

Coevolution in multidimensional trait space favours escape from parasites and pathogens

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Almost all species are subject to continuous attack by parasites and pathogens. Because parasites and pathogens tend to have shorter generation times^{1,2} and often experience stronger selection due to interaction than their victims do^{3,4}, it is frequently argued that they should evolve more rapidly and thus maintain an advantage in the evolutionary race between defence and counter-defence^{1,5}. This prediction generates an apparent paradox: how do victim species survive and even thrive in the face of a continuous onslaught of more rapidly evolving enemies? One potential explanation is that defence is physiologically, mechanically or behaviourally easier than attack, so that evolution is less constrained for victims than for parasites or pathogens⁶. Another possible explanation is that parasites and pathogens have enemies themselves and that victim species persist because parasites and pathogens are regulated from the top down and thus generally have only modest demographic impacts on victim populations^{7,8}. Here we explore a third possibility: that victim species are not as evolutionarily impotent as conventional wisdom holds, but instead have unique evolutionary advantages that help to level the playing field. We use quantitative genetic analysis and individual-based simulations to show that victims can achieve such an advantage when coevolution involves multiple traits in both the host and the parasite.

Most coevolutionary theory has focused on cases in which the interaction rate between two species is governed by a single trait in each species⁹ (but see refs 10–12). In nature, however, species–species interaction rates can depend on multiple traits¹³. For example, the resistance of wild parsnip to webworm attack depends on flowering phenology and on the concentrations of at least two different furanocoumarins in the plant¹⁴. Similarly, many teleost fish use both mucosal barriers and biocidal secretions to defend against monogenean and copepod parasites, and parasites must overcome both mechanisms to infect the host successfully¹⁵. Recent work has shown that the number of traits under selection can have qualitative effects on the outcome of evolution in single-species systems¹⁶. Thus, it is reasonable to ask whether the number of traits may also affect the outcome of coevolution.

To investigate the influence of the number of traits on coevolutionary trajectories, we developed a model of a victim–exploiter system in which the probability of a successful attack by an exploiter on a victim depends on n traits in each species. We assumed that each trait is functionally paired with a trait in the opposite species. When an exploiter encounters a potential victim, the probability of a successful attack depends on the suites of trait values in each individual. We call the probability of successful attack for a given encounter the ‘interaction probability’ to distinguish it from the interaction rate, which also depends on the densities of both species. The interaction probability may be highest when the exploiter’s trait value exceeds that of the victim (that is, difference traits) or when the individuals have similar trait values (that is, matching traits) at each functional pair. For example, the pericarp thickness of the Japanese camellia (*Camellia japonica*) and the rostrum length of its seed-parasitic weevil (*Curculio camelliae*) comprise a difference trait pair¹⁷, whereas the flowering phenology of *Heuchera*

grossulariifolia and the emergence time of its seed-parasitic moth *Greya politella* comprise a matching trait pair¹⁸. Differences in interaction probabilities between individuals with different trait values impose selection on traits and lead to coevolution between the species. We assumed that each trait affects the interaction probability independently. Thus, the victim can achieve a low interaction probability if it evolves at least one defence mechanism that avoids or overcomes the exploiter’s attack. Biologically, this corresponds to the common situation in which an attacker must overcome all of the chemical, morphological, physiological and behavioural defences of the victim for its attack to succeed^{13,15,19}. If the victim can evolve to lower its interaction probability with its exploiter, we say the victim ‘wins’ the evolutionary contest.

We used a quantitative genetic analysis^{20,21} of our model to extend Kirkpatrick’s concept of maximum evolvability²² for a single species to a maximum evolutionary escape rate for a victim–exploiter system (Methods). When the maximum evolutionary escape rate is greater than zero, the victim evolves to overcome or avoid the exploiter’s attack, and so wins the evolutionary contest. Our analysis assumes fixed genetic variance–covariance matrices (that is, G-matrices²⁰) in each species and weak selection due to interspecific interactions. For a very general class of interaction probability functions in the difference trait case, the maximum evolutionary escape rate is

$$\delta_{d,\max} = \max[-(s_v \mathbf{G}_v + s_e \mathbf{G}_e) \xi_a], \quad (1)$$

where \mathbf{G}_v and \mathbf{G}_e are the G-matrices of the victim and exploiter populations, s_v and s_e represent the effect of one interaction on the relative fitness of a victim or an exploiter, and ξ_a is a vector that captures the strength of effect of traits 1 to n on the interaction probability. For a very general class of interaction probability functions in the matching trait case, the maximum evolutionary escape rate is

$$\delta_{m,\max} = \max[\text{eig}[-(s_v \mathbf{G}_v + s_e \mathbf{G}_e) \xi_x]], \quad (2)$$

where ξ_x is a diagonal matrix in which the i th entry captures the strength of effect of trait i on the interaction probability.

