



# Symbiosis through exploitation and the merger of lineages in evolution

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A model for the coevolution of two species in facultative symbiosis is used to investigate conditions under which species merge to form a single reproductive unit. Two traits evolve in each species, the first affecting loss of resources from an individual to its partner, and the second affecting vertical transmission of the symbiosis from one generation to the next. Initial conditions are set so that the symbiosis involves exploitation of one partner by the other and vertical transmission is very rare. It is shown that, even in the face of continuing exploitation, a stable symbiotic unit can evolve with maximum vertical transmission of the partners. Such evolution requires that eventually deaths should exceed births for both species in the free-living state, a condition which can be met if the victim, in the course of developing its defences, builds up sufficiently large costs in the free-living state. This result expands the set of initial conditions from which separate lineages can be expected to merge into symbiotic units.

**Keywords:** adaptive dynamics; coevolution; evolutionary transitions; mutualism; symbiosis; vertical transmission

## 1. INTRODUCTION

Evolutionary biologists are accustomed to think of macroevolution as a branching process in which lineages diverge as they descend from common ancestors, giving rise to a tree-like phylogeny (Darwin 1859, p. 56). This picture is reinforced in many studies, a good example being the phylogeny of life based on comparisons of the small subunit of ribosomal RNA (Sogin 1991).

While in no way questioning the central role of this mode of evolution, here we consider the reverse process in which lineages, remote by descent, merge to form symbioses capable of reproducing themselves as a single unit. (In using the term 'symbiosis', we do not mean to imply a mutualistic association; we simply mean that the association is intimate and potentially long-lasting (Lewis 1985).) There is no doubt that such mergers have happened, a striking example being the evolution of the chloroplast of eukaryotes. This is thought to have begun with one or more mergers of photosynthetic Gram-negative bacteria and early eukaryotes arguably about 2000 million years ago (Dyer & Obar 1994, p. 12). Following this, there seems to have been a complex sequence of changes, perhaps involving the transfer of chloroplasts of one eukaryote to another (euglenoids and dinoflagellates), and uptake of complete photosynthetic eukaryotes by other eukaryotes (cryptomonads, diatoms and brown algae) (Cavalier Smith 1992; MacFadden & Gilson 1995).

The emergence of new, symbiotic units, built from independent subunits, lies at the heart of some of the major steps in the evolution of life (Buss 1987; Maynard

Smith & Szathmary 1995). How the transition is achieved is not at all obvious, as it is quite possible for natural selection, operating at the level of the subunits, to disrupt their integration into the larger unit. It is particularly difficult to see how it can come about in cases where the subunits are genetically unrelated and there is no opportunity for kin selection to take place. Attempts to find evolutionary paths leading to integration of unrelated organisms have usually presupposed that each subunit can provide some benefit to its partner so that the success of one is bound to the success of the other; the hypercycle of prebiotic evolution is a case in point (Eigen & Schuster 1977). But evolution of cooperative associations can be difficult to get started as the benefit each species provides to its partner may have to be greater than a threshold value (Frank 1995).

Arguably, a more likely starting point would involve the exploitation of one partner by the other. One way in which a symbiotic unit could emerge from such an initial state is through vertical transmission (Fine 1975); if the continued existence of the exploiter depends in part on its partner's survival, it will not pay to exploit the partner too heavily (Ewald 1987). A model presented by Yamamura (1993, 1996) indicated that an obligate parasite, which starts with enough vertical transmission, will cause evolution of greater vertical transmission and a decrease in exploitation, leading eventually to a mutualistic symbiosis.

For a stable symbiotic unit to emerge, an association is needed in which births exceed deaths in the symbiotic state of both partners, and correspondingly deaths exceed births in the free-living state. A symbiosis in which both species benefit from resources provided by the other will have this property. But such mutual

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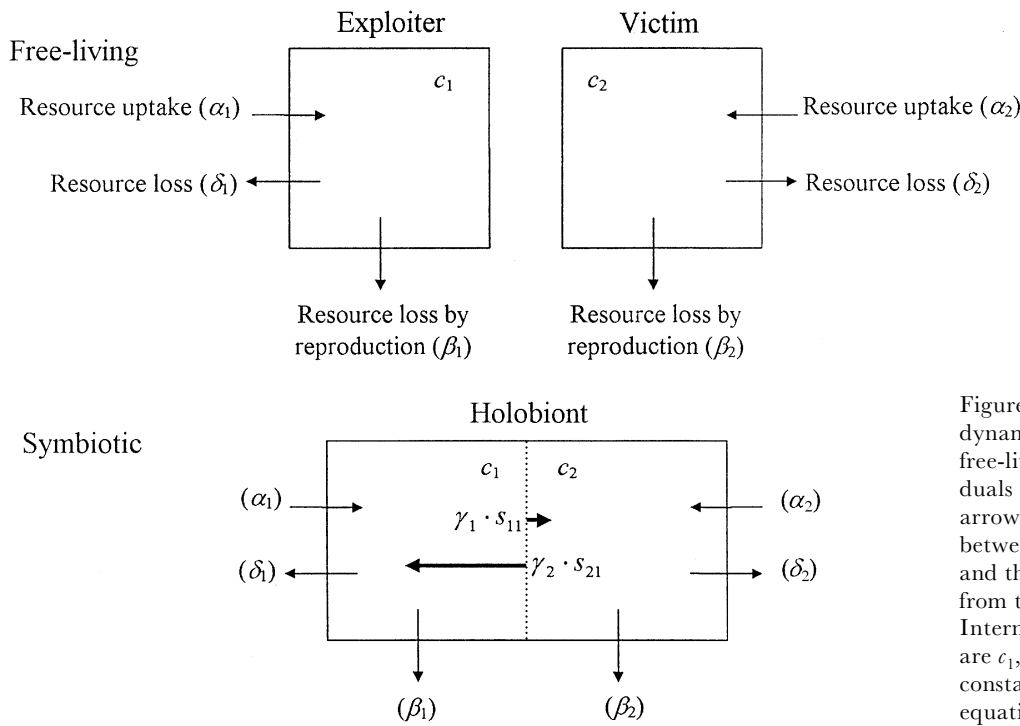


Figure 1. Model of resource dynamics across the boundaries of free-living and symbiotic individuals of two species. The heavy arrows refer to the flow of resources between individuals in symbiosis, and there is net flow of resources from the victim to the exploiter. Internal concentrations of resource are  $c_1, c_2$ . Greek symbols are rate constants used in Appendix A, equation (A1).

benefit is not necessary for merging of the lineages. We show here the existence of an evolutionary path from a facultative association to a stable symbiotic unit with coupled reproduction of the partners, in the face of continued exploitation of one partner by the other. This result expands the set of initial conditions from which separate lineages can be expected to merge into symbiotic units (Frank 1997).

