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Mutation rate increases in sexual populations during range expansion

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Abstract

The evolution of higher dispersal during range expansion increases invasion speed, provided that a species can adapt sufficiently fast to novel local conditions. Iterated founder effects during range expansion, however, cause low levels of local genetic diversity at these range margins. Mutation rates can evolve, too, and using an individual-based model we show that natural selection may lead to co-evolution of dispersal rates and mutation rates, which causes a faster range expansion and a larger species' range. Surprisingly, this also occurrs in sexual populations, due to the particular properties of spatial sorting. This co-evolution results in a long-lasting maintenance of high mutation rates in both sexual and asexual species. By this we extend the existing theory on the evolution of mutation rates, which was thought to be limited to asexual populations, with possibly far-reaching ecological consequences concerning invasiveness and the rate at which species can adapt to novel environmental conditions.

Introduction

Many species are currently expanding their ranges, both polewards and uphill, as a response to increasing global temperatures under climate change (Chen et al. 2011). Range expansions are known to have profound effects on the genetic composition of populations, regarding both neutral and adaptive genetic diversity (Hewitt 1996; Phillips et al. 2006; Excoffier et al. 2009; Cobben et al. 2012b). Traits that act to increase species' dispersal capabilities and population growth rates are selected for under range expansions due to spatial sorting (Hill et al. 2011; Shine et al. 2011) and kin competition (Kubisch et al. 2013b). This may lead to the higher dispersal rates (Thomas et al. 2001; Kubisch et al. 2010), dispersal distances (Phillips et al. 2006) and effective fertilities (Moreau et al. 2011) at the expanding front of species' ranges due to micro-evolution. An increasing dispersal rate under range expansion will increase the invasion speed (Phillips et al. 2006) , but only if the species is able to adapt sufficiently rapid to newly experienced local conditions. However, under range expansion the depletion of genetic diversity at the expanding range border due to iterated founder effects (Hewitt 1996; Excoffier et al. 2009; Cobben et al. 2011) can be expected to limit the invasion speed as low genetic diversity will lead to low rates of local adaptation and thereby delayed population establishment.

Evolvability, i.e. a set of mechanisms that facilitates evolution, has been shown to be subject to selection under conditions that favor an increased rate of local adaptation, e.g. under increasing environmental stochasticity and stress (Earl & Deem 2004; Kashtan et al.

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2007; Lee & Gelembiuk 2008). One example is the evolution of mutation rates, which can lead to increased levels of genetic diversity and thus increased evolvability (Kimura 1967; Leigh Jr 1970; Leigh Jr 1973; Sniegowski et al. 1997; Taddei et al. 1997; Metzgar & Wills 2000; Bedau & Packard 2003). In such a system a mutator gene codes for the rate of mutation at another gene under selection. In this latter gene, the number of mutations thus increases, generating more genetic variation for selection to act on, as such enabling adaptation to changing selection pressures (Kimura 1967; Leigh Jr 1970; Leigh Jr 1973; Taddei et al. 1997; Metzgar & Wills 2000; Sniegowski et al. 2000; Bedau & Packard 2003). During the colonization of a spatially heterogeneous environment, an increased mutation rate will be selected for as it generates more genetic diversity, provided that this results in the faster establishment of new populations by pre-adapted individuals. Further increased selection for high mutation rates can be expected due to the iterated founder effects (Cobben et al. 2011) and increased relatedness between individuals (Kubisch et al. 2013b) at the expansion front, in combination with the increased dispersal rates and higher potential invasion speed (Phillips et al. 2006; Phillips et al. 2010a). With the establishment of a stable range border, after range expansion, the selection pressures change and a return to lower mutation rates is expected.

The evolution of mutation rates has thus far mostly been associated with and only shown for asexual populations (Drake et al. 1998; Sniegowski et al. 2000). As selection acts on the mutation of the adaptation gene and not on the mutator gene, the evolution of mutation rates is the result of indirect selection and thus restricted to genetic hitchhiking, which is highly sensitive to recombination (Drake et al. 1998; Sniegowski et al. 2000). However, if an individual can only mate with genetically similar individuals, genetic information at the mutator gene and the adaptation gene can be reunited in the offspring despite their independent inheritance. Such conditions of genetic similarity are typical for range expansions due the low genetic diversity at the expanding range margin and the evolution of mutation rates in sexual populations might thus be possible there.

In this study, we use a spatially explicit individual-based metapopulation model of a sexual species establishing its range on a spatial gradient to investigate 1) whether there is co-evolution between dispersal rates and mutation rates during range expansion, 2) how this affects the genetic diversity across the range, and 3) the evolutionary dynamics under spatial equilibrium after range border establishment. The results show the joint evolution of dispersal rates and mutation rates in sexual populations resulting from the particular properties of spatial sorting. This co-evolution leads to a faster range establishment and a larger eventual species' range.

