A gene-regulatory network model for density-dependent and sex-biased dispersal evolution during range expansions.

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Abstract

Eco-evolutionary dynamics of range expansions are of great interest in the context of global change. Range expansions are spatial phenomena and critically depend on organisms' dispersal abilities. Dispersal has a genetic basis, it can evolve, but also can be plastic to external environmental conditions and the internal state of an organism. Importantly, dispersal plasticity itself can evolve which has most often been studied theoretically with a focus on optimal reaction norms under equilibrium conditions. However, under rapidly changing conditions, the rate of dispersal plasticity evolution will impact eco-evolutionary dynamics of range expansions. Rates of evolution in turn depend on the genetic architecture of underlying traits. To elucidate this interplay, we develop an individual-based metapopulation model of the evolution of density-dependent and sex-biased dispersal during range expansions. We represent the dispersal trait as a gene-regulatory network (GRN), which can take population density and an individual's sex as an input and analyse emergent context- and condition-dependent dispersal responses. We compare dispersal evolution and ecological dynamics in this GRN model to a standard reaction norm (RN) approach under equilibrium metapopulation conditions and during range expansions. We find that under equilibrium metapopulation conditions, the GRN model produces emergent density-dependent and sex-biased dispersal plastic response shapes that match theoretical expectation of the RN model. However, during range expansion, the GRN model leads to faster range expansion because GRNs can maintain higher adaptive potential. Our results imply that, in order to understand eco-evolutionary dynamics in contemporary time, the genetic architecture of traits must be taken into account.

Introduction

Dispersal is central to understanding the ecology and evolution of spatially structured populations. This is because it has consequences for population dynamics (ecology) and gene flow (evolution) within such populations. Under equilibrium metapopulation conditions, the evolutionary causes of dispersal are known and, in general, dispersal evolution is driven by spatio-temporal variation in fitness expectation, kin structure and inbreeding avoidance (Bowler and Benton, 2005). Not only can dispersal evolve, but it is now also recognised that dispersal is not random (Lowe and McPeek, 2014) and can be associated with a suite of phenotypic characteristics, or "dispersal syndromes" (Stevens et al., 2014; Cote et al., 2022). Dispersal can also respond to the internal state (condition-dependent dispersal; Clobert et al. 2009) and the external environment (context-dependent dispersal) of an organism (Fronhofer et al., 2018). As a consequence, the shape of the density-dependent dispersal reaction norm has been discussed extensively in the theoretical literature (Travis and Dytham, 1999; Poethke and Hovestadt, 2002; Kun and Scheuring, 2006). This is because the assumed reaction norm shape has consequences for predictions of overall dispersal rates and metapopulation dynamics (Bocedi et al., 2012; Poethke et al., 2016; Hovestadt et al., 2010). Harman et al. (2020) review the shape of density-dependent dispersal reaction norms found in the empirical literature and examine its relevance for predicting the stability of metapopulations. They find that positive density-dependent dispersal and density-independent dispersal are most commonly reported (however, mostly in laboratory studies) and theoretically show that these shapes are associated with population stability. Sex-biased dispersal has also experienced long-standing interest by both theoreticians and empiricists, as recently reviewed in detail by Li and Kokko (2019). In this context, the importance of the ordering of life-cycle events and mating systems has been discussed, but Li and Kokko (2019) point out that more work is needed. Importantly, while the optimal plastic response of dispersal to both internal state (e.g., sex-biased dispersal; Gros et al. 2008; Gros et al. 2009; Li and Kokko 2019) and external conditions (e.g., density-dependent dispersal; Travis and Dytham 1999; Gyllenberg and Metz 2001; Poethke and Hovestadt 2002) has been studied theoretically and empirically, the underlying mechanisms that generate dispersal plasticity have not been modelled.

Broadly, the question of modelling mechanisms underlying dispersal plasticity falls into a broader discussion of representing the genetic architecture of dispersal and the consequences of such modelling choices (Saastamoinen et al., 2018). In general, explicit genetic architecture of dispersal, plastic or constitutive, is not considered and highly simplifying assumptions, such as a single quantitative locus or standard adaptive dynamics assumptions (small mutation effects and rare mutation), are common. These approaches are useful to derive optimal dispersal rates or plastic responses under equilibrium metapopulation conditions. However, the genetic architecture of dispersal, which includes the number of

underlying loci, their effects and how they interact with each other (e.g., epistasis and pleiotropy), needs to be considered to make predictions of eco-evolutionary dynamics during rapidly changing conditions, such as rapid habitat fragmentation or range expansion. Under such conditions of rapid change, the ecological consequences and feedbacks do not only depend on the evolutionary optima but also the rate of evolution (Fronhofer et al., 2023). For example the number of loci that govern an additive dispersal trait may modify how the rate at which a spatially structured population responds to habitat fragmentation (Saastamoinen et al., 2018) and also the dynamics of range shifts (Weiss-Lehman and Shaw, 2022). Further, in a previous study, Deshpande and Fronhofer (2022) model constitutive dispersal and local adaptation using non-additive gene-regulatory networks, and find that this leads to faster and accelerated range expansions due to increased mutational sensitivity in the local adaptation trait, with the genetic architecture of dispersal having no effect.

In the context of dispersal plasticity, theoretical work has been able to derive optimal reaction norms for density-dependent dispersal from first principles (Gyllenberg and Metz, 2001; Poethke and Hovestadt, 2002). Alternatively, a function value trait approach has been used in which different "loci" represent the trait value corresponding to a given environment (Dieckmann et al., 2006) or differing internal conditions. Finally, some studies have relied on polynomials if the function-valued trait approach was too computationally demanding (Deshpande et al., 2021). However, fundamentally, these optimal reaction norms must have an underlying molecular and genetic basis, that is, there must be a genotype-to-phenotype map that can process internal states and environmental conditions, leading to the emergence of plastic responses at the phenotypic level.