## 2. A COEVOLUTIONARY MODEL OF SYMBIOSIS

We investigate the interaction of two species, indexed 1 and 2, using separate resources in the free-living state. When the species come together, they can form a symbiosis, and there is transfer of resources between the partners. Species 1, the 'exploiter', restricts the flow to its partner more than the other, the 'victim'. The composite, symbiotic unit may be temporary, or it may have a more extended existence; we emphasize its separate existence by calling it the 'holobiont', following Margulis (1993, p. 169).

To examine the evolution of the community, we use a dynamical system coupling two phenotypic traits in each species. The first affects the transfer of resources from the species to its partner; we refer to the value of this trait as  $s_{i1}$  for species  $i$ . The second affects the probability of coupled birth events of the partners in symbiosis. Such coupled births maintain the integrity of the holobiont from one generation to the next and are critical for merger of the lineages. We refer to the value of this second trait as  $s_{i2}$  for species  $i$ . The four trait values that predominate at a given time are collected into a vector  $\mathbf{s} = (s_{11}, s_{12}, s_{21}, s_{22})$ .

How the traits evolve depends on the abundance and phenotypic state of each species and its partner, an environment which itself is evolving. Disentangling the causal pathways involved is not trivial, and it helps to

think of a hierarchy of three separate time-scales: a microscopic (physiological) scale on which resources are taken up by individuals, a mesoscopic (ecological) scale on which the population dynamics determining abundance occur, and a macroscopic (evolutionary) scale on which phenotypic change takes place (Dieckmann & Law 1996; Marrow *et al.* 1996). Abundance of the species is then set by the current phenotypic states, but gradually changes as the system evolves.

### (a) Microscopic time-scale

We start with the smallest, physiological time-scale, on which abundances and trait values can be taken as constant. To keep a simple mechanistic underpinning for the phenotypic traits and their effects on birth and death events, we use a resource-based model; figure 1 shows the flows involved. We assume that there are two resources, 1 and 2, at an external concentration  $C_1, C_2$  in the environment; they might, for instance, be thought of as two sources of carbon. In the free-living state, species  $i$  uses resource type  $i$  only; in symbiosis, however, resource  $j$  can move into species  $i$ , in so doing being converted into resource  $i$ . The resource concentration within each individual comes rapidly to equilibrium, and the birth rate of the individual is proportional to this concentration. Details of resource flows in and out of individuals, and how these determine the per capita rates of reproduction are given in Appendix A.

### (b) Mesoscopic time-scale

On the time-scale of ecological dynamics, we define a system of equations for the dynamics of population size  $n_1, n_2$  and  $\bar{n}$  of the exploiter, victim and holobiont, respectively, still holding the trait values constant. The flows between these populations are shown diagrammatically in figure 2, and the dynamics are given by the following expressions:

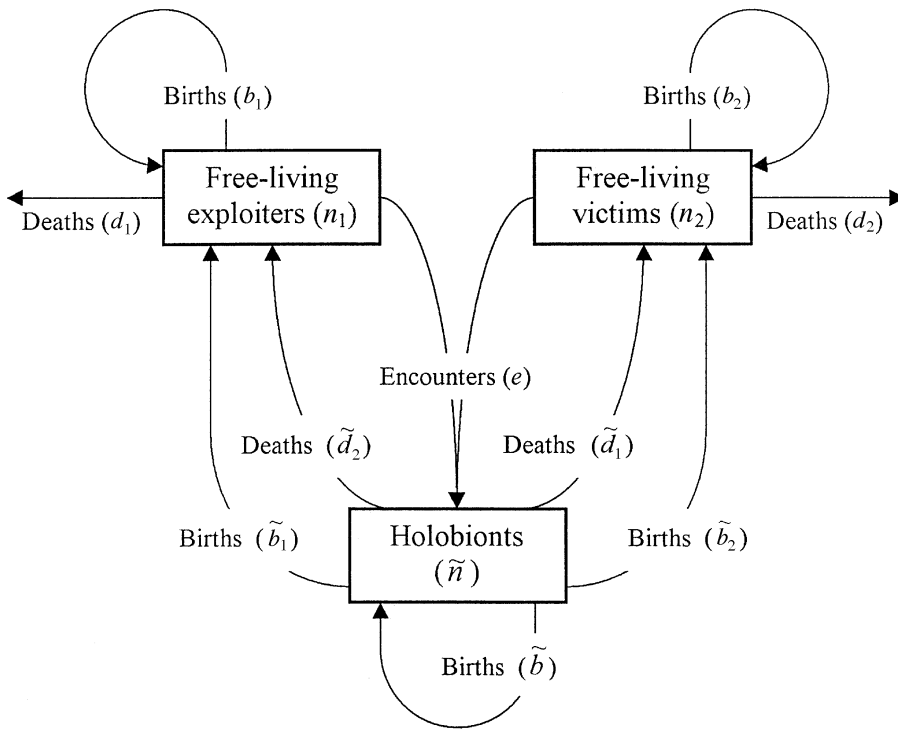


Figure 2. Model of population dynamics, showing the flows between populations of free-living exploiters, victims and holobionts, with population sizes  $n_1, n_2, \tilde{n}$ . Other symbols are rate constants used in equations (1).

