Chaotic Red Queen coevolution in three-species food chains

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Coevolution between two antagonistic species follows the so-called ‘Red Queen dynamics’ when reciprocal selection results in an endless series of adaptation by one species and counteradaptation by the other. Red Queen dynamics are ‘genetically driven’ when selective sweeps involving new beneficial mutations result in perpetual oscillations of the coevolving traits on the slow evolutionary time scale. Mathematical models have shown that a prey and a predator can coevolve along a genetically driven Red Queen cycle. We found that embedding the prey–predator interaction into a three-species food chain that includes a coevolving superpredator often turns the genetically driven Red Queen cycle into chaos. A key condition is that the prey evolves fast enough. Red Queen chaos implies that the direction and strength of selection are intrinsically unpredictable beyond a short evolutionary time, with greatest evolutionary unpredictability in the superpredator. We hypothesize that genetically driven Red Queen chaos could explain why many natural populations are poised at the edge of ecological chaos. Over space, genetically driven chaos is expected to cause the evolutionary divergence of local populations, even under homogenizing environmental fluctuations, and thus to promote genetic diversity among ecological communities over long evolutionary time.

Keywords: adaptive dynamics; arms race; chaos; coevolution; genetic divergence; predator–prey

1. INTRODUCTION

Antagonistic coevolution describes the reciprocal evolutionary interactions between populations belonging to an ‘exploiter’ (such as a predator or a parasite) and a ‘victim’ (such as a prey or a host). It is a change in the genetic make-up of a population in response to a genetic change in the antagonistic population (Thompson 1994). Antagonistic interactions have the potential to drive coevolutionary dynamics of adaptive traits: an evolutionary advantage gained by one antagonist is often associated with a disadvantage for the other antagonist, and may therefore prompt a counteradaptation. This may drive stabilizing selection and evolutionary specialization with extreme refinement of the coevolving traits (convergence to an evolutionary equilibrium); or runaway selection and evolutionary escalation with the exaggeration of traits (with the possible extinction of some or all coevolving populations; Matsuda & Abrams 1994; Ferri`ere 2000); or fluctuating selection and the so-called ‘Red Queen dynamics’ of perpetual reciprocal changes in the coevolving traits (convergence to a non-equilibrium evolutionary attractor; Van Valen 1973; Stenseth & Maynard Smith 1984; Vermeij 1994). It has been suggested that Red Queen dynamics underlie a large number of important biological processes, some of which are still poorly understood, such as genetic recombination and sexual reproduction (Hamilton et al. 1990), the extraordinary diversity of genes related to immune function, resistance and virulence (Salathe et al. 2008), and the spatial diversity and local adaptation of exploiter–victim systems (Gandon 2002).

An important dichotomy exists between two main types of Red Queen dynamics (Khibnik & Kondrashov 1997; Ebert 2008; Gaba & Ebert 2009): ecologically driven by negative frequency-dependent selection and genetically driven by beneficial mutations. This distinction is significant because the two types strongly differ in their mechanisms, their underlying genetic architecture, their ecological and evolutionary consequences, and the time scales on which they develop (Ebert 2008). With ecologically driven Red Queen dynamics, extant variants of the exploiter genotype that benefit the most from the numerically dominant victim genotypes are favoured, and, similarly, victim genotypes that best resist the numerically dominant exploiter genotypes are favoured. This pattern results in selection against common exploiter and victim genotypes in a time-lagged negative frequency-dependent fashion (ecological instability). A consequence of this form of fluctuating selection on extant genetic variation is that genetic polymorphism is maintained in the population for long periods (balanced selection) and that allele frequencies can oscillate considerably over time periods of a few generations.

In contrast, genetically driven Red Queen dynamics involve the repeated incidence, spread and fixation of new beneficial mutants in populations that stabilize at
ecological equilibria. Mutants are driven to fixation by
directional selection (selective sweeps). Thus, genetic
polymorphism is transient only, and the evolutionary
dynamics are slow—for two reasons. First, new mutations
causing variation in the adaptive traits involved are rare
events. Second, a new mutant starts with a very low fre-
quency (1/N, where N is the number of wild-type alleles
in the population); thus, empirically it can take hundreds
of generations until the mutant becomes recognizable
(e.g. 1%) at the population level (Elena et al. 1996).
Therefore, genetically driven Red Queen dynamics
develop on an evolutionary time scale that is several
orders of magnitude slower than the time scale of
ecological processes.

