence stable if a population with a nearby strategy can be invaded by a mutant host that is even closer to \(\beta^*\) \([52, 21, 34, 26, 23]\). In other words, if \(d_g(\beta)/d\beta \big|_{\beta=\beta^*} < 0\), then the singular strategy \(\beta^*\) is locally convergence stable. According to (10) and (14), we can see that if

\[ b''(\beta^*) < b_{\text{crit}}''(\beta^*), \tag{15} \]

then the singular strategy \(\beta^*\) is locally convergence stable \([53]\). Because the curve of critical function is always convex, the condition (15) implies that if the trade-off curve is less convex (or concave) than the curve of critical function in the vicinity of singular strategy \(\beta^*\), then the singular strategy can be reachable \([76, 77]\).

Thirdly, an evolutionarily singular strategy \(\beta^*\) is locally evolutionarily stable if no nearby mutant can invade \([52, 21, 34, 26, 23]\). In other words, if \(f(\beta_m,\beta^*) < 0\) for all \(\beta_m \neq \beta^*\) in a neighbourhood of \(\beta^*\), then the singular strategy \(\beta^*\) is locally evolutionarily stable. From (6), we can see that the singular strategy \(\beta^*\) is locally evolutionarily stable if

\[ \frac{\partial^2 f(\beta_m, \beta)}{\partial \beta_m^2} \bigg|_{\beta_m=\beta=\beta^*} = b''(\beta^*) < 0. \tag{16} \]

Therefore, if the trade-off curve is concave in the vicinity of \(\beta^*\), then the singular strategy \(\beta^*\) is locally evolutionarily stable. This implies that if there is an accelerating cost near the singular strategy \(\beta^*\), then the singular strategy \(\beta^*\) is evolutionarily stable \([76, 77]\).

Given an arbitrary trade-off curve, the approach of critical function analysis gives a simple way to identify the evolutionarily singular strategy and its stability \([53, 36, 75, 76, 77]\). Combining the results of convergence stability and evolutionary stability, we obtain the following results.

3. Results of monomorphic evolutionary dynamics.

3.1. Continuously stable strategy of host resistance. An evolutionarily singular strategy that is both convergence stable and evolutionarily stable is called a continuously stable strategy (CSS) \([30, 34, 36]\). A continuously stable strategy represents a finally evolutionary state of host resistance \([30, 34, 22]\). According to conditions (15) and (16), we obtain the following result.

**Theorem 3.1.** Assuming condition (2) holds. If one of the critical function \(b_{\text{crit}}(\beta)\) is tangential to the trade-off curve \(b(\beta)\) at a strategy \(\beta^*\) and \(b''(\beta^*) < 0\), then \(\beta^*\) is an evolutionarily singular strategy of system (11) and it is continuously stable.

From Theorem 3.1, we can see that if the trade-off curve is locally concave in the vicinity of \(\beta^*\), then the singular strategy \(\beta^*\) is a continuously stable strategy. This implies that if there is an accelerating cost near the singular strategy \(\beta^*\), then natural selection will drive the evolution of host resistance toward \(\beta^*\) and comes to a halt, namely, the singular strategy \(\beta^*\) represents a final endpoint of the
evolutionary process [30, 34, 36]. Thus the finally evolutionary outcome contains a single susceptible host with strategy $\beta^*$. As an example, the trade-off function is taken to be

$$b(\beta) = b_0 + \frac{b_1 \beta}{b_2 + \beta},$$

(17)

where $b_0 = 0.01, b_1 = 2.0$ and $b_2 = 0.1$. In this case, $b(\beta)$ is a monotonically increasing function and globally concave. Other parameter values are set to $\alpha = 0.01, m_0 = 0.005, m_1 = 0.0001, \mu = 0.01, \sigma = 0.00001$ (The values of these parameters and below are artificially determined according to the biological meaning of parameters and the time units, without reference to an actual situation). In this case, we can see that the evolutionarily singular strategy $\beta^*$ in Fig.1a is both convergence stable and evolutionarily stable, that is, the evolutionarily singular strategy $\beta^*$ in Fig.1a is a continuously stable strategy (see also Fig.1b). From Fig.1c, we can see that if the initial resistant ability is relatively weak ($\beta(0) = 0.0009$), then the resistant ability of host will gradually increase. In this case, the evolution of host resistance results in a decrease of basic reproduction number $R_0$ (see Fig.1d). During the evolutionary process of host resistance, the equilibrium population density of susceptible hosts will also gradually increase and finally reaches to a saturation state, but the equilibrium population density of infected hosts will gradually decrease as the host resistance evolves (see Fig.1e).

However, if the initial resistant ability is relatively strong ($\beta(0) = 0.0003$), then due to the trade-off relationship between the birth rate and resistance, the evolution will reduce the resistant ability of susceptible hosts, the transmission rate $\beta$ will gradually increase and converge to a saturation state (see Fig.2a). In this case, the evolution of host resistance leads to an increase of basic reproduction number $R_0$ (see Fig.2b). Particularly, in this case the equilibrium population density of susceptible hosts will gradually decrease, whereas the equilibrium population density of infected hosts will gradually increase and finally reaches to a saturation state (see Fig.2c).

Furthermore, we find that the basic reproduction number $R_0$ is a monotonically increasing function of transmission rate $\beta$, because

$$\frac{dR_0}{d\beta} = \frac{(b(\beta) - m_0)(\alpha + b(\beta)) + \beta b'(\beta)(\alpha + m_0)}{m_1 ((\alpha + b(\beta)))^2},$$

which is positive when $R_0 > 1$ (see Fig.2d). This implies that if there is a trade-off relationship between host resistance and its fertility, then there may exist a continuously stable strategy $\beta^*$. Depending on the initial resistant ability $\beta(0)$, the evolution of trait may increase or decrease the value of $R_0$, because $R_0$ is always a monotonically increasing function with respect to $\beta$.

### 3.2. Evolutionary branching of host resistance.

If the evolutionarily singular strategy $\beta^*$ is convergence stable, but not evolutionarily stable, then by the results of Geritz et al. [34], Dercole and Rinaldi [23] and Geritz [38], the mutant host and resident host with strategies $\beta_m$ and $\beta$ close to $\beta^*$ can coexist and diverge in their resistant ability, that is to say, the susceptible host population will undergo evolutionary branching. Therefore, we obtain the following result.

**Theorem 3.2.** Assuming condition (2) holds. If one of the critical function $b_{\text{crit}}(\beta)$ is tangential to the trade-off curve $b(\beta)$ at a strategy $\beta^*$ and $0 < b^"(\beta^*) < b_{\text{crit}}^"(\beta^*)$, then $\beta^*$ is an evolutionarily singular strategy of system (11) and it is an evolutionary branching point (EBP).
Figure 1. Continuously stable strategy of host resistance when the initial trait value $\beta(0) = 0.0009$. (a) A trade-off curve $b(\beta)$ described in (17) with $b_0 = 0.01, b_1 = 2.0$ and $b_2 = 0.1$ and a tangential critical function curve $b_{crit}(\beta)$. The filled circle $\beta^* = 0.000646$ is an evolutionarily singular strategy. The grey area indicates combinations of $\beta$ and $b(\beta)$ for which the endemic equilibrium, $(S^*(\beta), I^*(\beta))$, is globally asymptotically stable. (b) A pairwise invasibility plot (PIP) obtained with the trade-off function in (a). The grey areas indicate the mutant host can invade, while in green areas the mutant host becomes extinct. $\beta^* = 0.000646$ is a continuously stable strategy. (c) An evolutionary time series plot of transmission rate $\beta$ obtained through simulation of model (11) with initial condition $\beta(0) = 0.0009$. (d) The basic reproduction number $R_0$ against evolutionary time. (e) Equilibrium population densities of susceptible hosts $S^*(\beta)$ and infected hosts $I^*(\beta)$ when the transmission rate $\beta$ evolves. Other parameter values: $\alpha = 0.01, m_0 = 0.005, m_1 = 0.0001, \mu = 0.01, \sigma = 0.00001$. 

\[ \text{Figure 1. Continuously stable strategy of host resistance when the} \\ \text{initial trait value } \beta(0) = 0.0009. \] 

\[ \text{a) A trade-off curve } b(\beta) \text{ described} \] 

\[ \text{in (17) with } b_0 = 0.01, b_1 = 2.0 \text{ and } b_2 = 0.1 \text{ and a tangential critical function curve } b_{crit}(\beta). \] 

\[ \text{The filled circle } \beta^* = 0.000646 \text{ is an evolutionarily singular strategy. The grey area indicates combinations of } \beta \text{ and } b(\beta) \text{ for which the endemic equilibrium, } (S^*(\beta), I^*(\beta)), \text{ is globally asymptotically stable.} \] 

\[ \text{b) A pairwise invasibility plot (PIP) obtained} \] 

\[ \text{with the trade-off function in (a). The grey areas indicate the mutant host can invade, while in green areas the mutant host becomes} \] 

\[ \text{extinct. } \beta^* = 0.000646 \text{ is a continuously stable strategy.} \] 

\[ \text{c) An evolutionary time series plot of transmission rate } \beta \text{ obtained through simulation of model (11) with initial condition } \beta(0) = 0.0009. \] 

\[ \text{d) The basic reproduction number } R_0 \text{ against evolutionary time.} \] 

\[ \text{e) Equilibrium population densities of susceptible hosts } S^*(\beta) \text{ and infected hosts } I^*(\beta) \] 

\[ \text{when the transmission rate } \beta \text{ evolves. Other parameter values: } \alpha = 0.01, m_0 = 0.005, m_1 = 0.0001, \mu = 0.01, \sigma = 0.00001. \]
Figure 2. Continuously stable strategy of host resistance when the initial trait value $\beta(0) = 0.0003$. (a) An evolutionary time series plot of transmission rate $\beta$ obtained through simulation of model (11) with initial condition $\beta(0) = 0.0003$. (b) The basic reproduction number $R_0$ against evolutionary time. (c) Equilibrium population densities of susceptible hosts $S^*(\beta)$ and infected hosts $I^*(\beta)$ when the transmission rate $\beta$ evolves. (d) The basic reproduction number $R_0$ against transmission rate $\beta$. Other parameter values are the same as in Fig.1.