$$\dot{n}_1 = +b_1 n_1 - d_1 n_1 - e n_1 n_2 + \tilde{b}_1 \tilde{n} + \tilde{d}_2 \tilde{n}; \tag{1a}$$

$$\dot{n}_2 = +b_2 n_2 - d_2 n_2 - e n_1 n_2 + \tilde{b}_2 \tilde{n} + \tilde{d}_1 \tilde{n}; \tag{1b}$$

$$\dot{\tilde{n}} = -\tilde{d}_1 \tilde{n} - \tilde{d}_2 \tilde{n} + e n_1 n_2 + \tilde{b} \tilde{n}. \tag{1c}$$

The tildes here and below identify terms that apply to the symbiotic state. These equations are perhaps the simplest formulation that makes explicit both the free-living and symbiotic states. They include the rate at which free-living individuals of species  $i$  give rise to free-living offspring ( $b_i$ ), the rate at which symbiotic individuals of  $i$  give rise to free-living ( $\tilde{b}_i$ ) and symbiotic ( $\tilde{b}$ ) offspring, the death rates of species  $i$  in the free-living ( $d_i$ ) and symbiotic ( $\tilde{d}_i$ ) states, and encounters at rate  $e$  between free-living individuals creating holobionts.

The populations are regulated by the availability of resources  $C_1, C_2$  in the environment, as described in Appendix A. An effect of this regulation is the existence of an equilibrium point at which both species have positive population sizes, which is the solution in all our integrations that start with positive populations. Thus, on the mesoscopic time-scale, the populations tend to these equilibrium abundances for constant trait values. For interpretation of the conditions for increase of mutants used later, it should be noted that, once equilibrium has been reached, the following property applies to each species:

$$\tilde{d}_i < \tilde{b}_i + \tilde{b} \Leftrightarrow d_i > b_i; \tag{2}$$

in other words, if births exceed deaths in the symbiotic state, then deaths must exceed births in the free-living state.

(c) **Mutant trait values**

Consider now a community that has reached equilibrium population sizes for a given vector  $\mathbf{s}$  of resident trait values. To describe the evolutionary dynamics, we need to know whether a mutant trait  $s'_{ij}$  is able to spread when it enters the community. These mutants affect the birth rates in symbiosis, and we write the birth rates at ecological equilibrium as functions  $\hat{b}_i(s'_{ij}, \mathbf{s}), \hat{b}(s'_{ij}, \mathbf{s})$ , the first argument being the mutant trait value of the individual itself, and the second being the trait values of the resident community in which it occurs. In the free-living state, the birth rate  $\hat{b}_i(\mathbf{s})$  is unaffected by mutation and has only one argument, this being the state of the resident community.

How the traits affect birth rates in symbiosis is shown schematically in figure 3. The first trait  $s'_{i1}$  scales the rate at which the individual loses resource to its partner; this is a dimensionless quantity in the range  $[0, 1]$ . With the assumptions made above about resource flow between the symbionts, the total birth rate of a symbiotic individual  $\hat{B}_i(s'_{i1}, \mathbf{s})$ , which is defined by summing over the rate at which it produces both free-living and symbiotic offspring, decreases linearly as the rate at which it loses resource to its partner increases. An individual in the symbiotic state therefore produces more offspring the smaller  $s'_{i1}$  is. This effect is a passive consequence of the concentration at which resources equilibrate within individuals; we are not suggesting a ‘mafia’-like manipulation of the victim by the exploiter (Soler *et al.* 1995).

The second trait,  $s'_{i2}$ , affects the probability of a coupled birth event in symbiosis; this is also dimensionless in the range  $[0, 1]$ . This trait partitions the total birth rate of symbiotic individuals among free-living and symbiotic offspring. We make the assumption that the rate at which symbiotic offspring are born depends on the product  $s_{i2} s_{i22}$

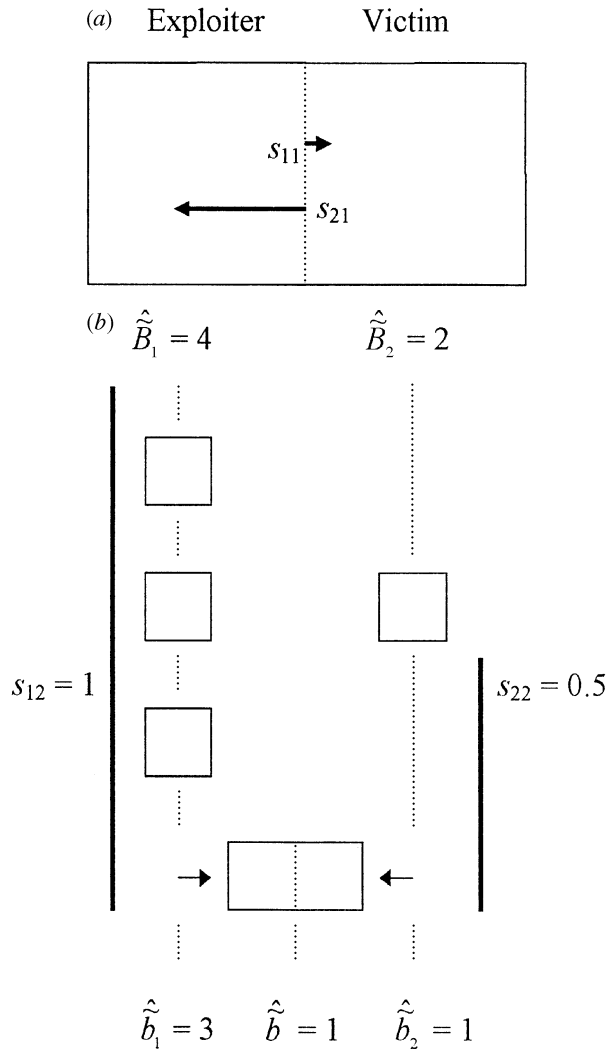


Figure 3. Model of adaptive dynamics, showing effects of traits  $s_{ij}$  on birth rates in symbiosis. (a) The first trait, affecting how much resource is lost to the partner, gives the exploiter a greater birth rate. (b) The second trait affects the proportion of births that are symbiotic; a numerical example is given showing how the total birth rate of symbionts is partitioned between symbiotic and free-living offspring.