Methods

We use a spatially explicit individual-based metapopulation model of a sexually reproducing species with discrete generations that expands its range along an elevational gradient, inspired by insects' ecology and parametrized using empirical data (Poethke et al. 1996; Amler et al. 1999). We allow the mutation rate of local adaptation to evolve, and investigate its interplay with the evolution of dispersal rate during and after range establishment.

Landscape

The simulated landscape consists of 250 columns (x-dimension) of 20 patches each (y-dimension). We assume wrapped borders in y-direction, building a tube. Hence, if an individual leaves the world in y-direction during dispersal, it will reenter the simulated world on the opposite side. However, if it leaves the world in the x-direction, it is lost from the simulation. To answer our research questions the model requires both a need for local adaptation and a relatively fast return to lower

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dispersal rates after population establishment. For this, we have chosen to use an altitudinal gradient, known to often be comprised of clines of decreasing temperature and increasing habitat fragmentation (Körner & Paulsen 2004). Thus firstly, in our model every column of patches (x-position) is characterized by its specific mean temperature τ_x. This mean local temperature is used for the determination of local adaptation of individuals. To simulate a large-scale habitat gradient, τ_x changes linearly from$\tau_{x=1} = 0$ to $\tau_{x=250} = 10$ along the x-dimension, i.e. by $\Delta_{\tau,x} = 0.04$ when moving one step in x-direction. Secondly, to account for habitat fragmentation in terms of patch isolation, each x-position is characterized by a certain degree of dispersal mortality. The probability to die upon dispersal, μ, changes linearly from $\mu_{x=1} = 0$ to $\mu_{x=250} = 1$ along the x-dimension.

Population dynamics and survival of offspring

Local populations are composed of individuals each of which is characterized by several traits: 1) their sex, 2) two genes at the dispersal locus l_d coding for the individual's dispersal probability, 3) two genes at the adaptation locus l_a coding for the individual's optimal temperature τ_{opt} , i.e. the temperature under which it survives best (see below for details), 4) another two genes at the mutator locus l_m coding for the mutation probability of the genes at locus l_a, so the mutation rate at the adaptation locus (see below under Genetics), and 5) a diploid neutral locus l_n, also mutating at the l_m mutation rate, for the sake of comparing with genetic diversity at the la locus.

Local population dynamics follow the time-discrete Beverton–Holt model (Beverton & Holt 1957). Each individual female in patch x, y is therefore assigned a random male from the same habitat patch (males can potentially mate several times) and gives birth to a number of offspring drawn from a Poisson distribution with mean population growth rate λ. The offspring's sex is chosen at random. Density-dependent survival probability s_1 of offspring due to competition is calculated as:

$$s_1 = \frac{1}{1 + \frac{\lambda - 1}{K} \cdot N_{x,y,t}} \tag{1}$$

with K the carrying capacity and $N_{x,y,t}$ the number of individuals in patch x, y at time t. Finally, the surviving offspring experience a further density-independent mortality risk $(1 - s_2)$ that depends on their local adaptation, so the matching of their genetically determined optimal temperature (τ_{opt}) to the temperature conditions in patch x, y (τ_x) according to the following equation:

$$s_2 = exp\left[-\frac{1}{2} \cdot \left(\frac{\tau_{opt} - \tau_x}{\eta}\right)\right] \tag{2}$$

where η describes the niche width or 'tolerance' of the species. We performed simulations for the species with a niche width of $\eta = 0.5$, equivalent to a decrease of survival probability of about 0.02 when dispersing one patch away from the optimal habitat. In this approach we assume that density-dependent mortality $(1 - s_1)$ acts before mortality due to maladaptation to local conditions $(1 - s_2)$. In addition, each population has an extinction probability ϵ per generation. Individual surviving offspring disperse with probability d that is determined by their dispersal locus (see below). If an individual disperses it dies with probability μ, which is calculated as the arithmetic mean of the dispersal mortality values of its natal and its target patch, respectively. This mortality accounts for various costs that may be associated with dispersal in real populations, like fertility reduction or predation risk (Bonte et al. 2012). We assume nearest-neighbor dispersal, i.e. successful dispersers settle randomly in one of the eight surrounding habitat patches.