The slow time scale involved hampers the empirical
investigation of genetically driven Red Queen dynamics,
and mathematical models have been useful to seek con-
ditions that could favour the Red Queen over
specialization or escalation. So far, the majority of these
models have focused on the two coevolving species and
ignored the community context in which coevolution
takes place. In this setting, genetically driven Red
Queen dynamics develop as regular, predictable cycles
in the adaptive trait space. However, pairs of coevolving
species are inevitably embedded in community-level
interactions of varying degrees of complexity. It is because
most species interact with suites of other species that vary
dynamically across geographical landscapes that coevolu-
tionary processes can be important in shaping the
structure and maintaining variability within specific pair-
wise interactions, such as predator–prey or host–parasite
systems (Abrams 1991, 1996; Strauss et al. 2005;
Thompson 2005; Thrall et al. 2007). For example, some
trematode parasites have strong effects on the evolutionary
dynamics of their snail hosts, but themselves are depend-
ent upon waterflow for completion of their life cycle
(Lively 1999). How the community context of coevolution
affects the occurrence and manifestation of genetically
driven Red Queen dynamics remains poorly known.

Seminal steps in the theoretical study of coevolution-
ary dynamics in the community context have been taken
recently (Caldarelli et al. 1998; Loeuille et al. 2002;
Gandon 2004; Niušmer & Doebeli 2004; Loeuille &
Loreau 2005; Kisdi & Liu 2006; Bell 2007; Ferrière
et al. 2007; Shores et al. 2008; Jones et al. 2009;
Stegen et al. 2009), but models of genetically driven
coevolutionary dynamics in which more than two species
coevolve in a multi-dimensional trait space are still
lacking. Here, we extend a simple two-species predator–
prey coevolutionary system (Dieckmann et al. 1995;
where genetically driven Red Queen cycles were
first documented) to model coevolution in a three-
dimensional trait space among three species forming a
food chain. The function of each species in the food
chain is determined by a continuous character subject
to rare and small genetic mutations. One may expect
that the addition of a coevolving species to a coevolving
pair could stabilize the evolutionary process at an evolu-
tionary equilibrium, thereby suppressing the Red
Queen dynamics (Vermeij 1982; Futuyma 1983), or
that the addition could destabilize the periodic evolution-
ary oscillation and drive the genetically driven Red Queen
into chaos (Gavrilents 1997). Here we show that con-
ditions leading to genetically driven periodic cycles in
the two traits of coevolving predator and prey favour
chaotic dynamics in the three coevolving traits of the
three-species food chain.

2. MODEL CONSTRUCTION

We focus on a single adaptive trait per species that charac-
terizes the function of the species in the food chain. The
trait determines competitive ability in the prey, and for-
aging success in the predator and superpredator. On the
evolutionary time scale, de novo trait variation is caused
by a rare genetic mutation. The current phenotypes
where genetically driven Red Queen cycles were
prevalent (if not towards extinction; Dieckmann

As in Dieckmann et al. (1995), Lotka–Volterra
equations are used to describe the ecological dynamics
of the food chain:

\[
\frac{dn_1}{dt} = n_1(r - cn_1 - a_2n_2), \tag{2.1a}
\]

\[
\frac{dn_2}{dt} = n_2(e_2a_2n_1 - d_2 - a_3n_3), \tag{2.1b}
\]

and

\[
\frac{dn_3}{dt} = n_3(e_3a_3n_2 - d_3). \tag{2.1c}
\]

where \(n_1, n_2\) and \(n_3\) are prey, predator and superpredator
densities, respectively; \(r\) and \(c\) are prey intrinsic \(\text{per capita}\)
growth rate and sensitivity to intraspecific competition,
respectively; and \(a_0, e_1\) and \(d_1\) are the attack rate, efficiency
and intrinsic death rate in the predator (\(i = 2\)) and
superpredator (\(i = 3\)), respectively. Each species is charac-
terized by one genetic trait \(x_i\) \((i = 1–3)\). The genetic
system is one-locus haploid; the genetic traits can influ-
ence the prey competition function \(c\) and the attack
rates \(a_2\) and \(a_3\), and trait dependencies are modelled
using the following functional forms:

\[
c = c_0 + c_2(x_1 - c_1)^2, \tag{2.2a}
\]

\[
a_2 = \exp \left( - \frac{x_1 - a_{24}}{a_{21}} \right)^2 + 2a_{23} \frac{x_1 - a_{24}x_2 - a_{25}}{a_{21}} \tag{2.2b}
\]

and

\[
a_3 = \exp \left( - \frac{x_2 - a_{34}}{a_{31}} \right)^2 + 2a_{33} \frac{x_2 - a_{34}x_3 - a_{35}}{a_{31}} \tag{2.2c}
\]

