Supporting Information. McManus, L.C., E.W. Tekwa, D.E. Schindler, T.E. Walsworth, M.A. Colton, M.M. Webster, T.E. Essington, D.L. Forrest, S.R. Palumbi, P.J. Mumby, and M.L. Pinsky. 2021. Evolution reverses the effect of network structure on metapopulation persistence. Ecology.

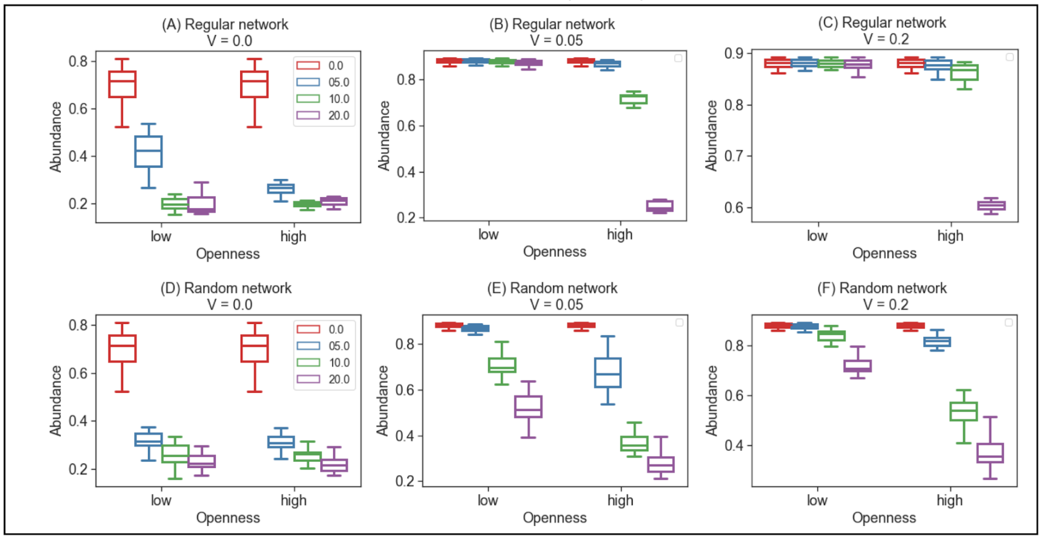
Appendix S1.

This PDF file includes:

Section S1: Additional figures
Section S2: Derivation of immigration and gene flow terms
Section S3: Alternative eco-evolutionary model formulation with quadratic fitness

Section S1. Additional figures.