Genetics

As mentioned above, each individual carries three unlinked, diploid loci coding for its dispersal probability, its optimum temperature

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(and thus its degree of adaptation), and the mutation rate of the optimum temperature gene, respectively, and an additional neutral locus. The phenotype of an individual is determined by calculating the arithmetic means of the two corresponding alleles, with no dominance effect involved. Hence, dispersal probability d is given by $d = \frac{l_{d,1}+l_{d,2}}{2}$ (with $l_{d,1}$ and $l_{d,2}$ giving the two 'values' of the two dispersal alleles), optimal temperature τ_{opt} is calculated as $\tau_{opt} = \frac{l_{a,1}+l_{a,2}}{2}$ (with $l_{a,1}$ and $l_{a,2}$ giving the 'values' of the two adaptation alleles), and similarly the mutation rate of the optimal temperature $m(\tau_{opt}) = 10^{-exp}$ (with $exp = \frac{l_{m,1}+l_{m,2}}{2}$, and $l_{m,1}$ and $l_{m,2}$ the 'values' of the two mutator alleles). At each of the four loci, newborn individuals inherit alleles, randomly chosen, from the corresponding loci of each of their parents. During transition from one generation to the next a gene may mutate. Genes at the dispersal locus and the mutator locus mutate with a probability of $m = 10^{-4}$. Genes at the adaptation and the neutral loci however, mutate with the probability m(τ_{opt}) given by the value based on the two alleles at the mutator locus l_m as elaborated above. Mutations are simulated by adding a random number to the value calculated from the mean of the inherited alleles. The mutation strengths depend on the value ranges of the specific genes and their genetic architectures. For the dispersal locus, they are drawn from a Gaussian distribution with mean 0 and standard deviation 0.2, for the adaptation and the neutral loci the standard deviation is 0.5 and for the mutator locus the standard deviation is 1. These standard deviations, i.e. the effect sizes of the mutations, differ per trait in line with the required range of values in the different traits, and have no other effect than a decrease of the computation time.

Simulation experiments

Simulations were initialized with a 'native area' (from $x = 1$ to $x = 50$) from where the species was able to colonize the world, while the rest of the world was initially kept free of individuals. Upon initialization, dispersal alleles ($l_{d,i}$) were randomly drawn from the interval $0 < l_{d,i} < 1$, and mutator alleles $l_{m,i}$ were set to 4, which set the initial mutation rate of the adaptation alleles and the neutral alleles to 10^{-4}. Populations were initialized with K locally optimally adapted individuals, i.e. adaptation alleles were initialized according to the local temperature τ_x. However, to account for some standing genetic variation we also added to every respective optimal temperature allele a Gaussian random number with mean zero and standard deviation 0.5. At the neutral locus, these individuals were initialized with random allele values with a mean of 0.5 and standard deviation 0.5. We performed 100 replicate simulations, which all covered a time span of 60 thousand generations. To establish demographic equilibrium, the individuals were confined to their native area during the first 1000 generations. After this burn-in period, the species was allowed to pass the $x = 50$ border. Table 1 summarizes all relevant model parameters, their meanings and the standard values used for the simulations. Serving as controls, the simulations were repeated with 100 replicates for fixed values of dispersal rate, $d = 0.05$, $d = 0.1$ and $d = 0.2$, while allowing the mutator locus to evolve, and reversely simulations with fixed values of the mutation rate of 10^{-4} and 10^{-5}, combined with evolving dispersal rate. In addition, we performed a control with fully linked mutator and adaptation loci.

Analysis

The individual phenotypes for the three traits were documented in time and space throughout the simulations. Genetic diversity was calculated as the variance in allelic values at the adaptation locus, the mutator locus and the neutral locus, per x-position.

Results

After the burn-in phase, the dispersal rate d in the core area, so under low dispersal mortality, is on average approximately 0.42. Maximum

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Table 1: *Parameter values.*

parameter / variable	(initialization) value	meaning
individual parameters:		
$l_{d,1}$,$l_{d,2}$	(0 to 1 and) evolving	alleles coding for dispersal propensity
$l_{a,1}$,$l_{a,2}$	(optimal with sd 0.5 and) evolving	alleles coding for optimal temperature
$l_{m,1}$,$l_{m,2}$	(4 and) evolving	alleles coding for mutation rate of optimal temperature
$l_{n,1}$,$l_{n,2}$	(0.5 with sd 0.5 and) evolving	neutral alleles as control
simulation parameters:		
K	100	carrying capacity
λ	2	per capita growth rate
ϵ	0.05	local extinction probability
m	10^{-4}	mutation rate for dispersal and evolvability alleles
μ_x	[0..1]	local dispersal mortality
τ_x	[0..10]	local temperature
η	0.5	niche width
x_{max}	250	extent of simulated landscape in x-direction
y_{max}	50	extent of simulated landscape in y-direction