(with \(0 < a_{23}, a_{33} < 1\) and \(c_0, c_2, a_{21}, a_{22}, a_{31}, a_{32}\) all
positive). Prey competition is minimum at \(x_1 = c_1,\) where
prey are best adapted to their environment, while
the attack rates \(a_2\) and \(a_3\) are bidimensional Gaussian
functions with elliptic contour lines centred at \((a_{24}, a_{25})\)
and \((a_{34}, a_{35})\), respectively, and controlled in amplitude and orientation by parameters \(a_{21} - a_{23}\) and \(a_{31} - a_{33}\), respectively. Differences \((x_1 - a_{24})\) and \((x_2 - a_{25})\) (respectively, \((x_2 - a_{34})\) and \((x_3 - a_{35})\)) measure the degree to which the predator (superpredator) ‘matches’ the prey (predator); that is, the attack rate is maximum when \(x_1 = a_{24}\) and \(x_2 = a_{25}\) (respectively, \(x_2 = a_{34}\) and \(x_3 = a_{35}\)), while parameters \(a_{21} - a_{23}\) (respectively, \(a_{31} - a_{33}\)) control the sensitivity of the attack rate to the mismatch.

When a mutation occurs in trait \(x_1\) and generates a new value \(x'_1\), the ecological system becomes

\[
\begin{align*}
\frac{dn_1}{dt} &= n_1 \left( r - c(x_1) \right) n_1 - c(x_1) n_1' - a_2(x_1, x_2)n_2, \quad (2.3a) \\
\frac{dn_1'}{dt} &= n_1' \left( r - c(x'_1) \right) n_1' - c(x'_1) n_1' - a_2(x'_1, x_2)n_2', \\
\frac{dn_2}{dt} &= n_2 \left( e_2 a_2(x_1, x_2) n_1 + e_2 a_2(x'_1, x_2) n_1' 
- d_2 - a_3(x_2, x_3) n_3 \right) \\
\text{and } \frac{dn_3}{dt} &= n_3 \left( e_2 a_3(x_2, x_3) n_2 - d_3 \right),
\end{align*}
\]

so that the fitness function of mutant \(x'_1\) is given by

\[
f_1(x_1, x_2, x_3, x'_1) = \frac{1}{n_1'} \left[ \frac{dn_1'}{dt} \right]_{n_1'=0}^{n_1=\hat{n}}
= \left( r - c(x'_1) \right) n_1(x_1, x_2, x_3) \\
- a_2(x'_1, x_2)n_2(x_1, x_2, x_3), \quad (2.4)
\]

where \(n = (n_1, n_2, n_3)\) and \(\hat{n}\) denotes the ecological equilibrium of model (2.1) at which the food chain stabilizes in the absence of mutants (§3).

Similar equations can be written when a mutation arises in the predator (trait \(x_2\)) or superpredator (trait \(x_3\); see appendix S1 in the electronic supplementary material) and yields the fitness functions of mutants \(x'_2\) and \(x'_3\):

\[
f_2(x_1, x_2, x_3, x'_2) = \frac{1}{n_2'} \left[ \frac{dn_2'}{dt} \right]_{n_2'=0}^{n_2=\hat{n}}
= e_2 a_2(x_2, x'_2) n_1(x_1, x_2, x_3) - d_2 \\
- a_3(x'_2, x_3)n_3(x_1, x_2, x_3), \quad (2.5)
\]

and

\[
f_3(x_1, x_2, x_3, x'_3) = \frac{1}{n_3'} \left[ \frac{dn_3'}{dt} \right]_{n_3'=0}^{n_3=\hat{n}}
= a_3(x'_3, x_3) n_2(x_1, x_2, x_3) - d_3. \quad (2.6)
\]

The right-hand sides are the product of mutation rates \((\mu_i, i = 1 - 3)\), mutational steps variances \((\sigma_i^2)\), equilibrium densities \((\hat{n}_i)\) and selection gradients (fitness derivatives). The latter explicit expressions are cumbersome and some were always generated and handled by means of symbolic computation.

### 3. MODEL ANALYSIS AND RESULTS

The ecological model (2.1) has a unique non-trivial equilibrium,

\[
\begin{align*}
\hat{n}_1 &= \frac{r - a_3 d_3}{c e_2 a_3}, \quad (3.1a) \\
\hat{n}_2 &= \frac{d_3}{e_2 a_3} \quad (3.1b) \\
\text{and } \hat{n}_3 &= \frac{e_2 a_2}{a_3} \left( \frac{r - a_2 d_3}{c e_2 a_3} \right) - \frac{d_2}{a_3}, \quad (3.1c)
\end{align*}
\]

which is positive if and only if \(\hat{n}_3 > 0\). When positive, the equilibrium \(\hat{n}\) is globally stable (in the positive orthant). Thus, the ecological model (2.1) is only viable within the region of the trait space defined by the condition \(\hat{n}_3 > 0\).