From Theorem 3.2, we can see that near the singular strategy $\beta^*$ if the trade-off curve is convex but less convex than the critical function curve, then this singular strategy $\beta^*$ is an evolutionary branching point (EBP). This means that in the vicinity of the singular strategy $\beta^*$ if there is a weakly decelerating cost, then evolutionary branching in the host resistance will occur.

As an example, we take the following trade-off function [72]

$$b(\beta) = \left( b_0 + \frac{b_1 \beta}{b_2 + \beta} \right) \left( 1 - b_3 \exp \left( \frac{- (\beta - \beta_0)^2}{\sigma_c^2} \right) \right).$$  \hspace{1cm} (18)
Figure 3. Evolutionary branching strategy of host resistance. (a) A trade-off curve $b(\beta)$ described in (18) with $b_0 = 0.055, b_1 = 4.0, b_2 = 0.05, \beta_0 = 0.0005, \sigma = 0.0002$ and a tangential critical function curve $b_{\text{crit}}(\beta)$. The filled circle $A = 0.000419$ is an evolutionarily singular strategy. The grey area indicates combinations of $\beta$ and $b(\beta)$ for which the endemic equilibrium, $(S^*(\beta), I^*(\beta))$, is globally asymptotically stable. (b) A pairwise invasibility plot (PIP) obtained with the trade-off function in (a). The grey regions indicate the mutant host can invade, while in green regions the mutant host becomes extinct. $A, B, C$ are three evolutionarily singular strategies. (c) A mutual invasibility plot obtained with the trade-off function in (a). In the grey regions, both $f(\beta_m, \beta) > 0$ and $f(\beta, \beta_m) > 0$. Other parameter values: $\alpha = 0.075, m_0 = 0.006, m_1 = 0.00014, \mu = 0.01, \sigma = 0.00001$.

The motivation for this choice of trade-off function lies in the flexibility with which we can manipulate its convexity [72]. The first bracket $(b_0 + b_1\beta/(b_2 + \beta))$ is a concave function of $\beta$ which approaches the upper limit $b_0 + b_1$ at a rate controlled by $b_2$. The second bracket allows us to manipulate this function in a controlled
manner, such that as $b_3$ is increased, (18) turns increasingly convex in the region around $\beta_0$. The width of this region is determined by the shape parameter $\sigma_c$. This type of trade-off function might be better to fit the experimental data. Here we choose parameter values $b_0 = 0.055, b_1 = 4.0, b_2 = 0.05, b_3 = 0.05, \beta_0 = 0.0005$ and $\sigma_c = 0.0002$. In this case, $b(\beta)$ is a monotonically increasing function and finally converges to a saturated state. Particularly, it is a concave-convex-concave trade-off curve (see Fig.3a). Other parameter values are set to $\alpha = 0.075, m_0 = 0.006, m_1 = 0.00014, \mu = 0.01, \sigma = 0.00001$. From Fig.3a, it can be seen that near the evolutionarily singular strategy $A = 0.000419$ the trade-off curve is less convex than the critical function curve, which implies that the evolutionarily singular strategy $A = 0.000419$ in Fig.3a is convergence stable but not evolutionarily stable. That is to say, the singular strategy $A$ in Fig.3a is an evolutionary branching point (see also Fig.3b), close to this singular strategy $A = 0.000419$ the mutant host and resident host can coexist and diverge in their resistant ability (see Fig.3c), the evolutionary branching in the host resistance will occur. From Fig.3b, we can also see that if the initial resistant ability is relatively strong (i.e., with a smaller value of transmission rate), then the susceptible host will firstly evolve towards the smaller singular strategy $A$, and then branch into two different types. However, if the initial resistant ability is relatively weak (i.e., with a larger value of transmission rate), then the susceptible host will evolve towards a continuously stable strategy $C$ and come to a halt.

3.3. Results of bifurcation analysis. How likely does the continuously stable strategy of host resistance evolve or how likely does the evolutionary branching in the host resistance strategy occur? This can be observed through the bifurcation analysis of evolutionary dynamics. In this section, by using the method of numerical simulation, we examine how the evolutionary singular strategy and its stability will change as the shape and strength of the trade-off curve is changed.

For the globally concave trade-off function (17), the bifurcation diagram of evolutionarily singular strategy $\beta^*$ versus the maximum birth rate $b_1$ is depicted in Fig.4a. Other parameter values are set to the same values as in Fig.1. We can see that if the trade-off function is globally concave, then the singular strategy $\beta^*$ is always convergence stable as well as evolutionarily stable, the natural selection will drive the evolution of host resistance towards $\beta^*$ and come to a halt. When the maximum birth rate $b_1$ increases continuously from zero, the value of continuously stable strategy $\beta^*$ will gradually increase and finally reaches to a saturation state. This implies that when there is an accelerating cost, then decreasing the host resistance (i.e., increasing continuously stable strategy $\beta^*$, accordingly increasing the fertility of host) will benefit the susceptible host population. In particular, for the globally concave trade-off function, we can see that the evolutionary branching in the host resistance strategy cannot occur.

In the case of a concave-convex-concave trade-off function (18), the bifurcation diagram of evolutionarily singular strategy $\beta^*$ versus the maximum birth rate $b_1$ is depicted in Fig.4b. Other parameter values are set to the same values as in Fig.3. In this case, if $0.69 < b_1 < 8.0$, then the trade-off function $b(\beta)$ is monotonically increasing and finally converges to a saturation state. It can be seen that when $1.29 < b_1 < 4.64$, then the smaller singular strategy $\beta^*$ is convergence stable but not evolutionarily stable, close to this singular strategy, evolutionary branching in the host resistance strategy will occur. Particularly, we can see that when the maximum birth rate $b_1$ gradually increases, the value of evolutionary branching
Figure 4. Bifurcation diagram of evolutionary dynamics when the parameter of trade-off function is changed. (a) Evolutionarily singular strategy $\beta^*$ versus the maximum birth rate $b_1$ when the trade-off function is the same as in Fig. 1a. (b) Evolutionarily singular strategy $\beta^*$ versus the maximum birth rate $b_1$ when the trade-off function is the same as in Fig. 3a. (c) Evolutionarily singular strategy $\beta^*$ versus the trade-off strength $b_3$ when the trade-off function is the same as in Fig. 3a. (d) Evolutionarily singular strategy $\beta^*$ versus the shape parameter $\sigma_c$ when the trade-off function is the same as in Fig. 3a. In (a), (b), (c) and (d), arrows indicate the direction of evolutionary change. The black solid curves indicate the evolutionarily singular strategies which are both convergence stable and evolutionarily stable; the red dashed curves indicate the evolutionarily singular strategies which are not evolutionarily stable. CSS denotes the continuously stable strategy, EBP denotes the evolutionary branching point. The grey region indicates combination of $\beta$ and $b(\beta)$ for which the endemic equilibrium $(S^*(\beta), I^*(\beta))$ is globally asymptotically stable. In non-grey region, $I^*(\beta)$ equals to zero, the evolution of host resistance can not occur. In (a), other parameter values are the same as in Fig. 1. In (b), (c) and (d), other parameter values are the same as in Fig. 3.
point will also gradually increase. However, when $2.69 < b_1 < 4.64$ whether or not the evolutionary branching occurs also depends on the initial host resistance strategy, because in this case there also exists a continuously stable strategy for the host resistance.

Moreover, based on the trade-off function (18), Fig.4c depicts the bifurcation diagram of evolutionarily singular strategy $\beta^*$ versus the trade-off strength $b_1$. Other parameter values are set to the same values as in Fig.3. In this case, when $0.0 < b_1 < 0.15$, the trade-off function $b(\beta)$ is monotonically increasing and finally converges to a saturation state. From Fig.4c, we can see that when $0.0014 < b_1 < 0.086$, that is, for a moderately strong trade-off function, the smaller singular strategy $\beta^*$ is convergence stable but not evolutionarily stable, close to this singular strategy, evolutionary branching in the host resistance will occur. However, when $0.031 < b_1 < 0.086$, that is, the convexity of trade-off function becomes relatively strong, then whether evolutionary branching occurs or not also depends on the initial host resistance strategy, because in this case there also exists another continuously stable strategy (CSS) for the host resistance (see Fig.4c).

