

Figure S1: Even with no selection, the cline width w_{pq} stays finite, $\langle w_{pq} \rangle \rightarrow 8\sigma^2\rho$ (black dot) as time t goes to infinity. The black dotted line shows the prediction, $\langle w_{pq} \rangle = 8\sigma^2\rho \left(1 - \exp\left(-\frac{t}{16\sigma^2\rho^2}\right) \operatorname{erfc}\left(\frac{\sqrt{t}}{4\rho\sigma}\right)\right)$, where erfc is the complementary error function. The replicates are shown in coloured lines, their average cline width w_{pq} in a black dashed line. The formulae are due to Hallatschek and Korolev (2009, p. 2, where $I(t) \equiv \langle w_{pq} \rangle/2$). At time zero, we assume the beginning of a secondary contact – i.e. the allele frequency changes abruptly from 0 to 1 in the middle of the habitat. Over the time of 10 000 generations, the cline moves about in a random walk but does not get to the margins of the habitat range of 500 demes. Parameters: migration rate $\sigma^2 \rightarrow m = 1/2$, haploid deme size $2\rho \rightarrow N = 30$, deme spacing $\delta x = 1$.

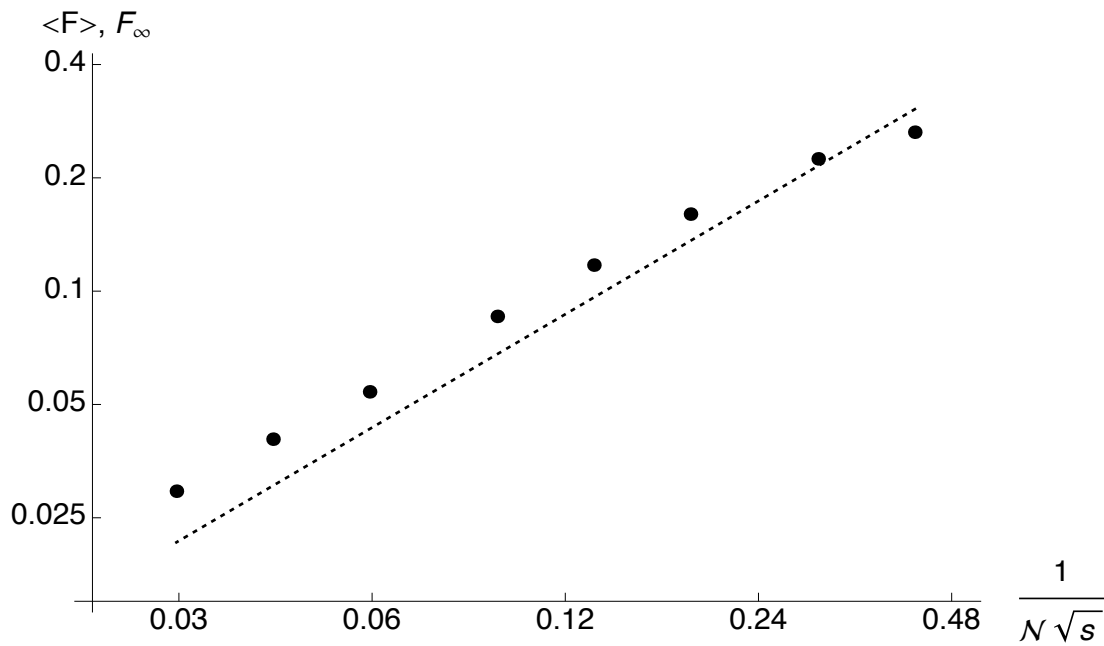


Figure S2: The standardized variance at the margin of the cline, and the expected one over the range, are close (notice the logarithmic scale). The dotted line shows the $F_\infty = 1/(\rho\sigma\sqrt{6s})$, as derived by Luskin and Nagylaki (1979). The dots are the measured expected $\langle F \rangle$ for the model with step change. Selection coefficient s ranges from 0.001 to 0.2, haploid deme size is $N = 60$; number of replicates is 100. Generations time is 1000; the equilibrium in the extent of fluctuations is reached by generation 1000 even for $s = 0.001$ (visual check); at time zero the cline is at deterministic equilibrium.