If the superpredator and the predator are able to simultaneously match the predator and the prey, respectively (i.e. \(a_{25} = a_{34}\)), and if, at the same time, the prey is able to minimize its sensitivity to intraspecific competition (i.e. \(c_1 = a_{2k}\)), then \(x_1 = c_1, x_2 = a_{25}, x_3 = a_{35}\) is an equilibrium of the evolutionary model (2.7). Starting from these conditions, and fixing parameters at values corresponding to evolutionary cycles in the ditrophic model (Dieckmann et al. 1995), we performed the numerical continuation of the equilibrium \(\bar{x}\) with respect to several parameters.

As expected, evolutionary stability was sensitive to the mutation rate \(\mu_1\) of the prey. As \(\mu_1\) increases, the evolutionary equilibrium loses stability through a supercritical Hopf bifurcation that yields a small-amplitude stable evolutionary cycle (see appendix S3 in the electronic supplementary material). Starting from the Hopf bifurcation, we numerically continued the cycle, while monitoring its stability through the computation of the associated Floquet multipliers (i.e. the three eigenvalues of the linearized Poincaré map associated with the cycle; one of them is structurally equal to 1, and therefore its estimated value is a measure of computation accuracy; the other two determine the stability of the cycle). Again, by increasing \(\mu_1\), evolutionary stability was easily lost through a series of period-doubling bifurcations (a negative Floquet multiplier passing through −1; see appendix S3 in the electronic supplementary material). At each period-doubling bifurcation, the cycle becomes unstable, and a new stable cycle (which traces twice the bifurcating cycle) appears. Switching to the continuation of the new stable cycle allowed us to find the next period-doubling bifurcation. Because the sequence of bifurcation parameter values \(\mu_1^i, i = 1, 2, \ldots\), accumulates geometrically at the frontier \(\mu_1^\infty\) of the chaotic region of the Feigenbaum period-doubling cascade, only a limited number of bifurcations in the sequence could be detected (\(\mu_1^i, i = 1, 2, 3\), are reported in figure 1). The robustness of the cascade has been checked through the continuation of the period-doubling bifurcations with respect to various pairs of parameters (details will be published elsewhere).
In order to estimate \( \lambda^m \), we computed the full spectrum of the attractor’s Lyapunov exponents \( L_1 \geq L_2 \geq L_3 \) for finely incremented values of \( \mu_1 \) (step \( 10^{-3} \); see appendix S2 in the electronic supplementary material). \( L_1 > 0 \) implies that \( \mu_1 \) is in the chaotic region, whereas \( L_1 = 0 \) in periodic windows (figure 1); in the chaotic region, \( L_3 \) is structurally equal to 0 (its estimated value measures computation accuracy), while \( L_3 \) is negative. The attractor’s fractal dimension then follows from the Kaplan–Yorke formula (figure 2). In this example, the dominant Lyapunov exponent equals \( 0.0081321 \) and the fractal dimension of the attractor is 2.0176 (the attractor lies roughly on a two-dimensional Møbius strip). Typically, the prey and predator characters oscillate with small irregular fluctuations in amplitude and frequency, while variation in the amplitude of the oscillations in the superpredator trait is more pronounced.

Our analysis shows that the genetically driven Red Queen turns chaotic under conditions similar to those leading to genetically driven Red Queen cycles, provided that the mutation time scale of the prey is short enough compared with the mutation time scales of the predator and the superpredator. That is (Dieckmann et al. 1995; Dercole et al. 2003), the predator efficiency should be great enough to drive the prey away from its genetic optimum; and there should be sufficient need for the predator to track the prey’s character change. As the prey departs from its optimum, its population density drops, which causes a reversal of selection on the predator’s trait, followed by a reversal of selection on the prey’s character. If the prey evolves fast enough, it will not be ‘caught up’ by the predator and permanent trait oscillations will evolve; the system ends up in chaos because the predator is also engaged in a coevolutionary chase with the superpredator. Broad comparative analyses (e.g. Martin & Palumbi 1993) have established a strong relationship between nucleotide substitution rate and body size. For instance, rates of nuclear and mtDNA evolution are slow in whales, intermediate in primates and fast in rodents, and a similar effect of body size also exists in poikilothermic vertebrates. Thus, trophic chains with smaller prey (and hence faster mutagenesis) may be more prone to coevolutionary chaos.