One such representation of a genotype-to-phenotype map is the gene-regulatory network (GRN) model proposed by Wagner (1994). Wagner's gene-regulatory network model assumes that a developmental phenotype is a vector of expression states of regulatory genes and the genotype is a matrix that contains the interactions between these genes. The Wagner model can be modified such that the regulatory genes can receive internal or environmental cues (Espinosa-Soto et al., 2011; Draghi and Whitlock, 2012; van Gestel and Weissing, 2016; Brun-Usan et al., 2021), and produce a quantitative phenotype (Draghi and Whitlock, 2012). Indeed, representing plasticity using gene-regulatory networks not only provides a mechanism for it (Chevin et al., 2022), but also reveals how phenotypic plasticity modifies evolvability by introducing developmental constraints (Draghi and Whitlock, 2012; Brun-Usan et al., 2021). For example, under conditions of rapid environmental change, Draghi and Whitlock (2012) model phenotypic plasticity of two correlated quantitative traits using a model combining GRN and quantitative genetics approaches. They find that plastic populations, which evolve in heterogeneous environments and have genes that receive an input from the external environment, exhibit evolvability in the direction of the environmental variation and adapt most easily. van Gestel and Weissing (2016) model bacterial sporulation using a GRN

approach, incorporating phenotypic plasticity by allowing the regulatory genes to receive environmental inputs, and find that a GRN approach allows for greater diversity in the response to novel conditions than a classical reaction norm approach, capturing a greater adaptive potential.

Building on this work, we posit that gene-regulatory networks can be used to model dispersal plasticity. Using this bottom-up approach, we here seek to understand whether processes at the molecular level, particularly, gene-regulation, yield a similar plastic response to the phenotypically predicted optimal reaction norm (Poethke and Hovestadt, 2002) in the case of density-dependent dispersal. Hence, we develop an individual-based metapopulation model, in which dispersal can evolve to be plastic to local population density. We represent the genetic architecture of density-dependent dispersal using a GRN, that takes as an input the local population density, regulatory genes process this input and finally output a continuous dispersal probability trait. We compare the GRN model to the theoretically expected reaction norm (RN) shape proposed by Poethke and Hovestadt (2002). Finally, we also investigate whether such a match to theoretical expectations holds if dispersal can additionally be sex-biased (Li and Kokko, 2019), that is, plastic to an organism's internal state.

To highlight how the genetic architecture of dispersal plasticity impacts predictions under conditions of rapid change, we model range expansions (Miller et al., 2020). How quickly organisms spread in space depends, besides on reproduction, centrally on dispersal. Since dispersal has a genetic basis (Saastamoinen et al., 2018) and can evolve (Ronce, 2007), potentially rapid evolution of dispersal ability can impact range expansion dynamics, but, vice versa, range expansions can also drive dispersal evolution by spatial sorting and selection, wherein more dispersive individuals end up at the range expansion front (Shine et al., 2011). It has also been shown that the speed of range expansions depends critically on whether dispersal increases or decreases with population density (Altwegg et al., 2013). In theoretical work, density-dependent dispersal can lead to accelerating range expansions (Travis et al., 2009), due to the evolution of decreased positive density-dependence of dispersal at range fronts. Yet, experimental studies have shown both, reductions (Fronhofer et al., 2017; Dahirel et al., 2021, 2022) and increases (Mishra et al., 2020) in positive density-dependence in dispersal during range expansion.

Thus, concretely in this study we address the following questions: 1) Does a more mechanistic GRN model of plasticity lead to the emergence of what is predicted from first principles at the RN level? 2) What are the ecological and evolutionary consequences of a more complex but mechanistic model under native equilibrium metapopulation conditions and during range expansions?

Model description

General description

We develop a discrete-time and discrete-space individual-based metapopulation model of a sexually reproducing, diploid species in which dispersal can evolve and be plastic to certain external cues and internal states. We represent the genetic basis of an individual's dispersal trait by a gene-regulatory network (GRN), that takes as input and processes external cues and internal states producing as an output its dispersal probability (Fig. 1 A, C). Particularly, we assume that the individuals can sense the local population density (density-dependent dispersal), or both the local population density and their own sex (density-dependent and sex-biased dispersal). In order to compare our model to the theoretically expected plastic response in the cases of density-dependent dispersal and density-dependent and sex-biased dispersal, we develop additional models (Fig. 1 B, D) using the reaction norm approach described in Poethke and Hovestadt (2002).

Individuals are initially present in the central 10×5 grid out of a 500×5 landscape, for 20000 generations (time-steps), in order for the dispersal genotypes to reach (quasi)-equilibrium. We then compare the plastic responses when dispersal plasticty is represented by a GRN (GRN model) and when it is represented by the theoretically expected reaction norm (RN model) from Poethke and Hovestadt (2002). To explore the consequences of these modelling choices in a scenario in which the evolutionary potential of dispersal is relevant, we assume that individuals with these optimised plastic responses can start range expansion in the x-dimension after 20000 generations. Therefore, the boundary conditions in the x-direction are reflecting for the first 20000 generations. In the y-direction, boundary conditions are periodic, hence the landscape resembles a hollow tube. Range expansions can take place till the expanding population has moved 245 patches from the central 10×5 patches in either direction along the x-dimension.

Life cycle

Dispersal

We assume that dispersal is natal. The probability that an individual disperses is given by its genetically encoded plastic response to local population density (Fig. 1 A–B) alone or local population density and sex (Fig. 1 C–D). The plastic response may either be encoded by a GRN or the threshold (Fig. 1 A, C) of a theoretically expected reaction norm (Fig. 1 B, D). If an individual disperses, one of the eight nearest neighbouring patches is chosen as the target patch. Dispersal costs (Bonte et al., 2012) are captured by the dispersal mortality μ, which is the probability that an individual dies while dispersing.