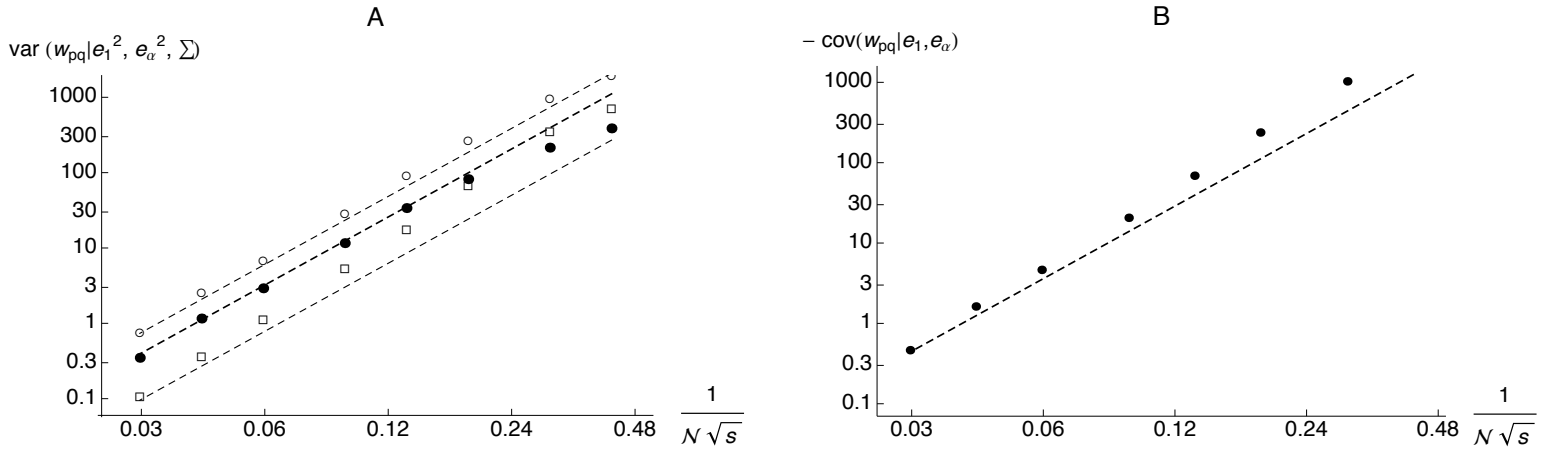


Figure S3: A: Variance in cline width (●) increases with the strength of drift as $w_{pq} = 4.21 \frac{\sqrt{2\pi} l^2}{N\sqrt{s}} = 4.21 \frac{\sqrt{m}}{2\rho\sqrt{2s^{3/2}}}$ (middle dashed line). The prediction is a sum of components of variance in cline width due to the second eigenfunction, representing changes in the slope of the cline (○, top dashed line: $w_{pq|e_1} = 4\pi^2/5 \frac{\sqrt{2\pi} l^2}{N\sqrt{s}}$), variance due to fluctuations at higher frequencies (□, bottom dashed line: $w_{pq|e_\alpha} = 1.02 \frac{\sqrt{2\pi} l^2}{N\sqrt{s}}$) and (B:) negative covariance between the component due to second eigenfunction and higher order terms, $w_{pq|e_1, e_\alpha} = 4.71 \frac{\sqrt{2\pi} l^2}{N\sqrt{s}}$. Parameters as for Figure 5.

Eigenfunction expansion for growth of a perturbation to a cline

$$\frac{\partial p(x, t)}{\partial t} = \frac{\sigma^2}{2} \frac{\partial^2 p(x, t)}{\partial x^2} + s(p, x)p(x, t)q(x, t) + \zeta(x, t) \quad (\text{S1})$$

where σ is the standard deviation of dispersal distance, and the selective advantage $s(p, x)$ (to the first order) of an allele varies across space and may depend on allele frequency (p). Whereas one cannot solve the spatial diffusion equation with selection and drift, because the fluctuations due to genetic drift $\zeta(x, t)$ depend in general on both time and space, the equation for expected change in the allele frequency in a one dimensional habitat can be solved analytically when selection depends only on location, $s(x)$.

We consider a model of a linear frequency-dependent selection, where the fitness of the allele with frequency p is $1 - qs$ (and vice versa) – as would be the marginal fitness with “underdominance” of selection strength s in a diploid model. To the first order of s , allele frequency p changes according to

$$\frac{\partial p}{\partial t} = \frac{\sigma^2}{2} \frac{\partial^2 p}{\partial x^2} + spq(p - q) \quad (\text{S2})$$

where σ is the standard deviation of dispersal distance, and x denotes space, t time. As usual, $q(x, t) = 1 - p(x, t)$ - and we drop the (x, t) unless we want to specifically highlight the dependency.

Scaling time with selection $T = st$ and distance relative to the dispersal, $X = x\sqrt{\frac{2s}{\sigma^2}}$ gives $\frac{\partial p}{\partial T} = \frac{\partial^2 p}{\partial X^2} + pq(p - q)$. The equilibrium solution is $p_0 = \frac{1}{1 + \text{Exp}[-(X - X_0)]}$ (and the mirror image, $1 - p_0$). The position of the cline, X_0 , is arbitrary.