over both species; it is then enough for one species to have a trait value  $s_{22}=0$  for there to be no coupled births. The rate at which these holobiont births occurs is taken to be  $\hat{b}(s'_{i2},s) = \min(\hat{B}_i(s'_{i2},s)s'_{i2}s_{k2}, \hat{B}_k(s_{k2},s)s'_{i2}s_{k2})$ , where  $k \neq i$ ; the reason for using this function is that the holobiont cannot reproduce itself faster than any of its components. So the rate at which symbiotic offspring are born is the same for both species (there is one individual of each species in the offspring), and we adjust the rate at which free-living offspring are born accordingly:  $\hat{b}_i(s'_{i2},s) = \hat{B}_i(s'_{i2},s) - \hat{b}(s'_{i2},s)$ . A numerical illustration of how this works is given in figure 3.

A cost to evolution will also be considered below. This is motivated by costs found in an experimental study on the evolution of a bacterial infection of *Amoeba* (Jeon 1972, see §4). We introduce the cost as a death rate  $d_i(s'_{i1})$  in the free-living state, which increases as  $s'_{i1}$  diverges from the value  $s_{i1}^{(0)}$  before evolution starts, and use a function symmetric around  $s_{i1}^{(0)}$ :

$$d_i(s'_{i1}) = D_i \exp(\omega_i (s'_{i1} - s_{i1}^{(0)})^2), \tag{3}$$

where  $D_i$  is the free-living mortality rate before evolution starts, and  $\omega_i$  is a constant scaling how fast the cost grows.

(d) **Macroscopic time-scale**

We now turn to a longer, evolutionary time-scale on which mutations occur and replace resident traits. In making this separation of time-scales, we are assuming that mutations are sufficiently rare for the populations to get close to their equilibrium sizes between mutation events.

At a qualitative level, quite a lot about phenotypic evolution of a symbiotic system can be learnt simply from the sign of the average initial rate of increase of a mutant (Metz *et al.* 1992; Genkai-Kato & Yamamura 1998). Specifically, writing  $N'_i = (n'_i, \tilde{n}'_i)$  as the size of the mutant population, the average rate  $\dot{N}'_i$  at which it grows when rare is given by

$$\dot{N}'_i = N'_i L_i, \tag{4a}$$

from equations (1), where

$$L_i = \begin{pmatrix} \hat{b}_i(s) - d_i(s'_{i1}) - e\hat{n}_k(s) & e\hat{n}_k(s) \\ \hat{b}_i(s'_{ij},s) + \tilde{d}_k & \hat{b}(s'_{ij},s) - \tilde{d}_i - \tilde{d}_k \end{pmatrix}, \tag{4b}$$

and  $k \neq i$ . (The resident community can be taken as remaining at the equilibrium abundances  $\hat{n}_1(s), \hat{n}_2(s), \hat{n}(s)$ , set by the resident trait values, when the mutant is rare.) The average initial rate of increase  $\lambda$  of the mutant (i.e. the dominant eigenvalue of  $L_i$ ) must be positive for the mutant to stand any chance of becoming established. For a mutation of small enough effect on the phenotype,  $\lambda$  is given to a good approximation by the determinant and trace of  $L_i$  (Genkai-Kato & Yamamura 1998), so the condition for a mutant to increase, on average, when rare is

$$\lambda = \det L_i / \text{tr} L_i > 0. \tag{5}$$

Generically, this approximation for the eigenvalue becomes exact for  $s'_{ij} \rightarrow s_{ij}$ . With this expression it is possible to find relatively simple conditions for the spread of mutants.

To step from a qualitative condition to the quantitative dynamics of phenotypic evolution, we use a deterministic approximation to a stochastic mutation-selection process. The first source of stochasticity is mutation itself; a mutant birth, with trait value  $s'_{ij}$ , is drawn at random from a mutation distribution symmetric around the current resident trait value  $s_{ij}$  and with small variance. The second source is the chance of extinction of the mutant when rare. A mutant that escapes extinction when rare is assumed to go to fixation. Evolution of the traits can be approximated by the mean path of the stochastic process, using a system of four equations (A 6a) derived in Appendix A. These equations describe the coupled, adaptive dynamics of the four traits. As each trait evolves, it changes the environment in which the species live, and this affects the future path of evolution of each trait; each species both constructs and is

changed by its environment (Lewontin 1983; Odling-Smee *et al.* 1996).

**3. RESULTS**

We can now determine conditions needed for development of a holobiont which, by means of coupled births, maintains its integrity as a symbiotic unit from one generation to the next. Below, two cases are considered: (a) evolution with no costs, in which the rate of coupled births does not increase substantially, and (b) evolution with costs, where it can become advantageous to both partners to remain in symbiosis from one generation to the next.

In describing these cases, we assume that the following starting conditions apply.

1. Mixing between the free-living and symbiotic states is large enough for  $\text{tr}L_i < 0$ ; our numerical studies indicate that this is readily satisfied even for small  $e$  (in the numerical example below  $e=0.005$ ), which means that a mutant can spread if and only if  $\det L_i < 0$  (see inequality (5)).
2. Traits affecting resource flow begin with values  $s_{11}=0, s_{21}>0$ ; species 1 is then the exploiter and species 2 the victim.
3. Traits affecting coupled births ( $s_{12}, s_{22}$ ) start close to zero; as a result it is initially very rare for continuity of the symbiosis to be maintained from one generation to the next.

Throughout it is assumed that mutants cause no more than small effects on the phenotype.

