Ecology Letters, (2002) **5**: 246–256

REPORT

Local adaptation and the geometry of host–parasite coevolution

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Abstract

Metapopulation dynamics can strongly affect the ecological and evolutionary processes involved in host–parasite interactions. Here, I analyse a deterministic host–parasite coevolutionary model and derive analytic approximations for the level of local adaptation as a function of (1) host migration rate, (2) parasite migration rate, (3) parasite specificity and (4) parasite virulence. This analysis confirms the results of previous simulation studies: the difference between host and parasite migration rates may explain the level of local adaptation of both species. I also show that both higher specificity and higher virulence generally lead to higher levels of local adaptation of the species which is already ahead in the coevolutionary arms race. The present analysis also provides a simple geometric interpretation for local adaptation which captures the complexity of the temporal dynamics of host–parasite coevolution.

Keywords

Coevolution, migration, metapopulation, virulence, local adaptation.

Ecology Letters (2002) 5: 246–256

INTRODUCTION

In coevolutionary host–parasite systems each species may constitute an ever changing environment to which its opponent has to adapt. Such coevolutionary processes have been extensively studied at the scale of the population (Hamilton 1980, 1993; Nee 1989; Haraguchi & Sasaki 1996; Sasaki 2000) but interspecific coevolution may also take place at a larger spatial scale involving several populations connected by gene flow (a geographical mosaic of coevolution; Thompson 1994, 1999). The recognition of the role of spatial structure in coevolutionary interactions led to several empirical (Parker 1985; Lively 1989; see review by Kaltz & Shykoff 1998) and theoretical (Frank 1991a, 1991b, 1997; Judson 1995; Gandon *et al.* 1996; Morand *et al.* 1996; Lively 1999; Gomulkiewicz *et al.* 2000; Nuismer *et al.* 2000) studies of the emerging pattern of adaptation. It is conventional wisdom that parasites have greater evolutionary potential than their hosts since they often have larger population sizes and shorter generation times. As a consequence, parasites may have an evolutionary advantage and are expected to be adapted to their sympatric hosts. Several experiments support this view. Indeed, most transplant experiments have shown that parasites perform better on sympatric than on allopatric hosts (Parker 1985; Lively 1989; Ebert 1994; Manning *et al.* 1995; Morand *et al.* 1996; Lively & Dybdhal 2000). However, other experiments did not find any evidence of parasite local adaptation (Morand *et al.* 1996; Dufva 1996; Mutikainen *et al.* 2000) or even found local maladaptation of the parasite (Imhoof & Schmid-Hempel 1998; Kaltz *et al.* 1999; Oppliger *et al.* 1999). These results suggest that the parasite might not always be ahead in the coevolutionary arms race.

Using a simulation model of host–parasite coevolution, Gandon *et al.* (1996, 1998) showed that the ratio of host to parasite migration rates strongly affected the pattern of local adaptation. For intermediate or low migration rates, if parasites (or hosts) migrate more than hosts (or parasites), parasites (or hosts) are locally adapted. In contrast, if the species have similar or high migration rates, there is no differential response (i.e. equal performance in sympatry or allopatry). These predictions have been tested in different biological systems through comparison of the level of local adaptation (obtained by transplant experiments) and host and parasite migration rates (inferred from the analysis of genetic structure in host and parasite populations). As expected from the theory, these comparisons revealed a relatively high migration rate (compared to host migration rates) of locally adapted parasites (Dybdhal & Lively 1996; Davies *et al.* 1999) and a relatively low migration rate of locally maladapted parasites (Kaltz *et al.* 1999; Delmotte *et al.* 1999).

This consistency between theoretical predictions and empirical results is encouraging. However, the theory underlying these predictions is far from satisfactory because it is almost exclusively based on simulation studies. Simulations are useful for exploring the effects of some parameters (e.g. host and parasite migration rates), but they fail to provide a general understanding of the processes involved in the emergence of local adaptation. The mosaic *theory* of coevolution (Thompson 1999) requires a more formal basis and the precise aim of this paper is to provide a first step in this direction. Using a slightly modified version of Nee's model of antagonistic coevolution (Nee 1989), I present a simplified deterministic metapopulation model of host–parasite coevolution. This yields analytical approximations of the level of local adaptation as a function of (1) host migration, (2) parasite migration, (3) parasite specificity and (4) parasite virulence (deleterious effect on host fitness). The analysis of this model also yields a geometric presentation of this measure of local adaptation. A geometrical view has heuristic value because it captures most of the complexity involved in these dynamical systems and, in particular, the effects of host and parasite migration rates on adaptation.

THE MODEL

Life cycle

I will assume that both the host and the parasite are haploid, reproduce asexually, and have constant and very large population sizes (such that the effect of genetic drift on the dynamics of gene frequencies is assumed to be negligible). The genetic determinism of host resistance (or parasite infectivity) is governed by a single locus, H (P for the parasite) and two alleles, H_1/H_2 (P_1/P_2 for the parasite). The interaction follows the assumptions of a modified Matching Allele Model (Nee 1989; Frank 1991a, b, 1994; Gandon *et al.* 1996). A host H_1 confers resistance against a parasite P_2 (such that infection occurs with a probability $1 - S$) but is fully susceptible to a parasite P_1 (for the host H_2, replace the subscript 1 by 2, and vice versa). The parameter S refers to parasite specificity. When $S = 0$, there is no specificity and each host type is equally susceptible to both parasite types. When $S = 1$, a given type of parasite can only infect one type of host, and we recover the classical Matching Allele Model. Parasite virulence, V, measures the deleterious effect of parasites on infected hosts. At the scale of the metapopulation, I further assume that the habitat consists of a very large number, n, of populations and that host and parasite migration rates (m_H and m_P, respectively) are independent and do not vary with the distance between populations (island model of dispersal).