4. DISCUSSION

Even though quantitative data on long-term predator–prey coevolutionary dynamics remain elusive (Barnosky 2001), the fossil record supports the view that predation is an important driver of evolutionary change (Kelley et al. 2003). Moreover, palaeontological and phylogenetic analyses gather increasing evidence for the role of three-level chain interactions in coevolution (Currie et al. 2003; Kelley et al. 2003). These empirical findings have been paralleled by extensions of coevolutionary theory beyond pairwise interactions (Abrams 1996; Caldarelli et al. 1998; Loeuille et al. 2002; Gandon 2004; Nuismer & Doebeli 2004; Loeuille & Loreau 2005; Kisdi & Liu 2006; Bell 2007; Ferrière et al. 2007; Shoresh et al. 2008; Jones et al. 2009; Stegen et al. 2009), but so far the complexity of evolutionary dynamics among more than two species coevolving in a multi-dimensional trait space has been little explored. As a step forward in that direction, we added a superpredator, as a third coevolving species, to coevolution between a prey and a predator.

Prey– predator–superpredator trophic chains have long attracted the attention of ecologists as they occur by diverse mechanisms, can cross ecosystem boundaries and have practical importance; for example, in the management of fisheries or biological control of crop pests (Cohen et al. 2009). Our model descends from the lineage of two-species models that addressed genetically driven predator–prey coevolution (Stenseth & Maynard Smith 1984; Rosenzweig et al. 1987; Rand & Wilson 1991; Marrow et al. 1992; Dieckmann et al. 1995; Doebeli 1997; Gavrilts 1997; Khibnik & Kondrashov 1997; Dercole et al. 2003, 2006) and specifically extends the analysis of Dieckmann et al. (1995), where stable cycles in adaptive dynamics were first documented.

We searched for strange attractors in the three-trait, three-species coevolutionary model by weaving intuition and theory. Theory was telling us that in third-order dynamical systems the most common route to chaos is the Feigenbaum period-doubling cascade (see appendix S3 in the electronic supplementary material), and we knew that evolutionary stability in predator–prey models was especially sensitive to the mutation rate of the prey (Dieckmann et al. 1995; Dercole et al. 2003). Thus, our analysis of the tritrophic evolutionary dynamics was organized by looking for parameters that caused evolutionary cycles in the lower ditrophic model (and such that increasing the prey mutation rate could trigger doubling of the cycle period) and then tracking the period-doubling cascade. The strategy was successful at detecting transitions towards evolutionary chaos in the three-species system.

Our analysis of three-species coevolution was intended as an extension of Dieckmann et al.’s (1995) two-species model. This is the technical motivation for our choice of the type I functional response to describe trophic interactions, hence the Lotka–Volterra structure of the
ecological model. This has the important consequence of ensuring that the food chain always stabilizes at an equilibrium on the ecological time scale. Therefore, oscillations predicted by the evolutionary model could only be due to nonlinear interactions between selective pressures acting on genetic variation in the adaptive traits—not to trait variation induced by instabilities in the ecological dynamics (Abrams & Matsuda 1997a). More realistic food chain models with, for example, saturating (type II) functional responses or self-limitation at higher trophic levels can also stabilize at ecological equilibria, though ecological cycles and ecological chaos are also expected in viable regions of the trait space. This opens the possibility of Red Queen chaotic dynamics that would be ‘ecogenetically driven’ (sensu Khibnik & Kondrashov 1997; for the two-species case see Dercole et al. 2003; Dercole et al. 2006).

Another fundamental feature of the model is the definition of the adaptive traits. We keep the ‘matching model’ used in Dieckmann et al. (1995), which has long been popular in the theory of predator–prey coevolution (Cohen et al. 1993; Abrams 2000; Loeuille & Loreau 2005; Stegen et al. 2009). The matching model assumes that the traits of a species and its prey jointly determine the attack (and capture) rate on the former by the latter, and that the attack rate is maximized when the two traits match. Scaled body size is a commonly used surrogate measure for such traits (Williams & Martinez 2000). Defining the adaptive traits according to the matching model is known to promote genetically driven Red Queen cycles in the two-species predator–prey coevolutionary model (Marrow et al. 1992, 1996; Dieckmann et al. 1995; Abrams & Matsuda 1997b; Doebeli 1997; Gavrilets 1997), and thus provided us with the appropriate framework to answer our main question—how are two-species Red Queen cycles affected by the coevolution of a third species?