Fig.4d describes the bifurcation diagram of evolutionarily singular strategy $\beta^*$ versus the shape parameter $\sigma_c$. Other parameter values are set to the same values as in Fig.3. In this case, when $0.002 < \sigma_c < 0.00168$, the trade-off function $b(\beta)$ is monotonically increasing and finally converges to a saturation state. From Fig.4d, we can see that when $0.000168 < \sigma_c < 0.00178$, that is, for a moderate width of convex region, the smaller singular strategy $\beta^*$ is convergence stable but not evolutionarily stable, close to this singular strategy, evolutionary branching in the host resistance will occur.

From Fig.4, we can see that given the environmental conditions and the functional form of trade-off relationship, there may exist a wide range of parameter values (such as $b_1$, $b_3$ and $\sigma_c$) which can lead to evolutionary branching in the host resistance. Next, we further discuss the impact of changes of demographic parameters on the evolutionary behaviour of host resistance.

### 3.4. Effect of demographic parameters

In this section, by using the method of implicit differentiation, we discuss how likely the evolutionary branching in the host resistance will occur independent of the trade-off function, and how changes in the demographic parameters will affect the evolutionary behaviour of host resistance.

First of all, we consider the impact of the strength of density-dependent mortality $m_1$ on the continuously stable strategy (CSS) and evolutionary branching point (EBP) of host resistance. This can be determined by the sign of the derivative of $\beta^*$ with respect to $m_1$. On the basis of the selection gradient $g(\beta, m_1)$ in (10), by implicitly differentiating the equation $g(\beta^*, m_1) = 0$ with respect to $m_1$, and treating $\beta^*$ as a function of $m_1$ [76, 77], this gives

$$
\frac{\partial g(\beta^*, m_1)}{\partial \beta^*} \frac{d\beta^*}{dm_1} + \frac{\partial g(\beta^*, m_1)}{\partial m_1} = 0.
$$

Using the definition of $g(\beta, m_1)$, we rewrite (19) as

$$
d\beta^* = \left( \frac{\partial}{\partial m_1} \left( \frac{\partial f(\beta_m, \beta)}{\partial \beta_m} \bigg|_{\beta_m=\beta} \right) \right)_{\beta=\beta^*} \left( \frac{\partial}{\partial \beta} \left( \frac{\partial f(\beta_m, \beta)}{\partial \beta_m} \bigg|_{\beta_m=\beta} \right) \right)_{\beta=\beta^*}.
$$

Because both ‘CSS’ and ‘EBP’ are convergence stable, which means that the denominator of equation (20) is always negative. Therefore, the sign of $d\beta^*/dm_1$ is
determined by the numerator of equation (20). By direct calculations, the numerator of equation (20) is given by

\[
- \left( \frac{\partial}{\partial m_1} \left( \frac{\partial f(\beta_m, \beta)}{\partial \beta_m} \bigg|_{\beta_m=\beta} \right) \right)_{\beta=\beta^*} = -\frac{b(\beta^*) + \alpha}{(\beta^*)^2},
\]

which is always negative when condition (2) holds. Therefore, for both the continuously stable strategy (CSS) and evolutionary branching point (EBP) \( \beta^* \), \( d\beta^*/dm_1 > 0 \) is always true, that is to say, the evolutionarily singular strategy \( \beta^* \) will always increase as the parameter \( m_1 \) increases. This means that if the strength of density-dependent mortality \( m_1 \) becomes strong, then the susceptible host population will increase its birth rate \( b(\beta) \) (because the transmission rate \( \beta \) will increase) and accordingly decrease its resistant ability, no matter the exact relationship between \( b(\beta) \) and \( \beta \).

Two typical examples are depicted in Figs.5c and 5f. Based on the globally concave trade-off function (17), we obtain the bifurcation diagram of evolutionarily singular strategy \( \beta^* \) versus the mortality strength \( m_1 \) (see Fig.5c). From Fig.5c, we can see that if the strength of density-dependent mortality \( m_1 \) gradually increases, then the continuously stable strategy (CSS) \( \beta^* \) will always increase and the susceptible host population will evolve to a state at which it has a lower resistant ability but with a higher birth rate and come to a halt. In this way the evolution of host resistance may benefit the whole susceptible host population. Moreover, based on the concave-convex-concave trade-off function (18), we obtain the bifurcation diagram of evolutionarily singular strategy \( \beta^* \) versus the mortality strength \( m_1 \) (see Fig.5f). From Fig.5f, we can see that for fixed other parameter values evolutionary branching of host resistance is possible when 0.00013 < \( m_1 \) < 0.000144. Particularly, it can be seen that if \( m_1 = 0 \), that is, there is no density-dependent mortality, then the evolutionary branching in the host resistance can not occur. If the strength of density-dependent mortality \( m_1 \) gradually increases, then the value of evolutionary branching point (EBP) will increase and the susceptible hosts will firstly evolve to a state at which it has a lower resistant ability but with a higher birth rate and then branches into two different types. However, if the strength of density-dependent mortality \( m_1 \) becomes relatively strong, then numerical simulation analysis shows that the evolutionarily singular strategy regains the evolutionary stability and becomes a ‘CSS’ (see Fig.5f).

Similarly, we examine the influence of the natural death rate \( m_0 \) and the pathogen-induced mortality rate \( \alpha \) on the continuously stable strategy (CSS) and evolutionary branching point (EBP) of host resistance. By the same argument as above, we can see that for both ‘CSS’ and ‘EBP’, \( d\beta^*/dm_0 > 0 \) and \( d\beta^*/d\alpha > 0 \), which means that the value of continuously stable strategy or evolutionary branching point \( \beta^* \) will gradually increase as the parameter \( m_0 \) or \( \alpha \) increases (see Figs.5a, 5b, 5d and 5e). In particular, from Fig. 5d and Fig.5e, we can see that when parameters \( m_0 \) and \( \alpha \) take the middle range values, the evolutionary branching in the host resistance is possible. When the parameter \( m_0 \) or \( \alpha \) increases, the susceptible host population will firstly evolve to a state at which it has a lower resistance ability but with a higher birth rate and then branches into two different types. This means that in order to determine whether the evolutionary branching occurs, the susceptible host population must balance the costs and benefits based on the resistance ability, reproductive ability and other demographic conditions [10].
Figure 5. Bifurcation diagram of evolutionary dynamics when the demographic parameter is changed. (a) Evolutionarily singular strategy $\beta^*$ versus the pathogen-induced mortality rate $\alpha$ when the trade-off function is the same as in Fig.1a. (b) Evolutionarily singular strategy $\beta^*$ versus the natural death rate $m_0$ when the trade-off function is the same as in Fig.1a. (c) Evolutionarily singular strategy $\beta^*$ versus the strength of density-dependent mortality $m_1$ when the trade-off function is the same as in Fig.1a. (d) Evolutionarily singular strategy $\beta^*$ versus the pathogen-induced mortality rate $\alpha$ when the trade-off function is the same as in Fig.3a. (e) Evolutionarily singular strategy $\beta^*$ versus the natural death rate $m_0$ when the trade-off function is the same as in Fig.3a. (f) Evolutionarily singular strategy $\beta^*$ versus the strength of density-dependent mortality $m_1$ when the trade-off function is the same as in Fig.3a. In (a), (b), (c), (d), (e) and (f), the arrows indicate the directions of evolutionary change. The black solid curves indicate the evolutionarily singular strategies which are both convergence stable and evolutionarily stable; the red dashed curves indicate the evolutionarily singular strategies which are not evolutionarily stable. CSS denotes the continuously stable strategy, EBP denotes the evolutionary branching point. The grey region indicates combination of $\beta$ and $b(\beta)$ for which the endemic equilibrium is globally asymptotically stable. In (a), (b) and (c), other parameter values are the same as in Fig.1. In (d), (e) and (f), other parameter values are the same as in Fig.3.
By the above analysis, we can see that if the constraint function is weakly convex in the vicinity of evolutionarily singular strategy, i.e., there is a weakly decelerating cost near the singular strategy $\beta^*$, then evolutionary branching in the host resistance is possible. From the bifurcation diagrams (see Figs. 4 and 5), it can be seen that for a given trade-off function the evolutionary branching behavior can occur over a large range of demographic parameter values. After branching has occurred in the host resistance strategy, it becomes more interesting to study the further coevolution of such a dimorphic susceptible host. Next, we use a similar approach to investigate the evolutionary dynamics of such a dimorphic susceptible host and find the finally evolutionary outcome.

4. Dimorphic evolutionary dynamics. In this section, we extend the analysis to host population with two resident resistance strategies $\beta_1$ and $\beta_2$, and investigate whether the two types of susceptible hosts with different resistant abilities can evolve to an evolutionarily stable equilibrium at which they can stably coexist on the much longer evolutionary timescale [76, 77]. We assume that the dimorphic susceptible host shares all the properties except for resistant ability and natural birth rate. Moreover, it is assumed that mutations are very rare and very small.