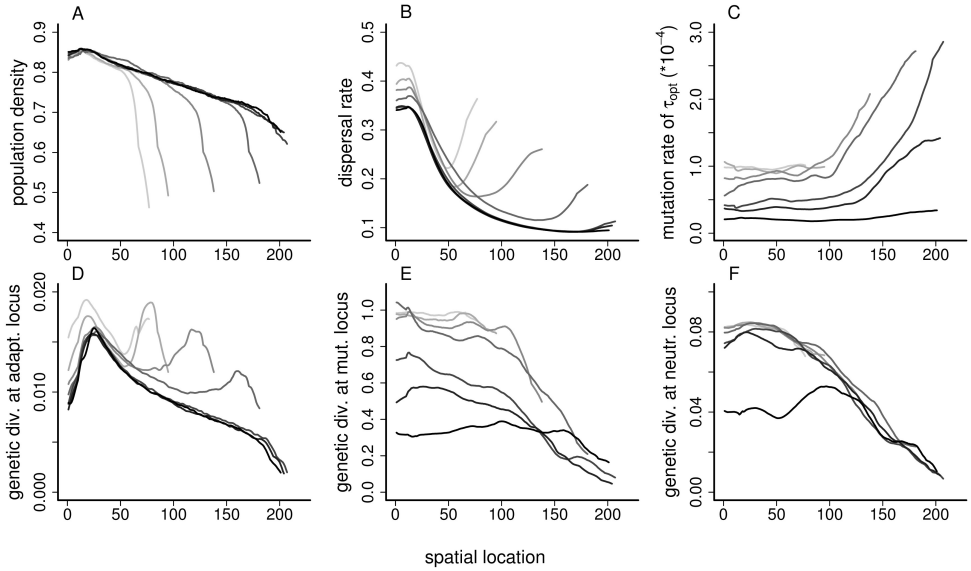

Figure 1: *The average values over 100 simulations during and after range expansion across the gradient (horizontal axis) in time (gray scaling from light to dark, as time proceeds, which is given in a sequence of generations 100, 200, 500, 1000, 5000, 10000, 50000) of A. population density, B. dispersal rate, C. the mutation rate of the adaptation alleles, D. genetic diversity at the adaptation locus, E. genetic diversity at the mutator locus, and F. neutral genetic diversity, all measured as the variance in allele values. For reasons of clarity, a moving average with a window size of 20 has been applied (data were present in 10-generation intervals).*

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population density is around 0.85 here, accompanied by a high level of local adaptation s2 (i.e. adaptation-dependent offspring survival probability) close to one (not shown), while the mutator values $m(\tau_{opt})$ is still at initialization values of 10^{-4} (Figure 1). Under range expansion, the dispersal rate d increases in the populations at the expansion front, and in time decrease again as these populations get older (Figure 1B). As the species expands its range further across the gradient of increasing dispersal mortality (and increasing temperature), the maximum established dispersal rates at the range front decrease (Figure 1B). The range border establishes at an average dispersal mortality of 0.8, and a temperature value of 8. After reaching spatial equilibrium, the spatial distribution of dispersal rates shows a decaying exponential trend. The mutator value $m(\tau_{opt})$ shows no spatial pattern before range expansion, but rapidly increases once the species invades the landscape (Figure 1C). At the range core the mutation rate decreases in time. After 5000 generations of expansion, this mutation rate is on average six times higher at the range margin than in the core. As a result of this increased mutation rate and the high local dispersal rates, genetic diversity at the adaptation locus is also increased at the range front, compared to regions which have been populated for a longer time (Figure 1D and 1B). At the very range margin the genetic diversity at the adaptation locus is lower, in line with the lower population densities here (Figures 1D and 1A). The diversity in the initial core area stays at fairly high levels, due to high local dispersal rates. In contrast, the neutral genetic diversity is five- to tenfold larger and shows a clear spatial pattern of a founder effect, with diversity decreasing with spatial location (Figure 1F). The same pattern can be seen in the genetic diversity at the mutator locus (Figure 1E), but despite the clear increase of the mutation rate due to selection and adaptation (Figure 1C) the genetic diversity at this locus remains relatively high, both in space and in time. Similar to the mean dispersal rate, mutation rates decrease again when the populations are getting older (Figure 1C). However, the time lag between the local decrease of the dispersal rate and the decrease of the mutation rate $m(\tau_{opt})$ steadily increase across space. At the range border it takes 35,000 generations for the mutation rate to decrease to equilibrium values after the dispersal rate has decreased.

From the control simulations with fixed values at the dispersal locus, it shows that the average maximum mutation rates increase with increasing (fixed) dispersal rates. This further leads to increased range sizes (Figures 2A-C). Mutation rates positively affect invasion speed, with decreasing (fixed) values of mutation rate causing a decreasing invasion speed (Figure 2D).

The control simulations with full linkage of the mutator locus and the local adaptation locus lead to a faster increase of the mutation rate during the range expansion, with a much higher maximum mutation rate (Figure 3C). Consequently, the level of genetic diversity at the adaptation locus is higher (Figure 3D). In contrast to the unlinked case, the increase of the mutation rate leads to a steep decline in the genetic diversity at the mutator locus (Figure 3E). The local level of adaptation s_2 is close to one in all simulations, throughout simulation time and across the complete species' range.

