SI Appendix: The Red Queen and King in finite populations

Carl Veller[*,†] Laura Hayward[‡] Christian Hilbe[§] Martin A. Nowak[*,†,¶]

Contents

[*]Department of Organismic and Evolutionary Biology, Harvard University, Massachusetts, U.S.A.
[†]Program for Evolutionary Dynamics, Harvard University, Massachusetts, U.S.A.
[‡]Department of Mathematics, Columbia University, New York, U.S.A.
[§]IST Austria, Am Campus 1, 3400 Klosterneuburg, Austria
[¶]Department of Mathematics, Harvard University, Massachusetts, U.S.A.

S1 Transition probabilities and time evolution of symbiotic dynamics

Here, we describe our full dynamical model of symbiosis evolution, calculate the probabilities of transitions from state to state, and use these to calculate the time evolution of the probability distribution over population states, given some initial distribution.

We suppose that the symbiosis is characterized by pairwise interactions according to the following asymmetric game:

		Player 2	
		C	D
Player 1	A	α_{AC}, β_{AC}	α_{AD}, β_{AD}
	B	α_{BC}, β_{BC}	α_{BD}, β_{BD}

(1)

Populations 1 and 2 (composed of player 1s and player 2s respectively) are of sizes N_1 and N_2, and have relative generation times g_1 and g_2. Each time-step, each individual receives its average payoff from interacting with a random member of the other population (each equally likely). If, in a given time-step, i members of population 1 play A, and j members of population 2 play C, then we may describe the population state in that time-step simply as (i, j), and the average payoff to individuals playing strategies A, B, C, and D are:

$$\pi_A(i,j) = \frac{j}{N_2}\alpha_{AC} + \frac{N_2 - j}{N_2}\alpha_{AD};$$
$$\pi_B(i,j) = \frac{j}{N_2}\alpha_{BC} + \frac{N_2 - j}{N_2}\alpha_{BD};$$
$$\pi_C(i,j) = \frac{i}{N_1}\beta_{AC} + \frac{N_1 - i}{N_1}\beta_{BC};$$
$$\pi_D(i,j) = \frac{i}{N_1}\beta_{AD} + \frac{N_1 - i}{N_1}\beta_{BD}.$$

If an individual in population l receives average payoff π, this translates to a positive fitness f via $f = 1 + w_l\pi$, so that $w_1, w_2 > 0$ calibrate the strength of selection in the two populations. The fitnesses of individuals playing the various strategies in population state (i, j) are $f_A(i,j) = 1 + w_1\pi_A(i,j)$, $f_B(i,j) = 1 + w_1\pi_B(i,j)$, $f_C(i,j) = 1 + w_2\pi_C(i,j)$, and $f_D(i,j) = 1 + w_2\pi_D(i,j)$

In each elementary time step, exactly one birth-death event occurs between the two populations. With probability $\frac{N_1/g_1}{N_1/g_1+N_2/g_2}$ this is in population 1, and with probability $\frac{N_2/g_2}{N_1/g_1+N_2/g_2}$ it is in population 2. If a birth-death event occurs in population l in a given time-step, then one individual in population l is chosen to reproduce, with probability proportional to fitness, and one individual is chosen to die, with each equally likely. The

same individual can be chosen to reproduce and die. The reproducing individual produces an offspring, which replaces the individual chosen to die. With probability $1-\varepsilon\mu_l$, the offspring inherits the strategy its parent plays, and with probability $\varepsilon\mu_l$ the offspring plays the other strategy instead (it 'mutates').

With populations of size N_1 and N_2, there are $n=(N_1+1)(N_2+1)$ possible populations states (i,j), which can be given some (arbitrary) enumeration $1,2,\ldots,n$. Let $P_{(i,j)\to(i',j')}$ be the probability that the system moves in one time-step from state (i,j) to step (i',j'). These one-step transition probabilities are:

$$P_{(i,j)\to(i+1,j)}=\frac{N_1/g_1}{N_1/g_1+N_2/g_2}\cdot\left[(1-\varepsilon\mu_1)\frac{if_A(i,j)}{if_A(i,j)+(N_1-i)f_B(i,j)}\frac{N_1-i}{N_1}+\varepsilon\mu_1\frac{N_1-i}{N_1}\right];$$
$$P_{(i,j)\to(i-1,j)}=\frac{N_1/g_1}{N_1/g_1+N_2/g_2}\cdot\left[(1-\varepsilon\mu_1)\frac{(N_1-i)f_B(i,j)}{if_A(i,j)+(N_1-i)f_B(i,j)}\frac{i}{N_1}+\varepsilon\mu_1\frac{i}{N_1}\right];$$
$$P_{(i,j)\to(i,j+1)}=\frac{N_2/g_2}{N_1/g_1+N_2/g_2}\cdot\left[(1-\varepsilon\mu_2)\frac{jf_C(i,j)}{jf_C(i,j)+(N_2-j)f_D(i,j)}\frac{N_2-j}{N_2}+\varepsilon\mu_2\frac{N_2-j}{N_2}\right];$$
$$P_{(i,j)\to(i,j-1)}=\frac{N_2/g_2}{N_1/g_1+N_2/g_2}\cdot\left[(1-\varepsilon\mu_2)\frac{(N_2-j)f_D(i,j)}{jf_C(i,j)+(N_2-j)f_D(i,j)}\frac{j}{N_2}+\varepsilon\mu_2\frac{j}{N_2}\right];$$

with $P_{(i,j)\to(i,j)}=1-P_{(i,j)\to(i+1,j)}-P_{(i,j)\to(i-1,j)}-P_{(i,j)\to(i,j+1)}-P_{(i,j)\to(i,j-1)}$, and $P_{(i,j)\to(i',j')}=0$ for all other states (i',j'). We refer to the $n\times n$ matrix P that contains these one-step transition probabilities as the transition matrix of the complete Markov chain.

Given some initial probability distribution over the set of population states, $\mathbf{v}^0=\left(v^0_{(i,j)}\right)$, we can compute the distribution over population states after t time-steps by taking t successive powers of the transition matrix P:

$$\mathbf{v}^t=\mathbf{v}^0P^t. \tag{2}$$

Note that $\mathbf{v}^t$ is a stochastic vector of length n, respecting the particular enumeration $1,2,\ldots,n$ chosen for the n population states.

The stationary distribution, $\mathbf{v}=\lim_{t\to\infty}\mathbf{v}^t$, is the unique stochastic vector that solves, for each state (i,j),

$$v_{(i,j)}=\sum_{(i',j')}v_{(i',j')}P_{(i',j')\to(i,j)}. \tag{3}$$

S1.1 Mutualistic symbioses

The payoff matrix of the mutualism game [game (2) in the Main Text] is

		Player 2	
		C	D
Player 1	A	$2,1$	$0,0$
	B	k,k	$1,2$

(4)

Among the two coordination matchings, (A, C) and (B, D), population 1 prefers (A, C) and population 2 prefers (B, D). The other matchings give the members of populations 1 and 2 equal payoff. Therefore, given a population state (i, j), a measure of the success of population 1 in that state is simply the average proportion of (A, C) matchings in that state minus the average proportion of (B, D) matchings: $\frac{ij}{N_1 N_2} - \frac{(N_1-i)(N_2-j)}{N_1 N_2}$. Given any distribution over population states $\mathbf{p}$, we may calculate the expected value of population 1's success, $\sum_{(i,j)} p_{(i,j)} \cdot \left(\frac{ij}{N_1 N_2} - \frac{(N_1-i)(N_2-j)}{N_1 N_2}\right)$.

Therefore, given an initial distribution over population states, $\mathbf{v}^0 = \left(v^0_{(i,j)}\right)$, making use of Eq. (2), the expected value of population 1's relative success after t time-steps is:

$$\sum_{(i,j)} v^t_{(i,j)} \cdot \left(\frac{ij}{N_1 N_2} - \frac{(N_1 - i)(N_2 - j)}{N_1 N_2}\right). \tag{5}$$

This is the basis of Figs. 2 and 3 in the *Main Text*, and Figs. S1, S6B,C, and S5B,C,E,F in this *SI Appendix*. For each possible starting point, these figures begin with a degenerate initial distribution that is one at that point and zero elsewhere, and calculate according to Eq. (5) the average relative success of population 1 after a short-run and long-run number of time-steps. The figures display the results for all possible initial starting points.

S1.2 Antagonistic symbioses

The payoff matrix of the antagonism game [game (1) in the Main Text] is

		Player 2	
		C	D
Player 1	A	$1, 0$	$0, 1$
	B	$0, 1$	$1, 0$

(6)

Among the four matchings, population 1 prefers (A, C) and (B, D) while population 2 prefers (A, D) and $B, C)$. Therefore, given a population state (i, j), a measure of the success of population 1 in that state is the average proportion of (A, C) and (B, D) matchings in that state minus the average proportion of (A, D) and $B, C)$ matchings: $\frac{ij+(N_1-i)(N_2-j)}{N_1 N_2} - \frac{i(N_2-j)+(N_1-i)j}{N_1 N_2}$. Given any distribution over population states $\mathbf{p}$, we may calculate the expected value of population 1's success, $\sum_{(i,j)} p_{(i,j)} \cdot \left(\frac{ij+(N_1-i)(N_2-j)}{N_1 N_2} - \frac{i(N_2-j)+(N_1-i)j}{N_1 N_2}\right)$.

Given an initial distribution over population states, $\mathbf{v}^0 = \left(v^0_{(i,j)}\right)$, making use of Eq. (2), the expected value of population 1's relative success after t time-steps is:

$$\sum_{(i,j)} v^t_{(i,j)} \cdot \left(\frac{ij + (N_1 - i)(N_2 - j)}{N_1 N_2} - \frac{i(N_2 - j) + (N_1 - i)j}{N_1 N_2}\right). \tag{7}$$

This is the basis of Fig. 1 in the *Main Text*, and S6A, and S5A,D here.

S2 Numerical analysis of the complete Markov chain

The stochastic process for the complete Markov chain defined by Eq. (2) does not make any restrictions on the evolutionary parameters. It applies for any choice of generation times, mutation rates, strengths of selection, and population sizes. But computation of the time evolution of the distribution over population states requires us to calculate powers of a transition matrix of dimension $n \times n$, where $n = (N_1 + 1)(N_2 + 1)$, and so analytical results for arbitrary parameter values quickly become infeasible. However, provided that the two populations are of moderate size, we can still use Eq. (2) to obtain exact numerical results, which we report in what follows.

S2.1 Short-run dynamics versus long-run dynamics

For the complete Markov chain, we can distinguish two timescales. In the short run, the fate of the two populations largely depends on the populations' initial composition. For example, when mutualistic symbioses start close to one of the two equilibria, (A,C) or (B,D), they can be expected to further approach that equilibrium in the short run. But as time goes by, mutations and random movements against the gradient of selection can lead populations to leave one equilibrium, and to move near the other one. In the long run, the process's dependence on initial conditions disappears: as the transition matrix P in Eq. (2) is primitive, the eventual success of a population is independent of where the populations have started.

Figs. 1-3 in the *Main Text*, and Figs. S1, S6 show how differences in generation times, mutation rates, selection strength and population sizes affect population 1's success [as measured by Eqs. (5) and (7)] for the two different timescales. In mutualistic symbioses where k is large, we observe that populations with a longer generation time, lower selection strength and smaller population size have an advantage in the short run (i.e., the respective population is favored for a majority of initial conditions; see *Main Text* Fig. 2). In the long run, however, differences in generation time become largely irrelevant, and the weaker strength of selection and the smaller population size turn out to put population 1 at a disadvantage. These results are reversed when k is small (*Main Text* Fig. 3), in which case weaker selection is a disadvantage in the short run, but an advantage in the long run.

In antagonistic symbioses, the effect of the evolutionary parameters is unambiguous. Here, the population with shorter generation time, higher mutation rate, higher selection strength or larger population size is favored for all time scales.