End of constant temperature period



End of increasing temperature period

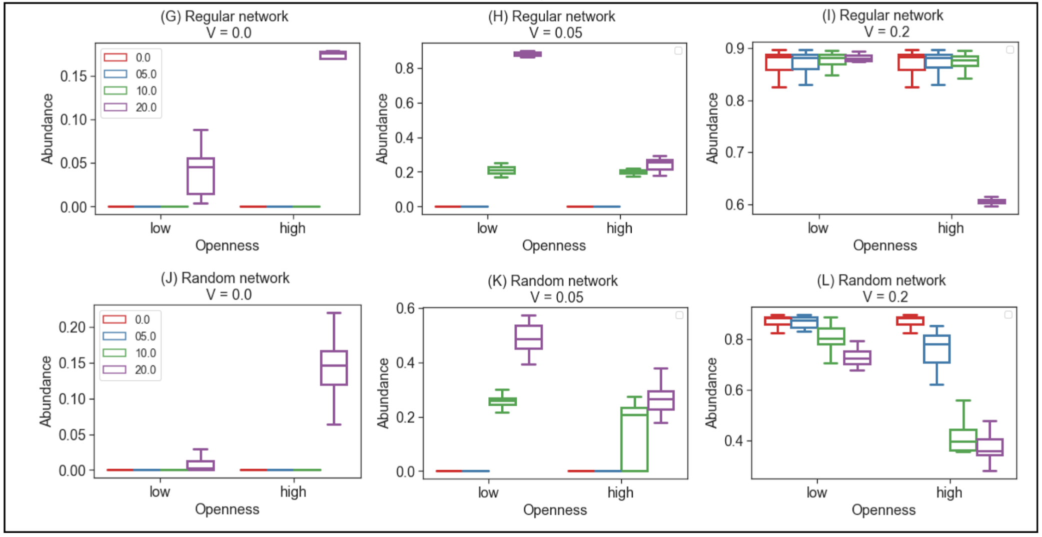
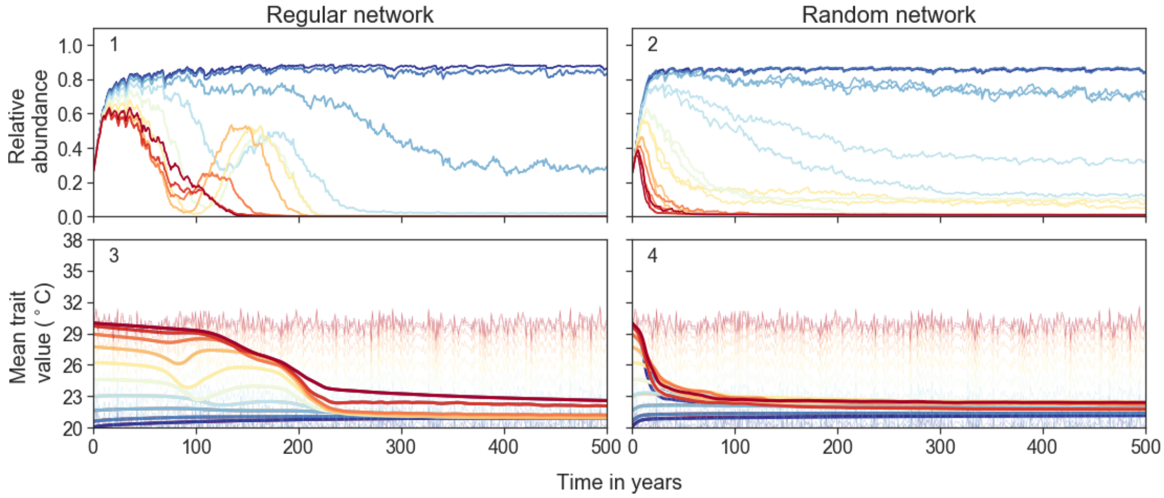
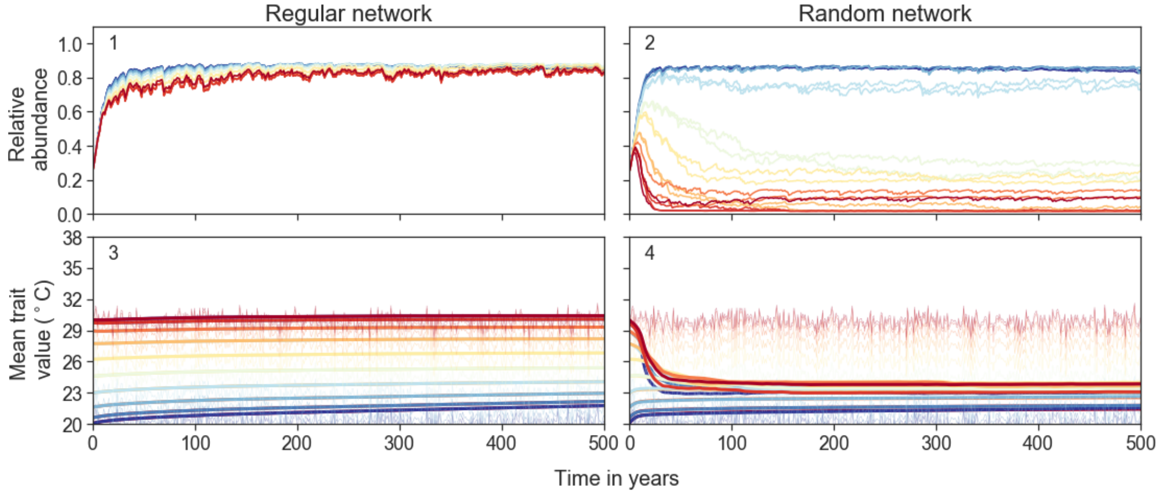


Figure S1. Evolutionary capacity dictates whether increasing steepness of the environmental gradient is beneficial or detrimental to the network. Final mean abundance by environmental steepness gradient: 0 °C (red), 5 °C (blue), 10 °C (green) and 20 °C (purple). Results are shown for the end of the constant temperature period (A-F) and the temperature increase period (G-L) averaged across 20 iterations. Low openness condition was γ=0.14 and high openness condition was γ=1.0.