In representative systems where victim and exploiter G-matrices were randomly and independently generated, increasing the number of traits or the strength of correlations between traits increased the probability that the maximum evolutionary escape rate would be greater than zero, and thus that the victim would win the evolutionary contest (Fig. 1). Intuitively, this is true because victims need to overcome their exploiters at only one trait if they are to escape, whereas exploiters must overcome their victims at all traits if they are to succeed. Each additional trait that affects the interaction probability provides the victim with an additional opportunity to evolve an effective escape mechanism. Correlations between traits constrain the evolution of some traits but facilitate the evolution of others. When correlations are strong, it is more likely that the victim’s evolution will be strongly facilitated or the exploiter’s evolution will be strongly constrained in at least one trait, and thus that the victim will evolve to escape the exploiter at that trait.

Our quantitative genetic analysis assumes that selection is weak and G-matrices are constant, but in nature selection due to interspecific

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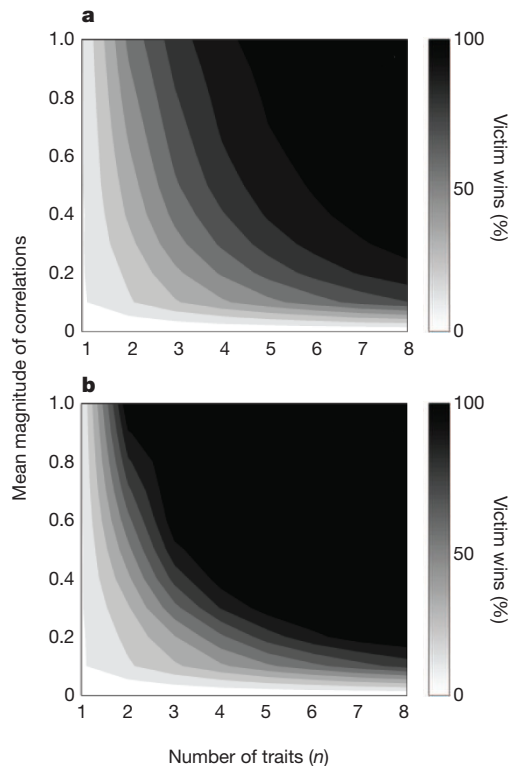


Figure 1 | Percentage victim wins as a function of the number of traits n and the mean magnitude of correlations between traits. **a**, The difference trait case. **b**, The matching trait case. In all simulations $s_e = 1$ and $s_v = -0.3$. In the difference trait case $\xi_{ai} = \xi_{aj}$ and in the matching trait case $\xi_{ai} = \xi_{aj}$ for all $[i, j]$.

interactions can be strong and G-matrices can evolve^{23–25}. We used genetically explicit individual-based simulations^{24,25} to test the robustness of our analytical results when the assumptions of our quantitative genetic analysis were violated (Methods). We initially assumed that the sizes of the victim and exploiter populations were independent of the interspecific interaction rate. This might be true, for example, if the exploiter has alternative victim species and if the victim population is regulated by something other than exploitation (for example, resource competition). As predicted, victims were more likely to evolve to lower their interaction probabilities with their exploiters when the number of traits governing the interaction probability was large and when the correlations between traits were strong (Tables 1 and 2). This result holds whether interaction probabilities are governed by difference traits, matching traits, or combinations of difference and matching traits (Methods and Supplementary Table 1).