S2.2 Robustness of results with respect to our modeling assumptions

In the Main Text, we predominantly considered in our long-run analysis the case where mutations are rare (i.e., where the parameter ε is very small). In addition, we assumed the fitness of an individual to be a *linear* function of its expected payoff, though other functions are also admissible. To show that these assumptions are not responsible for our

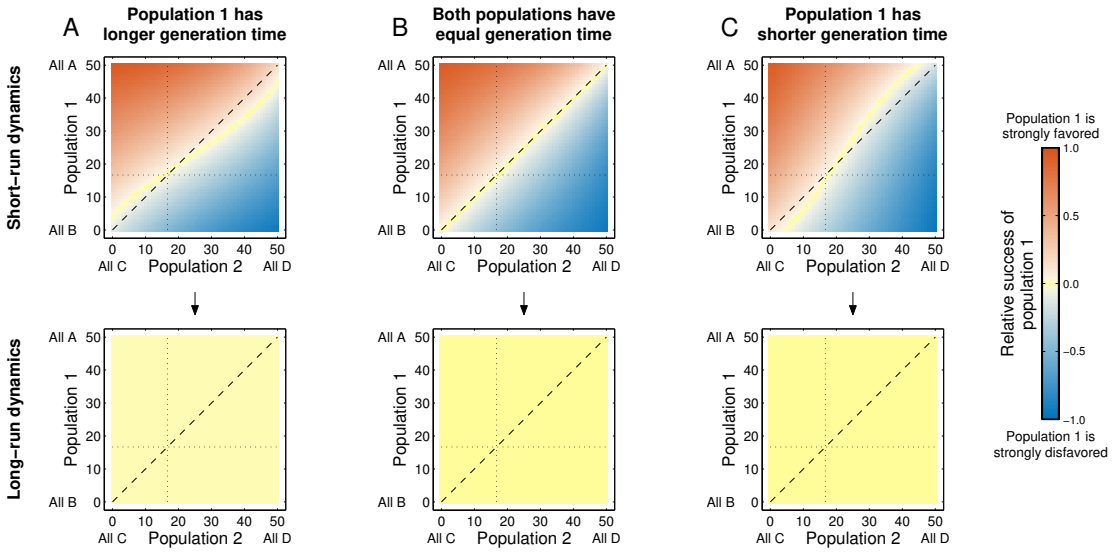


Figure S1: Mutualism dynamics when $k = 3/2$, and population 1 has (A) a longer generation time than population 2, (B) an equal generation time to population 2's, (C) a shorter generation time than population 2. For comparison with Fig. 2 in Bergstrom and Lachmann [1]. Each panel shows the numerically computed dynamics, assuming that both populations coincide in their other evolutionary parameters. The upper panels show population 1's success, as measured by Eq. (5), after 50 generations for every possible initial population (i.e., for each point in the squared state space). We observe a Red King effect: when population 1 has a longer generation time, the red area covers more than 50% of the square; the reverse is true when population 1 has a shorter generation time. These short-run results are similar to Bergstrom and Lachmann's, and indeed, the upper panels of this figure closely resemble their Fig. 2. The lower panels show the success of population 1 after 50,000 generations. By this time, selection-mutation equilibrium has been reached, so that the starting point no longer influences the dynamics: all lower panels have a uniform color. The populations are equally successful in the long run, no matter their relative generation times. Parameters: $k = 3/2$, $g_1 = g_2 = 1$, $N_1 = N_2 = 50$, $w_1 = w_2 = 0.05$, $g_1 = g_2 = 1$, $\mu_1 = \mu_2 = 1$, and $\varepsilon = 0.001$. (A) $g_1 = 10$; (C) $g_2 = 10$. A 'generation' is defined as $N_1 + N_2$ elementary updating events of the Moran process.

qualitative results, we have calculated the invariant distribution of the complete Markov chain for various values of ε (Figs. S2–S4), and using an exponential fitness function instead of the linear one (Fig. S5).

Figs. S2–S4 visualize the invariant distribution of the Markov chain for three different values of the baseline mutation rate, varying the parameter ε from $\varepsilon = 0.0001$ (top panels) to $\varepsilon = 0.01$ (bottom panels). When mutations are rare, the two populations are almost always situated at a boundary of the state space, and the states at the four corners are most abundant (as indicated by the red color). That is, in this regime, the two populations are usually monomorphic. Occasionally, a mutation introduces a new strategy into one of the two populations; this mutation typically goes extinct or fixes in that population before the next mutation occurs in either population. In this case, the weak-mutation methodology (as introduced in detail in Section S4) provides an excellent approximation of the dynamics of the complete Markov chain. We note that for mutualistic symbioses, the value of k in the payoff matrix controls the path that leads from one equilibrium to

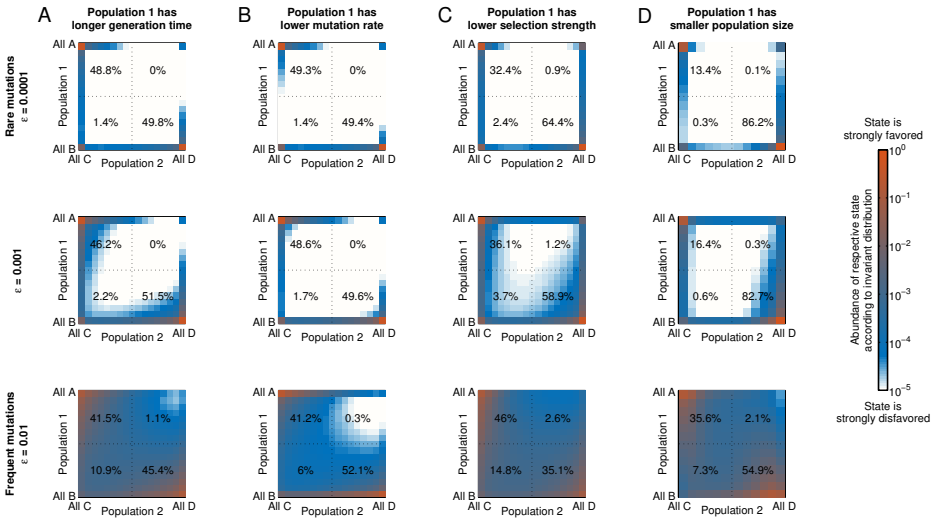


Figure S2: Effect of baseline mutation rate on the long-run abundance of strategies in mutualistic symbioses with $k = 3/2$. All panels show how abundant each population state is in the long run, according to the invariant distribution of the complete Markov chain. The numbers in each quadrant correspond to the fraction of time the respective quadrant is visited. Increases in the baseline mutation rate do not qualitatively change the weak-mutation conclusions for this game, except that differences in generation time and mutation rates lead to weak Red Queen effect [(A) and (B)]. With respect to differences in selection strength we find that a strong Red Queen effect for small mutation rates can reverse to a weak Red King effect when mutation rates are very large [(C), bottom panel]. For better visibility, we have increased the baseline strength of selection compared to the previous figures: $w_1 = w_2 = 0.2$ [and $w_1 = 0.05$, $w_2 = 0.5$ in (C)]. All other parameters are the same as before.

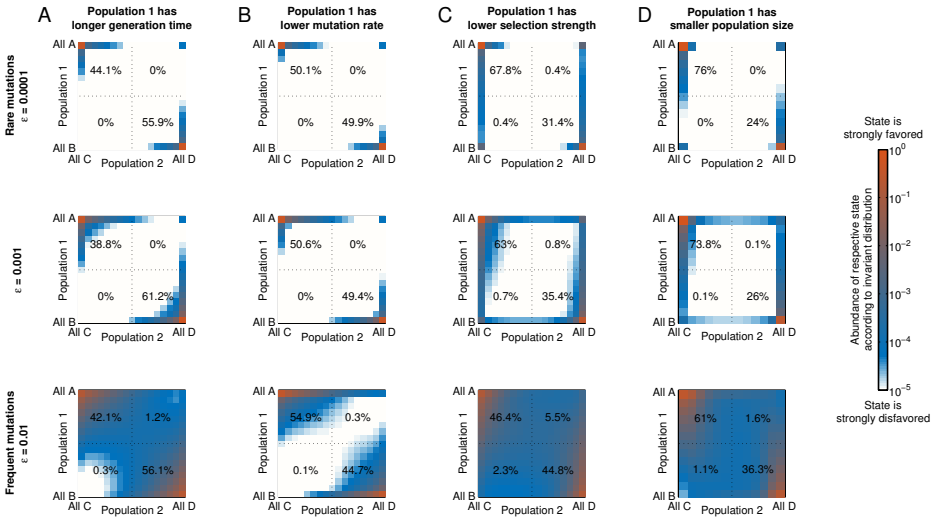


Figure S3: Effect of baseline mutation rate on the long-run abundance of strategies in mutualistic symbioses with $k = 1/2$. As in Fig. S2, the figure illustrates the invariant distribution of the complete Markov chain. Differences in selection strength and population size lead to a comparably strong Red King effect, whereas differences in mutation rates yield a weak Red King effect. Differences in generation time can result in a notable Red Queen effect. All parameters are the same as in the previous figure, except k.

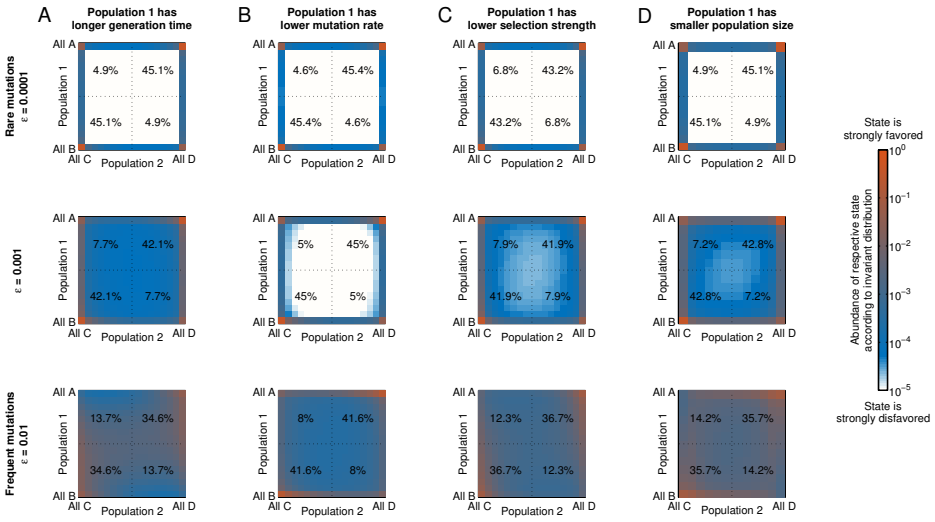


Figure S4: Effect of baseline mutation rate on the long-run abundance of strategies in antagonistic symbioses. In all panels, the invariant distribution puts less weight on states that are beneficial for population 1, i.e., states close to the (A,C) and (B,D) corners. This is as expected under Red Queen dynamics, as population 1 has a larger generation time (A), a lower mutation rate (B), weaker selection (C), or a smaller population size (D). All evolutionary parameters are the same as in Figs. S2 and S3.

another. For $k = 3/2$, transitions from (A,C) to (B,D) and back typically pass through the non-coordination state (B,C) (Fig. S2), whereas for $k = 1/2$, these transitions typically pass through the other non-coordination state (A,D) (Fig. S3).

As the mutation parameter ε increases, states in the interior of the state space occur more often, and the weak-mutation approximation is no longer an excellent quantitative match. Nevertheless, Figs. S2–S4 indicate that the qualitative predictions from the weak-mutation case are largely robust to changes in ε, in the sense that populations that are favored under the weak-mutation regime also tend to be favored as the baseline mutation rate is increased.

Similarly, we observe only a small quantitative change, and no qualitative change, when we assume that the fitness of an individual is defined as $f = \exp(w\pi)$, instead of the linear specification $f = 1 + w \cdot \pi$ used in the Main Text (Fig. S5).

S3 Mixing time of the Markov chain

We have distinguished the behavior of the dynamics in the 'short run' and the 'long run'. Here, we provide a more precise picture of how many generations it takes to be in the 'long run', for the two games we have studied. Since the object of interest in the long-run dynamics is the stationary distribution of the co-evolutionary process, the 'long run' should be defined as the number of generations required for the distribution over population states

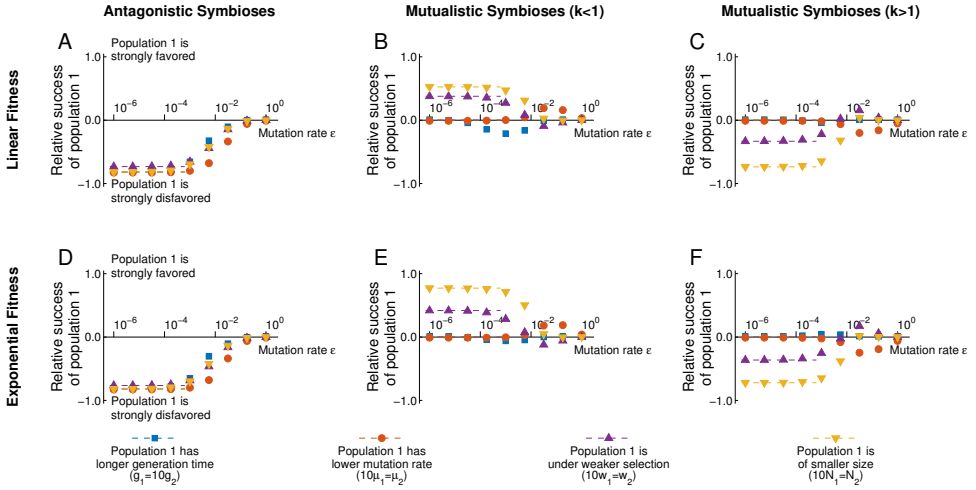


Figure S5: Impact of baseline mutation rate on the long-run relative success of population 1 in antagonistic and mutualistic symbioses. For various parameter combinations and two different fitness specifications, each panel shows the relative success of population 1, either using the payoff matrix for antagonistic symbioses (A), for mutualistic symbioses with $k = 1/2$ (B), or for mutualistic symbioses with $k = 3/2$ (C). We consider differences in generation time (blue), mutation rate (red), the strength of selection (purple), and population size (yellow). Dots show the numerically computed measures of population 1's success, as defined in (5) and (7) respectively. Dashed lines indicate the respective analytical solution in the limit of rare mutations. In antagonistic symbioses, all four dimensions put population 1 at a disadvantage when mutations become sufficiently rare. In mutualistic symbioses, only population size and selection strength have a notable effect; this effect is positive for $k = 1/2$ and negative for $k = 3/2$. The analytical solution provides a good approximation when $\varepsilon\mu \leq 10^{-4}$. Parameters are the same as in Figs. S2–S4.

to be close to the stationary distribution, i.e., the 'mixing time' of the process.