Several well-studied antagonistic pairwise interactions seem to conform to the matching model. This includes parasitic cuckoos and their hosts, in which the probability that a parasitic egg be rejected depends on the similarity of host and parasite egg morphologies (Robert & Sorci 1999); crossbills and lodgepole pines, for which fitnesses are influenced by matching between bill size and cone structure (Benkman 1999); feather lice and dove hosts, in which louse fitness at least is influenced by matching size with host size (and host size correlates with parasite size across species; Clayton et al. 2003). Other equally well-studied systems, however, better fit an alternative model in which the strength of between-species interactions is a monotonic function of the difference between the predator and prey’s traits. This is the case of parsnip web-worms and wild parsnips, in which feeding efficiency of defended plants increases with higher production of detoxifying enzymes (Berenbaum & Zangerl 1992). Likewise, the rate of successful attack in the Japanese-camellia—camellia-weevil system is a monotonic function of the difference between camelia fruit wall thickness and weevil mouthpart size (Toju & Sota 2006, 2009). The ‘difference model’ so defined also fits the trophic interaction between toxic newts as prey and potentially toxin-resistant garter snakes as predators (Brodie et al. 2002; Hanifin et al. 2008).

Nuismer et al.’s (2007) theoretical analysis of antagonistic coevolution under the difference model of attack rate shows that coevolutionary cycles are still possible with this model, provided that selection is strong enough and stabilizing selection acts on the traits. Thus, genetically driven coevolutionary cycles in pairwise antagonistic interactions appear to be at least possible under relatively broad conditions when the attack rate is described by the difference model. The question of whether coevolutionary cycles turn into chaos in the three-species food chain is open to investigation. Future models should also examine the coevolution of alternative or additional traits besides the attack rate. Dercole et al. (2003) and Kisdi & Liu (2006), for example, considered the evolution of handling time, a key factor of the functional response. As an
extension of our model, it would be interesting to account for genetic variation in predator and superpredator handling times, track the evolution of the functional responses themselves as a byproduct and monitor the potential bifurcations experienced by the coevolutionary dynamics as a consequence.

The possibility that natural selection acting on extant genetic variation drives community dynamics into chaos has been known since early analyses of host–pathogen models (May & Anderson 1983), and is not unexpected given that competition between multiple species or genotypes can easily destabilize population dynamics (Hofbauer & Sigmund 1998; Turchin 2003). This type of chaotic evolutionary dynamics has been found in theoretical studies of genetic polymorphisms under frequency-dependent selection (e.g. May & Anderson 1983; Seger 1992; Ferrière & Fox 1995; Solé & Sardanyés 2007), strategy frequencies in evolutionary games (Nowak & Sigmund 2003) and rapid evolution of a continuous trait in interaction with population dynamics (Abrams & Matsuda 1997a). All these are instances of evolutionary chaos on the ecological time scale. The system considered here is different since the time scales of ecology and evolution are separated: the population dynamics of different alleles stabilize on a monomorphic state over a time scale that is fast compared with the slow evolutionary time scale over which the dynamics of the adaptive traits develop. Thus, our analysis uncovers the first example of genetically driven chaotic Red Queen.

The genetically driven chaotic Red Queen implies that nonlinear interactions of selective pressures can drive phenotypic changes that are unpredictable over the slow time scale of long-term evolution, even in a perfectly constant abiotic environment. (Note that with chaos in allele or strategy frequencies driven by negative frequency dependence, there is unpredictability in the dynamics of frequencies, but the identity of alleles or strategies never changes.) This has implications for our understanding of the role of ‘chance’ in evolution (Travisano et al. 1995; Beatty 2006). Chance manifests itself when the evolutionary trajectories of adaptive traits diverge between replicated populations that were initiated in similar phenotypic and genotypic states. Experimental tests on bacterial systems have provided some of the best evaluations of the role that chance may play in evolution. Although founded by the same clone, and evolving in identical conditions, replicate populations often diverge from one another in their relative growth rate, demographic traits, morphological features and performance in other environments (Elena & Lenski 2003 and references therein). The conventional explanation for evolutionary divergence ‘by chance’ involves genetic stochasticity (the randomness of mutation and drift owing to demographic stochasticity) and environmental stochasticity (random changes in environmental conditions; Lenormand et al. 2008). However, models of adaptive trait dynamics derived from individual-level ‘first principles’ have shown that the effect of genetic stochasticity is often ‘smoothed out’ in the long term, with traits converging towards the attractor of a deterministic dynamical system, provided that there is some minimal separation between the time scales of mutation and selection (Champagnat et al. 2006). The present study shows that even if the randomness of genetic stochasticity is smoothed out, uncertainty can arise from the selection component of the evolutionary process: adaptive trait trajectories converge towards a deterministic attractor, yet the chaotic nature of the attractor renders the trait dynamics unpredictable beyond a short evolutionary time horizon. Thus, the nonlinearity of the selection gradient offers an alternative to genetic or environmental stochasticity to explain the chance component of evolutionary trajectories in real populations.