4.1. Coevolutionary model. Once the susceptible host population branches into two different types, $S_1$ and $S_2$, one with resistance strategy $\beta_1$ and the other with a slightly different resistance strategy $\beta_2$, then the population dynamics is given by

$$
\begin{align*}
\frac{dS_1}{dt} &= b(\beta_1)S_1 - \beta_1 S_1 I - m(N)S_1,
\frac{dS_2}{dt} &= b(\beta_2)S_2 - \beta_2 S_2 I - m(N)S_2,
\frac{dI}{dt} &= \beta_1 S_1 I + \beta_2 S_2 I - \alpha I - m(N)I,
\end{align*}
$$

(22)

where

$$
N = S_1 + S_2 + I, \ m(N) = m_0 + m_1 N,
$$

and $b(\beta)$ is a monotonically increasing function with respect to $\beta$ and eventually approaches to a state of saturation. For model (22), when the following condition (23) is true

$$
\begin{align*}
m_1(b(\beta_2) + \alpha)(\beta_1 - \beta_2) - (b(\beta_2) - m_0)\beta_1\beta_2 + (b(\beta_1) - m_0)(\beta_2)^2 > 0,
-m_1(b(\beta_1) + \alpha)(\beta_1 - \beta_2) - (b(\beta_1) - m_0)\beta_1\beta_2 + (b(\beta_2) - m_0)(\beta_1)^2 > 0,
\end{align*}
$$

(23)

we obtain an endemic equilibrium $(S_1^*(\beta_1, \beta_2), S_2^*(\beta_1, \beta_2), I^*(\beta_1, \beta_2))$, which is given by

$$
\begin{align*}
S_1^*(\beta_1, \beta_2) &= \frac{m_1(b(\beta_2) + \alpha)(\beta_1 - \beta_2) - (b(\beta_2) - m_0)\beta_1\beta_2 + (b(\beta_1) - m_0)(\beta_2)^2}{m_1(\beta_1 - \beta_2)^2}, \\
S_2^*(\beta_1, \beta_2) &= \frac{m_1(b(\beta_1) + \alpha)(\beta_2 - \beta_1) - (b(\beta_1) - m_0)\beta_1\beta_2 + (b(\beta_2) - m_0)(\beta_1)^2}{m_1(\beta_1 - \beta_2)^2}, \\
I^*(\beta_1, \beta_2) &= \frac{b(\beta_1) - b(\beta_2)}{\beta_1 - \beta_2}.
\end{align*}
$$

(24)
By using the method of Lyapunov function, we will show that the endemic equilibrium is globally asymptotically stable.

**Proposition 3.** If condition (23) holds, then the endemic equilibrium \((S^*_1(\beta_1, \beta_2), S^*_2(\beta_1, \beta_2), I^*(\beta_1, \beta_2))\) of model (22) is globally asymptotically stable in \(R^3_+ = \{S_1 > 0, S_2 > 0, I > 0\}\).

**Proof.** For simplicity, we use \((S^*_1, S^*_2, I^*)\) instead of \((S^*_1(\beta_1, \beta_2), S^*_2(\beta_1, \beta_2), I^*(\beta_1, \beta_2))\). Consider the following Lyapunov function

\[
V_3 = \left(S_1 - S^*_1 - S^*_1 \ln \frac{S_1}{S^*_1} \right) + \left(S_2 - S^*_2 - S^*_2 \ln \frac{S_2}{S^*_2} \right) + \left(I - I^* - I^* \ln \frac{I}{I^*} \right).
\]

It is clear that \(V_3 \geq 0\) and the equality holds only for \((S_1, S_2, I) = (S^*_1(\beta_1, \beta_2), S^*_2(\beta_1, \beta_2), I^*(\beta_1, \beta_2))\) in \(R^3_+ = \{S_1 > 0, S_2 > 0, I > 0\}\). Its time derivative along solutions of model (22) becomes

\[
\frac{dV_3}{dt} \bigg|_{\text{(22)}} = (S_1 - S^*_1) \frac{dS^*_1}{dt} + (S_2 - S^*_2) \frac{dS^*_2}{dt} + (I - I^*) \frac{dI}{dt} = -m_1((S_1 - S^*_1) + (S_2 - S^*_2) + (I - I^*))^2.
\]

It can be seen that \(dV_3/dt \leq 0\) in \(R^3_+\) and \(dV_3/dt = 0\) if and only if \((S_1, S_2, I) = (S^*_1, S^*_2, I^*)\). The globally asymptotical stability of \((S^*_1(\beta_1, \beta_2), S^*_2(\beta_1, \beta_2), I^*(\beta_1, \beta_2))\) follows from Lyapunov-LaSalle’s invariance principle.

Similar to the evolution of monomorphic host resistance, we separate the ecological timescale and evolutionary timescale. Before a mutant susceptible host appears, we assume that the resident hosts have reach to the endemic equilibrium \((S^*_1(\beta_1, \beta_2), S^*_2(\beta_1, \beta_2), I^*(\beta_1, \beta_2))\). Next, based on model (22) and the endemic equilibrium, we will derive the coevolutionary dynamics of dimorphic susceptible hosts. Because of the rarity of mutations, we assume that there is either a mutant host arising from susceptible hosts \(S_1\) or a mutant host arising from susceptible hosts \(S_2\), but not both at a time. By the same derivation as above, when a mutant susceptible host with a slightly different resistance strategy \(\beta_m\) enters into the resident community with a low density, the invasion fitness for the mutant host is then given by

\[
f(\beta_m, \beta_1, \beta_2) \begin{align*}
&= b(\beta_m) - \beta_m I^*(\beta_1, \beta_2) - (m_0 + m_1(S^*_1(\beta_1, \beta_2) + S^*_2(\beta_1, \beta_2) + I^*(\beta_1, \beta_2))),
\end{align*}
\]

where \(b(\beta_m)\) is the trade-off function and \(S^*_1(\beta_1, \beta_2), S^*_2(\beta_1, \beta_2), I^*(\beta_1, \beta_2)\) are respectively the equilibrium population densities of susceptible hosts \(S_1\), susceptible hosts \(S_2\) and infected hosts, which are described as in (24).

By using the same method as in Section 2.2, we can rigorously demonstrate that if \(f(\beta_m, \beta_1, \beta_2) > 0\), then the mutant susceptible host will invade and cause a trait substitution. The evolutionary direction of host resistance is determined by the sign of selection gradients \(g_1(\beta_1, \beta_2)\) and \(g_2(\beta_1, \beta_2)\), which are given by

\[
\begin{align*}
g_1(\beta_1, \beta_2) &= \left. \frac{\partial f(\beta_m, \beta_1, \beta_2)}{\partial \beta_m} \right|_{\beta_m = \beta_1} = b'(\beta_1) - I^*(\beta_1, \beta_2), \\
g_2(\beta_1, \beta_2) &= \left. \frac{\partial f(\beta_m, \beta_1, \beta_2)}{\partial \beta_m} \right|_{\beta_m = \beta_2} = b'(\beta_2) - I^*(\beta_1, \beta_2),
\end{align*}
\]

where \(b'(\cdot)\) is the derivative of the trade-off function. The evolutionary speed of host resistance is then given by

\[
\rho(\beta_1, \beta_2) = \frac{g_1(\beta_1, \beta_2) - g_2(\beta_1, \beta_2)}{g_1(\beta_1, \beta_2) + g_2(\beta_1, \beta_2)}.
\]
where \( b'(\beta_i) \) represents the first derivative of \( b(\beta_m) \) with respect to \( \beta_m \) evaluated at \( \beta_m = \beta_i, (i = 1, 2) \).

Furthermore, if the mutations are of small effect and rare, then the coevolutionary dynamics of host resistance is given by [27]

\[
\begin{align*}
\frac{d\beta_1}{d\tau} &= \frac{1}{2} \mu S_1^*(\beta_1, \beta_2) \sigma^2 g_1(\beta_1, \beta_2), \\
\frac{d\beta_2}{d\tau} &= \frac{1}{2} \mu S_2^*(\beta_1, \beta_2) \sigma^2 g_2(\beta_1, \beta_2),
\end{align*}
\]

(29)

where time \( \tau \) spans the evolutionary timescale and \( \mu \) denotes the probability that a birth event in susceptible hosts \( S_i \) is a mutant, \( (i = 1, 2) \). \( S_1^*(\beta_1, \beta_2) \) and \( S_2^*(\beta_1, \beta_2) \) are the equilibrium population densities of the two susceptible hosts which are described in (24). \( \sigma^2 \) denotes the variance of phenotypic effect of a mutation in susceptible hosts \( S_i \), \( (i = 1, 2) \). \( g_1(\beta_1, \beta_2) \) and \( g_2(\beta_1, \beta_2) \) are the selection gradients described in (28). Because we assume that the two host residents differ in only their birth rates and their resistance, they have the same \( \mu \) and \( \sigma^2 \). Moreover, we also assume that these two parameters do not depend on the trait values and are constants, therefore parameters \( \mu \) and \( \sigma^2 \) are the same as in the monomorphic host population. Model (29) tells us how the expected values of host resistance will change after evolutionary branching [76, 77].