Including random genetic drift $\epsilon(X, T)$, a small perturbation to the equilibrium of Eq. S2, Z , grows (to the first order) as

$$\frac{\partial Z}{\partial T} = \frac{\partial^2 Z}{\partial X^2} - (1 - 6p_0q_0)Z + \epsilon(X, T) \quad (\text{S3})$$

We look for a solution of the equation above in a form of $Z(X, T) = \sum_{i=1}^{\infty} \tilde{Z}_i(T)e_i(X)$ - i.e. decomposing Z with its time-dependent components $\tilde{Z}_i(T)$ and space-dependent

components $e_i(X)$. We choose the $e_i(X)$ so that they are the eigenfunctions of the corresponding homogeneous system (with $\epsilon(X, T) = 0$): $\frac{\partial Z}{\partial T} = LZ$, where L is the linear operator (here $L = \frac{\partial^2}{\partial X^2} - (1 - 6p_0q_0)$) - hence, $Le_i = \lambda_i e_i$, where λ_i are eigenvalues and e_i the eigenfunctions of L .

Normalizing so that $\int e_i(X)e_j^*(X)dX = \delta_{ij}$, the eigenfunctions and respective eigenvalues are:

$$e_0(X) = \sqrt{6p_0q_0} \quad \lambda_0 = 0 \quad (\text{S4})$$

$$e_1(X) = (p_0 - q_0)\sqrt{3p_0q_0} \quad \lambda_1 = -3/4 \quad (\text{S5})$$

$$e(\alpha, X) = \frac{3\alpha i(p_0 - q_0) + 2\alpha^2 - (1 - 6p_0q_0)}{\sqrt{2\pi(1 + \alpha^2)(1 + 4\alpha^2)}} \text{Exp}(i\alpha X) \quad \lambda(\alpha) = -1 - \alpha^2 \quad (\text{S6})$$

Apart from the first two, the eigenfunctions form a continuum along α . The transformed perturbation components are: $\tilde{Z}_0(T) = \int_{-\infty}^{\infty} Z(X, T)e_0^*(X)dX$, $\tilde{Z}_1(T) = \int_{-\infty}^{\infty} Z(X, T)e_1^*(X)dX$, $\tilde{Z}(\alpha, T) = \int_{-\infty}^{\infty} Z(X, T)e^*(\alpha, X)dX$.

Substituting to the above equation (Eq. S3) the eigenfunction transformation of Z , ϵ and using $Le_i = \lambda_i e_i$, gives (as \tilde{Z} is constant with respect to L):

$$\begin{aligned} \frac{\partial}{\partial T}(\tilde{Z}_0(T)e_0(X) + \tilde{Z}_1(T)e_1(X) + \int_{-\infty}^{\infty} \tilde{Z}(\alpha, T)e(\alpha, X)d\alpha) = \\ \lambda_0 \tilde{Z}_0(T)e_0(X) + \lambda_1 \tilde{Z}_1(T)e_1(X) + \int_{-\infty}^{\infty} \lambda(\alpha) \tilde{Z}(\alpha, T)e(\alpha, X)d\alpha + \\ \tilde{\epsilon}_0(T)e_0(X) + \tilde{\epsilon}_1(T)e_1(X) + \int_{-\infty}^{\infty} \tilde{\epsilon}(\alpha, T)e(\alpha, X)d\alpha \end{aligned} \quad (\text{S7})$$

As the eigenfunctions are orthogonal, we get

$$\begin{aligned} \frac{\partial}{\partial T}(\tilde{Z}_0(T) + \tilde{Z}_1(T) + \int_{-\infty}^{\infty} \tilde{Z}(\alpha, T)d\alpha) = \\ \lambda_0 \tilde{Z}_0(T) + \lambda_1 \tilde{Z}_1(T) + \int_{-\infty}^{\infty} \lambda(\alpha) \tilde{Z}(\alpha, T)d\alpha + \tilde{\epsilon}_0(T) + \tilde{\epsilon}_1(T) + \int_{-\infty}^{\infty} \tilde{\epsilon}(\alpha, T)d\alpha \end{aligned} \quad (\text{S8})$$