(A) Constant temperature
V = 0.0 & $\gamma = 1.0$



(B) Constant temperature
V = 0.06 & $\gamma = 1.0$



(C) Increasing temperature
V = 0.2 & $\gamma = 1.0$

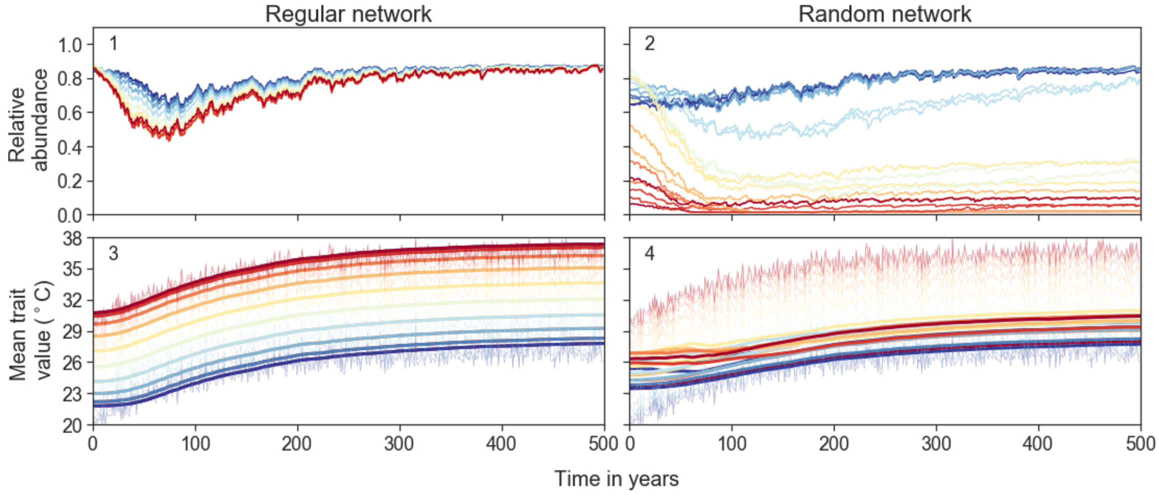


Figure S2. Representative trajectories under different levels of relative abundance and average trait value by patch for regular and random networks under high openness (γ=1.0) and different levels of additive genetic variance. Simulations during constant temperature with no genetic variance (V=0) (A), constant temperature with low genetic variance (V=0.06) (B), and increasing temperature with high genetic variance (V=0.2). -Trajectories are colored by relative patch temperature, where warmer and cooler colors represent higher and lower temperatures, respectively. Lines are mean trajectories averaged across 20 runs. Translucent lines in the bottom row are the temperature time series.