Discussion

In this study we investigate whether an increase in the dispersal rate (and thus a potential increase of the invasion speed) under range expansion of a sexual species can lead to the evolution of a higher mutation rate at the adaptation locus. We observe an increase of the mutation rate, positively dependent on the dispersal rate. This co-evolution results in a faster range expansion and a larger ultimate species' range. The increase of the mutation rate occurrs despite the recombination in sexual populations due to the particular properties of spatial sorting during range expansion. After range establishment the evolved high mutation rates take an extensive period

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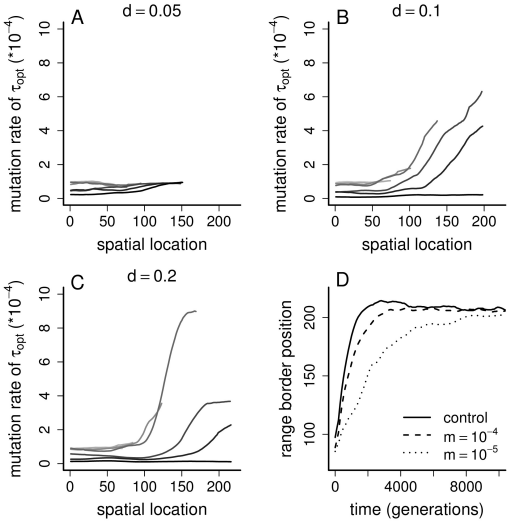

Figure 2: *The results of the control simulations, with the average values of the mutation rate (A-C) during and after range expansion across the gradient (horizontal axis) in time (gray scaling from light to dark, as time proceeds, which is given in a sequence of generations 100, 200, 500, 1000, 5000, 10000, 50000) under A. a fixed dispersal rate of 0.05, B. a fixed dispersal rate of 0.1, and C. a fixed dispersal rate of 0.2. In panel D the range border position in time (horizontal axis) is shown, averaged over 100 simulations for the original experiment with evolving mutation rate (here called 'control') and fixed mutation rates of* 10^{-4} *and* 10^{-5}.

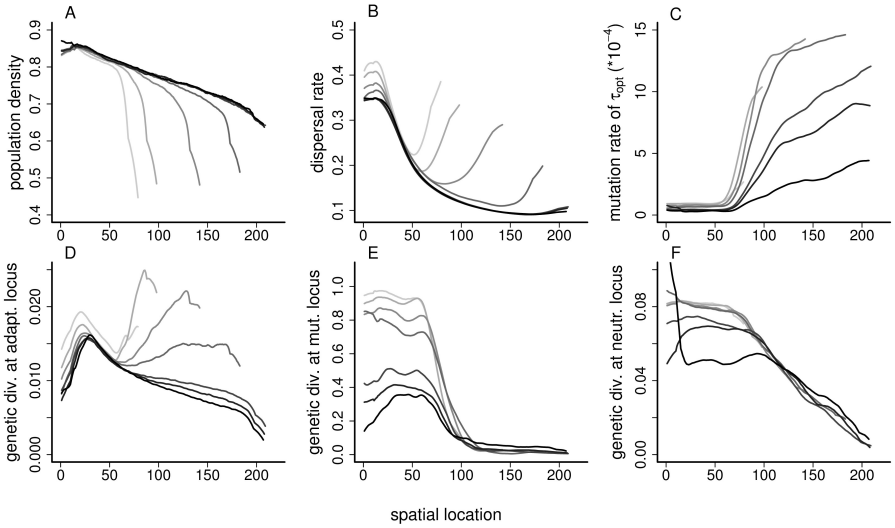

Figure 3: *The results of the control simulation with the fully linked mutator and adaptation loci. The average values over 100 simulations during and after range expansion across the gradient (horizontal axis) in time (gray scaling from light to dark, as time proceeds, which is given in a sequence of generations 100, 200, 500, 1000, 5000, 10000, 50000) of A. population density, B. dispersal rate, C. the mutation rate of the adaptation alleles, D. genetic diversity at the adaptation locus, E. genetic diversity at the mutator locus, and F. neutral genetic diversity, all measured as the variance in allele values. For reasons of clarity, a moving average with a window size of 20 has been applied (data were present in 10-generation intervals).*

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of time to decrease. This is the result of the limited selection against high mutation rates, and in addition correlated with the availability of genetic diversity at the mutator gene.

During range expansion the dispersal rate shows a clear signal of spatial sorting (Shine et al. 2011) and kin competition (Kubisch et al. 2013b), with good dispersers gathering at the expanding wave front (Phillips et al. 2010a). We observe that mutation rate can increase in combination with the increased dispersal rates and spatial variation, as experienced under range expansion. High dispersal rates, i.e. the immigration of many individuals, is expected to maintain a high local level of genetic variation (Holt & Barfield 2011), from which one would expect high levels of dispersal to be accompanied by a low local mutation rate. At the margin, however, relatedness amongst individuals increases at an advancing range front (Kubisch et al. 2013b), reducing both local genetic diversity and the diversity of immigrants. Under these conditions an increase in the mutation rate of local adaptation evolves, which allows faster adaptation to the experienced spatial variation in local temperature, causing a faster range expansion across the spatial gradient.