For small populations, such as those for which we have displayed results in our various figures, the time evolution of the probability distribution can be computed exactly, and so we can directly see how rapidly it converges to being stationary (Fig. S6). We see that, for the parameters we have studied in the Main Text figures and in Figs. S1-6 here (i.e., all with small population sizes, of order 50), the long run in antagonistic symbioses can be thought to be after about 10^2-10^3 generations (Fig. S6A), while in mutualistic symbioses, the long run is after about 10^3-10^4 generations (Fig. S6B,C).

For larger population sizes, direct computation of the time evolution of the evolutionary process is not feasible, since it involves taking successive powers of very large matrices. Moreover, numerical estimation of the mixing time is computationally very difficult, and in fact not feasible for our purposes, which are to see how the mixing time changes as we vary key parameters like population size. Therefore, we resort to approximate analytical arguments. We shall focus on the case where mutations are rare in both populations, so that there are seldom several mutations segregating in the populations.

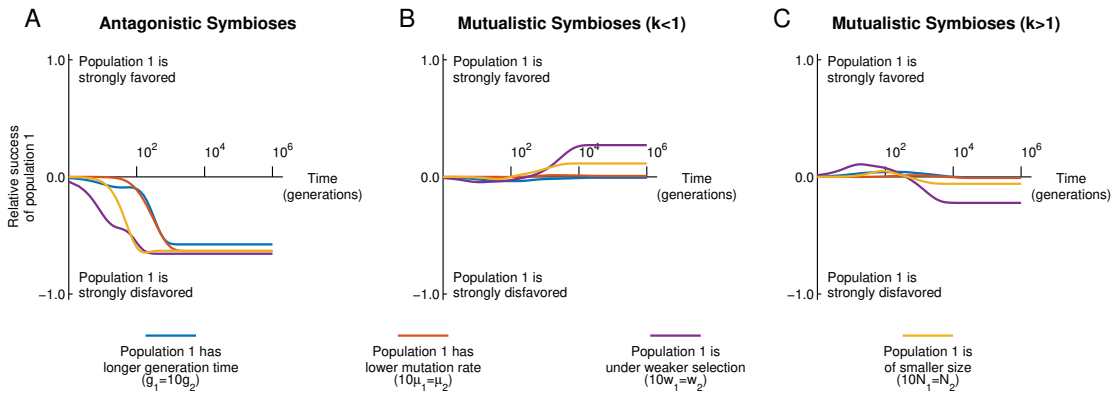


Figure S6: Dynamics of mutualistic and antagonistic symbioses over time. For various parameter combinations, the three plots show the relative success of population 1, using the payoff matrix for antagonistic symbioses (A), for mutualistic symbioses with $k = 1/2$ (B), and for mutualistic symbioses with $k = 3/2$ (C). The panels illustrate the temporal effects of differences in generation time (blue), mutation rate (red), the strength of selection (purple), and population sizes (yellow). The curves show the expected evolution of population 1's relative success, as measured by the quantities (5) for mutualistic symbioses and (7) for antagonistic symbioses. (A) In the long run, antagonistic symbioses disfavor the population with longer generation time, lower mutation rate, weaker selection strength and smaller population size. (B) In mutualistic symbioses with $k = 1/2$, the population with longer generation time and weaker selection strength is disfavored in the intermediate run. However, in the long run, differences in generation time have a negligible impact on the success of a population, and the effect of weaker selection becomes positive. The other two dimensions have either no substantial effect (differences in mutation rates) or they have a positive effect as well (smaller population size). (C) When $k = 3/2$, the effects of weaker selection and smaller population size are reversed from the case of $k = 1/2$. Parameters are the same as in Figs. 1-3 in the *Main Text*.

S3.1 Antagonistic symbioses

In antagonistic symbioses, when the mutation rate is small, the probability distribution over time is influenced predominantly by those transitions from pure state to pure state that are driven by positive selection (i.e., the 'arms race'). Given some initial starting point, the dynamics quickly move towards one of the pure states, after which the cycle from pure state to pure state begins. Having moved to some new pure state, how quickly the dynamics subsequently move to a new pure state is a random variable, but after sufficiently many such transitions, we expect the proportion of time that has been spent in each state to be close to that in the stationary distribution.

Therefore, the mixing time should be proportional to the time it takes to move from one pure state to another. Starting from a pure state, this requires a mutation to *substitute*, i.e., to arrive and fix, in the presently disfavored population. If the mutation rate is low enough, then the rate-limiting part of this process is the arrival time of a mutation destined to fix, and not the time it takes the mutation to fix (which occurs relatively quickly). Mutations arrive in this population i at rate $N_i\varepsilon\mu_i$, and have selective advantage w_i $(= [1 + w_i(1)] - [1 + w_i(0)])$.

We may distinguish two cases: weak selection and strong selection. Weak selection applies when $N_i w_i < 1$, in which case the fixation probability of beneficial mutations is

approximately $1/N_i$ (i.e., they are nearly neutral). So, under weak selection, the substitution rate of beneficial mutations in population i is approximately $N_i\varepsilon\mu_i/N_i = \varepsilon\mu_i$, and so the mixing time of the process will be approximately proportional to $1/\min_i(\varepsilon\mu_i)$. That is, the mixing time should decrease as the mutation rates of the populations increase. This approximation should be good as long as the waiting time for a mutation destined to fix in a population, $1/\varepsilon\mu_i$, is significantly longer than the time it takes that mutation to fix, which in the case of weak selection is about $2N_i$ generations, on average. So, our above analytical reasoning should be valid when is $N_i\varepsilon\mu_i \ll 1$.

Strong selection applies when $N_i w_i > 1$, and if w_i is small, the fixation probability of beneficial mutations with selective advantage w_i is approximately w_i [3]. Under strong selection, therefore, the substitution rate of beneficial mutations in population i is approximately $N_i\varepsilon\mu_i w_i$, and so the mixing time of the process will be proportional to $1/\min_i(N_i\varepsilon\mu_i w_i)$. That is, the mixing time should decrease as the sizes, mutation rates, and selection strengths of the populations increase. Again, this approximation will be good if the waiting time for a mutation destined to fix in a population, here $1/(N_i\varepsilon\mu_i w_i)$, is much larger than the time it takes to fix, which is $\log(N_i)/w_i$ on average. So, we require $N_i \log(N_i)\varepsilon\mu_i \ll 1$.

S3.2 Mutualistic symbioses

For the evolutionary process to mix in the case of the mutualism game also requires that each pure state be visited sufficiently often, the equilibria (A, C) and (B, D), as well as the non-equilibria (A, D) and (B, C).

In the case of weak selection in both populations, $N_1 w_1, N_2 w_2 < 1$, substitutions that drive the population state from one pure state to the other occur at rate $\varepsilon\mu_i$ if in population i, and so the mixing time of the process should be proportional to $1/\min_i(\varepsilon\mu_i)$, as in the case of antagonistic symbioses with weak selection.

In the case of strong selection in at least one population, the mixing time of the evolutionary process will be determined by how long it takes to substitute *against* selection in that population (or both), i.e., to substitute out of equilibrium. This is because substitutions into equilibrium, under positive selection, occur on a much faster timescale than substitutions out of equilibrium when the mutation rates in the two directions are equal. Another way of saying this is that the evolutionary process will spend most of the time in equilibrium states.

For example, consider the substitution rate from the equilibrium state (A, C) to the non-equilibrium state (A, D). This involves the arrival in an all-C population 2 of a D mutant, and the subsequent fixation of the D mutant. D mutants arrive at rate $N_2\varepsilon\mu_2$. They receive payoff 0 versus the incumbent strategy C's payoff of 1, and are therefore at relative selective disadvantage $-w_2/(1 + w_2)$. Under strong selection, the fixation probability of such a mutant is approximately $\frac{w_2}{1+w_2}\exp\left(-N_2\frac{w_2}{1+w_2}\right)$ [5], and so the substitution rate from (A, C) to (A, D) is approximately $N_2\varepsilon\mu_2\frac{w_2}{1+w_2}\exp\left(-N_2\frac{w_2}{1+w_2}\right)$. The substitu-

tion rates from (A,C) to (B,C), from (B,D) to (B,C), and from (B,D) to (A,D) can be estimated similarly as $N_1\varepsilon\mu_1\frac{w_1(2-k)}{1+2w_1}\exp\left(-N_1\frac{w_1(2-k)}{1+2w_1}\right)$, $N_2\varepsilon\mu_2\frac{w_2(2-k)}{1+2w_2}\exp\left(-N_2\frac{w_2(2-k)}{1+2w_2}\right)$, and $N_1\varepsilon\mu_1\frac{w_1}{1+w_1}\exp\left(-N_1\frac{w_1}{1+w_1}\right)$ respectively.

The mixing time under strong selection should be proportional to the inverse of the smallest of these four substitution rates. In each case, the properties of the mixing time will be similar. Suppose, for instance, that the (A,C) to (A,D) substitution is slowest. Then the mixing time of the process is proportional to

$$\frac{\exp\left(N_2\frac{w_2}{1+w_2}\right)}{N_2\frac{w_2}{1+w_2}\varepsilon\mu_2}.$$

For large $N_2\frac{w_2}{1+w_2}$, the exponential term in the numerator dominates, and the mixing time becomes very large. In such cases, the stationary distribution is unlikely to be approached on realistic timescales. For smaller values of $N_2\frac{w_2}{1+w_2}$, mixing will occur on realistic timescales.

S4 Weak-mutation methodology

A general description of the weak-mutation methodology that we have employed can be found in ref. [9]. The inclusion of generation rates is the only difference between this and the methodology set out there. Here, we shall give the method in full for the particular case of 2-player, 2-strategy games that we have studied. We alter the notation a little from the previous section, so that the payoff to a member of population i playing strategy X who encounters a member of the other population playing strategy Y is denoted $\pi_i(X,Y)$

In the weak mutation limit, $\varepsilon\to 0$, the evolutionary dynamics converge to an embedded dynamics over just the pure states (in which each population is monomorphic). These pure states can be labelled (A,C), (A,D), (B,C), and (B,D), which we shall, for notational convenience, enumerate as pure states 1, 2, 3, and 4. We write $\rho_i(x,y)$ for the fixation probability of a single payoff-x mutant in population i otherwise pure for a payoff-y strategy. In the Moran process that we have predominantly used, and which is described in the previous section,

$$\rho_i(x,y)=\frac{1-\left(\frac{1+w_ix}{1+w_iy}\right)^{-1}}{1-\left(\frac{1+w_ix}{1+w_iy}\right)^{-N_i}}.$$

The dynamics can also easily be extended to other processes. For example, it could be that population i experiences a full-population Wright-Fisher update with probability proportional to g_i. In this case, applying to the above, we write $s(x,y)=1-\frac{1+w_ix}{1+w_iy}$ and

make use of Kimura's diffusion approximation

$$\rho_i(x,y) = \frac{1-e^{-s(x,y)}}{1-e^{-N_i s(x,y)}}.$$

In fact, we may make use of any process that satisfies the properties that, without mutations, (a) absent strategies would remain absent, and (b) any strategy that is present but not fixed has positive probability of increasing its representation in the next generation. Given such a process, and therefore fixation probability functions $\rho_1(\cdot,\cdot)$ and $\rho_2(\cdot,\cdot)$ for the two populations, the one-step transition probabilities in the embedded dynamics are:

$$\begin{aligned}
&P_{1\to2} = \frac{N_2\mu_2}{g_2}\rho_2\Big(\pi_2(D,A),\pi_2(C,A)\Big); \quad P_{2\to1} = \frac{N_2\mu_2}{g_2}\rho_2\Big(\pi_2(C,A),\pi_2(D,A)\Big);\\
&P_{1\to3} = \frac{N_1\mu_1}{g_1}\rho_1\Big(\pi_1(B,C),\pi_1(A,C)\Big); \quad P_{3\to1} = \frac{N_1\mu_1}{g_1}\rho_1\Big(\pi_1(A,C),\pi_1(B,C)\Big);\\
&P_{2\to4} = \frac{N_1\mu_1}{g_1}\rho_1\Big(\pi_1(B,D),\pi_1(A,D)\Big); \quad P_{4\to2} = \frac{N_1\mu_1}{g_1}\rho_1\Big(\pi_1(A,D),\pi_1(B,D)\Big);\\
&P_{3\to4} = \frac{N_2\mu_2}{g_2}\rho_2\Big(\pi_2(D,B),\pi_2(C,B)\Big); \quad P_{4\to3} = \frac{N_2\mu_2}{g_2}\rho_2\Big(\pi_2(C,B),\pi_2(D,B)\Big);\\
&P_{1\to4} = P_{4\to1} = P_{2\to3} = P_{3\to2} = 0;\\
&P_{1\to1} = 1 - P_{1\to2} - P_{1\to3}; \;\; P_{2,2} = 1 - P_{2\to1} - P_{2\to4};\\
&P_{3\to3} = 1 - P_{3\to1} - P_{3\to4}; \;\; P_{4\to4} = 1 - P_{4\to2} - P_{4\to3}.
\end{aligned}$$

The stationary distribution over the states, $\lambda = [\lambda_1, \lambda_2, \lambda_3, \lambda_4]$, is the stochastic vector that solves

$$\lambda_i = \sum_{j=1}^{4} \lambda_j P_{j\to i} \quad \text{for } i = 1,2,3,4.$$

S5 Antagonistic symbioses, weak-mutation limit

We consider here the antagonistic symbiosis payoff matrix (game [1] in the *Main Text*).