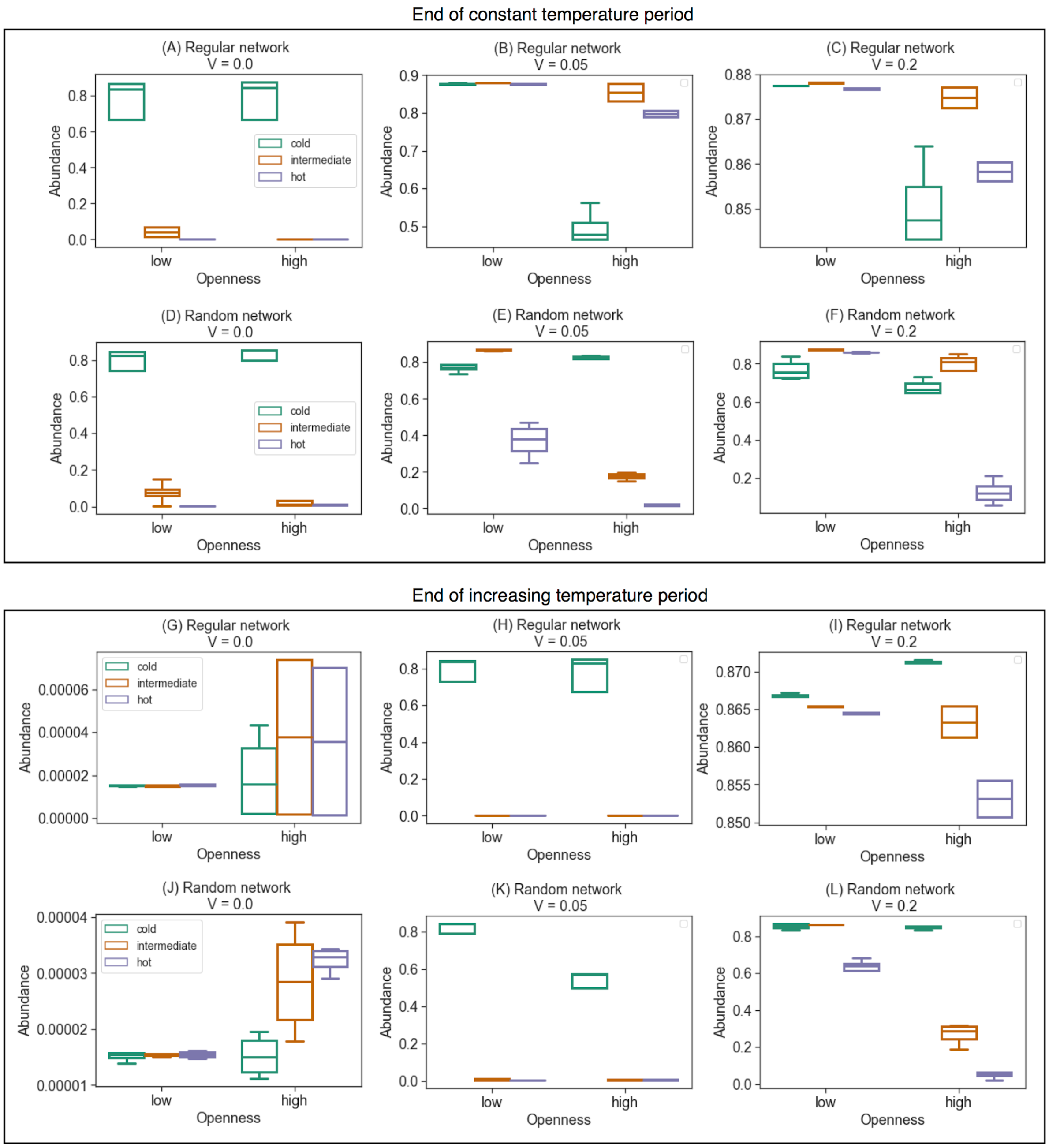


Figure S3. Hot and intermediate patches reach lower abundance in random networks. Final mean abundance of the four coldest (green), intermediate (orange) and hottest (purple) patches in regular and random networks. Results are shown for the end of the constant temperature period (A-F) and the temperature increase period (G-L) averaged across 20 iterations. Low openness condition was γ=0.14 and high openness condition was γ=1.0.

Section S2. Derivation of immigration and gene flow terms

S2.1 Immigration

At the current time t , site i has relative abundance $N_i(t)$. Let β be the effective fecundity rate such that offspring are produced at rate $\beta N_i(t)$ at each site. Let connectivity matrix $\mathbf{D}$ contain the connection strengths among sites such that element D_{ij} is the probability of offspring reaching site i from site j. Focusing only on deterministic dispersal (and ignoring local population growth and stabilizing selection), the relative abundance due to immigration after a very short period of time, τ, is

$$N_i(t+\tau) = N_i(t) + \tau(1 - N_i(t))\beta \sum_j \mathrm{D}_{ij} N_j(t) \tag{S1}$$

Here, $(1 - N_i(t))$ is a density dependence term such that recruitment at a site slows as relative abundance approaches 1. (Note that $(1 - N_i(t))$ is equivalent to $\frac{K - N_i(t)}{K}$ if the carrying capacity, K, is set to 1.)

Using big O notation, the Taylor series expansion of $N_i(t+\tau)$ can be written as

$$N_i(t+\tau) = N_i(t) + \tau \left[\frac{\mathrm{d}N_i}{\mathrm{d}t}(t)\right] + \mathcal{O}(\tau^2), \tag{S2}$$

where $\mathcal{O}(\tau^2)$ signifies higher order terms. By combining equations Eqs. S1 and S2, we can solve for $\frac{\mathrm{d}N_i}{\mathrm{d}t}(t)$ as

$$\frac{\mathrm{d}N_i}{\mathrm{d}t}(t) = (1 - N_i(t))\beta \sum_j \mathrm{D}_{ij} N_j(t) + \mathcal{O}(\tau). \tag{S3}$$

Letting $l_i = \beta \sum_j \mathrm{D}_{ij} N_j(t)$ and τ go to 0, the instantaneous change in abundance from immigration becomes $l_i(1 - N_i(t))$, which is the second term in Eq. 1 from the main text. Note that we drop (t) in the main text for simplicity.