**(a) Cost-free evolution**

Consider a mutant  $s'_{i1}$  in species  $i$  that reduces the loss of resource to its partner in symbiosis, thereby gaining a small increment  $\delta\hat{b}_i + \delta\hat{b}$  to its birth rate in symbiosis. In the absence of any cost, the death rate of individuals in the free-living state is constant,  $d_i(s'_{i1}) = D_i$ , and, from inequality (5), the mutant can only increase if

$$0 < \underbrace{(D_i - \hat{b}_i(s))\delta\hat{b}}_I + \underbrace{e\hat{n}_k(s)(\delta\hat{b}_i + \delta\hat{b})}_{II}, \tag{6}$$

where  $k \neq i$ . This condition is satisfied for the exploiter: it has an excess of births over deaths in symbiosis, and correspondingly an excess of deaths over births in the free-living state (inequalities (2)), so term I is positive; term II, comprising only positive factors, is also positive. Thus  $s_{11}$  is held at zero by natural selection as the symbiosis evolves. In the case of the victim, our numerical results indicate that, because of the strong mixing, term II is large enough for the condition to be met for this species as well. This is just as one would expect: a mutant that reduces the loss of resources to its partner has a birth rate in symbiosis greater than that of the resident phenotype, irrespective of how these births are partitioned among free-living and symbiotic offspring. Evolution continues until the species have erected a complete barrier to resource flow in symbiosis, at which point the birth rates in symbiosis are the same as they are in the free-living state, and the symbiosis is neutral.

Consider now a mutant  $s'_{i2}$  in species  $i$  that redistributes births by symbiotic parents among free-living and symbiotic states, making a small increment  $\delta\hat{b}$  to the coupled births, and correspondingly a small reduction  $-\delta\hat{b}$  to free-living births. On average, such a mutant will increase if

$$0 < (D_i - \hat{b}_i(s))\delta\hat{b}. \tag{7}$$

What matters here is that deaths should exceed births in the free-living state. This property certainly holds for the exploiter: it has more births than deaths in symbiosis, and correspondingly more deaths than births when free-living (inequalities (2)); mutants with  $s'_{i2} > s_{i2}$  are therefore favoured. But the reverse applies to the victim, and mutants with  $s'_{i2} < s_{i2}$  are selected. The resulting conflict prevents a concerted shift towards more coupled births needed for the holobiont to maintain its integrity from one generation to the next. Eventually the symbiosis reaches a state in which the barriers to resource flow in symbiosis are complete ( $s_{11}=s_{21}=0$ ), at which point there is no further selection on coupled births at all.

An illustration of this evolution, obtained by integration of equations (A6), is shown in figure 4a. The downward path of  $s_{21}$  is evident;  $s_{11}$ , which starts at zero, is held at zero by selection. How the rate of coupled births changes depends quantitatively on the rate at which  $s_{12}$  increases and  $s_{22}$  decreases. But there is little change in these traits before  $s_{21}$ , like  $s_{11}$ , is zero, and  $s_{12}$  and  $s_{22}$  have become neutral.

**(b) Evolution with costs**

The evolutionary path above would end matters, were it not for costs associated with defence. However, the outcome can be quite different if, as in the case of Jeon's (1972) *Amoeba*, there is some loss of viability in the free-living state as the victim evolves in response to its symbiotic partner. To see the effect of such costs, we repeat the analysis above with a cost, as given in equation (3).

The condition for invasion by a mutant  $s'_{i1}$ , causing a small increment to reproduction in the symbiotic state (and now an increment  $\delta d_i$  to mortality in the free-living state as well) is

$$0 < \underbrace{(d_i(s_{i1}) - \hat{b}_i(s))\delta\hat{b}}_I + \underbrace{e\hat{n}_k(s)(\delta\hat{b}_i + \delta\hat{b})}_{II} + \underbrace{(\hat{b}(s_{i1},s) - \tilde{d}_i - \tilde{d}_k)\delta d_i}_{III}. \tag{8}$$

The exploiter, as before, remains at  $s_{11}=0$ , and experiences no cost. In the victim, two things happen. First, as  $s_{21}$  decreases, the victim's death rate in the free-living state increases, and term I becomes positive. Second, the increment in cost can become large enough for term III (which is negative) to come close to balancing terms I and II. Figure 4b illustrates the effect this has in arresting the downward trend of  $s_{21}$  before it reaches zero.

Such behaviour in trait  $s_{21}$  sets up the conditions needed for substantial increase in the rate of coupled birth events. Inequality (7) is replaced by