Imposing no restrictions on the rate parameters μ_1, μ_2, g_1, g_2, N_1, N_2, w_1, and w_2, the stationary distribution, calculated according to the method described in the previous section, is

$$\lambda = [s_1, 1, 1, s_1]/\bar{\lambda},$$

where $\bar{\lambda} = 2 + 2s_1$, and

$$s_1 = \frac{\frac{N_1\mu_1}{g_1}\rho_1(1,0) + \frac{N_2\mu_2}{g_2}\rho_2(0,1)}{\frac{N_1\mu_1}{g_1}\rho_1(0,1) + \frac{N_2\mu_2}{g_2}\rho_2(1,0)}.$$

The long-run success of population 1 relative to population 2 is proportional to $\lambda_1 - \lambda_4 = (s_1 - 1)/\bar{\lambda}$, which is increasing in s_1.

Holding the rate parameters of population 2 constant, and focusing on the rate pa-

rameters of population 1, a sufficient condition for the success of population 1 to increase is therefore that the term $\frac{N_1\mu_1}{g_1}\rho_1(1,0)$ increases and the term $\frac{N_1\mu_1}{g_1}\rho_1(0,1)$ decreases. The former term is the substitution rate of beneficial mutations in population 1, while the latter is the substitution rate of deleterious mutations.

S5.1 Selection strength

A higher selection strength w_1 increases the fixation probability of beneficial mutations $\rho_1(1,0)$ and decreases the fixation probability of deleterious mutations $\rho_1(0,1)$ for any reasonable evolutionary process (this is, after all, a plausible *definition* of selection strength), but has no effect on the arrival rate of these mutations. It therefore increases the substitution rate of beneficial mutations and decreases the substitution rate of deleterious mutations, and therefore increases s_1 and thus the relative success of population 1.

S5.2 Population size

It follows that, if the evolutionary process is such that beneficial mutations have a faster and deleterious mutations a slower substitution rate in larger populations (loosely, if natural selection acts more efficiently in larger populations), then a larger population size for population 1 is associated with a larger value of s_1, i.e., greater long-run success. It is folk knowledge that this property holds of the Wright-Fisher and Moran processes, though we have been unable to find direct proofs in the literature, and so provide them here.

We should note that the usual statement of the result that beneficial mutations substitute at a higher rate in larger populations assumes that the beneficial mutations in question confer a selective advantage $s \ll 1/N_e$ while $N_e s \gg 1$, so that their fixation probability in isolation can be approximated by s (in a haploid population) or $2s$ (in a diploid population, where s is the haploid fitness contribution). It follows directly that the substitution rate, $\mu N s$ (haploid) or $4\mu N s$ (diploid), is increasing in N.

In contrast, the results below hold for *all* selection coefficients s (including $s < 0$) and population sizes N.

Moran: Suppose that mutants are of relative fitness $r \neq 1$. Then, if independent (no interference of any sort), they arrive and fix at rate

$$\mu N \frac{1 - r^{-1}}{1 - r^{-N}}.$$

The proportional change of this quantity with respect to change in N is

$$\frac{\partial}{\partial N} \ln\left(\mu N \frac{1 - 1/r}{1 - 1/r^N}\right) = \frac{1}{N} - \frac{\ln r}{r^N - 1} \overset{\text{sign}}{=} \operatorname{sgn}(r-1)[r^N - 1 - N \ln r] \overset{\text{sign}}{=} \operatorname{sgn}(r-1)$$

where the second step is the result of multiplying through by $N(r^N - 1)$, which is positive if $r > 1$ and negative if $r < 1$, and the last step follows from $x > 1 + \ln(x)$ for all $x \neq 1$.

Therefore,

$$\operatorname{sgn}\left[\frac{\partial}{\partial N}\left(\mu N\frac{1-r^{-1}}{1-r^{-N}}\right)\right]=\operatorname{sgn}(r-1),$$

and so beneficial mutations ($r>1$) arrive and fix at a higher rate in a larger population, while detrimental mutations ($r<1$) arrive and fix at a lower rate in a larger population.

Wright-Fisher (diffusion approximation): For a Wright-Fisher process, in the diffusion limit, writing $s=r-1$, the arrival-fixation rate varies with N according to

$$\begin{aligned}\frac{\partial}{\partial N}\left(\mu N\frac{1-e^{-s}}{1-e^{-Ns}}\right)&=\mu\left(\frac{1-e^{-s}}{1-e^{-Ns}}-N\frac{1-e^{-s}}{(1-e^{-Ns})^2}se^{-Ns}\right)\\&\overset{\text{sign}}{=}\operatorname{sgn}(s)\left[1-e^{-Ns}-Nse^{-Ns}\right]=\operatorname{sgn}(s)\left[1-\frac{1+Ns}{e^{Ns}}\right].\end{aligned}$$

But $e^x>1+x$ for all $x\neq 0$, and so

$$\operatorname{sgn}\left[\frac{\partial}{\partial N}\left(\mu N\frac{1-e^{-s}}{1-e^{-Ns}}\right)\right]=\operatorname{sgn}(s).$$

Though they do not bear on the problem considered in our *Main Text*, it is nonetheless worth noting some implications of the above results. One major implication concerns the rate at which populations of different size are expected to adapt; that is, the average rate at which fitness increases in populations of differing size. Again, the result below is folk knowledge in population genetics, but we have been unable to find a general proof.

Assume that mutations arise at rate μ per replication, and sufficiently infrequently at the population level that their fate, extinction or fixation, is almost always determined before the arrival of the next mutation in the population—this is the commonly-assumed 'sequential fixations' model [6]. We study a haploid population of size N, where the next mutation that appears in the population is drawn from some fitness effect distribution $f(s)$, where s is the fitness difference between current members of the population and the potential mutant. We assume this distribution to be atomless in what follows, but this is not necessary in general. Writing $\rho(s,N)$ for the fixation probability of a mutant of fitness effect s in a population of size N (as written for the Moran and Wright-Fisher processes above), the current rate of fitness increase of the population can then be written

$$R_{\text{fitness}}=N\mu\int_{-\infty}^{\infty}sf(s)\rho(s,N)ds.$$

This changes with N according to

$$\begin{aligned}\frac{\partial}{\partial N}R_{\text{fitness}} &= \frac{\partial}{\partial N}\left[N\mu\int_{-\infty}^{\infty} sf(s)\rho(s,N)ds\right] \\ &= \frac{\partial}{\partial N}\left[-\int_{-\infty}^{0} -|s|f(s)\mu N\rho(s,N)ds + \int_{0}^{\infty} sf(s)\mu N\rho(s,N)ds\right] \\ &= \int_{-\infty}^{0} -|s|f(s)\mu\left[\frac{\partial}{\partial N}N\rho(s,N)\right]ds + \int_{0}^{\infty} sf(s)\mu\left[\frac{\partial}{\partial N}N\rho(s,N)\right]ds.\end{aligned}$$

From what we showed earlier, we note that if the evolutionary process is a Wright-Fisher or a Moran process, then both integrands in this last line are positive, and so $\frac{\partial}{\partial N}R_{\text{fitness}} > 0$.

S5.3 Mutation rate and generation time

Finally, write $r_1 = (\mu_1/g_1)/(\mu_2/g_2)$, so that $s_1 = \frac{N_1 r_1 \rho_1(1,0)+N_2\rho_2(0,1)}{N_1 r_1\rho_1(0,1)+N_2\rho_2(1,0)}$. Then

$$\frac{\partial s_1}{\partial r_1} = N_1 N_2 \frac{\rho_1(1,0)\rho_2(1,0) - \rho_1(0,1)\rho_2(0,1)}{[N_1 r_1\rho_1(0,1) + N_2\rho_2(1,0)]^2},$$

which is positive if $\rho_1(1,0) > \rho_1(0,1)$ and $\rho_2(1,0) > \rho_2(0,1)$, i.e., if, in both populations, beneficial mutations have higher fixation probability than deleterious mutations. Again, this is true of all reasonable evolutionary processes.

S5.4 Moran process

In the special case of a Moran process operating in each population, and assuming $N_1 = N_2 = N$ and $w_1 = w_2 = w$, we have $\rho_1 \equiv \rho_2 = \rho$, and $\frac{\rho(1,0)}{\rho(0,1)} = (1+w)^{N-1} =: \gamma$. Then

$$s_1 = \frac{Nr_1\rho(1,0) + N\rho(0,1)}{Nr_1\rho(0,1) + N\rho(1,0)} = \frac{r_1\frac{\rho(1,0)}{\rho(0,1)} + 1}{r_1 + \frac{\rho(1,0)}{\rho(0,1)}} = \frac{r_1\gamma + 1}{r_1 + \gamma}.$$

This is the basis of Eq. [3] in the Main Text.

S6 Mutualistic symbioses, weak-mutation limit

The mutualism payoff matrix (game [2] in the *Main Text*) is

		Player 2	
		C	D
Player 1	A	$2,1$	$0,0$
	B	k,k	$1,2$

The stationary distribution, calculated according to the method above, is

$$\lambda = \left[\tilde{\lambda}_1, \tilde{\lambda}_2, \tilde{\lambda}_3, \tilde{\lambda}_4\right] / \bar{\lambda},$$

where $\bar{\lambda}$ is a normalization constant and

$$\begin{aligned}
\tilde{\lambda}_1 &= \rho_1(2,k)\left[\rho_2(k,2)\rho_1(1,0) + \rho_2(1,0)\rho_1(0,1)\right] + r_1\rho_2(1,0)\left[\rho_2(2,k)\rho_1(0,1) + \rho_2(k,2)\rho_1(2,k)\right] \\
\tilde{\lambda}_2 &= \rho_1(0,1)\left[\rho_2(2,k)\rho_1(k,2) + \rho_2(0,1)\rho_1(2,k)\right] + r_1\rho_2(0,1)\left[\rho_2(2,k)\rho_1(0,1) + \rho_2(k,2)\rho_1(2,k)\right] \\
\tilde{\lambda}_3 &= \rho_1(k,2)\left[\rho_2(k,2)\rho_1(1,0) + \rho_2(1,0)\rho_1(0,1)\right] + r_1\rho_2(k,2)\left[\rho_2(0,1)\rho_1(1,0) + \rho_2(1,0)\rho_1(k,2)\right] \\
\tilde{\lambda}_4 &= \rho_1(1,0)\left[\rho_2(2,k)\rho_1(k,2) + \rho_2(0,1)\rho_1(2,k)\right] + r_1\rho_2(2,k)\left[\rho_2(0,1)\rho_1(1,0) + \rho_2(1,0)\rho_1(k,2)\right]
\end{aligned}$$

Here, $r_1 = (\mu_1 N_1/g_1)/(\mu_2 N_2/g_2)$ (this definition is slightly different from that we employed in the antagonistic symbiosis section above). Notice that the dependence on r_1 is not necessarily as simple as it immediately appears from the expressions for the $\tilde{\lambda}_i$, because the normalizing constant $\bar{\lambda}$ also depends on r_1.

S6.1 Mutation rate and generation time

If we fix $N_1 = N_2 = N$ and $w_1 = w_2 = w$, then the fixation probability functions of the two populations coincide: $\rho_1 \equiv \rho_2 =: \rho$. The stationary distribution takes on the simple form

$$\lambda = \left[1, \frac{\rho(0,1)}{\rho(1,0)}, \frac{\rho(k,2)}{\rho(2,k)}, 1\right] / \bar{\lambda},$$

where $\bar{\lambda}$ normalizes that λ sums to one. The stationary distribution is therefore independent of the mutations rates and generation times of the two populations.

In the case of the Moran process, on which we focused in the *Main Text*, the stationary distribution simplifies to Eq. [5] in the Main Text:

$$\lambda = \left[1, \left(\frac{1}{1+w}\right)^{N-1}, \left(\frac{1+kw}{1+2w}\right)^{N-1}, 1\right] / \bar{\lambda}.$$

Why do the mutation rate and generation time have no effect on the stationary distribution when mutation is weak? This result is a special case of the following general statement: For any 4-state Markov chain, if

$$\begin{aligned}
P_{1\to2}/P_{2\to1} = P_{2\to4}/P_{4\to2} &= A, \\
P_{1\to3}/P_{3\to1} = P_{4\to3}/P_{3\to4} &= B, \\
\text{and } \; P_{1\to4} = P_{4\to1} = P_{2\to3} = P_{3\to2} &= 0,
\end{aligned}$$

then the stationary distribution is simply $\lambda = [1, A, B, 1]/\bar{\lambda}$, where $\bar{\lambda} = 2 + A + B$.