4.2. Evolutionarily singular dimorphism. We firstly identify the specific feature of a trade-off function that can support an evolutionarily singular dimorphism. The directional evolution may come to a halt at an evolutionarily singular dimorphism \( (\beta_1^*, \beta_2^*) \). From (28), we can see that the condition for a positive singular dimorphism \( (\beta_1^*, \beta_2^*) \) is given by

\[
b'(\beta_i^*) = I^*(\beta_1^*, \beta_2^*), \quad (i = 1, 2).
\]

(30)

From (30), we can see that a trade-off function that can support a singular dimorphism must have two points at which it has the same slope, which cannot be the case for a globally concave trade-off function (such as (17)). If a singular dimorphism does not exist, then in simple trade-offs two host strains may continue to coexist indefinitely at the respective maximum and minimum trait values. By inserting (24) into (30), we obtain a specific expression for the required slope

\[
b'(\beta_i^*) = \frac{b(\beta_2^*) - b(\beta_1^*)}{\beta_2^* - \beta_1^*}, \quad (i = 1, 2).
\]

(31)

Therefore, a necessary condition for \( b(\beta) \) to support a positive singular dimorphism is that it is tangential to a straight line at two separate points [72, 41]. The simplest case is a concave-convex-concave trade-off function.

4.3. Continuously stable coexistence. If the singular dimorphism \( (\beta_1^*, \beta_2^*) \) is both convergence stable and evolutionarily stable, it is called a continuously stable dimorphism and it represents the finally evolutionary outcome, at which the dimorphic susceptible host can stably coexist on the long-term evolutionary timescale [72, 76, 77, 41].

Specifically, the convergence stability of \( (\beta_1^*, \beta_2^*) \) can be seen from the Jacobian matrix of system (29) at the singular dimorphism [49, 22]. Using (24) and (31), we obtain

\[
\frac{\partial I^*(\beta_1, \beta_2)}{\partial \beta_i} \bigg|_{\beta_i = \beta_i^*} = 0, \quad (i = 1, 2).
\]
Therefore, the Jacobian matrix $J_1$ of system (29) at $(\beta_1^*, \beta_2^*)$ is given by

$$J_1 = \begin{bmatrix} V_1(\beta_1^*, \beta_2^*)b''(\beta_1^*) & 0 \\ 0 & V_2(\beta_1^*, \beta_2^*)b''(\beta_2^*) \end{bmatrix},$$

where $V_i(\beta_1^*, \beta_2^*) = \mu \sigma^2 S_i(\beta_1^*, \beta_2^*)/2$, $(i = 1, 2)$. $S_i(\beta_1^*, \beta_2^*)$ $(i = 1, 2)$ are described in (24) with $(\beta_1, \beta_2) = (\beta_1^*, \beta_2^*)$. We can see that if $b''(\beta_i^*) < 0$ for $i = 1$ and 2, then the determinant of Jacobian matrix $J_1$ is positive and its trace is negative. Therefore, if the trade-off function is concave at both $\beta_1^*$ and $\beta_2^*$, then the evolutionarily singular dimorphism $(\beta_1^*, \beta_2^*)$ is locally convergence stable [72, 76, 77, 41].

Besides, if

$$\frac{\partial^2 f(\beta_m, \beta_1^*, \beta_2^*)}{\partial \beta_m^2} \bigg|_{\beta_m = \beta_1^*} = b''(\beta_1^*) < 0, \text{ for } i = 1 \text{ and } 2,$$

then the singular dimorphism $(\beta_1^*, \beta_2^*)$ is locally evolutionarily stable. This condition is satisfied if the trade-off function is concave at both $\beta_1^*$ and $\beta_2^*$. This means that once a positive singular dimorphism exists and is convergence stable, then it is always evolutionarily stable, and no further evolutionary branching is possible [72, 76, 77, 41]. Therefore, we obtain the following result.

**Theorem 4.1.** Assuming condition (23) holds. If condition (31) is satisfied and $b''(\beta_i^*) < 0$ for $i = 1$ and 2, then the evolutionarily singular dimorphism $(\beta_1^*, \beta_2^*)$ of system (29) is continuously stable.

From Theorems 3.2 and 4.1, we can see that if there is a weakly decelerating cost near the singular strategy, then evolutionary branching in the host resistance will occur. After branching, for a concave-convex-concave trade-off function, there may exist a continuously stable singular dimorphism, the susceptible host population will finally evolve into two different types, which can stably coexist on the much longer evolutionary timescale [72, 41]. In this case, the finally evolutionary outcome contains two types of hosts with different susceptibility.

As an example, we take the same trade-off function as in Fig.3. From Figs.4b and 4d and Figs.5c and 5f, we can see that for fixed other parameter values, when $1.29 < b_1 < 4.64$ or $0.000168 < \sigma_c \leq 0.000282$ or $0.00183 < m_0 < 0.0074$ or $0.00013 < m_1 < 0.000144$, the evolutionary branching in the host resistance is possible. After branching, through numerical simulation we find that the dimorphic susceptible host can continuously stable coexist on the long-term evolutionary timescale. Specifically, when $b_1 = 4.0, \sigma_c = 0.0002, m_0 = 0.006$ and $m_1 = 0.00014$, then the trade-off curve is concave-convex-concave (see Fig.3a). From Figs.3b and 3c, it can be seen that evolutionary branching in the host resistance can occur. After branching has occurred in the host resistance, the two types of susceptible hosts evolve according to model (29). By numerical simulation, we find an interior evolutionarily singular dimorphism $E_1 = (0.000932, 0.000103)$ and its reflection point $E_2 = (0.000103, 0.000932)$ (depending on the initial trait value, the dimorphic susceptible hosts will evolve towards the singular strategy $E_1$ or $E_2$). At the evolutionarily singular strategy we find that $b''(\beta_i^*) < 0$ for $i = 1$ and 2, thus the evolutionarily singular dimorphism is continuously stable. Fig.6a shows that the evolutionarily singular dimorphism is convergence stable and Fig.6b shows that the evolutionarily singular dimorphism $E_1 = (0.000932, 0.000103)$ is evolutionarily stable. Therefore, after branching in the host resistance has occurred, depending on the initial resistant ability, the dimorphic susceptible host will evolve towards the
Figure 6. Continuously stable coexistence of dimorphic susceptible hosts. The trade-off function is given by (18) with parameters $b_0 = 0.055, b_1 = 4.0, b_2 = 0.05, b_3 = 0.05, b_0 = 0.0005, \sigma_c = 0.0002$. (a) A trait evolution plot. The singular strategy $A = 0.000419$ is an evolutionary branching point. After the branching has occurred, there exist an interior dimorphic singular strategy $E_1 = (0.000932, 0.000103)$ and its reflection point $E_2 = (0.000103, 0.000932)$. The vector fields obtained from the deterministic model (29) indicate the directions of evolutionary change of traits $\beta_1$ and $\beta_2$. The black curves and red curves indicate the isoclines of traits $\beta_1$ and $\beta_2$, respectively. The solid curves indicate the evolutionarily singular strategies which are evolutionarily stable, whereas the dashed curves indicate the evolutionarily singular strategies which are not evolutionarily stable. (b) A fitness landscape plot when $(\beta_1^*, \beta_2^*) = (0.000932, 0.000103)$. (c) A simulated evolutionary tree obtained through simulation of models (11) and (29) with the initial condition $\beta(0) = 0.0005$. At evolutionary time $\tau_1$ evolutionary branching occurs. (d) Equilibrium population densities of susceptible hosts when the traits $\beta_1$ and $\beta_2$ evolve. (e) Equilibrium population density of infected hosts when the traits $\beta_1$ and $\beta_2$ evolve. Other parameter values: $\alpha = 0.075, m_0 = 0.006, m_1 = 0.00014, \mu = 0.01, \sigma = 0.00001$. 

\[ \begin{align*} 
& b_0 = 0.055, b_1 = 4.0, b_2 = 0.05, b_3 = 0.05, b_0 = 0.0005, \sigma_c = 0.0002. 
\end{align*} \]
evolutionarily singular dimorphism $E_1$ or $E_2$ and come to a halt. The finally evolutionary outcome contains two types of susceptible hosts, which can stably coexist on a long-term evolutionary timescale.

The evolutionary tree of host resistance obtained through simulation of models (11) and (29) with initial trait value $\beta(0) = 0.0005$ is depicted in Fig.6c. At evolutionary time $\tau_1$, the susceptible host branches into two different types. After branching has occurred, we can see that the trait in one branch initially increases, whereas in the other branch it initially decreases. This was expected because at a branching point the resident and mutant susceptible hosts coexist under opposite selection pressure and diverge in their resistant strategies [23, 72, 76, 77, 41]. Finally, the susceptible host evolves into two different types, one is a relatively higher susceptible strain, the other is a relatively higher resistant strain. The corresponding equilibrium population densities of susceptible hosts and infected hosts along the evolutionary tree are depicted in c and 6e. It can be seen that the equilibrium population densities of the two types of susceptible hosts differ very much just after the branching. The susceptible host $S_1$ associated with the upper branch has a lower equilibrium density, but its population equilibrium density initially gradually increases as its trait evolves. This maybe because with the increase of transmission rate $\beta_1$ (i.e., with the decrease of resistant ability), the birth rate of susceptible hosts $S_1$ will also increase, the advantage far outweighs its disadvantage. By comparison, the susceptible host $S_2$ associated with the lower branch has a higher equilibrium density, but its equilibrium density initially gradually decreases as its trait evolves (the equilibrium densities immediately after branching depend on how the initial trait values of the dimorphic population are chosen; a different initial point in the vicinity of the branching point may lead to the opposite results). Finally, at the evolutionarily stable dimorphism $E_1 = (0.000932, 0.000103)$ the equilibrium population densities of the two types of susceptible hosts are very close to each other.