Reproduction and inheritance

After dispersal, individuals reproduce. The population dynamics in a patch follow the Beverton-Holt model (Beverton and Holt, 1957):

$$N_{x,y,t+1} = N_{x,y,t} \frac{\lambda_0}{1 + \alpha N_{x,y,t}}. \tag{1}$$

Here, λ_0 is the intrinsic growth rate and α is the intra-specific competition coefficient. A female first chooses a mate at random, and then produces a number of offspring drawn from Poisson distribution with mean $\frac{2\lambda_0}{1+\alpha N_{x,y,t}}$. The factor 2 corrects for that fact that only females reproduce and keeps λ_0 interpretable at the population level. The offspring inherit the alleles to the various parameters to the GRN or the threshold of the theoretically expected reaction norm, one from each parent at each locus. In the GRN model, we assume that mutation rate decreases in the first 5000 time steps and is constant after (Deshpande and Fronhofer, 2022). Since the GRN model has a large number of parameters, using larger mutation rates initially allows the fitness landscape to be coarsely explored quickly without the trait value getting stuck in a local optimum.

The parental generation then dies and is replaced by the offspring. In addition, we assume that there may be random patch extinctions every generation with a probability ϵ per patch. These extinctions represent density-independent, catastrophic external impacts.

GRN model

We assume that dispersal probability (d) is genetically encoded and plastic to external conditions and internal states. Particularly, we represent the genotype-to-phenotype map of dispersal probability using a gene-regulatory network (Deshpande and Fronhofer, 2022). Since in our model dispersal probability is plastic and and a quantitative trait, we follow the modifications made to the Wagner (1994) model by Draghi and Whitlock (2012). We assume that individuals can sense their external conditions (here, local population density but this can be extended to other cues such as predator presence) and can also receive internal cues (here, sex but this can also be extended to for example, body condition). These cues are then processed by a Wagner-like (Wagner, 1994) gene-regulatory network, which characterised by a vector of gene expression states at the end of a dynamic developmental process. The linear combination of these equilibrium gene-expression states is the dispersal phenotype.

More concretely, the gene-regulatory network has three layers: an input layer (which takes the external cue and/or internal state), a regulatory layer (vector of gene expression states) and an output layer (the trait) (van Gestel and Weissing, 2016). These layers are connected to each other by matrices of weights: the input weights ($\boldsymbol{U}_d$), regulatory weights ($\boldsymbol{W}_d$) and output weights ($\boldsymbol{V}_d$). Each gene has its own

properties: a slope ($\mathbf{r}_d$) and a threshold ($\boldsymbol{\theta}_d$). Therefore, the genotype of an individual is given by these weights and gene properties. The subscript d indicates that the trait under study is dispersal, but more generally such a GRN can be used to study plasticity in other quantitative traits. The regulatory genes process the external environmental cues or internal states ($\mathbf{x}_d$) that they receive as an input. In the case of density-dependent dispersal, organisms can, for example, sense reduced resource availability due to intra-specific competition or might have quorum sensing mechanisms (Fellous et al., 2012; Fronhofer et al., 2015). We assume that any such external cue of population density increases linearly with it, therefore, the GRN takes the local population density $N_{x,y,t}$ normalised by the expected equilibrium density of the Beverton-Holt model $\hat{N} = \frac{\lambda_0 - 1}{\alpha}$ as an input. Further, when dispersal can be sex biased, along with population density, the individual's sex (0 for females 1 for males) is taken as an input. This may represent sex hormones or any other sex-dependent developmental cue.

Thus, the developmental process for the dispersal trait is characterised by the following difference equation (Deshpande and Fronhofer, 2022) where $\mathbf{S_d}(I)$ is the vector of gene expression states at each iteration of the developmental process:

$$S_{d,i}(I+1) = \frac{2}{1 + \exp(-r_{d,i}(\sum_{j=1}^{j=m} U_{d,j,i} x_{d,j} + \sum_{k=1}^{k=n} W_{d,k,i} S_{d,k}(I) - \theta_{d,i})} - 1. \tag{2}$$

Therefore, the expression state of a gene is a sigmoid function of the input it receives from the environment and other genes (Siegal and Bergman, 2002) and can take values between -1 and 1. The equilibrium gene expression states $\mathbf{S}_d^*$ are obtained after $I = 20$ iterations. We discard GRNs that do not reach a fixed point steady state equilibrium by this time (Wagner, 1994). The dispersal probability is then calculated as:

$$d = \sum_{i=1}^{i=n} V_{d,i} * S_{d,i}. \tag{3}$$

RN model

Many different models have been used to represent density-dependent dispersal reaction norms. Travis and Dytham (1999), assume a threshold function, in which dispersal probability is zero below the threshold and increases linearly beyond it, and optimise the parameters representing this line. The theoretical model in Poethke and Hovestadt (2002) derives the optimal reaction norm of dispersal probability as a function of local population density to be a threshold function, which is zero below the threshold but has a saturating increase beyond it. Kun and Scheuring (2006) assume a sigmoid relationship in their model, which is represented by three parameters that are optimised. We here choose to use the model by Poethke and Hovestadt (2002) as a control because it is derived from first principles, and it has been