In the mutualism game, when $N_1 = N_2 = N$ and $w_1 = w_2 = w$, the fixation probability functions $\rho_1(\cdot,\cdot)$ and $\rho_2(\cdot,\cdot)$ are identical (not just for the Moran process, but for any

evolutionary process whose fixation probability function depends only on population size and selection strength). Let $\rho(\cdot,\cdot) = \rho_1(\cdot,\cdot) = \rho_2(\cdot,\cdot)$. Then

$$\frac{P_{1\to2}}{P_{2\to1}} = \frac{\frac{N_2\mu_2}{g_2}\rho_2(0,1)}{\frac{N_2\mu_2}{g_2}\rho_2(1,0)} = \frac{\rho(0,1)}{\rho(1,0)} = \frac{\frac{N_1\mu_1}{g_1}\rho_1(0,1)}{\frac{N_1\mu_1}{g_1}\rho_1(1,0)} = \frac{P_{2\to4}}{P_{4\to2}}.$$

So $P_{1\to2}/P_{2\to1} = P_{2\to4}/P_{4\to2} = A$, where $A = \rho(0,1)/\rho(1,0)$ is independent of the mutation rates and generation rates of the two populations. Similarly, $P_{1\to3}/P_{3\to1} = P_{4\to3}/P_{3\to4} = B$, where $B = \rho(k,2)/\rho(2,k)$ too depends only on N and w.

So the stationary distribution does not depend on μ_1, μ_2, g_1, or g_2. This result stems from consideration of probabilities of transitions against selection (e.g., $P_{1\to2} > 0$); it cannot be found using methods that rule out such transitions, such as deterministic dynamics like the replicator equation.

S6.2 Selection strength

In order to explore the effect of selection strength on how the populations fare (in the case of a Moran process) we look at the effect of this parameter on $\lambda_{(A,C)}$ and $\lambda_{(B,D)}$, i.e., λ_1 and λ_4. Using the expression given above for the stationary distribution, we calculate that

$$\begin{aligned}\lambda_{(A,C)} - \lambda_{(B,D)} \overset{\text{sign}}{=} &\left(\frac{1}{\rho_2(2,k)} + r_1\frac{1}{\rho_1(2,k)}\right)\left(\left(\frac{1}{1+w_1}\right)^{N_1-1} - \left(\frac{1}{1+w_2}\right)^{N_2-1}\right)\\ &- \left(\frac{1}{\rho_2(1,0)} + r_1\frac{1}{\rho_1(1,0)}\right)\left(\left(\frac{1+kw_1}{1+2w_1}\right)^{N_1-1} - \left(\frac{1+kw_2}{1+2w_2}\right)^{N_2-1}\right) =: g(w_1,w_2).\end{aligned}$$

Fix $N_1 = N_2 = N$ and $w_2 = w$, and assume a slight increase in w_1 from this value ($w_1 \to w + \Delta w$). Define

$$c_1(x) := \frac{1 - \left(\frac{1+kx}{1+2x}\right)^{-1}}{1 - \left(\frac{1+kx}{1+2x}\right)^{-N}};\quad g_1(x) := \left(\frac{1}{1+x}\right)^{N-1};$$

$$c_2(x) := \frac{1 - \left(\frac{1}{1+x}\right)^{-1}}{1 - \left(\frac{1}{1+x}\right)^{-N}};\quad g_2(x) := \left(\frac{1+kx}{1+2x}\right)^{N-1},$$

and note that $c_1(w) = 1/\rho_2(2,k)$ and $c_2(w) = 1/\rho_2(1,0)$. Then

$$g(w_1,w) = \left[c_1(w) + r_1c_1(w_1)\right]\left(g_1(w_1) - g_1(w)\right) - \left[c_2(w) + r_1c_2(w)\right]\left(g_2(w_1) - g_2(w)\right).$$

Let $w_1 = w + \Delta w$. Taylor expanding c_1, c_2, g_1 and g_2 around $\Delta w = 0$,

$$g(w + \Delta w, w) = \underbrace{(1 + r_1)\left[c_1(w)g_1'(w) - c_2(w)g_2'(w)\right]}_{\text{First order term}} \Delta w + o(\Delta w)$$

Hence, the sign of $\lambda_{(A,C)} - \lambda_{(B,D)}$ for Δw sufficiently small (and positive) will be determined by the sign of the first order term:

$$\lambda_{(A,C)} - \lambda_{(B,D)} \overset{\text{sign}}{=} \frac{1}{\rho_2(2,k)} g_1'(w) - \frac{1}{\rho_2(1,0)} g_2'(w)$$

When $w = w^* := \frac{1-k}{k}$, $\rho_2(2,k) = \rho_2(1,0)$ and $g_1(w) = g_2(w)$. This suggests that a useful reparameterization is $w = \frac{1-k+\eta}{k}$. Then $\eta > 0$ corresponds to $w > w^*$ and $\eta < 0$ corresponds to $w < w^*$. Since w is constrained to be positive, we must have that $\eta > k-1$. With this reparameterization we have

$$\begin{aligned}
\tilde{c}_1(\eta) &:= c_1\left(\frac{1-k+\eta}{k}\right) = \frac{1 - k^{-N}\left(1 - \frac{\eta}{2-k+2\eta}\right)^{-N}}{1 - k^{-1}\left(1 - \frac{\eta}{2-k+2\eta}\right)^{-1}}; \\
\tilde{g}_1(\eta) &:= g_1\left(\frac{1-k+\eta}{k}\right) = k^{N-1}\left(1 - \frac{\eta}{1+\eta}\right)^{N-1}; \\
\tilde{c}_2(\eta) &:= c_2\left(\frac{1-k+\eta}{k}\right) = \frac{1 - k^{-N}\left(1 - \frac{\eta}{1+\eta}\right)^{-N}}{1 - k^{-1}\left(1 - \frac{\eta}{1+\eta}\right)^{-1}}; \\
\tilde{g}_2(\eta) &:= g_2\left(\frac{1-k+\eta}{k}\right) = k^{N-1}\left(1 - \frac{\eta}{2-k+2\eta}\right)^{N-1}.
\end{aligned}$$

Define $v_1(\eta) := k\left(1 - \frac{\eta}{2-k+2\eta}\right)$ and $v_2(\eta) := k\left(1 - \frac{\eta}{1+\eta}\right)$. Then

$$\begin{aligned}
\lambda_{(A,C)} - \lambda_{(B,D)} &\overset{\text{sign}}{=} \frac{1 - v_2^{-1}(\eta)}{1 - v_2^{-N}(\eta)} \frac{d}{d\eta}\left(v_2^{N-1}(\eta)\right) - \frac{1 - v_1^{-1}(\eta)}{1 - v_1^{-N}(\eta)} \frac{d}{d\eta}\left(v_1^{N-1}(\eta)\right) \\
&\overset{\text{sign}}{=} \frac{1 - v_2^{-1}(\eta)}{1 - v_2^{-N}(\eta)} v_2^{N-2}(\eta) v_2'(\eta) - \frac{1 - v_1^{-1}(\eta)}{1 - v_1^{-N}(\eta)} v_1^{N-2}(\eta) v_1'(\eta)
\end{aligned}$$

It can easily be verified that $v_1'(\eta) < 0$ and $v_2'(\eta) < 0$. Writing $f(x) := \frac{1-x^{-1}}{1-x^{-N}} x^{N-2}$,

$$\lambda_{(A,C)} - \lambda_{(B,D)} \overset{\text{sign}}{=} f(v_2(\eta)) v_2'(\eta) - f(v_1(\eta)) v_1'(\eta)$$

Let

$$h_1(\eta) := \frac{\eta}{2-k+2\eta} \qquad \left[\Rightarrow h_1'(\eta) := \frac{2-k}{(2-k+2\eta)^2} = \frac{(2-k)}{\eta^2}\left(1-\frac{v_1(\eta)}{k}\right)^2\right]$$

$$h_2(\eta) := \frac{\eta}{1+\eta} \qquad \left[\Rightarrow h_2'(\eta) := \frac{1}{(1+\eta)^2} = \frac{1}{\eta^2}\left(1-\frac{v_2(\eta)}{k}\right)^2\right].$$

Clearly $h_1'(\eta) = -v_1'(\eta)/k$ and $h_2'(\eta) = -v_2'(\eta)/k$, so

$$\begin{aligned}\lambda_{(A,C)} - \lambda_{(B,D)} &\overset{\text{sign}}{=} f(v_1(\eta))h_1'(\eta) - f(v_2(\eta))h_2'(\eta) \\ &\overset{\text{sign}}{=} (2-k)f(v_1(\eta))\left(1-\frac{v_1(\eta)}{k}\right) - f(v_2(\eta))\left(1-\frac{v_2(\eta)}{k}\right)\end{aligned}$$

Setting $t_k(x) := \left(1-\frac{x}{k}\right)^2 f(x)$,

$$\lambda_{(A,C)} - \lambda_{(B,D)} \overset{\text{sign}}{=} (2-k)t_k(v_1(\eta)) - t_k(v_2(\eta)).$$

We note that for any fixed values of x_1 and x_2 — for example, $x_1 = v_1(\eta)$ and $x_2 = v_2(\eta)$ — and any k, if $x_1 < x_2$, then

$$\begin{aligned}\frac{t_k(x_1)}{t_k(x_2)} &= \left(\frac{x_1}{x_2}\right)^{N-2}\left(\frac{1-\frac{1}{x_2}^N}{1-\frac{1}{x_1}^N}\cdot\frac{1-\frac{1}{x_1}}{1-\frac{1}{x_2}}\cdot\left[\frac{1-\frac{x_1}{k}}{1-\frac{x_2}{k}}\right]^2\right) \\ &= \left(\frac{x_1}{x_2}\right)^{2N-2}\left(\frac{1-x_2^N}{1-x_1^N}\cdot\frac{1-\frac{1}{x_1}}{1-\frac{1}{x_2}}\cdot\left[\frac{1-\frac{x_1}{k}}{1-\frac{x_2}{k}}\right]^2\right) \xrightarrow[N\to\infty]{} 0\end{aligned}$$

It can also be verified that $v_1(\eta) < v_2(\eta)$ when $\eta < 0$, while $v_1(\eta) > v_2(\eta)$ when $\eta > 0$. Therefore, for large enough N:

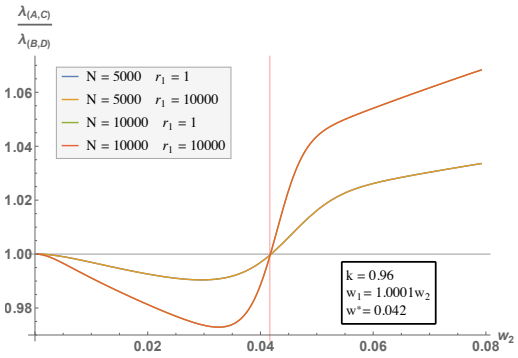
$$\begin{aligned}&\text{if } \eta > 0, \;\; (2-k)t_k(v_1(\eta)) > t_k(v_2(\eta)) \qquad \left[\Rightarrow \lambda_{(A,C)} - \lambda_{(B,D)} > 0\right]; \\ &\text{if } \eta < 0, \;\; (2-k)t_k(v_1(\eta)) < t_k(v_2(\eta)) \qquad \left[\Rightarrow \lambda_{(A,C)} - \lambda_{(B,D)} < 0\right].\end{aligned}$$

In the special case $\eta = 0$ (that is, $w = w^*$) we have that $t_k(v_1(\eta)) = t_k(v_2(\eta))$ so

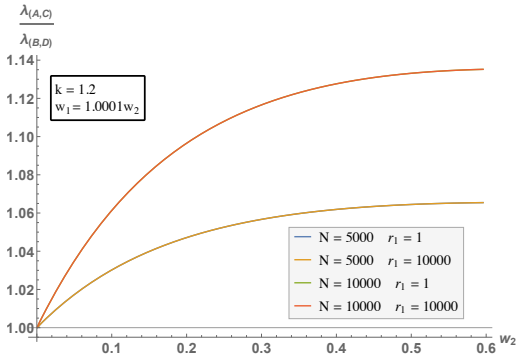
$$\lambda_{(A,C)} - \lambda_{(B,D)} \overset{\text{sign}}{=} 1-k$$

In summary, in the limit of large N, when $w_1 = w + \Delta w > w = w_2$,

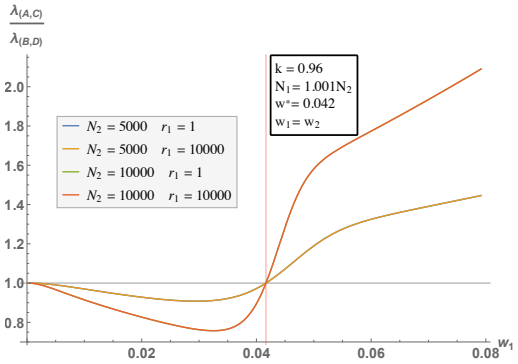
1. If $k \in (0,1)$, then
$$\lambda_{(B,D)} < \lambda_{(A,C)} \qquad \text{if } w \geq \frac{1-k}{k}$$
That is, the increase in the strength of selection in population 1 is beneficial.



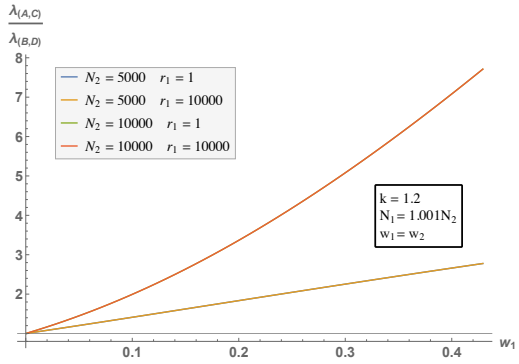
(a) Increasing the strength of selection when $k \in (0, 1)$.