Local adaptation

By definition, the level of local adaptation, Δ_s, of the species s (where s = host or parasite) refers to the difference between (1) the performance in the population of origin, P_s[home], and (2) the performance in a remote population, P_s[away]:

$$\Delta_S \equiv P_S[\text{home}] - P_S[\text{away}] \qquad (1)$$

If host performance is measured as the probability of resistance and parasite performance as the probability of infection, then the level of host adaptation is equal to the opposite of the parasite's level of local adaptation. In the following, I drop the subscripts of these variables and only focus on the analysis of parasite local adaptation, referring to it as $\Delta \equiv P[\text{home}] - P[\text{away}] = \Delta_{\text{parasite}}$. The first measure of parasite performance, P[home], depends on the local dynamics of gene frequencies of both species. The second, P[away], is the performance of a parasite from a given population that is placed in a randomly chosen population among the $n - 1$ remaining ones. This second measure is an *average* of the performance over these $n - 1$ populations.

The pattern of adaptation will strongly depend on the distribution of the genetic variability for resistance and infectivity within and among populations. Indeed, a prerequisite for local adaptation is the occurrence of genetic differentiation among both host and parasite populations (Gandon *et al.* 1998). Two very different situations may lead to such distribution of genetic diversity. First, each population may fix different alleles. This would lead to differentiation among populations and, consequently, to host or parasite local adaptation. This situation is, however, very unlikely if some migration occurs between populations. Migration can reintroduce alleles that have gone extinct at a particular location and, because of negative frequency-dependence, these alleles will increase in frequency and restore polymorphism.

A second situation may arise in which all populations are polymorphic but vary in their allele frequencies. This may lead to complicated dynamics, with allele frequencies that vary both over space and time. Classically, these dynamics have been analysed through computer simulations (Frank 1991a, b, 1997; Gandon *et al.* 1996; Lively 1999). However, the ergodic property of these coevolutionary systems may yield convenient simplifications. Indeed, using a similar coevolutionary model, Frank (1991b) showed that the pattern of variation of genotype frequencies over several populations (across space) at a particular point in time is equivalent to the pattern emerging over several generations for a single population (across time). In the present model, the negative frequency-dependent dynamics of these models and the symmetry of the fitness functions ensure that the expected frequencies (over time) of host and parasite alleles

in a given population are equal to ½. The expected gene frequencies among host and parasite immigrants are also equal to ½ since immigrants are randomly sampled over the whole metapopulation (expected gene frequency over space). This yields the following recurrence equations for changes in gene frequencies in both species (Appendix A):

$$x_{t+1} = \frac{(1-m_H)(2x_t(1-V)+SV(x_t-y_t))}{2(1-V)+SV(1-4x_ty_t)}$$
$$y_{t+1} = \frac{(1-m_P)(2y_t+S(x_t-y_t))}{2-S(1-4x_ty_t)} \quad (2)$$

where x is the departure of the frequency of host H_1 from ½, such that x is positive when there is an excess of host H_1. y has a similar interpretation for the parasite population. The subscripts t and $t + 1$ refer to the values of x and y at two successive generations.

MODEL ANALYSIS

Local stability analysis

The point $x = y = 0$ represents a trivial equilibrium of eqns 2. The analysis of the local stability of this point yields the following condition for stability (Appendix B):

$$(1-m_H)(1-m_P) < \frac{(2-V(2-S))(2-S)}{(2-V(2-S))(2-S)+VS^2} \quad (3)$$

Consequently, when migration rates are above some threshold values (m_H^* for the host and m_P^* for the parasite, see Appendix B), the above equilibrium is stable. Note that these threshold values increase with both parasite virulence and parasite specificity (see Fig. 1).

The above analysis of the stability condition is particularly relevant for the study of local adaptation. Indeed, in the absence of temporal variation in gene frequencies (limit cycles), all the populations have the same gene frequencies. The absence of genetic differentiation among populations implies that there is no spatial variation of the environment of the species and, consequently, no local adaptation. Note, however, that the absence of local adaptation does not imply maladaptation (maladaptation also requires some genetic differentiation among populations). In other words, local adaptation (or maladaptation) may only occur below the threshold values of host and parasite migration rates. In the following, I will focus on the analysis of the dynamics of gene frequencies in this region of the parameter space.

Local dynamics of gene frequencies

Numerical simulations using the recurrence eqns 2 show that when condition 3 is not met, the gene frequencies in each species oscillate and converge rapidly towards a stable limit cycle. Following Nee (1989), it is possible to derive an approximate solution for such dynamics. The linearization of system 2 (provided in Appendix B) yields the following solutions for the variations of gene frequencies:

$$x_t = A\sin(\theta t)$$
$$y_t = B\sin(\theta t+\phi) \quad (4)$$

A and B refer to the amplitude of gene frequency oscillations in host and parasite populations, respectively. θ determines the period of the oscillations and ϕ is the phase difference between the parasite and its host. The phase difference depends on host and parasite migration rates, on parasite specificity and on parasite virulence (see Appendix C):

$$\phi = \arccos \times \left(\frac{m_P - m_H}{2S\sqrt{V(1-m_P)(1-m_H)/((2-S)(2(1-V)+SV))}}\right) \quad (5)$$