The mechanisms that promote evolutionary escape in the quantitative genetic analysis also operate in numerical simulations. However, numerical simulations revealed an additional mechanism: G-matrices in the victim and exploiter populations evolve to favour the victim

Table 1 | Outcome of coevolution in the difference trait case

n	$r_p = 0.00$	$r_p = 0.08$	$r_p = 0.26$	$r_p = 1.00$
1	0.7222* (17*)	–(–)	–(–)	–(–)
2	0.6703 (17)	0.6295 (18)	0.5963 (32)	0.4621 (39)
4	0.5633 (19)	0.5267 (31)	0.3304 (63)	0.1745 (77)
8	0.4639 (26)	0.4024 (34)	0.1789 (82)	0.0336 (96)

We conducted 100 simulations for each combination of trait number n and correlation strength r_p . We recorded a victim win if the mean interaction probability decreased over 2,000 generations of interaction. Results are shown as mean final interaction probability (percentage victim wins). The parameter r_p is the mean magnitude of correlations between pairs of traits in the same species at the beginning of each simulation. Biologically, r_p can be interpreted as the expected magnitude of correlations between traits due to pleiotropy alone. The magnitude and direction of correlations can change as G-matrices evolve (see Methods), and we measured r_p at the beginning of each simulation to capture correlation strength before selection had altered G-matrices.

*Correlation is not meaningful when $n = 1$.

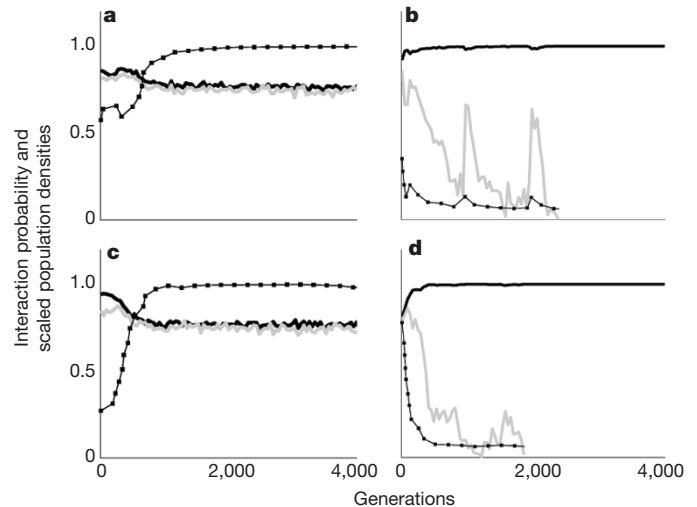


Figure 2 | Interaction probabilities and population densities in representative numerical simulations. Beaded lines show the mean interaction probability in each generation. Black lines show the victim density, and grey lines the exploiter density, with densities scaled to the carrying capacity of the victim. **a**, **b**, The difference trait case for $n = 1$ (**a**; $\delta_{d,max} = -0.012$) and $n = 4$ (**b**; $\delta_{d,max} = 0.046$). **c**, **d**, The matching trait case for $n = 1$ (**c**; $\delta_{m,max} = -0.029$) and $n = 4$ (**d**; $\delta_{m,max} = 0.069$). Maximum evolutionary escape rates were calculated in the first pictured generation of each simulation, but changed as G-matrices evolved.

species increasingly as the number of traits in the system increases. In the difference trait case, this happens because antagonistic interspecific interactions cause negative correlations to evolve between the victim's defensive traits. These negative correlations constrain victim evolution. As the number of traits in the system increases, these negative correlations dissipate, and the constraint on victim evolution is removed (Methods and Supplementary Table 5). In the matching trait case, antagonistic interactions cause increased variance in the traits of the victim population and decreased variance in the traits of the exploiter population^{10,26}. Greater genetic variance in the victim population allows the victim to evolve more rapidly relative to the exploiter. As the number of traits in the system increases, the genetic variance in the victim population increases relative to that in the exploiter population (Methods and Supplementary Table 6). As a result, the victim can evolve away from the exploiter more rapidly when the number of traits in the system is large.

In nature, victim and exploiter population sizes can be sensitive to interaction rates, and therefore coevolution can affect population dynamics. To test whether our qualitative results hold in such cases, we performed additional simulations in which the absolute fitnesses of individuals in each population depended on the number of interactions in which those individuals participated (Methods). These simulations showed two qualitatively different ecological outcomes (Fig. 2). In the first, the exploiter evolves faster than the victim in all traits. The interaction probability approaches one, and the exploiter wins the evolutionary contest (Fig. 2a, c). In the second, the victim evolves faster than the exploiter in at least one trait. The interaction probability declines and the exploiter population shrinks. As exploiters become less common, selection for increased victim defence is reduced, and the

Table 2 | Outcome of coevolution in the matching trait case

n	$r_p = 0.00$	$r_p = 0.08$	$r_p = 0.26$	$r_p = 1.00$
1	0.7447* (22*)	–(–)	–(–)	–(–)
2	0.6700 (22)	0.6602 (25)	0.5724 (37)	0.2980 (59)
4	0.5262 (26)	0.4633 (33)	0.2373 (76)	0.0583 (92)
8	0.3239 (43)	0.2425 (55)	0.0399 (98)	0.0074 (98)

We conducted 100 simulations for each combination of trait number n and correlation strength r_p . We recorded a victim win if the mean interaction probability decreased over 2,000 generations of interaction. Results are shown as mean final interaction probability (percentage victim wins).