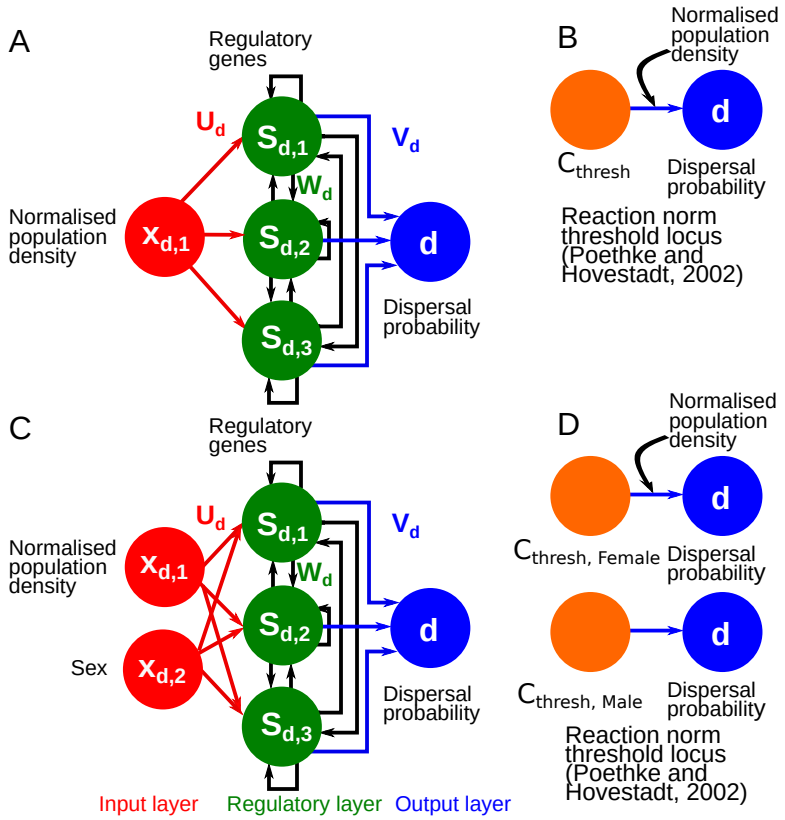

Figure 1: GRN (A, C) and RN (B, D) models for density-dependent (A–B) and density-dependent and sex-biased dispersal (C–D). The assumed GRN model has an input layer which is a vector $\mathbf{x}_d$ of external states or external cues, in our case, population density alone (A), and population density and sex (B). The regulatory genes receive this input via the input weights $\boldsymbol{U}_d$. Genes have expression states denoted by $\mathbf{S}_d$, and interactions between these genes are encoded by a regulatory matrix $\boldsymbol{W}_d$. The effects of these genes are encoded by the matrix $\boldsymbol{V}_d$. In the case of density-dependent dispersal, the RN model is represented by a single quantitative locus which is the threshold of the function derived by Poethke and Hovestadt (2002) and for density-dependent and sex biased dispersal, two loci with sex dependent expression encode the threshold. We compare both, evolution of dispersal plasticity and range expansion dynamics, between the reaction norm and GRN approaches.

shown to out-compete the other models in pairwise competition simulation experiments (Hovestadt et al., 2010). The threshold C_{thresh} is encoded by a single locus with two alleles. $\hat{N}$ is the expected equilibrium population density.

$$d = \begin{cases} 0 & 0 \leq \frac{N_{x,y,t}}{\hat{N}} < C_{thresh} \\ 1 - \hat{N}\frac{C_{thresh}}{N_{x,y,t}} & otherwise \end{cases} \tag{4}$$

$\frac{N_{x,y,t}}{\hat{N}}$ is the local population density normalised by the expected equilibrium population density. We also extend this to sex-biased and density-dependent dispersal by encoding two different threshold normalised densities as two loci, $C_{thresh,M}$ and $C_{thresh,F}$. $C_{thresh,M}$ is expressed if the individual is a male, and $C_{thresh,F}$ is expressed if the individual is female.

Analysis

We analyse both GRN and RN models for density-dependent dispersal (GRN DDD and RN DDD) alone and for density-dependent and sex-biased dispersal (GRN DDD + sex bias and RN DDD + sex bias). Model parameters are found in Table 1. Since dispersal evolution ultimately is driven by costs and benefits, we run 50 replicate model simulations for dispersal costs $\mu = 0.01, 0.1, 0.3$ and a random patch extinction risk of $\epsilon = 0, 0.05, 0.1$.

Results and discussion

Evolution of the density-dependent dispersal plastic response in the GRN and RN models.

Our model shows that the plastic response of a trait (here, dispersal) can indeed emerge from cellular and molecular processes, namely gene-regulatory network dynamics (Fig. 2). Thus, this is an instance of a complex system model which leads to the emergence of trait plasticity.

Poethke and Hovestadt (2002) derived from first principles, in metapopulations with discrete-time logistic dynamics (as assumed in our individual-based model), that the optimal plastic response of dispersal to local population density is a threshold function, in which there is no dispersal below a threshold, but a saturating increase beyond it. Fig. 2 shows that the optimal density-dependent dispersal plastic response produced by the GRN DDD model matches this theoretically expected reaction norm (Poethke and Hovestadt, 2002). However, the concurrence between the GRN DDD and the Poethke and Hovestadt (2002) RN DDD model only holds for those population densities that occur during the course of the simulation, since these are the conditions for which the trait can be optimized. Therefore, Fig. 2 shows the plastic response only at those population densities that occur frequently in each scenario. The histograms of densities that occur during the equilibrium metapopulation phase of the simulation can be found in Fig. S1.

Our results also contribute to the discussion on the shapes of functions assumed while modelling density-dependent dispersal reaction norms in individual-based simulations (Bocedi et al., 2012; Poethke et al., 2016; Hovestadt et al., 2010). Various density-dependent dispersal reaction norm shapes have been assumed so far, as discussed above. Our results concur with Hovestadt et al. (2010), supporting the shape of the plastic response (threshold function) derived by Poethke and Hovestadt (2002). Hovestadt et al. (2010) show that the theoretically expected reaction norm shape (Poethke and Hovestadt, 2002) wins in pairwise competition simulation experiments between individuals with genotypes encoding the various reaction norm shapes described when dispersal costs are not too high. We re-capture these results

Table 1: Model Parameters/Variables

Model Parameter/Variable	Description	Values
$N_{x,y,t}$	Population density in the patch x, y at time t	dynamical
λ_0	Intrinsic growth rate in Beverton-Holt model	2
α	Intra-specific competition coefficient in Beverton-Holt model	0.01
μ	Dispersal mortality	0.01, 0.1, 0.3
ϵ	Local patch extinction probability	0, 0.05, 0.1
m_{min}	Mutation rate at equilibrium	0.0001
m_{max}	Mutation rate at the beginning	0.1 for GRN, $m_{max} = m_{min}$ for others
σ_m	Effect size (standard deviation) of mutations	0.1
$\mathbf{x}$	Vector of inputs to the GRN	in simulation
n	Number of regulatory genes	4
$\mathbf{S}_{d,I}$	Vector of expression states of regulatory genes at iteration I	in simulation
$\boldsymbol{U}_d$	$m \times n$ matrix with each element U_{ji} representing the connection between the input j and gene i	evolves, initialised from a normal distribution with sd = 1
$\boldsymbol{W_d}$	$n \times n$ matrix with each element W_{ki} representing the connection between the gene k and gene i	evolves, initialised from a normal distribution with sd = 1
$\boldsymbol{V}_d$	$1 \times n$ matrix with each element V_i representing the connection between the gene k and the output	evolves, initialised from a normal distribution with sd = 1
$\boldsymbol{\theta}_d$	Thresholds of regulatory genes	evolves, initialised from a normal distribution with sd = 1
$\mathbf{r}_d$	Slopes of regulatory genes	evolves, initialised from a normal distribution with sd = 1
C_{thresh}	Threshold for density-dependent dispersal in RN model	evolves, initialised from a uniform distribution between 0 to 1
$C_{thresh,F}$	Threshold for density-dependent and sex-biased dispersal in RN model for females	evolves, initialised from a uniform distribution between 0 to 1
$C_{thresh,M}$	Threshold for density-dependent and sex-biased dispersal in RN model for males	evolves, initialised from a uniform distribution between 0 to 1