S2.2 Gene flow

At the current time step, *t*, site i has mean trait value $z_i(t)$. From the previous section, we know that the increase in abundance at site i after a short duration τ that is attributed to new individuals is $\tau l_i(1 - N_i(t)) + \mathcal{O}(\tau^2)$(Eqs. S1 and S2) . Based on the migrant pool model of colonization (Slatkin, 1977; Hanski et al., 2011), the mean trait value at site i of immigrants with abundance $\tau l_i(1 - N_i(t)) + \mathcal{O}(\tau^2)$ before density dependence is

$$z_i^c(t) = \frac{\beta \sum_j \mathrm{D}_{ij} N_j(t) z_j(t)}{l_i}. \tag{S4}$$

To calculate the new mean trait value after a short time period τ, we need to average the current trait weighted by the relative abundance of individuals (local+immigrant). As such, the mean trait value due to gene flow after duration τ is:

$$z_i(t+\tau) = \frac{N_i(t)}{N_i(t) + \tau l_i(1 - N_i(t))} z_i(t) + \frac{\tau l_i(1 - N_i(t))}{N_i(t) + \tau l_i(1 - N_i(t))} z_i^c(t). \tag{S5}$$

The Taylor series expansion of $z_i(t+\tau)$ can be written as

$$z_i(t+\tau) = z_i(t) + \tau \left[\frac{\mathrm{d}z_i}{\mathrm{d}t}(t)\right] + \mathcal{O}(\tau^2). \tag{S6}$$

We can then combine Eqs. S5 and S6 and solve for $\frac{\mathrm{d}z_i}{\mathrm{d}t}(t)$ as

$$\frac{\mathrm{d}z_i}{\mathrm{d}t}(t) = \frac{z_i(t+\tau) - z_i(t)}{\tau} + \mathcal{O}(\tau), \tag{S7}$$

$$\frac{\mathrm{d}z_i}{\mathrm{d}t}(t) = \frac{1}{\tau}\left[\frac{N_i(t)z_i(t) + \tau l_i(1-N_i(t))z_i^c(t) - (N_i(t) + \tau l_i(1-N_i(t)))z_i(t)}{N_i(t) + \tau l_i(1-N_i(t))}\right] + \mathcal{O}(\tau) \tag{S8}$$

and

$$\frac{\mathrm{d}z_i}{\mathrm{d}t}(t) = \frac{l_i(1 - N_i(t))(z_i^c(t) - z_i(t))}{N_i(t) + \tau l_i(1 - N_i(t))} + \mathcal{O}(\tau). \tag{S9}$$

Letting τ go to 0, we find

$$\frac{\mathrm{d}z_i}{\mathrm{d}t}(t) = (z_i^c(t) - z_i(t)) \frac{l_i}{N_i(t)} (1 - N_i(t)). \tag{S10}$$

The instantaneous rate of change in mean trait value due to colonization is therefore $(z_i^c(t) - z_i(t)) \frac{l_i}{N_i(t)} (1 - N_i(t))$, which is the first term in Eq. 2 from the main text. This term can be interpreted as the difference between the incoming mean colonization trait value and the current mean trait $(z_i^c(t) - z_i(t))$, which is then scaled by the fraction of the population attributed to new immigrants ($\frac{l_i}{N_i(t)}$) and the abundance of the population relative to the overall carrying capacity $(1 - N_i(t))$. Again, we drop (t) in the main text notation for simplicity.

Section S3. Alternative eco-evolutionary model formulation with quadratic fitness

S3.1 Introduction

A common approach used to model quantitative trait dynamics is to assume a quadratic fitness function. Traditionally, quantitative genetics models in discrete time with non-overlapping generations assume a Gaussian formulation, which is equivalent to a quadratic in continuous time with overlapping generations (e.g., Kirkpatrick & Barton, 1997; Lande, 1976; Pease et al., 1989). Therefore, an alternative approach to the model in the main text incorporates a quadratic function for growth r_i at each patch *i*.