*Correlation is not meaningful when $n = 1$.

rate of victim evolution slows. As a result, the exploiter may be able to persist with a low interaction probability and a low population density (Fig. 2b, d). If the populations are sufficiently small, the chance fixation of favourable mutations in the victim or unfavourable mutations in the exploiter can reduce the interaction probability until the exploiter cannot achieve a positive population growth rate. If this happens, the exploiter population crashes and there is little opportunity for new favourable mutations to rescue the rapidly shrinking exploiter population from extinction. In the difference trait, matching trait and mixed trait cases, the probability that the victim evolves to lower its interaction probability with its exploiter, and the probability that the exploiter goes extinct, increase as the number of traits or the strength of the correlations between traits increases (Methods and Supplementary Tables 2–4). This supports the results of our fixed-population analyses.

Our study is motivated by host–parasite systems, but our models are general to any victim–exploiter species pair. For example, in nature predators must first detect, then capture, and finally subdue their victims, and victims have defensive traits to thwart their predators at each stage of the attack¹³. The presence of multiple defence mechanisms may help prey species to evolve and maintain low interaction rates with their predators. Similarly, herbivores often experience meaningful loss of fitness as a result of the various defence mechanisms of their host plants^{27,28}. Coevolution in highly dimensional trait space may help plants to limit the damage they receive from herbivores, and so may help to explain why the world is green²⁹.

METHODS SUMMARY

We modelled a victim–exploiter system in which selection is due only to inter-specific interactions. Exploiters encounter potential victims at random, and they interact with a probability that depends on a suite of n genetically determined traits in each individual.

Quantitative genetic analysis. Under appropriate assumptions (Methods), the change in population mean trait values during one generation is^{20,21}

$$\begin{aligned}\Delta \bar{z}_e &= \mathbf{G}_e \boldsymbol{\beta}_e \\ \Delta \bar{z}_v &= \mathbf{G}_v \boldsymbol{\beta}_v\end{aligned}\quad (3)$$

where each $\boldsymbol{\beta}_x$ is a vector of selection gradients that depends on the interaction probability function, the fitness effect of interactions and the trait values in each population. For difference trait systems, we determined whether the victim wins by analysing the conditions under which $\Delta \bar{z}_{vi} > \Delta \bar{z}_{ei}$ for at least one i . For matching trait systems, (3) has an equilibrium at $\bar{z}_e = \bar{z}_v$. We determined whether the victim wins by analysing the conditions under which the maximum eigenvalue of the Jacobian of (3) evaluated at $\bar{z}_e = \bar{z}_v$ is greater than zero.

Numerical simulations. We complemented our analytical approach with genetically explicit individual-based simulations^{21,22}. Trait values in either species were governed by a set of unlinked, diallelic loci with pleiotropic alleles. Pleiotropy and linkage disequilibria caused correlations between trait values in each population. We considered two well-studied heuristic interaction probability functions. An exploiter with trait values ($z_{e1}, z_{e2}, \dots, z_{en}$) interacts with a victim with trait values ($z_{v1}, z_{v2}, \dots, z_{vn}$) with probability

$$P(I|z_{e1}, z_{e2}, \dots, z_{en}, z_{v1}, z_{v2}, \dots, z_{vn}) = \prod_{i=1}^n (1 + \exp(-g_i(z_{ei} - z_{vi})))^{-1} \quad (4)$$

in the difference trait case and

$$P(I|z_{e1}, z_{e2}, \dots, z_{en}, z_{v1}, z_{v2}, \dots, z_{vn}) = \prod_{i=1}^n \exp(-\gamma_i(z_{ei} - z_{vi})^2) \quad (5)$$

in the matching trait case. Parameters g_i and γ_i determine the sensitivity of the interaction probability to trait i . Reproduction is sexual, and individuals produce offspring in proportion to their fitnesses after interactions. This framework allows trait means, variances and covariances to evolve. We iterated generations and recorded whether the interaction probability between exploiters and victims increased (that is, the exploiter won) or decreased (that is, the victim won) over time.

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