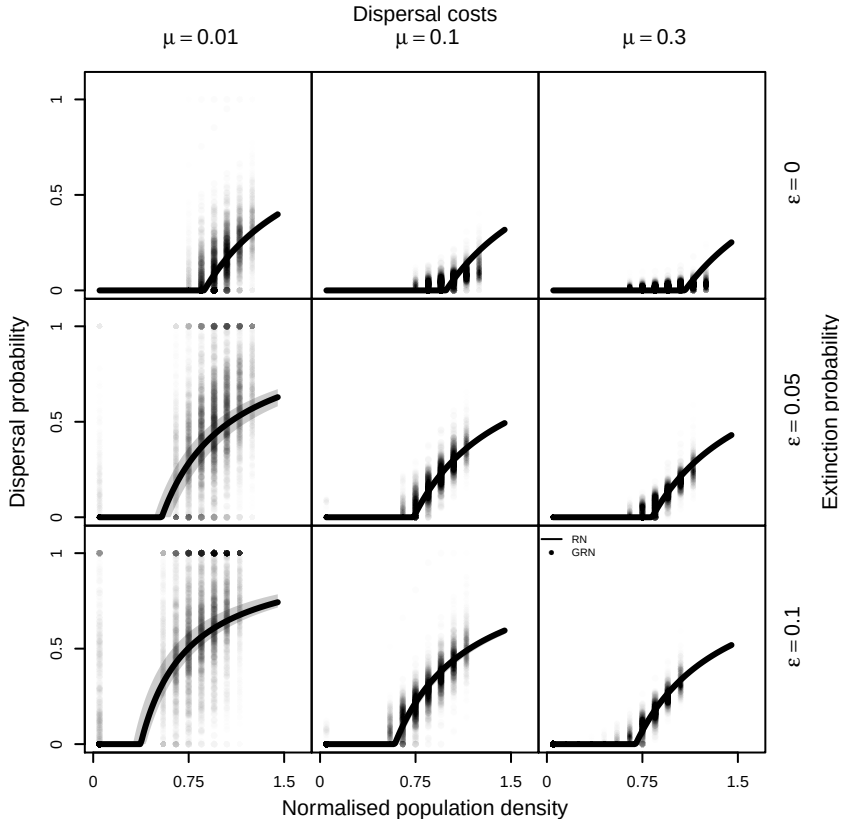

Figure 2: Comparison between density-dependent dispersal plastic response in the GRN and RN models. Dispersal costs increases from left to right ($\mu = 0.01, 0.1, 0.3$), from top to bottom, extinction probability increases ($\epsilon = 0, 0.05, 0.1$). ES dispersal probability as a function of population density normalised by the expected equilibrium population density ($\hat{N} = \frac{\lambda_0 - 1}{\alpha}$). The black lines lines represent the median, and shaded region the inter-quartile range of the ES reaction norms in the RN model from Poethke and Hovestadt (2002). The black points represent the calculated GRN output for 1000 randomly chosen individuals at the end of 20000 time steps. The transparency of the points is weighted by the frequency of occurrence of the population density so as to only represent the GRN plastic response for those densities that occur during the simulation. Fixed parameters: $\lambda_0 = 2$ and $\alpha = 0.01$. Number of regulatory genes $n = 4$.

without the need for pairwise competition experiments, since the GRN approach allows for a flexibility of density-dependent dispersal plastic response shapes.

More importantly, the GRN model also provides a mechanistic basis for plasticity. While the GRN is likely to be more complicated in reality, the different layers of the gene-regulatory network that produce the plastic response can be interpreted biologically. For example, the input layer represents the external environmental cue, population density, which can be sensed as, for example, the reduced availability of resources, or other chemical and mechanical cues (Fellous et al., 2012; Fronhofer et al., 2015) resulting from larger local density of individuals. The regulatory layer can be interpreted as the gene expression states in cells of a relevant developmental stage that respond to local population density. A very clear example of this is the case of dispersal polyphenism in pea aphids, a system in which female winged

phenotypes specialise in dispersal as opposed to un-winged phenotypes (Brisson et al., 2010). Finally, the output weights are the linear downstream effects of this developmental GRN, including structural genes and metabolic pathways.

Evolution of the density-dependent and sex-biased dispersal plastic response in the GRN and RN models.