$$0 < (d_i(s_{i1}) - \hat{b}_i(s))\delta\hat{b}, \tag{9}$$

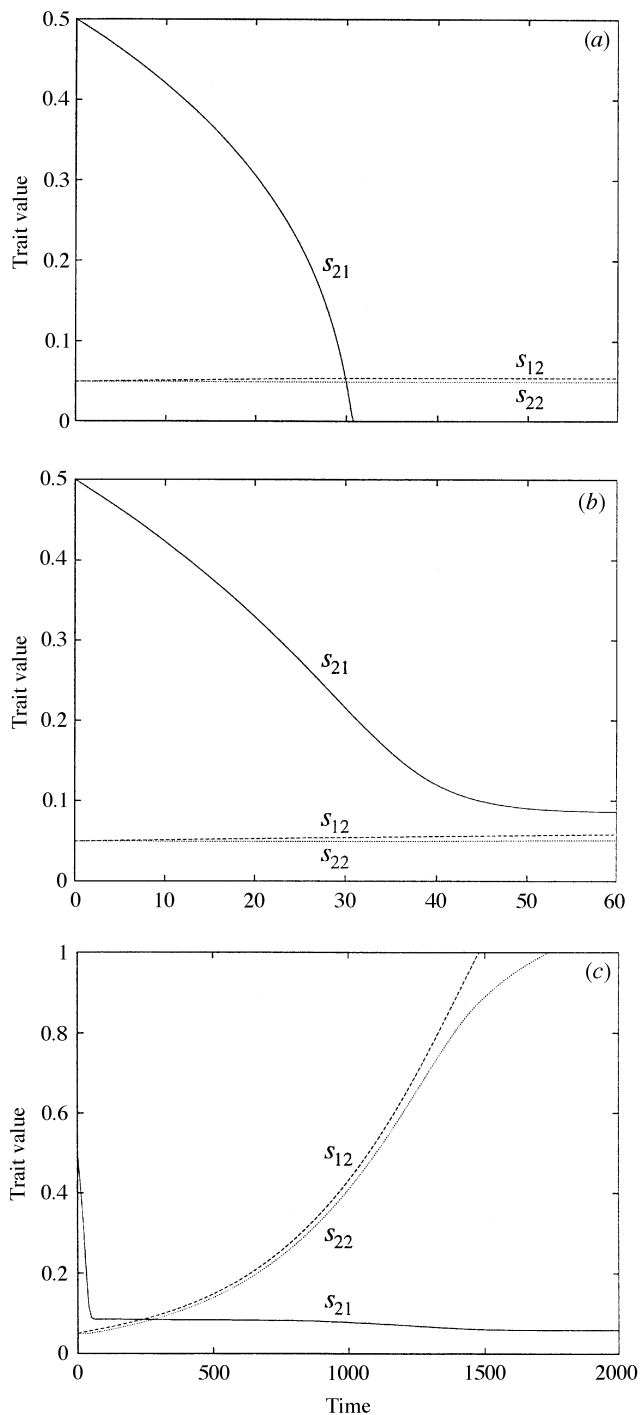


Figure 4. Evolution of trait  $s_{12}$  affecting resource transfer, and traits  $s_{21}$  and  $s_{22}$  affecting the probability of coupled births, in symbiosis: (a) without a cost ( $D_i=1, \omega_i=0$ ), and (b) and (c) with a cost ( $D_i=1, \omega_i=10$ ) to evolution;  $s_{11}$  remains at zero throughout. Constants set as follows:  $\alpha_i=2, \beta_i=1, \gamma_i=10, \delta_i=1, \epsilon_i=1, \ell=0.005, \tilde{d}_i=1, I_i=10, g_i=1, a_i=0.002, \mu_{ij}=0.001, \sigma_{ij}^2=0.01$ .

which, after some evolution, is now satisfied for the victim as well as the exploiter. Increased coupled births are now advantageous to both species, and there is a concerted shift towards a symbiotic unit capable of reproducing itself as a whole. This switch in direction of selection on the victim comes about, not through any benefit it gets from the exploiter, but because the costs associated with defence make the victim's free-living state less and less viable.

Table 1. Data for distinguishing between dependence and benefit of species in symbiosis

		model of symbiosis <sup>1</sup>		viability of <i>Amoeba</i> clones <sup>2</sup> (%)
		exploiter	victim	
before evolution	partner absent	4500	4500	93
	partner present	7001	1154	
after evolution	partner absent	4500	212	7
	partner present	5482	2531	82
	partner present			

<sup>1</sup>This refers to abundance of species at equilibrium in the simulation in figure 4c before evolution (time 0) and after evolution (time 2000).

<sup>2</sup>This summarizes information on the proportion of viable clones in an experiment on evolution of *Amoeba proteus* infected by bacteria (Jeon 1972).

Figure 4c gives an example of this evolution. The early decline in  $s_{21}$  corresponds to that in figure 4b. After this early rapid change, both  $s_{12}$  and  $s_{22}$  increase, and continue to do so until they have both reached their maximum values. By time 1750, all births by the victim in the symbiotic state give rise to holobiont offspring. The same applies to most births by the exploiter, although the small remaining flow of resource from the victim to the exploiter gives some excess offspring to the exploiter which are inevitably free-living. As one would expect, the rate of evolution of  $s_{12}$  is of a lower order than that of  $s_{ij}$ ; trait 2 does no more than redistribute a constant birth rate among free-living and symbiotic states, whereas the other trait affects birth and death rates directly.

Notice that large changes in abundance come about over the course of evolution. Equilibrium values at the start and end of the evolutionary process in figure 4c are shown in table 1; this gives both the total abundance in the presence of the other species, and the abundance that would be achieved if the other species were absent. The victim's free-living death rate becomes so high that this species can barely maintain a population at all in the absence of its partner.

It should be understood that the main results in this section, the invasion criteria in inequalities (6)–(9), are based simply on the ecological dynamics as described in equations (1) and figure 2. The more detailed specifications of resource flow, density regulation, and effects of phenotypic traits are needed for deriving the adaptive dynamics. But the invasion criteria themselves apply to much more general settings.

#### 4. DISCUSSION

The results above show that separate lineages can merge into symbioses capable of reproducing as a single unit even if resource transfer is entirely unidirectional from a victim to its exploiter. This happens if, in the course of developing defences against the exploiter, the costs experienced by the victim in the free-living state

and the increments in these costs become sufficiently large. There is then a sustained increase in vertical transmission such that the symbiosis reproduces more and more as a single unit. Increasingly, the continuity of the association is maintained from generation to generation. The critical feature is that there should be more deaths than births in the free-living state (and correspondingly, fewer deaths than births in symbiosis) for both species; whether this is achieved by increased benefits to each partner, or by costs that one or other partner incurs in defending itself, is immaterial.

There has been debate for over a century as to whether particular evolved symbioses could be said to be mutualistic (Sapp 1994), and our results illustrate why it can be so difficult to achieve a consensus. A physiologist would observe the completely unidirectional flow of resources in the resulting evolved symbiosis, and would probably conclude that the association is not mutualistic (Douglas & Smith 1989). An ecologist, less concerned with the proximal mechanisms of interaction, might carry out a perturbation experiment on the evolved symbiosis, observing the consequences of reducing the abundance of each species in turn: the abundance of the other species will fall in each case, indicating that the association is mutualistic (Odum 1971). See Hurst (1996) for an evolutionary definition of mutualism.