(b) Increasing the strength of selection when $k \in [1, 2)$.



(c) Increasing the population size when $k \in (0, 1)$.



(d) Increasing the population size when $k \in [1, 2)$.

Figure S7: The effect of a slight increase in the population size or selection strength of population 1 for different values of k. In each case, the blue and green lines are invisible because they coincide with the yellow and red lines respectively. This highlights the insensitivity of effects to large changes in r_1.

$$\lambda_{(B,D)} > \lambda_{(A,C)} \qquad \text{if } w < \frac{1-k}{k}$$

That is, the increase in the strength of selection in population 1 is detrimental.

2. If $k \in [1, 2)$:

$$\lambda_{(B,D)} < \lambda_{(A,C)}$$

That is, the increase in the strength of selection in population 1 is beneficial.

To see a graphical representation of this behaviour refer to Figures S7a and S7b.

Numerical calculations suggest that for a large enough population size a generalization of the above findings hold, beyond the marginal ($w_1 = w_2 + \Delta w$) effects we have studied analytically above. That is, for fixed w_2 we have

1. If $k \in (0, 1)$, then

   (a) If $w_2 > w^*$

   $$\lambda_{(B,D)} < \lambda_{(A,C)} \qquad \text{if } w_1 > w_2 \text{ or } w_1 < w^*$$

   That is, if w_2 is above the threshold then population 1 can do better either by having a selection strength below the threshold or by having a selection strength greater than that in population 2.

   $$\lambda_{(B,D)} > \lambda_{(A,C)} \qquad \text{if } w^* < w < w_2$$

   That is, having stronger selection in population 1 is detrimental.

   (b) If $w_2 < w^*$

   $$\lambda_{(B,D)} < \lambda_{(A,C)} \qquad \text{if } w_1 < w_2$$

   That is, having weaker selection in population 1 is beneficial.

   $$\lambda_{(B,D)} > \lambda_{(A,C)} \qquad \text{if } w_1 > w_2$$

   That is, having stronger selection in population 1 is detrimental.

2. If $k \in [1, 2)$:

   $$\lambda_{(B,D)} < \lambda_{(A,C)} \qquad \text{if } w_1 > w_2$$

   That is, having stronger selection in population 1 is beneficial.

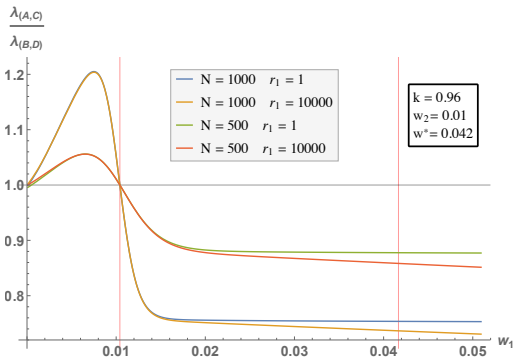
   $$\lambda_{(B,D)} > \lambda_{(A,C)} \qquad \text{if } w_1 < w_2$$

   That is, having weaker selection in population 1 is detrimental.

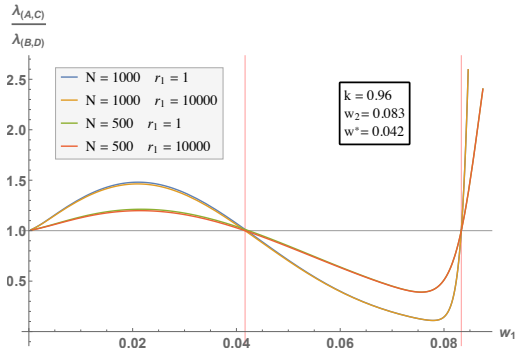
A graphical illustration of these results can be seen Figure S8.

S6.3 Population size

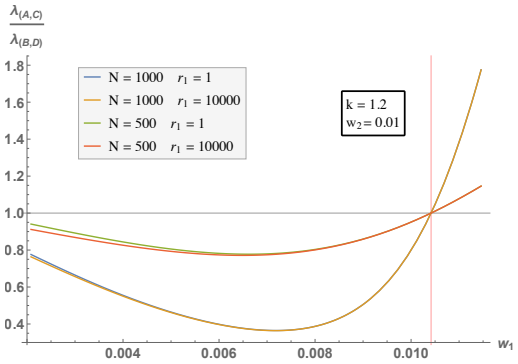
To investigate the effect of population size we fix $w_1 = w_2 = w$ and $N_2 = N = lN_0$, and assume a slight increase in N_1 ($N_1 \to lN_0 + \Delta N$). Or rather, $l_1 \to l + \Delta l$ so that $N_1 \to N_0(l + \Delta l)$. Using the same methods and definitions as in the investigation of the



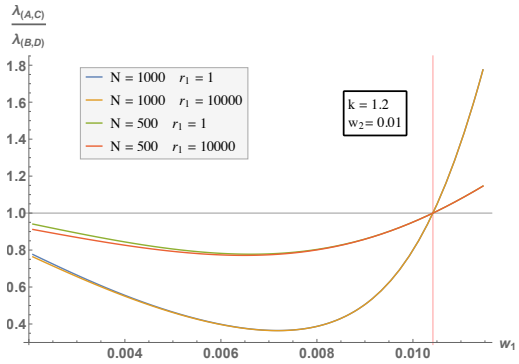
(a) Varying the strength of selection in population 1 when $k \in (0,1)$ and $w_2 < w^*$.



(b) Varying the strength of selection in population 1 when $k \in (0,1)$ and $w_2 > w^*$.



(c) Varying the strength of selection in population 1 when $k \in [1,2)$.



(d) Varying the strength of selection in population 1 when $k \in [1,2)$.

Figure S8: The effect of changing the strength of selection in population 1, with selection strength in population 2 held constant, for different values of k. The two populations are of equal size. Again, note the insensitivity of effects to large changes in r_1.

effect of selection strength, we arrive at

$$\begin{aligned}
\lambda_{(A,C)} - \lambda_{(B,D)} &\overset{\text{sign}}{=} \frac{(1 - v_2^{-1}(\eta))}{1 - v_2^{-lN_0}(\eta)} \frac{d}{dl}\left(v_2^{lN_0-1}(\eta)\right) - \frac{(1 - v_1^{-1}(\eta))}{1 - v_1^{-lN_0}(\eta)} \frac{d}{dl}\left(v_1^{lN_0-1}(\eta)\right) \\
&\overset{\text{sign}}{=} \frac{(1 - v_2^{-1}(\eta))}{1 - v_2^{-lN_0}(\eta)} v_2^{lN_0-1}(\eta) \ln\left(v_2(\eta)\right) - \frac{(1 - v_1^{-1}(\eta))}{1 - v_1^{-lN_0}(\eta)} v_1^{lN_0-1}(\eta) \ln\left(v_1(\eta)\right) \\
&\overset{\text{sign}}{=} \frac{(1 - v_2^{-1}(\eta))}{1 - v_2^{-N}(\eta)} v_2^{N-1}(\eta) \ln\left(v_2(\eta)\right) - \frac{(1 - v_1^{-1}(\eta))}{1 - v_1^{-N}(\eta)} v_1^{N-1}(\eta) \ln\left(v_1(\eta)\right)
\end{aligned}$$

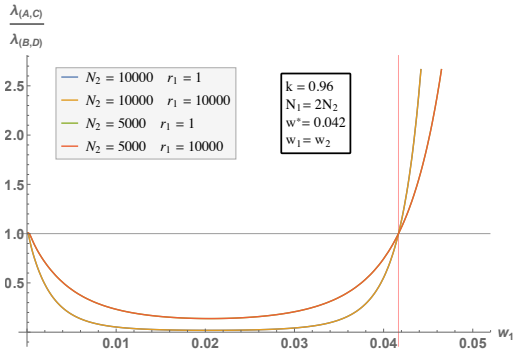
Setting $h(x) := \frac{1-x^{-1}}{1-x^{-N}} x^{N-1} \ln(x)$,

$$\lambda_{(A,C)} - \lambda_{(B,D)} \overset{\text{sign}}{=} h(v_2(\eta)) - h(v_1(\eta)).$$

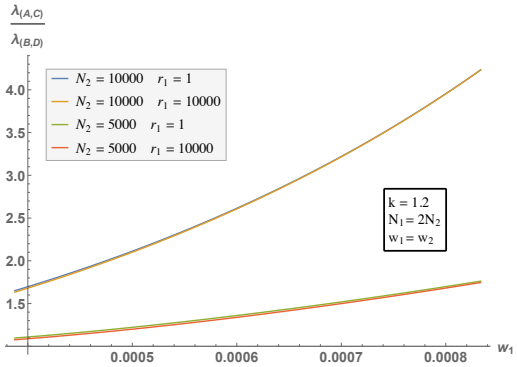
For $0 < x < 1$

$$h^{'}(x) \overset{\text{sign}}{=} x^N(1-x)(1-x^N) - \ln(x)(2-x)(1-x^N) + N\ln(x)\left(\frac{1-x}{1-x^N}\right),$$

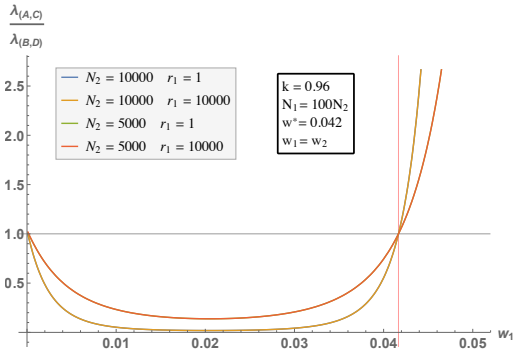
which is decreasing on any fixed interval $[x_1, x_2]$, where $0 < x_1 < x_2 < 1$, for N large enough. We use once again that $v_1(\eta) < v_2(\eta)$ when $\eta < 0$, while $v_1(\eta) > v_2(\eta)$ when $\eta > 0$.



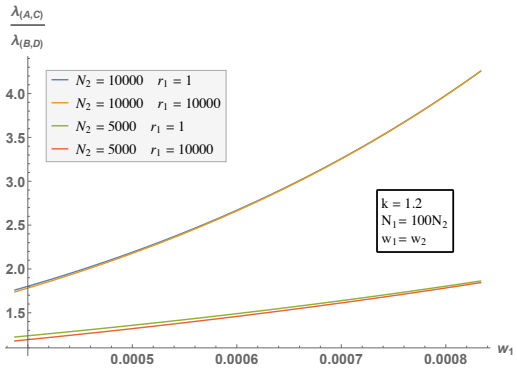
(a) A twofold difference in population sizes when $k \in (0, 1)$.



(b) A twofold difference in population sizes when $k \in [1, 2)$.



(c) A hundredfold difference in population sizes when $k \in (0, 1)$.



(d) A hundredfold difference in population sizes when $k \in (0, 1)$.

Figure S9: The effect of large differences in population size for different values of k. Note the insensitivity of effects to r_1.

In summary we find that if N is sufficiently large, and $N_1 = N + \Delta N > N = N_2$,

1. If $k \in (0, 1)$

$$\lambda_{(B,D)} < \lambda_{(A,C)} \qquad \text{if } w > \frac{1-k}{k}$$

That is, the increase in population 1's size is beneficial.

$$\lambda_{(B,D)} > \lambda_{(A,C)} \qquad \text{if } w < \frac{1-k}{k}$$

That is, the increase in population 1's size is detrimental.

2. If $k \in [1, 2)$:

$$\lambda_{(B,D)} < \lambda_{(A,C)}$$

That is, the increase in population 1's size is beneficial.

To see a graphical representation of this behaviour refer to Figures S7c and S7d.

As in the case of selection strength, numerical calculations suggest that for a large enough population size a generalization of the above findings hold. That is, for fixed $w_1 = w_2 = w$, the above summary holds for any $N_1 > N_2$ (N_2 large enough).

A graphical illustration of these results can be seen Figure S9.

S6.4 Summary of results

A summary of our weak-mutation results for the mutualism game is found in Fig. S10.

S7 Mutualistic symbioses, weak-selection limit

We have shown that, when mutation rates are very small, they (and generation times) have no effect on the stationary distribution of the evolutionary process. To explore how this result changes when mutation rates are allowed to be appreciably large, we resort to an alternative simplification, allowing mutation rates to be large, but forcing selection to be weak.

Since we are interested in the effect of mutation rates in the two populations, we set their sizes (N), selection strengths, and generation times equal. We make use of the two-population Moran process studied elsewhere in this paper, which is identical to that studied by Ohtsuki [8] when selection is weak. (In fact, Ohtsuki uses an exponential translation of payoffs to fitnesses, $f = \exp(w\pi)$, while we have used a linear translation, $f = 1 + w\pi$. These translations coincide in the weak-selection limit, $w \to 0$, for which Ohtsuki derives results, and which we consider here. This can easily be seen by Taylor expanding the exponential translation around $w = 0$. Therefore, Ohtsuki's weak-selection results hold also for the linear fitness translation.)