Following Kirkpatrick & Barton (1997), the intrinsic growth rate as a function of mean trait value, z_i, is

$$r_i = r_{max} - \frac{(T_i - z_i)^2}{2\sigma}. \tag{S11}$$

The strength of selection is σ, which is equivalent to the variance in a Gaussian fitness function. In our main formulation (Eq. 4 in the main text), the variance is $\frac{w^2}{2}$. T_i is the current temperature. Letting $r_{max} = \frac{r_0}{\sqrt{2\pi w^2}}$, Eq. S11 can be rewritten as

$$r_i = \frac{r_0}{\sqrt{2\pi w^2}} - \frac{1}{w^2}(T_i - z_i)^2. \tag{S12}$$

The overall fitness equation, g_i, includes this growth rate as well as the effects of intraspecific competition, where the strength of the latter is denoted by α (in our original formulation, $\alpha = r_i$):

$$g_i = r_i - \alpha N_i. \tag{S13}$$

Note that we do not include additional mortality in this formulation, as compared to exponential mortality in the main text model (Eq. 5). Finally, population dynamics without dispersal can be written as

$$\frac{\mathrm{d}N_i}{\mathrm{d}t} = g_i N_i - \frac{1}{w^2}V, \tag{S14}$$

where V is the additive genetic variance (as in our main text equations) and genetic load is captured by the second term in Eq. S14. This is equivalent to the genetic load term in Eq. 1: $\frac{1}{2}V\frac{\partial^2 g_i}{\partial z^2}$.

Following Pease and Lande (1989), the effect of selection on mean trait value assuming normally distributed phenotypes is $\frac{\mathrm{d}z_i}{\mathrm{d}t} = V\frac{\partial g_i}{\partial z_i}$. Incorporating Eq. S13 from above and adding a term (q_i) to reduce selection at low abundance, the effect of selection is then

$$\frac{\mathrm{d}z_i}{\mathrm{d}t} = 2q_i V\frac{(T_i - z_i)}{w^2} \quad . \tag{S15}$$

To account for dispersal, we use the same immigration and gene flow terms used in the main text (second term in Eq. 1 and first term in Eq. 2), which were derived in Supporting Information B. The full model is then

$$\frac{\mathrm{d}N_i}{\mathrm{d}t} = g_i N_i + l_i(1 - N_i) \tag{S16}$$

$$\frac{\mathrm{d}z_i}{\mathrm{d}t} = (z_i^c - z_i)\left(\frac{l_i}{N_i}\right)(1 - N_i) + 2q_i V\frac{(T_i - z_i)}{w^2} \tag{S17}$$

where l_i is the immigration rate (Eq. 6) and z_i^c is the population-weighted mean trait of immigrating individuals (Eq. 7).

S3.2 Results from the alternative model

Parameter values used were from Table 1 unless explicitly stated in the figure caption. We found that our main conclusions were robust to the alternative quadratic fitness formulation. First, random networks led to greater abundance at low V, but regular networks led to greater abundance at higher V (Figs. S4 and S5). Second, we found that regular networks promote local adaptation while random networks are susceptible to gene swamping from sites with the highest abundance. This is evident in the maintenance of a wide set of trait values in the regular network and a narrowing of values in the random networks (Fig. S6).