In addition, based on the numerical bifurcation analysis and Fig.4d we find that when $0.000282 < \sigma_c < 0.00178$, that is, the convex region of trade-off curve is relatively wider, then the evolutionary branching in the host resistance is possible. However, in this case, after branching there is no interior dimorphic singular strategy. By numerical simulation, we find that when $0.000282 < \sigma_c < 0.00178$, one of the two host strains will evolve towards the boundary of $(\beta_1, \beta_2)$ phase-plane, at which the dimorphic susceptible host can continuously stably coexist. Specifically, when $\sigma_c = 0.0005$, then the trade-off curve is concave-convex-concave (see the trade-off curve II in Fig.12a). Through numerical simulation, we find that after branching has occurred in the host resistance, depending on the initial trait value, one of the dimorphic susceptible host will evolve towards the boundary of $(\beta_1, \beta_2)$ phase-plane, at which one host strain tends to be maximally resistant, the other host strain may have a moderate resistance (see Fig.7). They can also continuously stably coexist on a long-term evolutionary timescale. On the whole, from Figs.4, 5, 6 and Fig.7, we can see that for a larger range of parameter values the dimorphic susceptible host may continuously stably coexist on a long-term evolutionary timescale [76, 77]. Particularly, for the parameter values in Fig.4 and Fig.5, it can be seen that the evolutionary trade-off curve is concave-convex-concave (see the
Figure 7. Continuously stable coexistence of boundary dimorphism. The trade-off function and parameter values are the same as in Fig. 6 except for $\sigma_c = 0.0005$. (a) A trait evolution plot. The singular strategy $A = 0.000492$ is an evolutionary branching point. After the branching has occurred, there is no interior dimorphic singular strategy. The vector fields obtained from the deterministic model (29) indicate the directions of evolutionary change of traits $\beta_1$ and $\beta_2$. The black curves and red curves indicate the isoclines of traits $\beta_1$ and $\beta_2$, respectively. The solid curves indicate the evolutionarily singular strategies which are evolutionarily stable. (b) A fitness landscape plot when $(\beta_1^*, \beta_2^*) = (0.000113, 0)$. (c) A simulated evolutionary tree obtained through simulation of models (11) and (29) with the initial condition $\beta(0) = 0.0006$. (d) Equilibrium population densities of susceptible hosts when the traits $\beta_1$ and $\beta_2$ evolve. (e) Equilibrium population density of infected hosts when the traits $\beta_1$ and $\beta_2$ evolve.
trade-off curves \( I \) and \( II \) in Fig.12a). In other words, under certain demographic conditions the two host strain may continuously stably coexist if the trade-off relationship looks like a concave-convex-concave curve, even though there may not exist an interior evolutionarily singular dimorphism.

4.4. **Extinction of one evolutionary branch.** From Theorem 3.2 and numerical bifurcation analysis, we can see that the evolutionary branching in the host resistance is possible for many different types of trade-off curves and different demographic conditions. However, the evolutionary branching does not ensure that the dimorphic susceptible host can continuously stably coexist on a long-term evolutionary timescale. The further coevolution of the dimorphic susceptible host may result in loss of one or two evolutionary branches and thus the dimorphic susceptible host will go back to a monomorphism or become extinct [23, 76, 77, 4, 41].

In the present model, we find that after branching has occurred in the host resistance, the condition (31) in Theorem 4.1 may not be satisfied, thus there may not exist an interior singular dimorphism in system (29). In this case, the dimorphic susceptible host may not persistently coexist on the long-term evolutionary timescale. Through numerical simulation analysis, we find that after the branching has occurred, depending on the specific shape and strength of trade-off relationship between host resistance and its fertility, one of the two evolutionary branches may become extinct, and the dimorphic susceptible host finally falls back to a monomorphism [23, 76, 4, 77, 41]. In particular, through the analysis of the vector field (29) and coexistence region, we find that after branching if the vector field increases along both the \( \beta_1 \)-axis and \( \beta_2 \)-axis, then one of the two evolutionary branches may go extinct (see Figs.7, 9, 11). Furthermore, from (24) we can see that after branching if \( \beta_1 < \beta_2 \), then \( m_1(b(\beta_2) + \alpha)(\beta_1 - \beta_2) < 0 \) and \( b(\beta_1) < b(\beta_2) \), thus the equilibrium population density of susceptible host \( S_1 \) will firstly becomes zero. In contrast, after branching if \( \beta_2 < \beta_1 \), then the equilibrium population density of susceptible hosts \( S_2 \) will firstly becomes zero. This implies that after the branching has occurred, due to the trade-off relationship between host resistance and its fertility, the evolutionary branch with relatively stronger resistance (smaller \( \beta \)) will go extinct. However, it’s worth noting that it is not necessary that the two host strains will evolve outside of the coexistence region whenever there is no dimorphic singular point. Depending on the evolutionary speed and trade-off function, they may just sit at their maxima and minima provided there is a route through the coexistence region.

As an example, we take the same trade-off function as in (18). However, the parameter values are assumed to be \( b_0 = 0.05, b_1 = 5.5, b_2 = 0.05, b_3 = 0.8, \beta_0 = 0.0018, \sigma_c = 0.008 \) and \( \alpha = 0.075, m_0 = 0.0055, m_1 = 0.000098, \mu = 0.01, \sigma = 0.00005 \). From Fig.8, we can see that for fixed other parameter values, when \( 3.826 < b_1 < 9.177 \) or \( 0.007 < \sigma_c < 0.008347 \) or \( 0.00462 < m_0 < 0.00567 \) or \( 0.000089 < m_1 < 0.000101 \), the evolutionary branching of host resistance is possible. After branching has occurred, through numerical simulation analysis, we find that for all parameter values in Fig.8 the evolutionary branch with smaller \( \beta \) will go extinct and the remaining branch with bigger \( \beta \) will continue to evolve to a continuously stable strategy (CSS). Specifically, when \( b_1 = 5.5, \sigma_c = 0.008, m_0 = 0.0055 \) and \( m_1 = 0.000098 \), then the trade-off function \( b(\beta) \) in (18) is monotonically increasing and finally converges to a saturation state, which looks like a sigmoidal curve (see the trade-off curve \( I \) in Fig.12b). The pairwise invasibility plot is shown in Fig.9a, which indicates the evolutionarily singular strategy \( A \) is an evolutionary branching
Figure 8. Bifurcation diagram of monomorphic evolutionary dynamics when one of the parameters in the model is changed. The trade-off function is given by (18) with parameters $b_0 = 0.05, b_1 = 5.5, b_2 = 0.05, b_3 = 0.8, \beta_0 = 0.0018$ and $\sigma_c = 0.008$. (a) Evolutionarily singular strategy $\beta^*$ versus the maximum birth rate $b_1$. (b) Evolutionarily singular strategy $\beta^*$ versus the shape parameter $\sigma_c$. (c) Evolutionarily singular strategy $\beta^*$ versus the natural death rate $m_0$. (d) Evolutionarily singular strategy $\beta^*$ versus the strength of density-dependent mortality $m_1$. In (a), (b), (c) and (d), arrows indicate the direction of evolutionary change. The black solid curves indicate the evolutionarily singular strategies which are both convergence stable and evolutionarily stable; the red dashed curves indicate the evolutionarily singular strategies which are not evolutionarily stable. CSS denotes the continuously stable strategy, EBP denotes the evolutionary branching point. The grey region indicates combination of $\beta$ and $b(\beta)$ for which the endemic equilibrium $(S^*(\beta), I^*(\beta))$ is globally asymptotically stable.
point (EBP). After branching has occurred in the host resistance, the two types of susceptible hosts evolve according to model (29). However, in this case, by numerical simulation analysis we do not find any positive evolutionarily singular dimorphism (see Fig.9b). Therefore, after branching has occurred, the dimorphic susceptible host may evolve towards the edge of coexistence region (see Fig.9b). Near the edge of coexistence region, the next successful mutant host will drive the population outside the coexistence region, so that the dimorphic susceptible host will go back to a monomorphism. In particular, by numerical simulation, we find that independent of the initial resistant ability, always the evolutionary branch with the lower $\beta$ goes extinct and the remaining branch with higher $\beta$ will continue to evolve to a continuously stable strategy (CSS). In this case, the finally evolutionary outcome contains a monomorphic susceptible host with a relatively weaker resistance, but it has a relatively higher birth rate. The evolutionary tree of host resistance obtained through simulation of models (11) and (29) with initial trait value $\beta(0) = 0.0015$ is depicted in Fig.9c. At evolutionary time $\tau_2$, the susceptible host population experiences evolutionary branching. After branching, we can see that the trait in one branch initially increases and finally evolves to a continuously stable strategy, while in the other branch it initially decreases and at evolutionary time $\tau_2$ it becomes extinct. This phenomenon can be seen as an typical example of ‘evolutionary murder’ [35, 42, 62, 23, 5, 77, 41]. Particularly, from Figs.9a, 9b and 9c, we can see that even if all mutations are small, the combination of evolutionary branching and loss of one emerging branch has efficiently allowed the initially monomorphic susceptible host to jump across the repellor $B$ and to continue its monomorphic evolution on the other side [35, 42, 62, 23, 5, 41].