When host and parasite migration rates are equal, $\phi = \pi / 2$. When the parasite migration rate is higher than the host migration rate, $\phi < \pi / 2$ and, finally, when the parasite migration rate is lower than the host migration rate, $\phi > \pi / 2$. These results have heuristic value since the length of the lag measures the speed at which the parasite tracks the evolutionary changes of its host. When $\phi = \pi / 2$, the parasite tracks a new host type precisely when it becomes

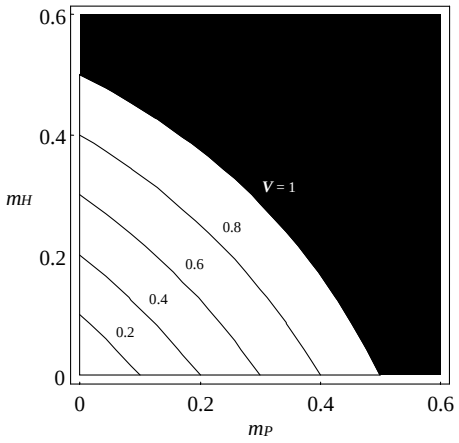

Figure 1 Effects of host migration rate, m_H, parasite migration rate, m_P, and parasite virulence, V, on the local stability of the equilibrium $\{x = 0, y = 0\}$. The black area indicates the parameter space where the equilibrium is always locally stable. In the white area, this equilibrium is locally unstable under the curve which indicates the threshold values of host and parasite migration rates (see eqns B3). These threshold values decrease with parasite virulence, as indicated on the figure for five different levels of parasite virulence ($V = 1$, 0.8, 0.6, 0.4, 0.2 and $S = 1$). Parasite specificity has very similar effects to parasite virulence (not shown).

the most common host. In other words, the evolutionary dynamics are governed by negative frequency-dependence. This occurs whenever the migration rates of the coevolving species are equal. When there is a bias in migration rates, however, the evolutionary dynamics result from a balance between the effects of negative frequency-dependence (leading towards $\phi = \pi / 2$) and the perturbations induced by biased migration rates. The gene frequency of the species with the higher rate of migration will return to the equi-frequency point sooner. For instance, a higher rate of migration will allow the parasite to track a new host type before it actually becomes the most common (i.e. when $\phi < \pi / 2$). The sign of δ, the departure of the phase difference from $\pi / 2$ ($\delta \equiv \pi / 2 - \phi$), depends only on the difference between host and parasite migration rates. In particular, the sign of δ is independent of parasite virulence and parasite specificity. However, a drop in either virulence or specificity decreases the *absolute* value of δ. This effect, again, can be explained by the balance between the effects of negative frequency-dependent selection and migration. When virulence and/or specificity decrease, the strength of selection is reduced and the effects of biased migration dominate, yielding higher absolute values of δ.

Note that when either parasite virulence or parasite specificity becomes very low, the approximation of the phase difference given by eqn 5 fails. Indeed, in the extreme cases where $V = 0$ ($S = 0$), the polymorphism in the host (parasite) population becomes neutral, which prevents the occurrence of stable limit cycles (see also condition 3 and Fig. 1).

A GEOMETRICAL VIEW OF LOCAL ADAPTATION

Local adaptation approximation

The above analysis can now be used to study the effects of migration rates and parasite virulence on the level of local adaptation. The derivation of parasite local adaptation requires a measure of parasite performance in the population of origin, which is easily derived from the local gene frequencies: $P[\text{home}] = 2Sx_t y_t + 1 - S / 2$. It also requires a measure of parasite performance in a remote population. As explained above, because of the negative frequency-dependence of the model, the expected allele frequencies at the scale of the metapopulation are all equal to ½ (i.e. $\bar{x} = \bar{y} = 0$). This yields $P[\text{away}] = 1 - S / 2$, and, using eqn 1:

$$\Delta_t = 2Sx_t y_t \qquad (6)$$

where Δ_t is the level of parasite local adaptation for a focal parasite population at time t. This expression of parasite local adaptation will oscillate across time. In particular, the sign of $\bar{\Delta}_t$ depends on the signs of x_t and y_t. When they have the same (different) sign(s) the parasite is locally adapted (maladapted). Averaging this measure of local adaptation over several generations, $\bar{\Delta}$, or over several populations, $\bar{\Delta}_t$, will give similar results if the dynamics of the different populations are not synchronized (Frank 1991b). Such an average measure is particularly relevant because it refers to a general property of the metapopulation (Δ_t only refers to local adaptation at a particular point in space and time). An analytic expression of $\bar{\Delta}$ can be derived from the approximation of the local dynamics of gene frequencies:

$$\bar{\Delta} = 2S\frac{AB}{2\pi}\int_0^{2\pi}(\sin(\theta t)\sin(\theta t + \phi)\mathrm{d}t = SAB\cos(\phi) \qquad (7)$$

Combining eqns 5 and 7 yields:

$$\bar{\Delta} = AB\frac{m_P - m_H}{2\sqrt{V(1-m_P)(1-m_H)/((2-S)(2(1-V)+SV))}} \qquad (8)$$

Therefore, $\bar{\Delta}$ depends on the amplitude of the oscillations over time, as well as the phase difference between the evolutionary dynamics of the host and the parasite. The amplitude of the oscillations will only affect quantitatively the level of local adaptation. The phase difference, however, may affect the results qualitatively. In other words, whether host or parasites are locally adapted depends only on the phase difference between host and parasite gene frequencies oscillations.