The evolutionary process is an irreducible, aperiodic Markov chain over the state space S of all possible population states. Ohtsuki [8] shows that, when the selection strength w is small ($w \to 0$), the stationary distribution of this process, $\lambda(s), s \in S$, simplifies significantly. Denote by $\langle x \rangle_w$ the expectation of x, taken with respect to the stationary distribution; i.e., $\langle x \rangle_w = \sum_{s \in S} x(s)\lambda(s)$. Then, for example, the long run frequency of members of population 1 who play strategy A is $\langle p_A \rangle_w = \sum_{s \in S} p_A(s)\lambda(s)$, where $p_A(s)$ is

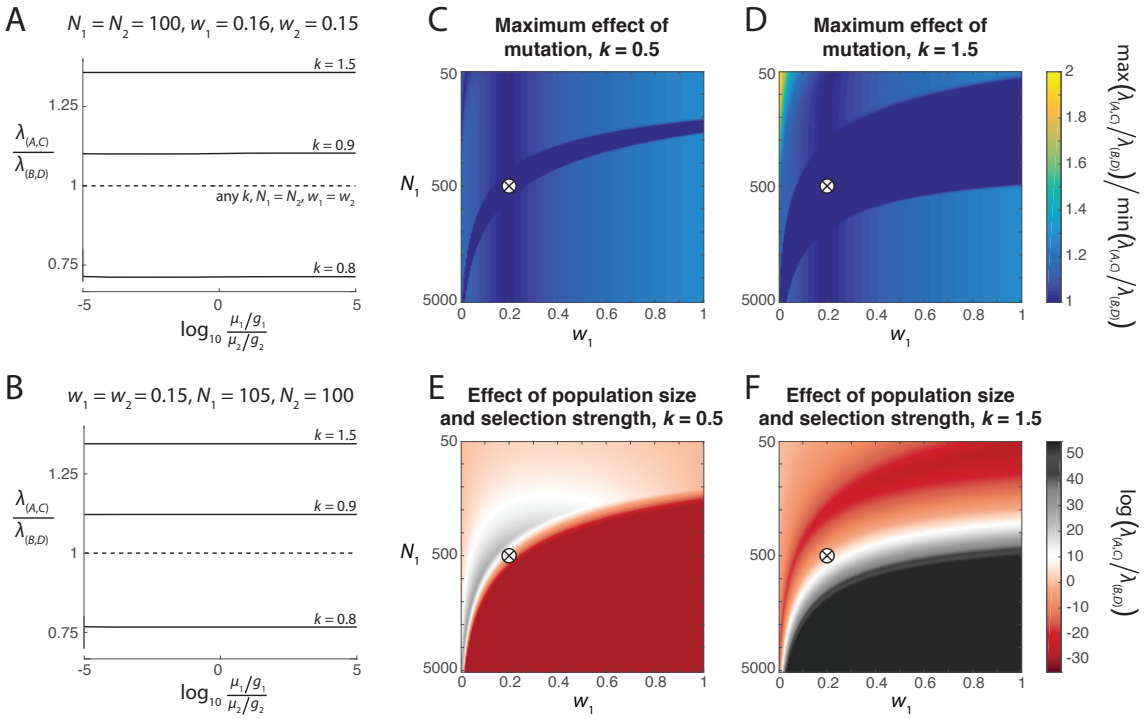


Figure S10: Long-run evolutionary dynamics of mutualisms, when mutations are rare ($\varepsilon \to 0$). (*A*) Setting the populations' sizes equal, we increase population 1's selection strength slightly above population 2's value of $w_2 = 0.15$. Then population 1 does better ($\lambda_{(A,C)} > \lambda_{(B,D)}$) when $k = 0.9$ [because then $w_2 = 0.15 > (1-k)/k = 0.11$], and when $k > 1.5$, but worse when $k = 0.8$ [because then $w_2 = 0.15 < (1-k)/k = 0.25$]. The populations do equally well when $N_1 = N_2$ and $w_1 = w_2$, no matter their relative mutation rates or generation times. (*B*) Setting the populations' selection strengths equal, we increase population 1's size slightly above population 2's. Again, population 1 benefits from its greater rate of evolution when $k = 1.5$ and $k = 0.9$, but not when $k = 0.8$. (*C, D*) We fix population 2's size at $N_2 = 500$ and selection strength at $w_2 = 0.2$ (marked by the cross), set equal population 1 and 2's generation times, and vary population 1's size N_1 and selection strength w_1. For each (N_1, w_1) combination, we vary the relative rate of mutation of the two populations across ten orders of magnitude, and calculate the ratio of the largest and smallest values of $\lambda_{(A,C)}/\lambda_{(B,D)}$, i.e., the maximum effect of mutation on the long-run relative success of the two populations. (*E, F*) For the same parameters as in (*C, D*), we set equal the population's mutation rates, and plot the natural logarithm of $\lambda_{(A,C)}/\lambda_{(B,D)}$ for each (N_1, w_1) combination.

the proportion of population 1 playing strategy A in population state s. For population 2, we denote strategy frequencies by q_C and q_D.

The quantities we are interested in are the long-run frequencies of (A, C) and (B, D) pairings/interactions. If the former frequency is larger than the latter, then we say that population 1 is more successful (recall that all other pairings yield the same payoff for the population 1 and 2 interactants). These quantities, $\langle p_A q_C \rangle_w$ and $\langle p_B q_D \rangle_w$, can be

calculated from Eq. (29) in ref. [8]. Writing $\hat{\mu}_1 = (N-1)\varepsilon\mu_1$ and $\hat{\mu}_2 = (N-1)\varepsilon\mu_2$,

$$\langle p_A q_C \rangle_w = \frac{1}{4}\left\{1 + w\frac{N-1}{(\varepsilon\mu_1+\varepsilon\mu_2)(1+\hat{\mu}_1)(1+\hat{\mu}_2)}\left[\varepsilon\mu_1(1-\varepsilon\mu_1)\frac{2-k}{2} + \varepsilon\mu_2(1-\varepsilon\mu_2)\frac{1}{2} + \frac{1-k}{4}(\varepsilon\mu_2-\varepsilon\mu_1)[1+\hat{\mu}_1+\hat{\mu}_2]\right]\right\};$$

$$\langle p_B q_D \rangle_w = \frac{1}{4}\left\{1 + w\frac{N-1}{(\varepsilon\mu_1+\varepsilon\mu_2)(1+\hat{\mu}_1)(1+\hat{\mu}_2)}\left[\varepsilon\mu_1(1-\varepsilon\mu_1)\frac{1}{2} + \varepsilon\mu_2(1-\varepsilon\mu_2)\frac{2-k}{2} - \frac{1-k}{4}(\varepsilon\mu_2-\varepsilon\mu_1)[1+\hat{\mu}_1+\hat{\mu}_2]\right]\right\}.$$

From these expressions, we calculate the long run advantage to population 1,

$$\begin{aligned}
\langle p_A q_C \rangle_w - \langle p_B q_D \rangle_w &= \frac{w}{4}\frac{N-1}{(\varepsilon\mu_1+\varepsilon\mu_2)(1+\hat{\mu}_1)(1+\hat{\mu}_2)}\left[\varepsilon\mu_1(1-\varepsilon\mu_1)\left(\frac{2-k}{2}-\frac{1}{2}\right)\right. \\
&\qquad \left. +\varepsilon\mu_2(1-\varepsilon\mu_2)\left(\frac{1}{2}-\frac{2-k}{2}\right) + \frac{1-k}{2}(\varepsilon\mu_2-\varepsilon\mu_1)(1+\hat{\mu}_1+\hat{\mu}_2)\right] \\
&= \frac{w}{4}\frac{N-1}{(\varepsilon\mu_1+\varepsilon\mu_2)(1+\hat{\mu}_1)(1+\hat{\mu}_2)}\left[\varepsilon\mu_1(1-\varepsilon\mu_1)\frac{1-k}{2} - \varepsilon\mu_2(1-\varepsilon\mu_2)\frac{1-k}{2}\right. \\
&\qquad \left. +\frac{1-k}{2}(\varepsilon\mu_2-\varepsilon\mu_1)[1+(N-1)(\varepsilon\mu_1+\varepsilon\mu_2)]\right] \\
&= \frac{w}{4}\frac{N-1}{(\varepsilon\mu_1+\varepsilon\mu_2)(1+\hat{\mu}_1)(1+\hat{\mu}_2)}\frac{1-k}{2}\left[N(\varepsilon\mu_2-\varepsilon\mu_1)(\varepsilon\mu_1+\varepsilon\mu_2)\right] \\
&= \frac{w}{8}\frac{N(N-1)}{(1+\hat{\mu}_1)(1+\hat{\mu}_2)}(1-k)\varepsilon(\mu_2-\mu_1) \\
&= A(1-k)\varepsilon(\mu_2-\mu_1),
\end{aligned}$$

where $A = \frac{w}{8}\frac{N(N-1)}{(1+\hat{\mu}_1)(1+\hat{\mu}_2)} > 0$. Therefore, if $k < 1$, population 1 does better ($\langle p_A q_C \rangle_w - \langle p_B q_D \rangle_w > 0$) when it has the smaller mutation rate, $\mu_1 < \mu_2$. On the other hand, when $k > 1$, population 1 does better when it has the larger mutation rate, $\mu_1 > \mu_2$. So slower evolution, in terms of mutation rates, is favored when $k < 1$, and faster evolution is favored when $k > 1$.

When mutation rates are low ($\varepsilon \approx 0$), changes in relative mutation rates have very little effect on $\langle p_A q_C \rangle_w - \langle p_B q_D \rangle_w$, consistent with our weak-mutation results above.

S8 Mutualistic symbioses with continuous strategy spaces

So far, we have considered discrete-strategy games, where members of each population choose between two strategy options (A or B for population 1, and C or D for population 2). In the discrete mutualism game that we have studied, this discreteness results in there being two stable equilibrium outcomes, one preferred by population 1, and the other preferred by population 2. In the introductory section of our Main Text, we have dis-

cussed examples of mutualistic interactions where this strategy discreteness clearly applies. However, in many mutualisms, strategies are of a more continuous nature; for example, *how much* energy does one species devote to a certain mutually beneficial task, instead of reserving this energy for uses beneficial only to itself? In this section, we provide a preliminary setup and analysis of how stochastic evolutionary dynamics apply to such continuous-strategy mutualisms.

As before, we seek a game that describes interactions between two individuals drawn from two different populations. The game we shall study is a continuous version of the Nash bargaining game, which nests the classical 'divide-the-dollar' version [7] as a special case. The two individuals choose some activity level, $x \in [0,1]$ for individuals from population 1 and $y \in [0,1]$ for individuals from population 2. Depending on the parameterization, these activity levels may be thought of as contributions to a public good, for example, or the amount extracted from a joint resource. Payoffs are given by

$$\pi_1(x,y) = \begin{cases} \alpha x + (1-\alpha)y & \text{if } x+y \leq 1 \\ 0 & \text{otherwise} \end{cases} \quad \text{and} \quad \pi_2(x,y) = \begin{cases} (1-\alpha)x + \alpha y & \text{if } x+y \leq 1 \\ 0 & \text{otherwise} \end{cases} . \tag{8}$$

The parameter α measures to what extent individuals benefit from their own activity levels. The assumption $\alpha \in (0,1)$ ensures that the interaction can be interpreted as mutualistic: provided that the sum of both players' activities is at most 1, increasing one individual's activity increases both individuals' payoffs. As in many other studied bargaining games, the restriction that payoffs are positive only if $x+y \leq 1$ permits a simple characterization of the equilibrium set: any combination (x,y) with $x+y = 1$ is an equilibrium of the game. If $\alpha < 1/2$, an equilibrium favors population 1 if $x < y$ (i.e., the equilibrium favors the population that shows the lower activity level). Conversely, if $\alpha > 1/2$, an equilibrium favors population 1 if $x > y$. In the limiting case $\alpha \to 1$, the interaction reduces to 'divide-the-dollar': there is a resource worth a total of one unit in payoffs, and the individuals' activities represent what fraction of this resource they demand for themselves (with the convention that when the summed demands exceed the whole resource, both individuals get nothing).

To model the evolutionary dynamics, we consider a weak-mutation scenario similar to that we have employed in the discrete-strategy case—mutations are assumed to be rare, so that populations are almost always monomorphic for some strategy. The key difference between the previous analyses and that here is that, while in the discrete 2-strategy case, a mutation simply means switching to the other strategy, in the continuous case we need to specify the distribution of possible mutations. We employ a 'local mutations' model [4].

From any state (x,y) in which populations 1 and 2 are monomorphic for strategies x and y respectively, a mutation occurs in one of the populations; as before, the probability that this happens in population l is proportional to $N_l \mu_l / g_l$. Mutations are 'local', that is, of small effect: if the mutation appears in population 1 when it is fixed for strategy x, then the mutant's strategy is $x' = x + u$, where u is taken from the uniform distribution

on $[-\delta, \delta]$ (if x' happens not to be in the unit interval, another mutant strategy is drawn). The fitness of a resident x-player and of the mutant x'-player are $f_1 = 1 + w_1\pi_1(x, y)$ and $f_1' = 1 + w_1\pi_1(x', y)$, respectively. If, instead, the mutant appears in population 2, then the respective fitnesses f_2 and f_2' are calculated analogously (with the same maximum mutation effect δ applying to both populations, though their mutation *rates* can differ). As in the model with only two strategies, the mutant strategy fixes in its population l with probability $(1 - f_l/f_l')/[1 - (f_l/f_l')^{N_l}]$. This elementary updating process then iterates: another mutation occurs in one of the two population, and it again either fixes or goes extinct. Initially, individuals from both populations are assumed to show no activity $x=y=0$. By iterating this process for a sufficient timespan (for the simulations shown in the following we introduce 10^9 mutant strategies in total), we approximate the distribution of strategies in the mutation-selection equilibrium.