Such contrasting viewpoints suggest it would help to have other axes on which to evaluate the character of symbioses. Following an idea of Douglas & Smith (1989), consider how the properties of 'dependence' and 'benefit' evolve in the partners. A species can be said to have evolved greater dependence on its partner if its abundance, when measured in the absence of its partner, decreases during the course of evolution with the partner. Table 1 shows that this happens to the victim, as the victim declines from an equilibrium abundance of 4500 to 212 as a result of its greater death rate when free-living; the exploiter, on the other hand, does not change. Individuals from one species can be said to have come to benefit from those of the other species after evolution if their abundance in the presence of the partner after evolution is greater than it was in the absence of the partner before evolution. Table 1 shows that the outcome of evolution is to the benefit of the exploiter, as its abundance increases from 4500 to 5482, but not to the victim, as its abundance decreases from 4500 to 2531. (There is no implication of group selection in the argument: evolution can bring about the increase in benefit entirely by selection at the level of the individual.) A distinction between dependence and benefit is helpful because it indicates when the apparent success of one partner in symbiosis results from an increasing inability to live on its own, rather than from any direct benefit it gains from the interaction.

Evolution of dependence without benefit was observed in an experimental study of the evolution of a bacterial infection of *Amoeba* (Jeon 1972, 1983). This is of particular interest as the only detailed experimental study of evolution of a symbiosis. From an initial state in which *Amoeba* colonies were much more viable in the absence of the bacteria than in their presence, the *Amoeba* evolved to a state of low viability when deprived of the bacteria. Yet there was no sign that *Amoeba*'s viability in symbiosis

became greater than its viability before introduction of the bacteria (table 1). The cost assumed in our model and the evolutionary outcome is consistent with these qualitative features.

The modelling framework, based on adaptive dynamics, is designed to reflect as faithfully as possible the selection pressures generated in symbiosis. Inevitably though, the ecological setting is schematic, and it is important to be aware of its limitations. For instance, a full treatment of the ecological dynamics (equations (1)) would need to deal with more than two states (free-living and symbiotic), as holobionts could comprise multiple individuals of one or both partners. In reality, there would probably be further events, such as simultaneous death of both partners in symbiosis, and further traits under evolution, such as the rate at which holobionts are formed. Most important, the evolutionary path leading to merger of lineages under exploitation depends on victims incurring large enough costs in the free-living state as a result of evolution in symbiosis: a victim able to control its investment in defence, switching it on only in symbiosis, can escape this cost altogether. Such control could readily apply, but evidently does not do so in Jeon's (1972) symbiosis.

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## APPENDIX A. DERIVATION OF A MACROSCOPIC EVOLUTIONARY DYNAMIC

In this appendix we derive a dynamical system to describe the evolution of phenotypic traits in the symbiosis, using methods from adaptive dynamics (Dieckmann & Law 1996).

### (a) *Microscopic time-scale*

The derivation begins at the smallest time-scale of resource flux in and out of individuals; on this time-scale abundance of the species and their trait values are constant. The rate of change of the internal concentration  $c_i$  of an individual of species  $i$  is given by

$$\dot{c}_i = \alpha_i C_i - \beta_i b_i(c_i) + (\gamma_k c_k s_{k1} - \gamma_i c_i s_{i1}) - \delta_i c_i, \quad (\text{A1})$$

where  $\alpha_i$ ,  $\beta_i$ ,  $\gamma_i$  and  $\delta_i$  are rate constants for the flows as defined in figure 1,  $k \neq i$ , and the term in large brackets applies only in symbiosis. Birth rate is proportional to the internal resource concentration:  $b_i(c_i) = c_i \epsilon_i / \beta_i$ , where  $\epsilon_i$  is a positive constant.

The internal concentrations at equilibrium can be obtained by setting the right-hand side of equations (A1) to zero; this leaves expressions for the birth rates that depend on the external resource concentrations  $C_i$ . Because these concentrations become variables on the time-scale of population dynamics, we write the birth rates as  $b_1(C_1)$  and  $b_2(C_2)$  for free-living individuals,  $\tilde{b}_1(C_1, C_2)$  and  $\tilde{b}_2(C_1, C_2)$  for offspring of symbiotic individuals that are born free-living, and  $\hat{b}(C_1, C_2)$  for those that are born into the symbiotic state.

**(b) Mesoscopic time-scale**

The equations below show the full dependence of population dynamics on external resource concentrations, and incorporate the dynamics of these resources:

$$\dot{n}_1 = +b_1(C_1)n_1 - d_1n_1 - en_1n_2 + \tilde{b}_1(C_1, C_2)\tilde{n} + \tilde{d}_2\tilde{n} \quad (\text{A2a})$$

$$\dot{n}_2 = +b_2(C_2)n_2 - d_2n_2 - en_1n_2 + \tilde{b}_2(C_1, C_2)\tilde{n} + \tilde{d}_1\tilde{n} \quad (\text{A2b})$$

$$\dot{\tilde{n}} = -\tilde{d}_1\tilde{n} - \tilde{d}_2\tilde{n} + en_1n_2 + \tilde{b}(C_1, C_2)\tilde{n} \quad (\text{A2c})$$

$$\dot{C}_1 = +I_1 - g_1C_1 - a_1C_1(n_1 + \tilde{n}) \quad (\text{A2d})$$

$$\dot{C}_2 = +I_2 - g_2C_2 - a_2C_2(n_2 + \tilde{n}). \quad (\text{A2e})$$

The vital rates in equations (A2a–c) are defined in figure 2. Equations (A2d) and (A2e) describe the resource dynamics, and include a constant input rate  $I_i$ , loss due to uptake of resource  $i$  by individuals of species  $i$  with rate constant  $a_i$ , and loss from the ecosystem with rate constant  $g_i$ . All our numerical integrations of the system of equations (A2) come to equilibrium  $(\hat{n}, \hat{C}) = (\hat{n}_1, \hat{n}_2, \hat{\tilde{n}}, \hat{C}_1, \hat{C}_2)$  (we have used the fourth-order Runge–Kutta method for the purpose).