Equation 8 tells us that the average level of local adaptation of the parasite $\bar{\Delta}$ has the same sign as $m_P - m_H$. In other words, parasites are locally adapted when they migrate more than their hosts. Here, we recover the results obtained previously by Gandon *et al.* (1996) in a complicated stochastic simulation model.

This result has a useful geometrical interpretation. The oscillations of host and parasite types (see recurrence eqn 4) follow a limit cycle, which has an elliptical shape in the phase space. Figure 2 shows how host and parasite migration rates may distort the shape of this limit cycle through their effects on the phase difference. For example, when the parasites migrate more than the hosts, the shape of the limit cycle is modified so that most of the surface of the limit cycle lies in the first and third quadrants of the phase space. This yields an increase in the average level of parasite local adaptation. Analogous results were obtained by Nee (1989; p. 517) on mutation rates.

Equation 8 also shows that a drop in parasite virulence increases the absolute value of local adaptation. Lower virulence decreases the strength of negative frequency-dependent selection and, consequently increases the absolute value of δ (which could be viewed as a measure of the relative speed of the two species involved in the coevolu-

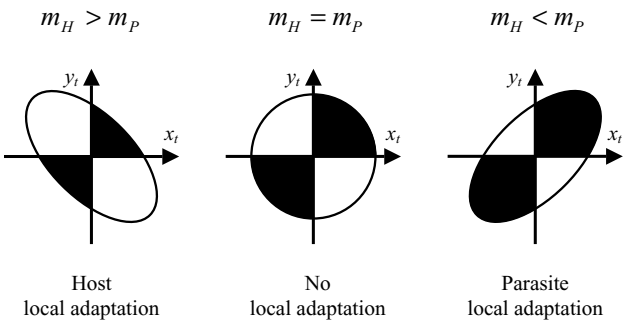

Figure 2 A geometric view of local adaptation. The black area (first and third quadrants) indicates the portion of the limit cycle where parasites are locally adapted. The white area (second and fourth quadrants) indicates the portion where hosts are locally adapted.

tionary race). Parasite specificity has a similar effect on δ (see eqn 5), but specificity has also a more direct effect on the measure of local adaptation (see eqn 6). In particular, when specificity is very low, any genetic differentiation among populations becomes undetectable and the absolute level of local adaptation drops. Ultimately, these two effects cancel out and specificity has only little effect on local adaptation.

But the above analysis ignores the potential effects of migration, virulence and specificity on local adaptation via the amplitude of gene frequency oscillations, A and B. I was unable to derive analytic expressions for these amplitudes but numerical simulations revealed that both values were always a decreasing function of migration rates. Combining this effect with the fact that the amplitude of the oscillations is equal to zero above some migration threshold value (see Appendix B and equation 3), I approximated the product of the amplitudes of gene frequency oscillations by the following quantity:

$$AB = \begin{cases} \left(1 - \frac{m_H}{m_H^*}\right)\left(1 - \frac{m_P}{m_P^*}\right) & \text{if } m_P < m_P^* \text{ and } m_H < m_H^* \\ 0 & \text{if } m_P > m_P^* \text{ or } m_H > m_H^* \end{cases} \quad (9)$$

The above expression ensures that oscillation amplitudes are maximized when there is no migration and that gene frequencies do not oscillate if host and/or parasite migration rates are above the threshold value specified in Appendix B.

Simulations

I checked the accuracy of the above approximations through numerical simulations of the system of recurrence eqn 2. The results of the simulation and the approximation were largely consistent. In particular, the approximation gives an accurate quantitative prediction of the level of local adaptation (Fig. 3).

The combination of simulations, approximations and stability analysis leads to the distinction of four different coevolutionary outcomes depending on both species' migration rates, parasite virulence and parasite specificity (Fig. 3A). In the absence of fluctuation of gene frequencies within populations, neither of the species is locally adapted (zone 1). When the gene frequencies do fluctuate, some

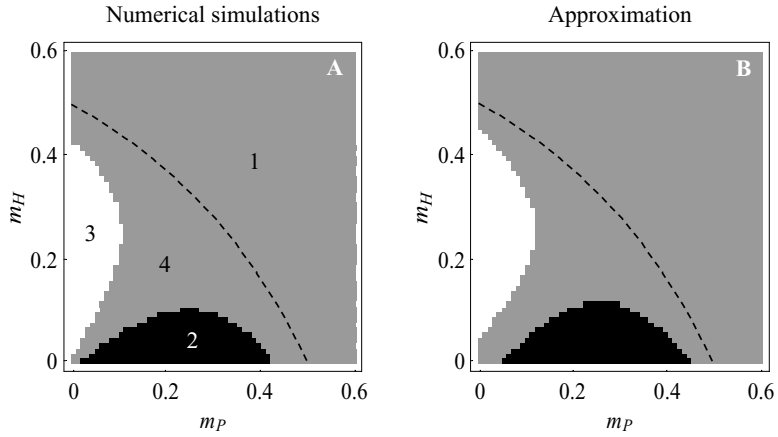

Figure 3 Host and parasite local adaptation as a function of host and parasite migration rates. In A, the results are obtained using the recurrence eqns 2, with randomly chosen initial gene frequencies and average levels of local adaptation between generations 1000 and 1500. In B, I approximated the level of local adaptation given by eqns 8 and 9. In the black area (zone 2) the parasite is locally adapted ($\bar{\Delta} > 0.02$). In the white area (zone 3) the host is locally adapted ($\bar{\Delta} < -0.02$). The grey area (zones 1 and 4) represents weak or absent local adaptation ($-0.02 < \bar{\Delta} < 0.02$). The dashed line (between zones 1 and 4) shows the threshold values of host and parasite migration rates above which there are no fluctuations in gene frequencies. $V = 1$ and $S = 1$.

local adaptation may occur. If parasites migrate more than their hosts, they tend to be locally adapted (zone 2) while the reverse is true when hosts migrate more than parasites (zone 3). Finally, when the host and the parasite have similar or large migration rates, neither species is locally adapted (zone 4). The above description leads to a useful distinction between zone 1 and zone 4, where a single pattern (the absence of local adaptation) can be caused by different processes.