The evolutionary dynamics of this model with continuous activity levels is different from the evolutionary dynamics of the discrete games studied in the Main Text, for at least three reasons: First, given our assumptions that mutant strategies are close to the strategies from which they mutated and that the payoff functions are continuous when total activity does not exceed 1, the difference between the fitness of a mutant strategy and of the strategy from which it mutated will usually be small, so that we are in a weak-selection regime [10]. Therefore, even mutants of reduced fitness may substitute at an appreciable rate. Second, while the discrete mutualism game had two distinct equilibria, in the continuous model there is a continuous path of equilibria (the line $x+y=1$); with local mutation and the associated weak selection, we may expect to see stochastic movement along this path. Third, in the discrete mutualism game, the Red King effect arose in a setting where it required *both* populations to evolve to reach an equilibrium—differences in their evolutionary rates then influenced the basins of attraction of the two equilibria. In the continuous strategy section that we are considering here, mutation and selection in one of the two populations would be sufficient to reach an equilibrium. For example, if population 1 has a very much shorter generation time than population 2, we may expect that, starting from the origin $(x, y) = (0, 0)$, the dynamics quickly move towards a state where individuals in population 1 show a much higher activity, $(x, y) \approx (1, 0)$. Whether we observe a Red King effect then depends on whether states close to $(1, 0)$ favor population 1 or population 2 (i.e., whether α is larger or smaller than $1/2$).

Figures S11 and S12 display simulation runs for two different values of α ($\alpha = 0.75$ and $\alpha = 0.25$). As for the discrete-strategy mutualism game studied in the Main Text, we consider how the dynamics are affected when the two populations differ in each of four different evolutionary rate parameters: generation time (first column in Figs S11 and S12), mutation rate (second column), selection strength (third column), and population size (fourth column). For all parameters, we assume that it is population 2 that evolves at a faster rate, either because it has a shorter generation time, a higher mutation rate, is under stronger selection, or is larger. We again distinguish between the short-run dynamics (here defined as the time it takes the populations to evolve to, or close to, one of the states on

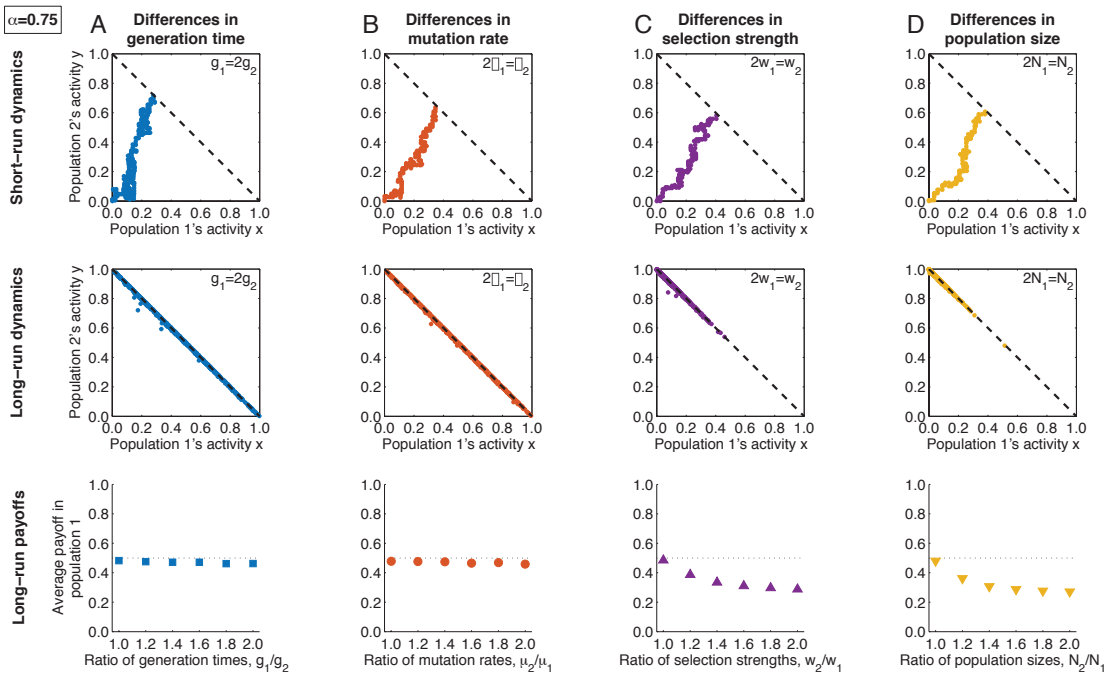


Figure S11: Short-run and long-run dynamics for continuous-strategy mutualisms, when α is large. Population 1 evolves slower owing to (A) a longer generation time, (B) a lower mutation rate, (C) weaker selection, and (D) a smaller population size. The top panels illustrate the short-run dynamics, showing typical evolutionary trajectories that the populations take from the initial state $(x, y) = (0, 0)$ to somewhere on or near the line of equilibria, $x+y = 1$ (the populations are considered near this line if $x + y \geq 0.98$). The middle panels show the long-run positions of the two populations over 10^9 elementary updating events. For clarity, these panels depict only those strategy combinations corresponding to the 10,000 most successful strategy combinations over time. The bottom panels depict the long-run average payoff of individuals in population 1, depending on how much the two populations differ in the relevant evolutionary rate parameter. Differences in generation time and mutation rate have little effect in the long run, but differences in selection strength and population size give rise to a strong Red Queen effect: the slower-evolving population 1 gets a lower share of the total payoff. This is similar to the results we obtained for the discrete-strategy mutualism game in the Main Text. Baseline parameters: $\alpha = 0.75$; $g_1 = g_2 = 1$, $\mu_1 = \mu_2 = 1$, $w_1 = w_2 = 0.5$ and $N_1 = N_2 = 100$; mutant strategies are at most a distance $\delta = 0.05$ from the strategy from which they mutated.

the equilibrium line) and the long-run dynamics (which corresponds to the 10^9 elementary updating events that we have simulated the evolutionary process for).

Independent of the value of α, and independent of the evolutionary rate parameter that is varied, we observe that the short-run dynamics are dominated by the population that evolves at a faster rate (see upper panels in Figs. S11 and S12). That is, when population 2 evolves faster, by the time the two populations reach the line of equilibria $x + y = 1$, we typically observe that $y > x$. The long-run dynamics depend on the evolutionary parameter that is varied (middle panels in Figs. S11 and S12). Differences

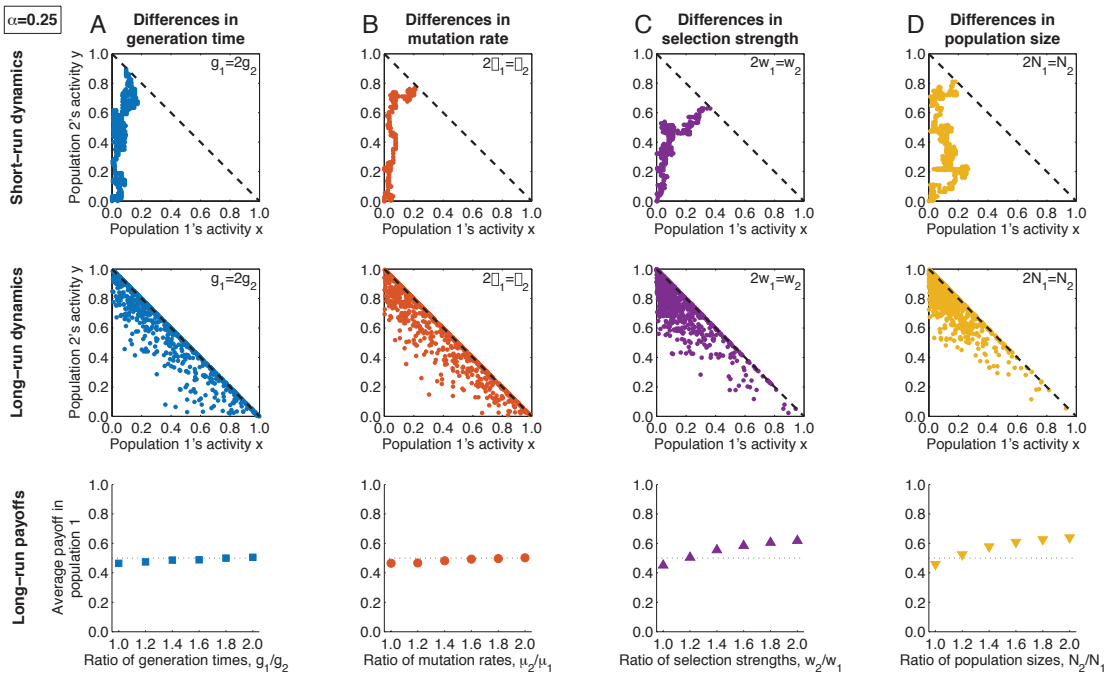


Figure S12: Short-run and long-run dynamics for mutualisms with a continuous trait space when α is small. The setup of the simulations is the same as in Fig. S11, except that here, $\alpha = 0.25$ (i.e., changes in own activity level usually have little influence on own payoff, but have a strong influence on payoffs of individuals in the other population). In this case, we observe a Red King effect when the populations differ in their selection strength or in their population size. Again, differences in generation time and mutation rate have little effect in the long run, similar to our results for the discrete-strategy mutualism game.

in generation time and mutation rate have little influence on the activity levels of the two populations, but differences in selection strength and population size create a bias towards higher activity levels in the faster-evolving population. To understand this, consider an arbitrary population state (x, y) on the equilibrium line (so that $x + y = 1$), and suppose that the two populations differ only in their selection strength: $w_2 > w_1$. In this case, the most likely evolutionary trajectory out of the present equilibrium state (x, y) involves the fixation in population 1 of a mutant with slightly reduced activity level $x' < x$ — such a mutant in population 1 is of reduced fitness, but is more likely to fix than an equivalent mutant in population 2 because selection is stronger in population 2 (and note that, in any population, a mutant with *increased* activity level is strongly selected against because it typically receives payoff 0). Then, again because $w_2 > w_1$, the next evolutionary step most likely involves population 2 slightly increasing its activity level y. Therefore, stochastic fluctuations off the equilibrium line tend to be in the direction of reduced x, and tend to return to the equilibrium line in the direction of increased y. In total, these two effects make the two populations move to the upper left corner, as depicted in the middle panels of Figs. S11 and S12. This is an example of drift-induced selection along an

equilibrium line that would otherwise be stationary under deterministic dynamics; drift-induced selection is a phenomenon of recent and growing interest in stochastic evolutionary dynamics (e.g., [2]).

In Fig. S11, we consider the case $\alpha = 0.75$, where the population that on average shows a higher activity level obtains higher average payoffs. We observe a Red Queen effect in this scenario when populations differ in their selection strengths or population sizes: the faster-evolving population 2 gets a higher share of the total payoff. In contrast, Fig. S12 shows the case $\alpha = 0.25$, where the population with the lower average activity level obtains higher average payoffs. Now, the slower-evolving population 1 outperforms population 2 when its slower evolution is due to reduced selection strength or smaller population size—a Red King effect. Again, differences in mutation rate and generation time have little effect. In addition, we note that for $\alpha = 0.25$, the two populations are more dispersed across the strategy space. Intuitively, because α is smaller, changes of own strategy within a population are under weaker selection, so that deviations below the equilibrium line are selected against less effectively.

References

[1] C. T. Bergstrom and M. Lachmann. The Red King effect: when the slowest runner wins the coevolutionary race. *Proceedings of the National Academy of Sciences*, 100(2):593–598, 2003.

[2] G. W. A. Constable, T. Rogers, A. J. McKane, and C. E. Tarnita. Demographic noise can reverse the direction of deterministic selection. *Proceedings of the National Academy of Sciences*, 113(32):E4745–E4754, 2016.

[3] J. B. S. Haldane. A mathematical theory of natural and artificial selection, part V: selection and mutation. *Mathematical Proceedings of the Cambridge Philosophical Society*, 23(07):838–844, 1927.

[4] L. A. Imhof and M. A. Nowak. Stochastic evolutionary dynamics of direct reciprocity. *Proceedings of the Royal Society of London B: Biological Sciences*, 277(1680):463–468, 2010.

[5] D. M. McCandlish, C. L. Epstein, and J. B. Plotkin. Formal properties of the probability of fixation: Identities, inequalities and approximations. *Theoretical population biology*, 99:98–113, 2015.

[6] D. M. McCandlish and A. Stoltzfus. Modeling evolution using the probability of fixation: history and implications. *The Quarterly review of biology*, 89(3):225–252, 2014.

[7] R. B. Myerson. *Game Theory: Analysis of Conflict*. Harvard University Press, 1991.

[8] H. Ohtsuki. Stochastic evolutionary dynamics of bimatrix games. *Journal of theoretical biology*, 264(1):136–142, 2010.

[9] C. Veller and L. K. Hayward. Finite-population evolution with rare mutations in asymmetric games. *Journal of Economic Theory*, 162:93–113, 2016.

[10] G. Wild and A. Traulsen. The different limits of weak selection and the evolutionary dynamics of finite populations. *Journal of Theoretical Biology*, 247(2):382–390, 2007.