**(c) Macroscopic time-scale**

Consider some point  $t$  in time on an evolutionary time-scale. At  $t$  the resident populations are assumed to be monomorphic with respect to phenotype, the phenotypic state being denoted  $s$ . Evolution comprises a sequence of trait substitutions (Metz *et al.* 1992), as mutations arise and go to fixation; we write  $w(s'_{ij}, s)$  as the probability per unit time of the trait substitution  $s_{ij} \rightarrow s'_{ij}$ .

The probability per unit time  $\mathcal{M}_{ij}$  of a mutant birth and the probability  $\mathcal{S}_{ij}$  that the mutant survives extinction when rare are statistically independent, so we may take their product and write for trait  $j$  in species  $i$

$$w_{ij}(s'_{ij}, s) = \mathcal{M}_{ij}(s'_{ij}, s)\mathcal{S}_{ij}(s'_{ij}, s) + \tilde{\mathcal{M}}_{ij}(s'_{ij}, s)\tilde{\mathcal{S}}_{ij}(s'_{ij}, s). \quad (\text{A3})$$

Notice that mutants born free-living ( $\mathcal{M}_{ij}, \mathcal{S}_{ij}$ ) have to be distinguished from those which are born into a symbiotic state ( $\tilde{\mathcal{M}}_{ij}, \tilde{\mathcal{S}}_{ij}$ ), as both the probability of the mutant occurring and its chance of survival depend on this initial state. The mutation probabilities are

$$\mathcal{M}_{ij}(s'_{ij}, s) = \mu_{ij}M_{ij}(s'_{ij} - s_{ij}) \left( \hat{b}_i(s)\hat{n}_i(s) + \hat{b}_i(s_{ij}, s)\hat{n}(s) \right) \quad (\text{A4a})$$

$$\tilde{\mathcal{M}}_{ij}(s'_{ij}, s) = \mu_{ij}M_{ij}(s'_{ij} - s_{ij}) \left( \hat{b}(s_{ij}, s)\hat{n}(s) \right), \quad (\text{A4b})$$

where  $\mu_{ij}$  is the fraction of births which are mutants, and the mutant trait value is drawn from a probability distribution  $M_{ij}(s'_{ij} - s_{ij})$ , which is symmetric around  $s_{ij}$  with constant, small variance  $\sigma_{ij}^2$  (the two traits in each species are assumed to be mutating independently). The term in large brackets in equation (A4a) (respectively (A4b)) gives the probability per unit time that a newborn individual appears in the free-living (respectively symbiotic) state.

To determine the probability that the mutant escapes extinction when rare, we employ a result from the theory of multitype branching processes based on the dominant eigenvalue  $\lambda$  and the corresponding right and left eigen-

vectors ( $u = (u_1, u_2)$  and  $v = (v_1, v_2)$  respectively) of the matrix  $L_i$  (equation (4b)); see Athreya & Ney (1972, p. 184). The probability that the mutant  $s'_{ij}$  does not ultimately become extinct is given by Theorem 1 of Athreya (1993) as

$$\mathcal{S}_{ij} = \lambda v_1 / \gamma, \quad (\text{A5a})$$

$$\tilde{\mathcal{S}}_{ij} = \lambda v_2 / \gamma, \quad (\text{A5b})$$

where  $\gamma = b_i(s'_{ij}, s)u_1v_1^2 + \tilde{b}_i(s'_{ij}, s)u_2v_1v_2 + \tilde{b}(s'_{ij}, s)u_2v_2^2$ , the right eigenvector being normalized as  $u_1 + u_2 = 1$ , and the left eigenvector as  $u_1v_1 + u_2v_2 = 1$ . This result applies to mutations of small effect; if the mutant is able to increase, the branching process is said to be slightly supercritical. A mutant that escapes extinction when rare is assumed to go to fixation.

Using equations (A3), (A4) and (A5), and carrying out a Taylor expansion for small deviations  $s'_{ij}$  around  $s_{ij}$ , gives the deterministic path

$$\frac{d}{dt}s_{ij} = \frac{1}{2}\mu_{ij}\sigma_{ij}^2 \left( \mathcal{B}_i(s_{ij}, s) + \tilde{\mathcal{B}}_i(s_{ij}, s) \right) \quad (\text{A6a})$$

The terms outside the large brackets come from the mutation process and scale the rate at which trait  $s_{ij}$  evolves;  $\mu_{ij}$  is the fraction of births that are mutants and  $\sigma_{ij}^2$  is the variance of the mutation distribution. The terms inside the brackets give the contribution to change in trait  $s_{ij}$  due to mutants that start as free-living ( $\mathcal{B}_i$ ) and symbiotic ( $\tilde{\mathcal{B}}_i$ ) individuals; these are

$$\mathcal{B}_i(s_{ij}, s) = \left( \hat{b}_i(s)\hat{n}_i(s) + \hat{b}_i(s_{ij}, s)\hat{n}_i(s) \right) \frac{\partial}{\partial s'_{ij}} \mathcal{S}_{ij}(s'_{ij}, s) \Big|_{s'_{ij}=s_{ij}} \quad (\text{A6b})$$

$$\tilde{\mathcal{B}}_i(s_{ij}, s) = \left( \hat{b}(s_{ij}, s)\hat{n}_i(s) \right) \frac{\partial}{\partial s'_{ij}} \tilde{\mathcal{S}}_{ij}(s'_{ij}, s) \Big|_{s'_{ij}=s_{ij}}. \quad (\text{A6c})$$

The first part of the right-hand side of equations (A6b) and (A6c) gives the rate at which offspring are produced; the second part is called a selection derivative (Marrow *et al.* 1992) and carries information about effects of traits on the ecological dynamics. For mutations with small enough effects on the phenotype, equation (A6) is a good approximation to the mean path of evolution.

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