Some differences between approximation and simulation results can be pointed out. For example, the approximated solution given by eqn 8 indicates that the sign of the average level of local adaptation only depends on the difference between host and parasite migration rates. Figure 4(A), however, shows that intermediate levels of virulence can lead to parasite local adaptation even when the host migrates more than its parasite. This effect can be explained by a selection asymmetry. When virulence decreases, the strength of selection becomes higher on the parasite because the cost for the parasite of an unsuccessful infection is higher than the cost for the host of becoming infected (a host–parasite version of the classical "life–dinner" asymmetry of predator–prey models). Therefore, even when the evolutionary potentials of the two species are equal (i.e. equal migration rates), the parasite may be locally adapted because of more intense selection on parasite populations. Note that this prediction only holds for relatively high values of virulence. Indeed, when virulence becomes very low, the decreased amplitude of the oscillations of gene frequencies may result in no local adaptation. Indeed, Fig. 4 A shows that, for low virulence values (i.e. $V < 0.4$) and whatever the bias in migration rates, a decrease in parasite virulence always leads to a reduction of local adaptation.

In contrast, a drop in parasite specificity induces a selection asymmetry in the opposite direction. When specificity decreases, the strength of selection becomes greater on the host than on the parasite population. Figure 4(B) shows that this may lead towards host local adaptation even if the parasite migrates more than its host. As for low virulence, low specificity always leads to very low levels of local adaptation.

Coevolutionary asynchrony

The above analysis (both approximations and numerical simulations of the recurrence eqns 2) relies on the assumption that the coevolutionary dynamics are asynchronous among populations (see Appendix A). This asynchrony has important implications for local adaptation, because under a synchronized regime of coevolution, the spatial variation of gene frequencies will vanish and, consequently, the local adaptation of both species will also disappear.

As pointed out by Nuismer *et al.* 2000) and Gomulkiewicz *et al.* (2000), genetic differentiation among populations could be produced by spatial variation in the strength and/or the type of selection (from antagonistic to mutualistic coevolution). Asynchrony and genetic differentiation, however, may be difficult to maintain in the *spatially homogeneous* model studied here (i.e. no variations in V and S among populations). In a fully deterministic model with no isolation by distance (i.e. island model of dispersal), host and parasite migration will tend to homogenize the spatial distribution of gene frequencies leading ultimately to coevolutionary synchrony. However, even if asynchrony cannot be maintained in the long term, the description of the pattern of adaptation before reaching coevolutionary synchrony (which may take a long time) may be of interest in itself. Numerical simulations (Fig. 5A) indicate that the analysis provided in this paper gives a good qualitative description of local adaptation in such a transitory phase (i.e. parasites are locally adapted during this transitory phase, as expected, since $m_p > m_h$).

Asynchrony can only be maintained in the long term if other forces act against the homogenizing effect of migration. In particular, genetic drift may decouple the dynamics of the different populations and counteract the

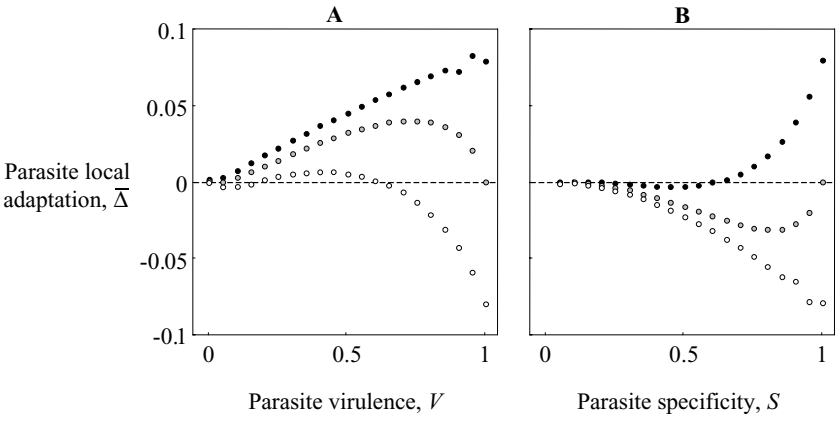

Figure 4 Parasite local adaptation as a function of (A) parasite virulence, V (with $S = 1$), and (B) parasite specificity, S (with $V = 1$). The results are obtained using numerical simulations of the recurrence eqns 2, with randomly chosen initial gene frequencies and average levels of local adaptation between generations 1000 and 5000. Three different migration cases are considered (from top to bottom): (1) $m_H = 10^{-4}$, $m_P = 10^{-2}$ (black dots), (2) $m_H = m_P = 10^{-2}$ (grey dots) and (3) $m_H = 10^{-2}$, $m_P = 10^{-4}$ (white dots).