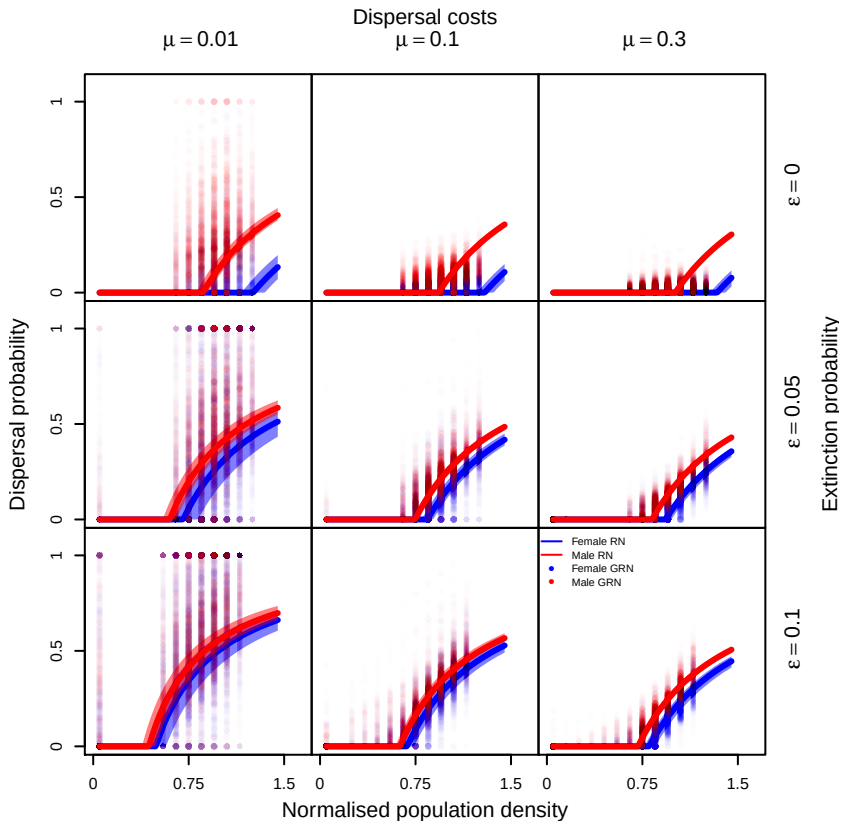

Figure 3: Comparison between density-dependent dispersal and sex-biased plastic response in the GRN and RN models. Dispersal costs increases from left to right ($\mu = 0.01, 0.1, 0.3$), from top to bottom, extinction probability increases ($\epsilon = 0, 0.05, 0.1$). ES dispersal probability as a function of population density normalised by the expected equilibrium population density ($\hat{N} = \frac{\lambda_0 - 1}{\alpha}$). The red and blue lines represent the ES reaction norms for males and females in the RN model from Poethke and Hovestadt (2002). The red and blue points represent the calculated GRN output for 1000 randomly chosen individuals at the end of 20000 time steps corresponding to male and female sex respectively. The transparency of the points is weighted by the frequency of occurrence of population density so as to only represent the GRN plastic response for those densities that occur during the simulation. Fixed parameters: $\lambda_0 = 2$ and $\alpha = 0.01$. Number of regulatory genes $n = 4$.

Dispersal may not only depend on the external context but also on internal conditions (Clobert et al., 2009), such as the sex of the potentially dispersing individual. Fig. 3 shows that including the input of an internal condition, sex, along with local population density, as explored in the previous subsection, leads to the emergence of a density-dependent and sex-biased dispersal plastic response. Again, this matches

the theoretically expected plastic response and the additional information of sex does not change the shape of the density-dependent dispersal reaction norm. Instead, the threshold is lower for males than for females leading to male-biased dispersal in our simulations.

Sex-biased dispersal is known to evolve due to asymmetry in limiting resources, kin competition, or inbreeding depression (Li and Kokko, 2019). In a similar simulation model by Gros et al. (2009), particularly one incorporating demographic stochasticity, it was shown that male-biased dispersal evolves because of between patch variation in the number of available females. The expected fitness of both males and females in a patch decreases with a smaller female population size since females actually bear the offspring. Therefore, the effect of demographic stochasticity dominates in patches with low female density. However, in a random mating system, males also experience a greater between patch variation in fitness depending on the female population size because of the variation in the availability of mates, which leads to an asymmetry in limiting resources, that is, mates, promoting male-biased dispersal.

Genetic architecture of dispersal plasticity impacts eco-evolutionary dynamics of range expansion

Under equilibrium metapopulation conditions, we have shown that both density-dependent dispersal and sex-biased dispersal reaction norms readily evolve in gene-regulatory network models and match theoretical predictions. But what are the ecological consequence of such plastic responses under novel conditions. In order to answer this questions, after 20000 time steps, we allow for range expansions in both, the GRN an RN models. We find that range expansion speeds are greater in the GRN model overall when local density alone (Fig. 4), and both local density and sex define dispersal decisions (Fig. 5). In general the difference between range expansion dynamics in the two models is greater when dispersal costs are low and rate of external patch extinctions is high (Fig. 4–5).

These patterns of faster range expansions speeds in the GRN model and the conditions of low dispersal mortality and extinction probability that produce them can be understood on the basis of the evolutionary history of the metapopulation before range expansions begin. Particularly, for an equilibrium metapopulation, Fig. S1–S2 show that individuals experience a set of conditions of population density that are around their expected equilibrium density $\hat{N}$. Even when there are patch extinctions, there is a bimodal distribution of population sizes, with one peak close to extinction and another at carrying capacity. This prevents optimisation by selection of the density-dependent dispersal and density-dependent and sex biased dispersal plastic response in the GRNs under densities that do not occur in the equilibrium metapopulation (Fig. S3–S4). At the same time, this implies that genetically based phenotypic variation in the plastic response can be maintained for these non-occurring density conditions, since individuals

are not exposed to them. Essentially, these parts of the plastic response in the GRN model are "hidden" to selection.

Under conditions of range expansion, however, dispersal evolution is known to be driven by the spatial sorting (Shine et al., 2011) of genetically encoded phenotypic variation at the range expansion front. Since in the reaction norm approach, selection optimises the threshold of the Poethke and Hovestadt (2002) function, variation is not maintained at low population densities. However, in the GRN model ample variation compared to the RN model (SI Fig. S3–S4) is maintained at those conditions that do not occur in equilibrium metapopulation conditions. This variation is then sorted, leading to evolution of greater dispersal rates at the range expansion front (SI Fig. S5–S6). Travis et al. (2009) have previously shown that accelerating invasions can be found in models assuming sigmoid density-dependent dispersal reaction norms. They argue that this allows them to have a relatively flexible function, where not just a threshold, as in Poethke and Hovestadt (2002), but also other properties of the reaction norm can evolve. We reconcile the two approaches because, at the equilibrium metapopulation level without assuming a particular shape of the plastic response, on an average the shape that emerges is the one predicted by Poethke and Hovestadt (2002) but the GRN approach has greater evolutionary flexibility as in Travis et al. (2009).