Further examples of genetically driven chaotic Red Queen dynamics are likely to be discovered in models of long-term evolution in which the adaptive process operates in a three- (or more) dimensional trait space—even if all traits (e.g. behavioural or life-history traits) pertain to the same single species. Genetically driven chaos might also arise in two-trait adaptive dynamics models, or even in one-trait systems showing ecological multistability (Dercole et al. 2002), that are subject to externally driven periodic fluctuations in mutation or selection. Besides its conceptual value, the genetically driven chaotic Red Queen suggests three new hypotheses (discussed below) about coevolutionary dynamics. Each hypothesis opens an avenue for future theoretical work.

(a) The intrinsic unpredictability of coevolutionary dynamics is widespread

In view of the general theory of dynamical systems, the existence of chaotic evolutionary attractors over some parameter region can affect the coevolutionary dynamics broadly outside that region. Even when the coevolutionary attractor of the food chain is an equilibrium or a cycle, the ‘shadow’ of evolutionary chaos will be seen in the form of long erratic transients (Hastings 2004). Genetic noise—owing, for example, to random drift or stochastic gene flow—or stochastic environmental fluctuations on the slow evolutionary time scale may actually maintain these transients for arbitrarily long evolutionary times. Such ‘noise-induced chaos’ illustrates the general fact that small amounts of exogenous noise can have disproportionate qualitative impacts on the long-term dynamics of a nonlinear system in which chaotic structures exist for some parameter values (Rand & Wilson 1991; Lai et al. 2003; Ellner & Turchin 2005).

(b) Coevolution can drive population dynamics to the edge of chaos

Looking at evolution on a slow time scale, in contrast with, or even completely separated from, the fast time scale of ecology, does not mean that the coevolutionary process has no effect on the ecological state of the system. In fact, the genetically driven chaotic Red Queen implies that the population size of each species also fluctuates chaotically, but these fluctuations develop on the slow, evolutionary time scale, because at each point in evolutionary time, the food chain model analysed here is at ecological equilibrium. In other food chain models, ecological cycles and chaos occur readily (Hastings & Powell 1991; Gross et al. 2005). In the light of this and other studies (Khibnik & Kondrashov 1997; Dercole et al. 2006), the trait domain corresponding to ecological chaos may contain part or all of the coevolutionary attractor (ecogenetically driven Red Queen). A sharp change in the selective regime at the
boundary between chaotic and non-chaotic ecological dynamics is expected in general (Ferrière & Gatto 1995; Dercole et al. 2006), and may poise the food chain near that boundary for long evolutionary times, in a process called ‘evolutionary sliding’ (Dercole et al. 2006). This would provide an evolutionary explanation for the standing puzzle that the abundance of many natural populations seemingly fluctuates ‘at the edge of chaos’ (Ellner & Turchin 1995; Turchin 2003).

(c) The chaotic Red Queen promotes genetic divergence in metacommunities

There is considerable interest in better understanding how coevolutionary processes work in geographically structured habitats (Thompson 2005). The arising of genetically driven chaos has direct implications for the origin and maintenance of genetic diversity in spatially extended communities. Let us consider the metaphor of a fragmented landscape in which all patches are identical and isolated. Genetically driven chaotic Red Queen dynamics imply that each local trophic chain evolves along the same strange attractor, but small ancestral differences in the genetic make-up of local communities will result in permanent genetic differences between patches. The magnitude of these differences will vary over time and sometimes be as large as the coevolutionary attractor. In contrast, small ancestral differences remain small in the case of periodic Red Queen dynamics (and the same would be true if the Red Queen were ecologically driven). In other words, local genetically driven coevolutionary chaos promotes spatial genetic divergence, even in the absence of environmental differences between patches. Red Queen dynamics in general can explain phenotypic mismatches between coevolving species even in the absence of spatial structure, gene flow or genetic drift (Berenbaum et al. 1986; Hanifin et al. 2008); the chaotic Red Queen, in particular, predicts the persistence of different degrees of mismatches between local communities, even if environmental conditions are spatially uniform.