This result is particularly interesting as selection for optimum mutation rate is associated with asexual populations (Kimura 1967; Leigh Jr 1970; Leigh Jr 1973; Sniegowski et al. 2000). Indeed, selection only operates on the adaptation locus, favoring mutations that increase local adaptation. In sexual populations, strong linkage is required for the (advantageous) alleles at the adaptation locus and the (high) mutation rate allele at the mutator locus to be inherited together, and as such to lead to indirect selection at the mutator locus (Sniegowski 2000). In our study, however, these two loci are genetically unlinked. Because the colonization of an empty patch requires new mutations to cope with the novel temperature, this on average occurrs by individuals carrying high mutation rate alleles. A high initial population growth rate and the specific requirements for invaders in such a newly established population lead to high relatedness between individuals, where the beneficial allele at the adaptation locus and high mutation rate alleles at the mutator locus are essentially 'soft-linked' for lack of availability of low mutation rate alleles.

Both high rate signals of dispersal and mutation disappear with time, as anticipated. High dispersal rates are only favorable with frequent population extinctions and low dispersal mortality (Ronce 2007). Once the range border is stabilized a low dispersal phenotype is more advantageous in this region of high dispersal mortality. However, these slow dispersers by definition take some time to reach the area (genetic signature of range expansion, Phillips et al. 2010b; Cobben et al. 2015). In addition they are hindered by the high dispersal mortality.

Once a population is well-adapted and dispersal rates are low, a high mutation rate is selected against because it causes deleterious mutations (Sniegowski et al. 2000). We, however, observe that after the dispersal rate decreases there is an extensive time lag of thousands of generations in the decrease of the mutation rate. The mutation rates are not under direct selection, as argued before. The difference with the simulations in which the loci are linked is very clear during range expansion, where the rate of increase and level of the mutation rate are much higher than in the unlinked case. We therefore expected the mutation rate to decline faster with linked loci as well, but this is not the case. Additional control simulations (Appendix A in the Supplementary material) show that an increased selection against high mutation rates after range establishments has hardly any effect (Figure S1), but that the speed of decrease of the mutation rate is highly correlated with the level of genetic diversity at the mutator locus (Figure S2). Due to the indirect selection a very high level of genetic diversity is required in this

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unlinked case. Since this level is much lower in the linked case compared to the case where both loci are unlinked (Figure 3E), the slow decrease of the mutation rates under linked loci conditions can likely be explained by the lack of genetic diversity as well. Since selection could act directly in this case, the required levels of genetic diversity are here, however, likely lower.

Holt and Barfield (2011) investigated niche evolution at species' range margins and found that local evolution was hampered when source populations of immigrating individuals were at low density, as a result of the stochastic processes in such populations (Pearson et al. 2009; Bridle et al. 2010; Turner & Wong 2010). The likelihood of observing niche evolution was further affected by the mutation rate, where dispersal limited local evolution in the sink population under a higher mutation rate, because of the increased numbers of maladapted individuals from the source (Holt & Barfield 2011). They did, however, not allow the joint evolution of mutation rate and dispersal rate, but instead used fixed rates. As a result, the dispersal rate did not decrease after colonization, while the conditions in the sink population made its persistence dependent on the constant influx of (maladapted) individuals, both in contrast to the model presented here.

Our results can be affected by the used genetic architecture, where linkage between traits (Blows & Hoffmann 2005; Hellmann & Pineda-Krch 2007), polygeny, and the magnitude of mutations can be of importance in range dynamics (Kawecki 2000, 2008; Gomulkiewicz et al. 2010). The used mutation model of adding values to the inherited values resulted in mutations that were at most mildly deleterious, while the distribution of random mutations would invoke a stronger selection pressure (Sanjuán et al. 2004). In our study we investigated the evolution of mutation rates. Dealing with novel environmental conditions or increased evolvability is, however, not restricted to mutation rates, but can be modeled in different ways, e.g. an increased magnitude of the phenotypic effect of mutations (Griswold 2006), an epigenetic effect, the evolution of modularity (Kashtan et al. 2009), degeneracy (Whitacre & Bender 2010), or the evolution of generalism or plasticity (Lee & Gelembiuk 2008). In a control simulation an increase of the niche width, i.e. increased generalism, uncouples the link between mutation and dispersal rates, allowing for a faster expansion and a larger range. With a much smaller niche width, the range expansion is hampered because of the strong selection against dispersal, which also leads to lower established mutation rates (Figure S1). In addition, Kubisch et al. (2013b) showed that when dispersal is a means of adaptation, by tracking suitable conditions during periods of change, this can prevent genetic adaptation altogether. Which kind of local adaptation can be expected under specific ecological and environmental conditions is an interesting field of future investigation.