The corresponding equilibrium population densities of susceptible hosts and infected hosts along the evolutionary tree are depicted in Figs.9d and 9e. We can see that the equilibrium population densities of the two types of susceptible hosts differ very much just after the branching and thereafter the equilibrium population density of susceptible hosts $S_2$ gradually decreases. At time $\tau_2$, due to the trade-off relationship between host resistance and its fertility, the equilibrium population density of susceptible hosts $S_2$ becomes zero [23, 76, 77, 41]. Finally, the susceptible host $S_1$ evolves to a continuously stable strategy, at which it has a relatively weaker resistance but with a relatively higher birth rate. Especially, from Figs.9d and 9e, we can see that the evolution of host resistance gradually reduces the equilibrium population density of susceptible hosts, on the contrary it gradually increases the equilibrium population density of infected hosts.

In order to show that the ‘evolutionary murder’ is a robust phenomenon, for the same trade-off function and parameter values as in Fig.9 except for $b_1 = 10.0$ and $\sigma_c = 0.0085$, through numerical bifurcation analysis, we can see that for fixed other parameter values, when $6.557 < b_1 < 12.46$ or $0.00815 < \sigma_c < 0.00885$ or $0.0051 < m_0 < 0.0058$ or $0.000094 < m_1 < 0.0001$, the evolutionary branching of host resistance is possible (see Fig.10). After branching has occurred, by numerical simulation, we also find that for all parameter values (EBP) in Fig.10 the evolutionary branch with smaller $\beta$ will go extinct and the remaining branch with bigger $\beta$ will continue to evolve to a continuously stable strategy (CSS). Specifically, when $b_1 = 10.0$ and $\sigma_c = 0.0085$, then the trade-off function $b(\beta)$ in (18) is monotonically increasing and finally converges to a saturation state, which also looks like a sigmoidal curve (see the trade-off curve $\Pi$ in Fig.12b). In this case, from Fig.11 it can be seen that at time $\tau_2$, the equilibrium population density of susceptible hosts
Figure 9. Evolutionary extinction of one emerging branch. The trade-off function is given by (18) with parameters $b_0 = 0.05, b_1 = 5.5, b_2 = 0.05, b_3 = 0.8, \beta_0 = 0.0018$ and $\sigma_c = 0.008$. (a) A pairwise invasibility plot. (b) A trait evolution plot. The vector fields obtained from the deterministic model (29) indicate the directions of evolutionary change of traits $\beta_1$ and $\beta_2$. The black curves and red curves indicate the isolines of traits $\beta_1$ and $\beta_2$, respectively. The solid curves indicate the evolutionarily singular strategies which are evolutionarily stable, whereas the dashed curves indicate the evolutionarily singular strategies which are not evolutionarily stable. (c) A simulated evolutionary tree obtained through simulation of models (11) and (29) with initial condition $\beta(0) = 0.0015$. At evolutionary time $\tau_1$ evolutionary branching occurs and at evolutionary time $\tau_2$ the emerging branch $\beta_2$ become extinct. (d) Equilibrium population densities of susceptible hosts when the traits $\beta_1$ and $\beta_2$ evolve. At evolutionary time $\tau_2$, the equilibrium population density of susceptible hosts $S_2$ becomes zero. The dashed curve indicates the total equilibrium population density of the two types of susceptible hosts. (e) Equilibrium population density of infected hosts when the traits $\beta_1$ and $\beta_2$ evolve. Other parameter values: $\alpha = 0.075, m_0 = 0.0055, m_1 = 0.000098, \mu = 0.01, \sigma = 0.00005$. 
Figure 10. Bifurcation diagram of monomorphic evolutionary dynamics when one of the parameters in the model is changed. The trade-off function and parameter values are the same as in Fig. 9 except for $b_1 = 10.0$ and $\sigma_c = 0.0085$. (a) Evolutionarily singular strategy $\beta^*$ versus the maximum birth rate $b_1$. (b) Evolutionarily singular strategy $\beta^*$ versus the shape parameter $\sigma_c$. (c) Evolutionarily singular strategy $\beta^*$ versus the natural death rate $m_0$. (d) Evolutionarily singular strategy $\beta^*$ versus the strength of density-dependent mortality $m_1$. In (a), (b), (c) and (d), arrows indicate the direction of evolutionary change. The black solid curves indicate the evolutionarily singular strategies which are both convergence stable and evolutionarily stable; the red dashed curves indicate the evolutionarily singular strategies which are not evolutionarily stable. CSS denotes the continuously stable strategy; EBP denotes the evolutionary branching point. The grey region indicates combination of $\beta$ and $b(\beta)$ for which the endemic equilibrium $(S^*(\beta), I^*(\beta))$ is globally asymptotically stable.
$S_1$ becomes zero, that is, at evolutionary time $\tau_2$ the host strain with relatively stronger resistance will become extinct. In summary, from Figs. 8, 9, 10 and Fig. 11, we can see that for a larger range of parameter values the evolutionary branch with stronger resistance may go extinct and the remaining branch with relatively weaker resistance may continue to evolve to a continuously stable strategy (CSS). Particularly, for the parameter values in Fig. 8 and Fig. 10 we find that the trade-off curve looks like a sigmoidal curve. In other words, under certain demographic conditions extinction of one evolutionary branch may occur for a sigmoidal trade-off curve.

By the above analysis, combining with the saturation characteristic of the trade-off function, we obtain the following results (see Table 1).

| Evolutionary outcomes | Evolutionary conditions | Shape of trade-off function |
|-----------------------|-------------------------|-----------------------------|
| CSS $\beta^*$        | $b'(\beta^*) < 0$       | Globally concave            |
| EBP $\beta^*$        | $0 < b'(\beta^*) < b''_{crit}(\beta^*)$ | Concave-convex-concave or sigmoidal |
| CSS $(\beta^*_1, \beta^*_2)$ | $b''(\beta^*_i) < 0, (i = 1, 2)$ | Concave-convex-concave |
| Extinction of one branch | No attracting singular strategies | Sigmoidal |

Note: CSS means continuously stable strategy; EBP means evolutionary branching point.

5. Discussion and conclusions. Understanding the evolutionary dynamics of host resistance in the light of ecological feedbacks has important implications for the prevention and control of infectious disease. In this paper, based on a classical susceptible-infected (SI) model with density-dependent mortality and the method of adaptive dynamics, we investigated the evolutionary dynamics of host resistance to pathogen infection. We assumed that only the host resistance-related traits can adaptively evolve, but there exists a trade-off relationship between the host resistance and its fertility. Particularly, it can be seen that the existence of density-dependent mortality on both infecteds and susceptibles allowed us to construct a standard Lyapunov function to prove the globally asymptotical stability of endemic equilibrium and the result of ‘invasion implies trait substitution’. If we ignored the density-dependent mortality on infected hosts, it was difficult to prove the globally asymptotical stability of endemic equilibrium and the result of ‘invasion implies trait substitution’.

Different from previous studies, by using the technique of critical function analysis, we identified the general features of trade-off function that allow for a continuously stable strategy and evolutionary branching of host resistance. Particularly, we showed that the critical function curve is always convex, near a singular strategy if the trade-off curve is convex but less convex than that of the critical function curve, then the singular strategy is an evolutionary branching point (EBP). This method helped us identify the general shapes of trade-off curve that will induce an evolutionary branching point or an evolutionarily stable strategy [36, 75, 76]. Using this method, the stability of evolutionarily singular strategy is also easily obtained through comparing the curvature of two curves, which is more intuitive. Specifically, we found that the finally evolutionary outcomes depend mainly on the shape and strength of trade-off function. In other words, which evolutionary outcome will occur relies largely on a balance between costs (here, reduction in birth rate) and benefits (here, resistance to transmission of the pathogen) [10, 4, 41]. We showed that if there is an accelerating cost, then a continuously stable strategy is
Figure 11. Evolutionary extinction of one existing branch. The trade-off function and parameter values are the same as in Fig. 9 except for $b_1 = 10.0$ and $\sigma_c = 0.0085$. (a) A pairwise invasibility plot. (b) A trait evolution plot. The vector fields obtained from the deterministic model (29) indicate the directions of evolutionary change of traits $\beta_1$ and $\beta_2$. The black curves and red curves indicate the isoclines of traits $\beta_1$ and $\beta_2$, respectively. The solid curves indicate the evolutionarily singular strategies which are evolutionarily stable, whereas the dashed curve indicates the evolutionarily singular strategies which are not evolutionarily stable. (c) A simulated evolutionary tree obtained through simulation of models (11) and (29) with initial condition $\beta(0) = 0.0006$. At evolutionary time $\tau_1$ evolutionary branching occurs and at evolutionary time $\tau_2$ the existing branch $\beta_1$ becomes extinct. (d) Equilibrium population densities of susceptible hosts when the traits $\beta_1$ and $\beta_2$ evolve. At evolutionary time $\tau_2$, the equilibrium population density of susceptible hosts $S_1$ becomes zero. The dashed curve indicates the total equilibrium population density of the two types of susceptible hosts. (e) Equilibrium population density of infected hosts when the traits $\beta_1$ and $\beta_2$ evolve.
Figure 12. The trade-off curve $b(\beta)$. The trade-off function is given by (18). (a) The trade-off curve $I$ is concave-convex-concave when $\sigma_c = 0.0002$. The trade-off curve $II$ is also concave-convex-concave, but with a wider convex region when $\sigma_c = 0.0005$. Other parameter values: $b_0 = 0.055, b_1 = 4.0, b_2 = 0.05, b_3 = 0.05, \beta_0 = 0.0005$. (b) The trade-off curve $I$ looks like a sigmoidal curve when $b_1 = 5.5$ and $\sigma_c = 0.008$. The trade-off curve $II$ looks also like a sigmoidal curve, but with a larger maximum birth rate when $b_1 = 10.0$ and $\sigma_c = 0.0085$. Other parameter values: $b_0 = 0.05, b_2 = 0.05, b_3 = 0.8, \beta_0 = 0.0018$.