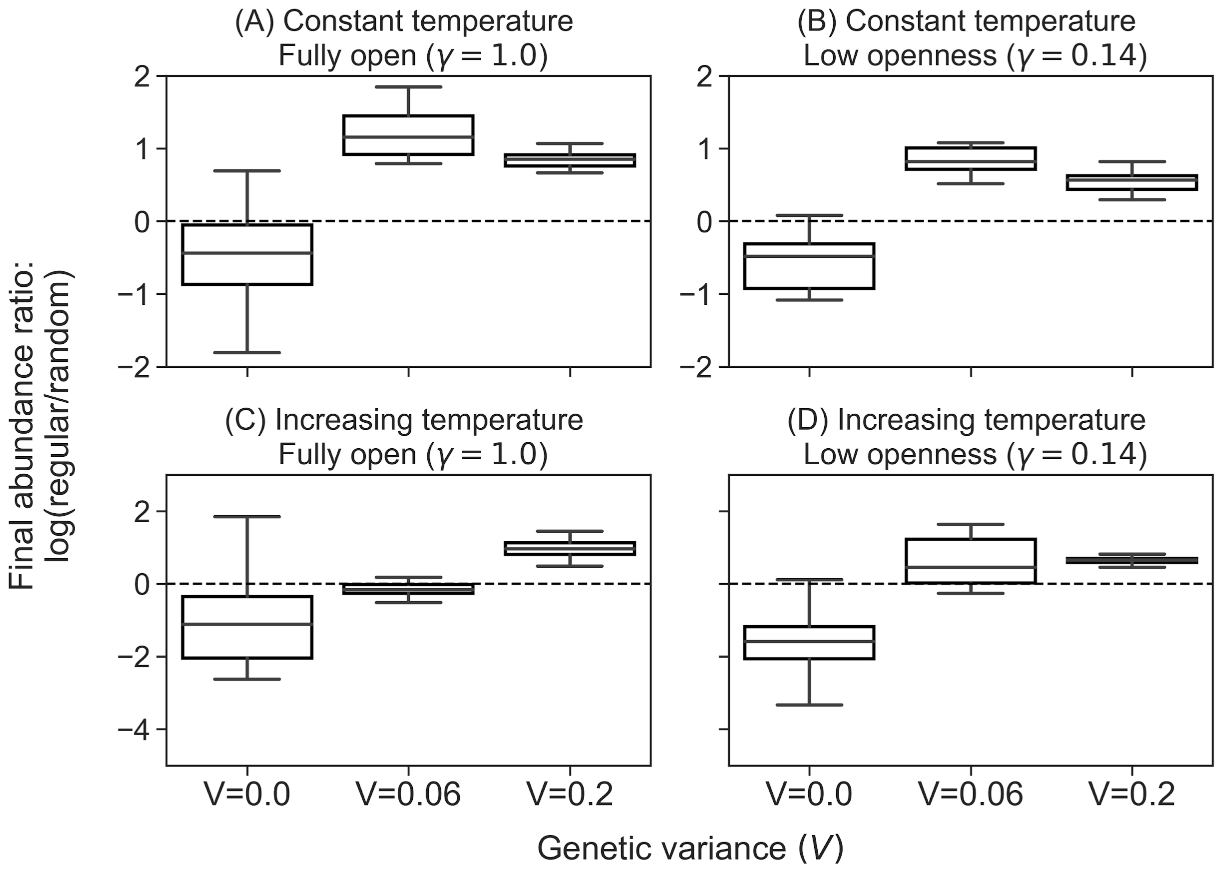


Figure S4. Influence of genetic variance on network-wide mean abundance at different levels of system openness. (Compare to Fig. 2 in the main text.) Results above the dashed horizontal line indicate that final abundance is higher in regular than random networks while results below the line indicate the opposite. Note the change in scale between top and bottom rows.