There is an ever-expanding pool of literature discussing the ecological and evolutionary dynamics of dispersal in the formation of species' ranges (reviewed in Kubisch et al. 2014). While individual-based models have recently largely extended our theoretical knowledge of interactions and evolution of traits during range expansion, empirical data have been restricted to a few well-known cases (Thomas et al. 2001; Phillips et al. 2006; Moreau et al. 2011). Increasing ecological realism in our models (Cobben et al. 2012a) can improve the predictability of theoretical phenomena, which can then be tested by data from field studies. So far, increased dispersal has been shown to increase invasion speeds (Thomas et al. 2001; Phillips et al. 2010a), affect the fate of neutral mutations (Travis et al. 2010), as well as the level of local adaptation (Kubisch et al. 2013a), and local population dynamics (Ronce 2007), and in addition causes strong patterns of spatial disequilibrium (Phillips et al. 2010b; Cobben et al. 2015).

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In this study we show new and unexpected consequences of the particular genetic properties of populations under spatial disequilibrium, i.e. the co-evolution of dispersal rates and mutation rates, even in a sexual species. This results in faster invasions and larger ultimate range sizes. In addition, the consequential local lack of genetic diversity maintains the mutation rates at a high level for a very long period of time. We conclude that range expansions can have important consequences for the evolution of mutation rates with possibly far-reaching ecological consequences concerning invasiveness and the adaptability of species to novel environmental conditions.

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References

1. Amler, K. et al. (1999). Die standardisierte populationsprognose (SPP): eine anwendung der zoologischen datenbanken am beispiel des NSG, Leutratal (Thüringen).

2. Bedau, M.A. & Packard, N.H. (2003). Evolution of evolvability via adaptation of mutation rates. Biosystems, 69, 143-162.

3. Beverton, R. & Holt, S. (1957). On the dynamics of exploited fish populations. Chapman and Hall.

4. Blows, M.W. & Hoffmann, A.A. (2005). A reassessment of genetic limits to evolutionary change. Ecology, 86, 1371-1384.

5. Bonte, D. et al. (2012). Costs of dispersal. Biol. Rev., 87, 290-312.

6. Bridle, J.R. et al. (2010). Why is adaptation prevented at ecological margins? New insights from individual-based simulations. Ecol. Lett., 13, 485-494.

7. Chen, I.C. et al. (2011). Rapid Range Shifts of Species Associated with High Levels of Climate Warming. Science, 333, 1024-1026.

8. Cobben, M.M.P. et al. (2011). Projected climate change causes loss and redistribution of genetic diversity in a model metapopulation of a medium-good disperser. Ecography, 34, 920-932.

9. Cobben, M.M.P. et al. (2012a). Landscape prerequisites for the survival of a modelled metapopulation and its neutral genetic diversity are affected by climate change. Landsc. Ecol., 27, 227-237.

10. Cobben, M.M.P. et al. (2012b). Wrong place, wrong time: climate change-induced range shift across fragmented habitat causes maladaptation and decreased population size in a modelled bird species. Glob. Change Biol., 18, 2419-2428.

11. Cobben, M.M.P. et al. (2015). Spatial sorting and range shifts: consequences for evolutionary potential and genetic signature of a dispersal trait. J. Theor. Biol.

12. Drake, J.W. et al. (1998). Rates of spontaneous mutation. Genetics, 148, 1667-1686.

13. Earl, D.J. & Deem, M.W. (2004). Evolvability is a selectable trait. Proc. Natl. Acad. Sci. U. S. A., 101, 11531-11536.

14. Excoffier, L. et al. (2009). Genetic Consequences of Range Expansions. Annu. Rev. Ecol. Evol. Syst., 40, 481-501.

15. Gomulkiewicz, R. et al. (2010). Genetics, adaptation, and invasion in harsh environments. Evol. Appl., 3, 97-108.

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16. Griswold, C. (2006). Gene flow's effect on the genetic architecture of a local adaptation and its consequences for QTL analyses. Heredity, 96, 445-453.

17. Hellmann, J.J. & Pineda-Krch, M. (2007). Constraints and reinforcement on adaptation under climate change: selection of genetically correlated traits. Biol. Conserv., 137, 599-609.

18. Hewitt, G.M. (1996). Some genetic consequences of ice ages, and their role in divergence and speciation. Biol. J. Linn. Soc., 58, 247-276.

19. Hill, J.K. et al. (2011). Climate change and evolutionary adaptations at species' range margins. Annu. Rev. Entomol., 56, 143-159.

20. Holt, R.D. & Barfield, M. (2011). Theoretical perspectives on the statics and dynamics of species' borders in patchy environments. Am. Nat., 178, S6-S25.