Furthermore, general results on the synchronization of dynamical systems subject to common fluctuating exogenous forces warn that the genetic divergence between local populations can be lost in the presence of long-term environmental fluctuations (this is known in ecology as the Moran effect; see Royama 1992 for a review). However, recent results (Colombo et al. 2008) show in great generality that this is possible only if environmental fluctuations are large and tuned specifically to the endogenous dynamics of the system. Genetically driven coevolutionary chaos could therefore play an important role in promoting genetic diversity in ecological communities threatened by environmental homogenization (Olden et al. 2004). We conclude that genetically driven Red Queen chaos might explain genetic differentiation of local communities without invoking local adaptation to different habitat conditions or to multiple steady states of local populations in the metacommunity. This points to the possibility that, in sexual species, the genetic divergence of local populations induced by complex adaptive dynamics might favour the evolution of reproductive isolation and hence parapatric speciation—even across relatively uniform habitats, as in marine species (Palumbi 1994). Extension of speciation models along ecological gradients (Doebeli & Dieckmann 2003) will help examine this hypothesis further.

5. CONCLUDING REMARKS

Here, we have extended Dieckmann et al.’s (1995) model of predator–prey genetically driven coevolution by adding a coevolving superpredator to the system. When Red Queen periodic cycles develop in the two-species model, the adaptive dynamics of the three coevolving species are often chaotic. A general condition for this to happen is that the evolutionary rate of the prey be large enough. The greatest irregularity is then predicted in the dynamics of the superpredator trait. Because the ecological model of the food chain is always at equilibrium throughout the trait space, instability in the ecological dynamics plays no role in generating this chaotic Red Queen, which is thus entirely driven by nonlinear interactions between the selective pressures acting on rare genetic variation of the traits.

The specificities of the model and the new hypotheses arising from the results call for continued theoretical investigation of chaotic dynamics in genetically driven coevolutionary processes. This theoretical endeavour should be paralleled by an empirical effort focusing on the patterns of temporal unpredictability and spatial heterogeneity of antagonistic coevolution and the consequences for population dynamics, genetic differentiation in metacommunities and macroevolutionary processes, including speciation.

A key difference between coevolutionary cycles and coevolutionary chaos lies in the expectation that geographically distinct communities subject to homogenizing factors of their environment (e.g. large-scale climatic fluctuations) should exhibit similar degrees of phenotype mismatching when coevolving cyclically, and persistently dissimilar degrees of mismatching when coevolving chaotically. Spatially heterogeneous mismatches have been documented recently in the camellia–weevil (Toju 2009) and newt–garter snake (Hanifin et al. 2008) systems. In the light of our results, the fine-scale divergence of coevolution in the former may not require geographical variation of environmental factors (Toju 2009). Molecular data supporting the role of beneficial mutations, rather than standing genetic variation, as fueling coevolution between newts and their snake predators (Feldman et al. 2009) offer promising evidence for the relevance of genetically driven Red Queen models to deepen our understanding of geographical patterns of coevolution in nature.

Besides trophic interactions, the Red Queen is expected to reign in many exploiter–victim systems (Lythgoe & Read 1998). Biomedical science has already revealed the potential ubiquity of the Red Queen in parasitic and pathogenic interactions (Moya et al. 2004). Experimental coevolution in host–pathogen systems is being used successfully to evidence the patterns and dissect the processes of ecologically driven Red Queen dynamics in laboratory systems (Koskella & Lively 2009) and in nature (Decaestecker et al. 2007). On the evolutionary time scale, antagonistic coevolutionary dynamics fuelled by de novo genetic variation have been studied experimentally using bacterial systems.
(Lenski & Levin 1985; Bohannan & Lenski 2000; Buckling & Rainey 2002; Gallet et al. 2009). The time-shift experimental design (Gaba & Ebert 2009) implemented to study ecologically driven Red Queen dynamics could be applied to measure how predictable genetically driven coevolutionary trajectories are under different experimental treatments, and thus to search for the essential property of chaotic dynamics—exponentially declining predictability of trajectories. Combining experiments with sufficiently detailed mathematical models of the study systems will be instrumental to identify relevant experimental treatments, to design data collection and analysis and to interpret the results (Decaestecker et al. 2007). If it were supported by such experiments on microbial systems, the genetically driven chaotic Red Queen might contribute to our understanding of the rapid and indeterminate evolution of viral pathogens (Kirkwood & Bangham 1994; Moya et al. 2004), and perhaps influence the study and control of emergent pathogens on large temporal and spatial scales.

Ultimately, the important question raised by the genetically driven chaotic Red Queen is unlikely to be whether or not long-term evolution in any specific ecological system is chaotic—a question that makes sense only in the realm of mathematical models. Population ecologists have long gone beyond that question—chaos versus non-chaos—to draw stunning insights from the nonlinear dynamics theory into how environmental forces and internal dynamics shape species abundance and distribution in nature (Allen et al. 1993; Ellner & Turchin 1995; Dixon et al. 1999; Turchin 2003). The same move could take place in evolutionary biology, as genetically driven Red Queen chaos challenges our ability to measure, compare and interpret coevolutionary patterns and processes in the real world.

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