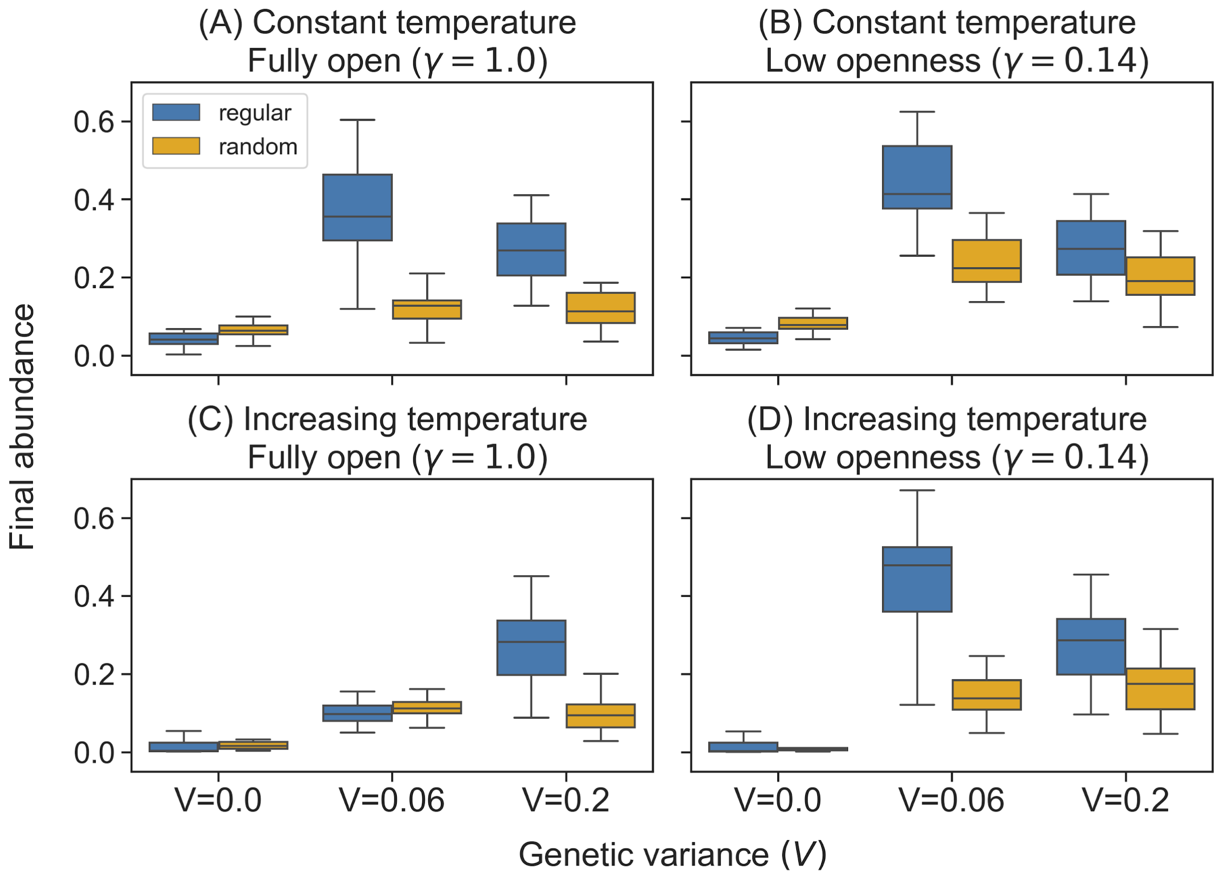


Figure S5. Final mean abundance across regular and random networks under constant (A, B) and increasing temperature scenarios (C,D). (Compare to Fig. 3 in the main text.) Results are shown for two levels of openness under different levels of additive genetic variance.

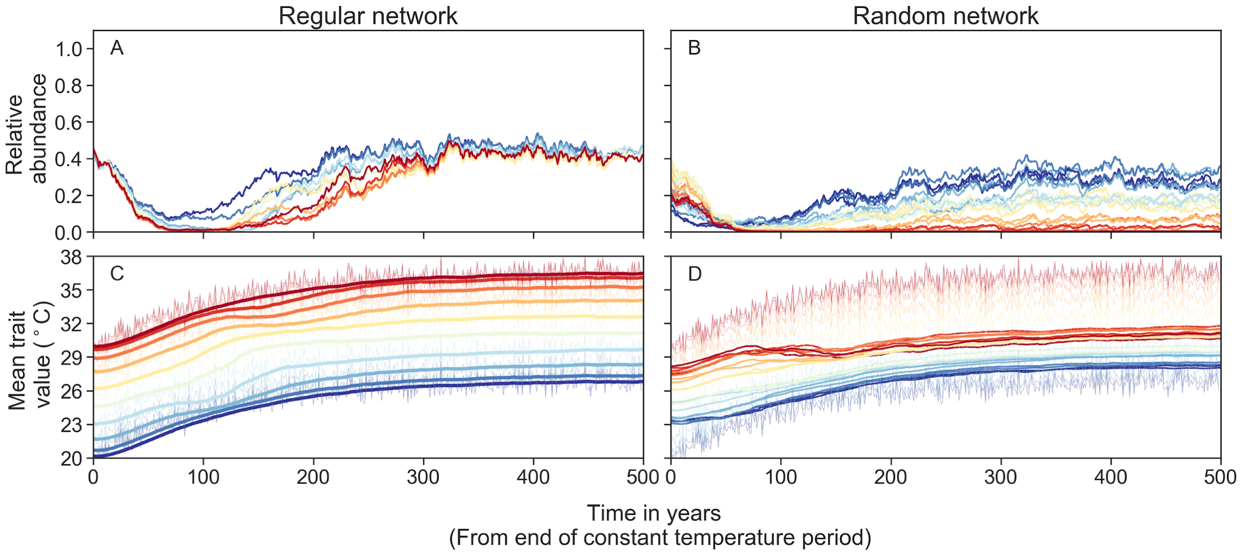


Figure S6. Illustrative trajectories of relative abundance (A, B) and average trait value by patch (C, D) for regular and random networks. (Compare to Fig. 4 in the main text.) Simulations during the temperature increase period in a system with low openness (γ=0.14) and low additive genetic variance (V=0.06). -Trajectories are colored by relative patch temperature, where warmer and cooler colors represent higher and lower temperatures, respectively. Lines are mean trajectories averaged across 20 runs. Translucent lines in the bottom row are the temperature time series.

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