Interestingly, the possibility for sex-biased and density-dependent dispersal increases the difference between the dynamics of the RN model and the GRN model. Generally, male-biased dispersal (Fig. 3) slows down range expansions (Miller et al., 2011) due to the fact that males cannot reproduce by themselves, implying that population, hence range expansion dynamics are female limited. Thus, the availability of variation at densities that do not occur in equilibrium metapopulation conditions in the GRN model further amplifies differences between the two models relative to density-dependent dispersal alone.

General discussion

In summary, we have developed a model for density-dependent and sex-biased dispersal that assumes that dispersal results from the effects of a gene-regulatory network. We find that under conditions that are experienced in equilibrium metapopulations, the emergent predicted plastic response matches existing theoretical predictions. We then compare range expansion dynamics between a GRN and an RN model and find that the GRN model leads to faster range expansions because of the availability of important cryptic variation.

The theoretical literature usually uses highly simplified representations of the genetic architecture of traits like dispersal, most often only representing them at the level of the phenotype (Saastamoinen

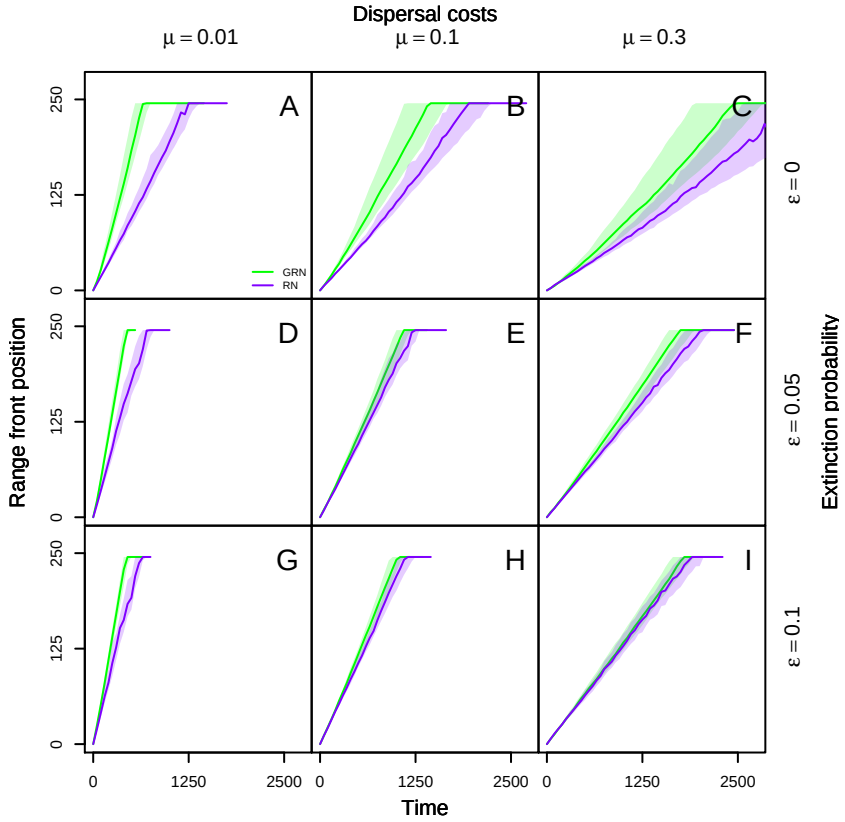

Figure 4: Range expansion dynamics in GRN vs RN model for DDD. Dispersal costs increase from left to right ($\mu = 0.01, 0.1, 0.3$), from top to bottom, extinction probability increases ($\epsilon = 0, 0.05, 0.1$). We plot the median and quartiles of range front position as a function of time for the GRN model and RN model. The range front is defined as the farthest occupied patch from the range core. Fixed parameters: $\lambda_0 = 2$ and $\alpha = 0.01$. Number of regulatory genes $n = 4$.

et al., 2018). Particularly, adaptive dynamics approaches, which assume small mutation effects and rare mutations, allow for optimal traits or reaction norms to be derived, analytically or by means of simulation, as a function of ecological equilibria (Govaert et al., 2019). Further, in simulations similar to ours, one quantitative locus with additive effects is often assumed (Saastamoinen et al., 2018). On the other hand, studies of genetic architecture rarely make ecological conditions explicit, with abstract representation of selection on traits by assuming a fitness function that is a priori defined rather than a result of underlying ecological processes (e.g., studies using the Wagner model; Wagner 1994). These approaches have been useful in highlighting key properties of genotype-to-phenotype relationship, such as robustness. Few studies highlight the advantage of incorporating both explicit ecological dynamics and genetic architectures. A notable exception is, for example, van Gestel and Weissing (2016), who compare GRN and RN approaches for bacterial sporulation, and show the GRN approaches maintain greater diversity of plastic responses under novel conditions.

In our study, we recapture the theoretically expected and known phenotypic relationships between