predicted. Alternatively, with a weakly decelerating cost, we found that evolutionary branching in the host resistance is possible [10, 76, 77, 4, 41]. Furthermore, for a globally concave trade-off function, we found that if the initial resistant ability is relatively strong, then the evolution of host resistance may lead to an increase of basic reproduction number $R_0$. However, if the initial resistant ability is relatively weak, then the evolution of host resistance may result in a decrease of basic reproduction number $R_0$. Particularly, in this model, we found that for any monotonically increasing function $b(\beta)$, $R_0$ is always a monotonically increasing function.
with respect to $\beta$, depending on the initial resistant ability, the evolution of trait may increase or decrease the value of $R_0$. Therefore, in general, we conjecture that if there is a trade-off relationship between the studied trait and another life-history trait, then $R_0$ may be a monotonic function with respect to the studied trait. $R_0$ is almost never maximized or minimized, which is consistent with previous studies [51].

Moreover, by using the method of implicit differentiation, we found that independent of the trade-off function, the values of continuously stable strategy (CSS) and evolutionary branching point (EBP) will always increase as the strength of density-dependent mortality or the natural death rate or the pathogen-induced mortality rate increases. Through evolutionary bifurcation analysis, it was also found that evolutionary branching in the host resistance is possible for a wide range of values of demographic parameters and different types of trade-off functions. Particularly, we found that the presence of a density-dependent mortality plays a crucial role in the evolutionary branching of host resistance. If there is no density-dependent mortality, then the evolutionary branching in the host resistance may not occur. This means that in order to determine whether the branching occurs, the susceptible host must balance the costs and benefits on the basis of the resistant ability, reproductive ability and other demographic conditions. It should be noted that in this paper we only considered a simple susceptible-infected (SI) model. It would be interesting to study the evolutionary branching in the host resistance based on a more realistic epidemic model, such as susceptible-infected-susceptible (SIS) model or susceptible-infected-recovered (SIR) model. In addition, defence mechanisms in hosts include not only avoiding becoming infected, but also recovering more quickly after infection or surviving longer once infected, therefore, it is also interesting to explore the evolution of costly host resistance with different defence mechanisms, such as recovery (increase in the clearance rate) or tolerance (reduction in the death rate due to infection) [16, 39, 10, 4, 41].

After evolutionary branching in the host resistance has occurred, we found that depending on the specific shape and strength of trade-off relationship, the susceptible host population may evolve into an evolutionarily stable dimorphism or the evolutionary branching is followed by the loss of one host strain. For one thing, different from previous studies, through rigorously mathematical analysis we found that if the trade-off curve is concave-convex-concave and tangential to a straight line at two separate points, then for a large range of demographic parameter values the susceptible host population will eventually evolve into two different types, which can continuously stably coexist on a much longer evolutionary timescale [3, 12, 72, 76, 77, 41]. Moreover, for a concave-convex-concave trade-off curve, if the width of convex region is relatively big, then after branching has occurred in the host resistance, by numerical simulation we found that one of the dimorphic susceptible host will evolve towards the boundary of $(\beta_1, \beta_2)$ phase-plane, at which one host strain tend to be maximally resistant, the other host strain may have a moderate resistance, which can also continuously stably coexist on a long-term evolutionary timescale, even though in this case there may not exist an interior evolutionarily singular dimorphism. After branching, numerical simulation analysis furthermore showed that the equilibrium population densities of the two types of susceptible hosts are finally very close to each other (whether this is a general phenomenon needs to further study), and the dimorphic evolution of susceptible
hosts may increase the equilibrium population density of infected hosts. Therefore, we can say that for a type of concave-convex-concave trade-off relationship, in the simple susceptible-infected community the monomorphic susceptible host can become dimorphic and the dimorphic susceptible host can continuously stably coexist on the long-term evolutionary timescale, no further evolutionary branching is possible \cite{72, 76, 77, 41}. In real world systems, the particular forms of the trade-off function that lead to the evolutionarily stable dimorphism might arise through pleiotropy or resource allocation. However, it should be noted that such coexistence is not necessarily stable against other life-history traits evolving on a much longer evolutionary timescale (such as recovery rate and pathogenicity) \cite{36, 77, 41}. Therefore, it remains interesting to investigate how robust the coexistence is and under what conditions the evolutionary branching in the host resistance can induce the secondary branching in the infected host population.

For another, Best et al. \cite{4} showed that for sufficiently complex polynomial trade-offs, this is, polynomials of degree three or higher, the resulting invasion boundaries may form closed ‘oval’ areas of invadability and strategy coexistence. If there are no attracting singular strategies existing within this region, then the evolution of dimorphic hosts is destined to result in the loss of one host strain. Different from the result of Best et al. \cite{4}, we found that if the saturated trade-off curve looks like a sigmoidal curve (may not be a polynomial trade-off of degree three or higher) and there is no straight line which is tangential to the trade-off curve at two separate points, then the evolutionary branching of host resistance may be possible, but it can not bring about an evolutionarily stable dimorphism. On the contrary, after branching has occurred, numerical simulation analysis showed that depending on the initial resistant ability, the dimorphic host will firstly evolve to the edge of coexistence region (the coexistence region may not be a closed ‘oval’ area), and then the evolutionary branch with stronger resistance will become extinct (i.e., the corresponding equilibrium population density will become zero) and the remaining branch will continue to evolve to a continuously stable strategy and come to a halt, which implies that the diversity is lost forever. In particular, for two different parameter sets, we found that the host with high resistance always evolved into extinction, whether this is a general phenomenon needs to be further studied. In real world systems, such a complex trade-off function is possible if defence is made up of multiple defence reactions, such as \textit{Drosophila melanogaster}, which uses local and systemic immune as well as physical barriers responses to pathogens \cite{4, 50}. Through numerical simulation, we found that for a large range of parameter values the phenomenon of ‘evolutionary murder’ may occur, which implies that the dimorphic susceptible hosts may be non viability on the long-term evolutionary timescale \cite{35, 42, 62, 23, 5, 4, 77, 41}. From the above specific examples, we can see that for the same trade-off function, different shapes and strengths may lead to entirely different evolutionary outcomes. Our results further highlight the importance of trade-offs to evolutionary behaviour of host resistance \cite{4, 41}. In particular, numerical simulations showed that the evolution of host resistance may reduce the equilibrium population density of susceptible hosts, in contrast it may increase the equilibrium population density of infected hosts. This phenomenon is a bit of a violation of our intuition and has not been observed in previous works. In addition, we also found that even though all mutations are small, the combination of evolutionary branching and loss of one host strain has effectively allowed the initially monomorphic host population to jump across the repellor and to continue
its monomorphic evolution on the other side [35, 42, 16, 62, 23, 5, 76, 77, 41]. It’s worth noting that if a singular dimorphism does not exist, then depending on the evolutionary speed and trade-off function, two host strains may just sit at their maxima and minima provided there is a route through the coexistence region or they may continue to coexist indefinitely at the respective maximum and minimum trait values. These are still interesting questions worth further studying.

To sum up, the novelty of this study is reflected in the following several aspects. Firstly, by using the method of Lyapunov function, we rigorously proved the globally asymptotical stability of endemic equilibrium and the result of ‘invasion implies substitution’, which is necessary for studying the evolutionary dynamics of host resistance step by step. Based on this population model, we can further study whether the evolutionary branching in the host may lead to evolutionary branching in the pathogen. Secondly, the main contribution of this paper was the use of critical function analysis to gain insight into the types of trade-offs that support different evolutionary outcomes for host resistance evolution. Thirdly, after branching we examined the coevolutionary dynamics of dimorphic susceptible hosts. We derived the demographic and evolutionary conditions that allow for a continuously stable coexistence of the dimorphic hosts and the loss of one host strain. Fourthly, we performed numerical bifurcation analysis of evolutionary dynamics and discussed the influence of demographic parameters on the evolutionary behaviour of host resistance, which is helpful for us to develop an analytical method for the bifurcation theory of evolutionary dynamics. In other words, based on a simple susceptible-infected (SI) model, we found a variety of evolutionary behaviour of host resistance. Therefore, this paper provided a typical example for analyzing the evolutionary invasion process of host resistance-related traits by using the method of adaptive dynamics.

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