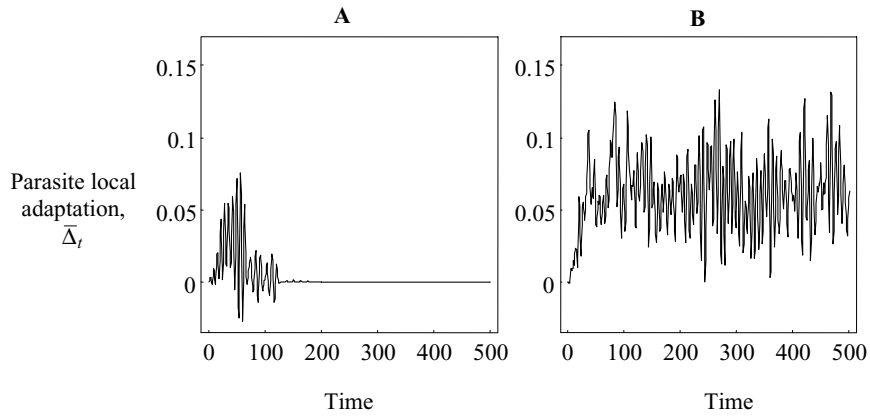

Figure 5 Genetic drift and coevolutionary asynchrony. Local adaptation (averaged over 50 coevolving populations) is plotted against time. At $t = 0$, each population is seeded with 100 hosts and 100 parasites, which are randomly chosen among the two different types. In (A) we assume that there is no genetic drift (i.e. host and parasite population sizes are assumed to be infinite for $t > 0$). In (B) host and parasite population are finite (100 parasites and 100 hosts in each population) and genetic drift maintains both coevolutionary asynchrony among populations and the pattern of local adaptation. Parameter values: $m_P = 10^{-1}$, $m_H = 10^{-3}$, $V = S = 0.8$.

effect of migration. Figure 5(B) shows how finite population sizes may allow asynchrony to be maintained. It is worth pointing out that genetic drift is classically viewed as a factor decreasing the level of local adaptation (Lande 1976). In contrast, in the present coevolutionary model, genetic drift can be a necessary condition for local adaptation because it maintains spatial variations among populations.

Isolation by distance may be another way to decouple the coevolutionary dynamics among populations that are far apart. This factor, alone (i.e. without genetic drift) could maintain some spatial variation among populations. Localized dispersal, however, generates spatial autocorrelation, since nearby populations tend to have similar gene frequencies. In two dimensions, the coevolutionary interaction can spontaneously gives rise to rotating spiral patterns (Fig. 6), where each spiral consists of two arms that differ in their gene frequencies. Spiral waves have been found in several population dynamics models (Hassell *et al.* 1991; Boerlijst *et al.* 1993) but, to my knowledge, such spatial patterns have never been described before in coevolutionary models.

Whatever the mechanism allowing the maintenance of spatial asynchrony (genetic drift, isolation by distance), it is important to note that the approximation derived in this paper provides an accurate description of the emerging pattern of local adaptation. Indeed, in both Figs 5(B) and 6, the average level of local adaptation is positive, as expected from eqn 8, since we used $m_p > m_h$ for these simulations.

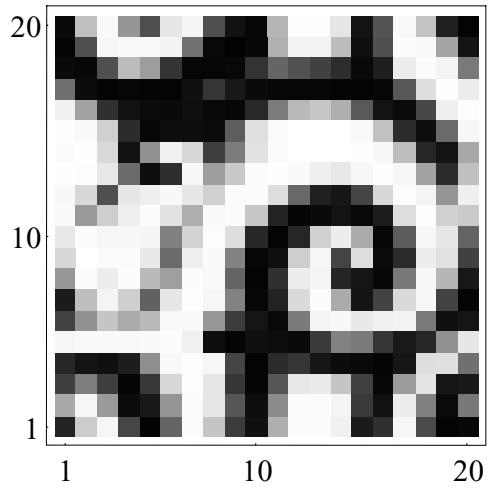

Figure 6 Typical spatial distribution of host gene frequencies (the darker the grey, the higher the H_1 allele frequency) in a two-dimensional habitat (similar spatial patterns emerge for the parasite). The habitat consists of 20×20 populations arranged in a torus where both host and parasite are allowed to disperse in the four nearest neighbouring populations. At $t = 0$, each population is seeded with 100 hosts and 100 parasites, which are randomly chosen from among the two different types. We assume that there is no genetic drift for $t > 0$. The parameter values used in these simulations ($m_P = 10^{-1}$, $m_H = 10^{-3}$, $V = S = 0.8$) led to parasite local adaptation: $\bar{\Delta} = 0.042$ (spatial average over the last 1000 generations of a 1500 generation simulation).

DISCUSSION

Metapopulation dynamics can strongly affect the ecological and the evolutionary processes involved in host–parasite interactions (Burdon *et al.* 1990; Frank 1991a, b, 1997; Thompson & Burdon 1992; Thompson 1994, 1999; Burdon & Thrall 1999). Recognition of the role of spatial structure

in coevolutionary interactions led to the study of (often complex and stochastic) simulation models (Frank 1991a, 1991b, 1997; Gandon *et al.* 1996; Lively 1999). These models are useful to explore the effects of some parameters but they do not allow detailed analyses of the processes involved. Here, I obtain insights into some metapopulation properties of host–parasite systems (particularly the level of local adaptation) from the analysis of the local dynamics of gene frequencies.