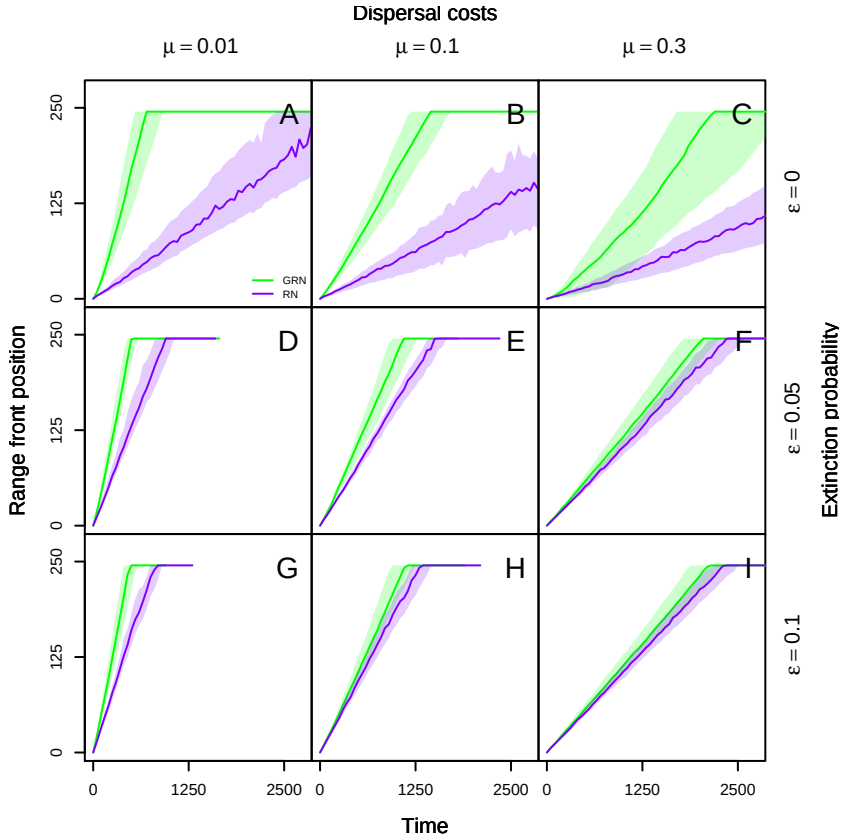

Figure 5: Range expansion dynamics in GRN vs RN model for DDD and sex bias. Dispersal costs increase from left to right ($\mu = 0.01, 0.1, 0.3$), from top to bottom, extinction probability increases ($\epsilon = 0, 0.05, 0.1$). We plot the median and quartiles of range front position as a function of time for the GRN model and RN model. The range front is defined as the farthest occupied patch from the range core. Fixed parameters: $\lambda_0 = 2$ and $\alpha = 0.01$. Number of regulatory genes $n = 4$.

population density and dispersal (Poethke and Hovestadt, 2002), confirming the validity of our approach. Importantly, under novel, low-density conditions experienced during range expansions, the differences observed between expansion dynamics in the different models make clear that approaches based on reaction norms may not be able to predict eco-evolutionary dynamics under novel conditions.

Our results underline the relevance of understanding genotype-to-phenotype (GP) maps for eco-evolutionary dynamics (Melián et al., 2018; Fronhofer et al., 2023), particularly for dispersal (Saastamoinen et al., 2018) and its response to internal and external cues (Clobert et al., 2009). While empirical evidence supporting our work is scarce, Brisson et al. (2010) showed differences in gene expression between winged and un-winged phenotypes of pea aphids, particularly in their wing development gene-regulatory network. In this system, winged morphs are often induced due to crowding and the relative production of dispersive and non-dispersive (reproductive) females depends on developmental cues, including crowding. More generally, our GRN approach can be used to understand how dispersal responds to other internal (e.g., infection state; Iritani and Iwasa 2014 or body condition; Baines et al. 2020) and external cues, for

example presence of parasites (Deshpande et al., 2021) or predators (Poethke et al., 2010).

GRN models and models of GP maps often use highly abstract representation of the environment (for example, Draghi and Whitlock 2012) and gene expression as phenotype under selection (for example Espinosa-Soto et al. 2011). These approaches have been useful in defining, for example, how evolvability of phenotypes is linked with phenotypic plasticity (van Gestel and Weissing, 2016) and the alignment between genetic, environmental perturbations and direction of selection, and how this impacts evolvability in multi-trait systems (Draghi and Whitlock, 2012; Brun-Usan et al., 2021).

However, in an eco-evolutionary framework (Govaert et al., 2019; Fronhofer et al., 2023), ecological interactions define selection on a trait. Ecological dynamics also define the trait that is under selection. Therefore, considering gene expression as phenotype directly under selection may not always be appropriate, and gene expression state to phenotype map must be included (Chevin et al., 2022). This is relevant because for example, the association of extremes of gene-expression (Rünneburger and Rouzic, 2016) with increased mutational sensitivity (decreased robustness) is actually reversed (Deshpande and Fronhofer, 2022). Further, while such a map is likely to be more complex than our assumed linear gene expression to phenotype map, approaches such as ours and that of van Gestel and Weissing (2016) also narrow the range of possible environments under native conditions and also help define phenotypes under selection that are ecologically informed.

The latter point becomes clear when considering our results on range expansion dynamics. Taking into account both genetic architecture and the ecological conditions that shape the evolution of dispersal plasticity, the GRN model leads to maintenance of variation in conditions (densities) that are not very frequent under equilibrium metapopulation conditions. This variation is then spatially sorted (Shine et al., 2011) during range expansion. However, in the RN approach, this maintenance of variation under equilibrium metapopulation conditions does not happen, since only the threshold to the reaction norm is under selection. We see the consequences of the spatial sorting of dispersal in the fact that range expansions are generally faster in GRN approaches, when dispersal is density-dependent alone, and sex-bias only increases the difference between the two models. This has previously been discussed in the literature as a form of cryptic variation particularly "hidden reaction norms" (Schlichting, 2008), which represents differences in genotypes that are not normally expressed at phenotypic level but might be expressed if the genotype is perturbed due to mutation or recombination, but also when the environment is perturbed. Our results are similar to the findings of van Gestel and Weissing (2016) who show that in their GRN model the release of cryptic variation in native environments can lead to more adaptive plastic responses in novel conditions.

Empirical studies of gene-regulation in a dispersal context remain rare. Yagound et al. (2022) have shown gene expression differences using mRNA sequencing in the brains of the invasive Australian cane

toad in few genes. In their study, dispersal-related genes generally showed elevated expression at the range front. This system and associated life-history and physiological changes is particularly well studied in terms of range expansion dynamics (Phillips et al., 2006; Perkins et al., 2013). Other examples include wing polyphenism in pea aphids (Brisson et al., 2010), and dispersal in yellow-bellied marmots (Armenta et al., 2019). This relative scarcity of empirical studies, together with the relatively important effects predicted by our model, clearly call for more work, both empirical and theoretical to understand how genotype-phenotype maps impact eco-evolutionary dynamics.

Author contributions

JND and EAF conceived the study. JND developed and analysed the models in collaboration with EAF. JND wrote the manuscript in collaboration with EAF.

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Data availability

Simulation code is available via GitHub and Zenodo (DOI: https://doi.org/10.5281/zenodo.8160132).

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