21. Kashtan, N. et al. (2007). Varying environments can speed up evolution. Proc. Natl. Acad. Sci. U. S. A., 104, 13711-13716.

22. Kashtan, N. et al. (2009). Extinctions in heterogeneous environments and the evolution of modularity. Evolution, 63, 1964-1975.

23. Kawecki, T.J. (2000). Adaptation to marginal habitats: contrasting influence of the dispersal rate on the fate of alleles with small and large effects. Proc. R. Soc. Biol. Sci. Ser. B, 267, 1315-1320.

24. Kawecki, T.J. (2008). Adaptation to marginal habitats. Annu. Rev. Ecol. Evol. Syst., 39, 321-342.

25. Kimura, M. (1967). On the evolutionary adjustment of spontaneous mutation rates. Genet. Res., 9, 23-34.

26. Körner, C. & Paulsen, J. (2004). A world-wide study of high altitude treeline temperatures. J. Biogeogr., 31, 713-732.

27. Kubisch, A. et al. (2013a). Predicting range shifts under global change: the balance between local adaptation and dispersal. Ecography, 36, 873-882.

28. Kubisch, A. et al. (2013b). Kin competition as a major driving force for invasions. Am. Nat., 181, 700-706.

29. Kubisch, A. et al. (2014). Where am I and why? Synthesizing range biology and the eco-evolutionary dynamics of dispersal. Oikos, 123, 5-22.

30. Kubisch, A. et al. (2010). On the elasticity of range limits during periods of expansion. Ecology, 91, 3094-3099.

31. Lee, C.E. & Gelembiuk, G.W. (2008). Evolutionary origins of invasive populations. Evol. Appl., 1, 427-448.

32. Leigh Jr, E.G. (1970). Natural selection and mutability. Am. Nat., 301-305.

33. Leigh Jr, E.G. (1973). The evolution of mutation rates. Genetics, 73, Suppl 73: 71.

34. Metzgar, D. & Wills, C. (2000). Evidence for the adaptive evolution of mutation rates. Cell, 101, 581-584.

35. Moreau, C. et al. (2011). Deep human genealogies reveal a selective advantage to be on an expanding wave front. Science, 334, 1148-1150.

36. Pearson, G.A. et al. (2009). Frayed at the edges: selective pressure and adaptive response to abiotic stressors are mismatched in low diversity edge populations. J. Ecol., 97, 450-462.

37. Phillips, B. et al. (2010a). Evolutionarily accelerated invasions: the rate of dispersal evolves upwards during the range advance of

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cane toads. J. Evol. Biol., 23, 2595-2601.

38. Phillips, B.L. et al. (2010b). Life-history evolution in range-shifting populations. Ecology, 91, 1617-1627.

39. Phillips, B.L. et al. (2006). Invasion and the evolution of speed in toads. Nature, 439, 803-803.

40. Poethke, H. J. et al. (1996). Gefährdungsgradanalyse einer räumlich strukturierten Population der Westlichen Beißschrecke (Platycleis albopunctata): ein Beispiel für den Einsatz des Metapopulationskonzeptes im Artenschutz. Zeitschrift für Ökologie und Naturschutz, 5, 229-242.

41. Ronce, O. (2007). How does it feel to be like a rolling stone? Ten questions about dispersal evolution. Annu. Rev. Ecol. Evol. Syst., 231-253.

42. Sanjuán, R. et al. (2004). The distribution of fitness effects caused by single-nucleotide substitutions in an RNA virus. Proc. Natl. Acad. Sci. U. S. A., 101, 8396-8401.

43. Shine, R. et al. (2011). An evolutionary process that assembles phenotypes through space rather than through time. Proc. Natl. Acad. Sci. U. S. A., 108, 5708-5711.

44. Sniegowski, P.D. et al. (2000). The evolution of mutation rates: separating causes from consequences. BioEssays, 22, 1057-1066.

45. Sniegowski, P.D. et al. (1997). Evolution of high mutation rates in experimental populations of E. coli. Nature, 387, 703-705.

46. Taddei, F. et al. (1997). Role of mutator alleles in adaptive evolution. Nature, 387, 700-702.

47. Thomas, C.D. et al. (2001). Ecological and evolutionary processes at expanding range margins. Nature, 411, 577-581.

48. Travis, J. et al. (2010). Mutation surfing and the evolution of dispersal during range expansions. J. Evol. Biol., 23, 2656-2667.

49. Turner, J.R. & Wong, H. (2010). Why do species have a skin? Investigating mutational constraint with a fundamental population model. Biol. J. Linn. Soc., 101, 213-227.

50. Whitacre, J. & Bender, A. (2010). Degeneracy: a design principle for achieving robustness and evolvability. J. Theor. Biol., 263, 143-153.