Migration rates and local adaptation

The above analysis confirms that the difference between host and parasite migration rates can strongly affect the level of local adaptation (Gandon *et al.* 1996). Here, I provide an analytic formulation of this result. The formulation shows that migration rates may act on the level of local adaptation by either acting on the amplitude of the gene frequency oscillations or on the phase difference between the trajectories of host and parasite gene frequencies. Only the effect of migration on the phase difference may shift the level of local adaptation from one species to another. Equal migration rates yield $\phi = \pi / 2$. Biased migration rates, however, allow the species with the higher migration rate to evolve faster. The departure, δ, from the situation where $\phi = \pi / 2$ can be viewed as a measure of the relative speed of the coevolutionary opponents. If $\delta > 0$ ($\delta < 0$) the parasite (the host) is ahead in the coevolutionary race.

Parasite virulence and local adaptation

Similarly, parasite virulence may affect local adaptation through an effect on either the amplitude of the gene frequency oscillations or on the phase difference. In contrast to the effect of migration rates, a change in virulence quantitatively affects the level of local adaptation without, in general, altering the qualitative pattern of adaptation (parasite or host local adaptation). Two main results are obtained. First, the parameter space where local adaptation may occur expands with higher parasite virulence (Fig. 1). Second, high virulence tends to promote local adaptation of the species that is already ahead in the coevolutionary race (i.e. the species with a higher migration rate, see Fig. 4). Note, however, that intermediate virulence induces an asymmetry in the strength of selection on the two coevolving species which biases the predictions (eqn 8) towards parasite local adaptation (see Fig. 4A).

Lively (1999) studied the effect of parasite virulence on the coevolutionary outcome of a very similar model. However, he assumed that the habitat consisted of two populations and that only the parasites could migrate between these populations. Under these assumptions, Lively (1999) showed that parasite virulence always increased parasite local adaptation. The present model extends the results of Lively to the case where hosts may also migrate between populations and shows that when the host migration rate is higher than the parasite migration rate, parasite virulence may also increase the level of host local adaptation (Fig. 4A).

Parasite specificity and local adaptation

Like parasite virulence, specificity is a necessary condition for coevolutionary dynamics. When specificity is very low any pattern of local adaptation vanishes. Higher specificity tends to promote local adaptation of the species that is already ahead in the coevolutionary race (Fig. 4B) but, in contrast with the effect of virulence, intermediate levels of specificity increase the strength of selection on the host population. Therefore, imperfect specificity ($S < 1$) may distort the predictions (eqn 8) towards host local adaptation. Interestingly, Kawecki (1998) showed that such a cost of low specificity on parasite adaptation may actually drive the evolution of more specialized parasites. Using a similar argument, the cost of high virulence on parasite adaptation that was identified above may favour lower virulence in the parasite population. However, the analysis of virulence evolution in a non-equilibrium coevolutionary context remains to be done.

It would also be interesting to extend the present analysis to other forms of specificity. The symmetry of the matching model assumed here is mathematically convenient but several authors have discussed the relevance of this form of specificity (Frank 1994, 1996; Parker 1994, 1996). In particular, Parker (1994) pointed out that the asymmetrical gene-for-gene (GFG) model originally proposed by Flor (1956) can prevent the occurrence of coevolutionary cycles and, consequently, may decrease the selection for sexual recombination (Parker 1994). More recently, Agrawal & Lively, 2002) studied a general model which allows the GFG of Flor (1956) and the matching allele model used here to appear as two extreme cases (two ends of a continuum). The analysis of this model showed that "the highly dynamical aspects of the matching-allele model were observed across most of the continuum" (Agrawal & Lively, 2002). This result suggests that the conclusions reached in the present paper may also apply across most of the continuum. The effects of the genetic basis of the infection, however, remain to be explored to check the generality of our predictions.

Evolutionary potential evolution

The present analysis yields a geometrical visualization of the results. This geometrical view has heuristic value because it describes accurately the effects of migration rates on the level of local adaptation (compare Figs 3 and 4). This result

had first been pointed out by Nee (1989), in a study of the effect of host and parasite mutation and recombination rates on coevolutionary dynamics. Mutation, recombination and migration rates, the main components of the evolutionary potential of a species, may indeed be viewed as alternative strategies in the face of a temporally variable environment (Hamilton 1980; Hamilton *et al.* 1990; Gandon *et al.* 1998). In such environments, it pays to evolve genotypic randomization mechanisms since randomization may increase the genetic variance and, consequently, the potential for adaptation to these variable environmental conditions.

The study of the coevolution among these alternative strategies remains to be carried out. One may expect a strong interaction among these strategies. For example, high migration rates may prevent the evolution of sexual reproduction (Ladle *et al.* 1993; Gandon *et al.* 1998). Coevolution among these traits may also occur between species. Haraguchi & Sasaki (1996) studied the coevolution of host and parasite mutation rates engaged in a gene-for-gene type of interaction. They showed that a typical coevolutionary outcome is that the parasite evolves high mutation rates while the host mutation rate is driven to zero. This result can be explained by a classical asymmetry in such interspecific interactions (the "life–dinner" principle in predator–prey interactions). As pointed out by Haraguchi & Sasaki, "the parasite mutates more frequently than the host, because the parasite is mutating for his life while the host is only mutating for his health". It would be interesting to verify whether this principle holds for other traits such as recombination or migration rates. Ultimately, the analysis of the "full model" (including coevolution of these different strategies in both the host and the parasite) may predict which randomization strategies (mutation, recombination or migration) are most likely to evolve.

ACKNOWLEDGEMENTS

V. Jansen, C. Lively, K. Lythgoe, A. Graham, Y. Michalakis, S. Nee, A. Read, F. Rousset, M. van Baalen and two anonymous referees provided thoughtful comments on the manuscript. In particular, I would like to thank Y. Michalakis for many inspiring discussions on host–parasite coevolution. I gratefully acknowledge financial support from The Wellcome Trust (grant 062429).

APPENDIX A

Derivation of the recurrence equations

Let the frequency of H_1 and H_2 be p and $(1-p)$, respectively, in a focal population. The frequencies of P_1 and P_2 are q and $(1-q)$. The fitnesses of the different alleles are:

$$\begin{aligned} W_{H_1} &= q(1-V) + (1-q)S + (1-q)(1-S)(1-V) \\ W_{H_2} &= (1-q)(1-V) + qS + q(1-S)(1-V) \\ W_{P_1} &= p + (1-S)(1-P) \\ W_{P_2} &= 1-p + (1-S)p \end{aligned} \tag{A1}$$

After selection and before migration the allele frequencies become:

$$\begin{aligned} p' &= \frac{pW_{H_1}}{pW_{H_1} + (1-p)W_{H_2}} = p\overline{W}_{H_1} \\ q' &= \frac{qW_{P_1}}{qW_{P_1} + (1-q)W_{P_2}} = q\overline{W}_{P_1} \end{aligned} \tag{A2}$$

After migration the allele frequencies become:

$$\begin{aligned} p'' &= p'(1-m_H) + m_H\bar{p}' \\ q'' &= q'(1-m_P) + m_P\bar{q}' \end{aligned} \tag{A3}$$

where $\bar{p}'$ and $\bar{q}'$ are, respectively, the average host and parasite gene frequencies (over the metapopulation). I further simplify the above recurrence equation by assuming asynchronous coevolutionary dynamics among the different populations which yields $\bar{p}' = \bar{q}' = 0.5$ (see further explanations in the main text) and

$$\begin{aligned} p'' &= p'(1-m_H) + m_H/2 \\ q'' &= q'(1-m_P) + m_P/2 \end{aligned} \tag{A4}$$

Following Nee (1989) I make the following substitutions:

$$\begin{aligned} p &= x + 1/2 \\ q &= y + 1/2 \end{aligned} \tag{A5}$$

This yields the system of recurrence eqns 2 given in the main text.

APPENDIX B

Local stability analysis

The point $x = y = 0$ is a trivial equilibrium of eqns 2. The stability of this equilibrium can be checked through the analysis of the Jacobian matrix, **J**, of the above system evaluated at $x = y = 0$:

$$\mathbf{J} = \begin{pmatrix} 1-m_H & (1-m_H)SV/(V(2-S)-2) \\ (1-m_P)S/(2-S) & 1-m_P \end{pmatrix} \tag{B1}$$

A necessary and sufficient condition for the stability of the equilibrium is:

$$2 > 1 + D > T$$

where

$$D = (1 - m_H)(1 - m_P)\frac{4(1 - S)(1 - V) + 2S}{(2 - V(2 - S))(2 - S)} \qquad \text{(B2)}$$
$$T = 2 - m_H - m_P$$

are the determinant and the trace, respectively, of **J**. This yields the local stability condition 3 given in the main text and the following two threshold values of host and parasite migration rates:

$$m_H^* = 1 - \frac{(2 - V(2 - S))(2 - S)}{(1 - m_P)(4(1 - V)(1 - S) + 2S)}$$
$$m_P^* = 1 - \frac{(2 - V(2 - S))(2 - S)}{(1 - m_H)(4(1 - V)(1 - S) + 2S)} \qquad \text{(B3)}$$

APPENDIX C

Approximation of the phase difference

When the dynamics of allele frequencies remain close to the equilibrium point $x = y = 0$ the linearization of the recurrence equations given in eqns 2 yields:

$$x_{t+1} = \frac{(1 - m_H)(2x_t(1 - V) + SV(x_t - y_t))}{2(1 - V) + SV}$$
$$y_{t+1} = \frac{(1 - m_P)(2y_t + S(x_t - y_t))}{2 - S} \qquad \text{(C1)}$$

Following the derivation of Nee (1989) the phase difference between hosts and parasites is (see A12 in Nee 1989):

$$\phi = \beta - \alpha \qquad \text{(C2)}$$

with

$$\alpha = \arctan\left(\frac{\sin(\psi_1 - \psi_2)}{\cos(\psi_1 - \psi_2) - \sigma_1/\sigma_2}\right)$$
$$\beta = \arctan\left(\frac{\sin(\psi_1 - \psi_2)}{\sigma_2/\sigma_1 - \cos(\psi_1 - \psi_2)}\right) \qquad \text{(C3)}$$

where $\{\sigma_1, \sigma_2\}$ and $\{\psi_1, \psi_2\}$ are the modulus and arguments, respectively, of the coordinates of the eigenvectors associated with the complex conjugate eigenvalues of **J** (see A10 in Nee 1989). After some rearrangements this yields:

$$\phi = \psi_1 - \psi_2 \qquad \text{(C4)}$$

It can be shown that:

$$\cos(\psi_1 - \psi_2) = \frac{m_P - m_H}{2S\sqrt{V(1 - m_P)(1 - m_H)/((2 - S)(2 - S)(2(1 - V) + SV))}} \qquad \text{(C5)}$$

yielding eqn 5 given in the main text.

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Edited, M.E. Hochberg
Received 28 September 2001
First decision made 7 November 2001
Second decision made 9 December 2001
Manuscript accepted 14 December 2001