There is a solution where all of the components with $i = 0, 1$ and all values of α sum to zero, i.e. $\frac{\partial \tilde{Z}_i(T)}{\partial T} = \lambda_0 \tilde{Z}_i(T) + \tilde{\epsilon}_i(T)$ for all i . Multiplying by $\text{Exp}(-\lambda_i T)$, using $\frac{\partial}{\partial T}(\tilde{Z}_i(T)\text{Exp}(-\lambda_i T)) = \text{Exp}(-\lambda_i T)(\frac{\partial}{\partial T} \tilde{Z}_i(T) - \lambda \tilde{Z}_i(T))$ and integrating $\int_{-\infty}^T d\tau$ (after $T \rightarrow \tau$) gives the time-dependent components of perturbations:

$$\tilde{Z}_i(T) = \int_{-\infty}^T \tilde{\epsilon}_i(\tau)\text{Exp}(-\lambda_i(\tau - T))d\tau.$$

And so for the covariance in the transformed fluctuations in allele frequencies,

$$\langle \tilde{Z}_i(T) \tilde{Z}_j(T') \rangle = \int_{-\infty}^T \int_{-\infty}^{T'} \langle \tilde{\epsilon}_i(\tau) \tilde{\epsilon}_j(\tau') \rangle \text{Exp}(-\lambda_i(\tau - T) - \lambda_j(\tau' - T')) d\tau d\tau' \quad (\text{S9})$$

Where $\langle \tilde{\epsilon}_i(\tau) \tilde{\epsilon}_j(\tau') \rangle = \int_{-\infty}^{\infty} \int_{-\infty}^{\infty} \langle \epsilon(X, \tau) \epsilon(X', \tau') \rangle e_i^*(X) e_j^*(X') dX dX'$ are the transformed noise components. We assume each deme is sampled independently, hence the fluctuation caused by random genetic drift can be described by white noise, uncorrelated in space and time: $\langle \epsilon(X, \tau) \epsilon(X', \tau') \rangle = \frac{\langle p(X)(1-p)(X) \rangle}{2\rho} \delta(X - X') \delta(\tau - \tau')$. Hence, at a given time $T = T'$, the covariance between the transformed components (with at least one $\lambda_i \neq 0$) is

$$\langle \tilde{Z}_i(T) \tilde{Z}_j(T) \rangle = -\frac{1 - \text{Exp}(T(\lambda_i + \lambda_j))}{2\rho(\lambda_i + \lambda_j)} \int_{-\infty}^{\infty} \langle p(X)(1-p)(X) \rangle e_i^*(X) e_j^*(X) dX \quad (\text{S10})$$

For eigenvalues $\lambda_i < 0$, the exponential term goes to zero. For the variance in fluctuations due to the shifts in position, where $\lambda_0 = 0$, $\langle \tilde{Z}_0(T)^2 \rangle = \frac{T}{2\rho} \int_{-\infty}^{\infty} \langle p(X)(1-p)(X) \rangle e_0^*(X)^2 dX$ - from Eq. S9 and below, integrating from 0 to T .

Transforming back, and denoting $\Lambda_{i,j} = \int_{-\infty}^{\infty} \langle p(X)(1-p)(X) \rangle e_i^*(X) e_j^*(X) dX$ gives the covariance in the fluctuations for the spatially aligned clines. (I.e., discounting the fluctuations in position, $\langle Z_0(X, T) Z_0(X', T) \rangle$. The covariance in fluctuations between position and width, $\Lambda_{0,1}$, is zero).

$$\begin{aligned} \langle Z(X, T) Z(X', T) \rangle = & -\frac{1}{2\rho} \left(\frac{\Lambda_{1,1}}{2\lambda_1} e_1(X) e_1(X') + \int_{-\infty}^{\infty} \int_{-\infty}^{\infty} \frac{\Lambda_{\alpha, \alpha'}}{\lambda(\alpha) + \lambda(\alpha')} e(\alpha, X) e(\alpha', X') d\alpha d\alpha' \right. \\ & + \int_{-\infty}^{\infty} \frac{\Lambda_{0, \alpha'}}{\lambda_0 + \lambda(\alpha')} e_0(X) e(\alpha', X') d\alpha' + \int_{-\infty}^{\infty} \frac{\Lambda_{0, \alpha}}{\lambda_0 + \lambda(\alpha)} e_0(X') e(\alpha, X) d\alpha + \\ & \left. + \int_{-\infty}^{\infty} \frac{\Lambda_{1, \alpha'}}{\lambda_1 + \lambda(\alpha')} e_1(X) e(\alpha', X') d\alpha' + \int_{-\infty}^{\infty} \frac{\Lambda_{1, \alpha}}{\lambda_1 + \lambda(\alpha)} e_1(X') e(\alpha, X) d\alpha \right) \end{aligned}$$

Scaling back to the original variables, and normalizing with average local allele frequency, we obtain standardized variance across space for aligned clines, F_A :

$$F_A = \frac{\sqrt{\pi/2}}{\mathcal{N}\sqrt{s}} \cdot \frac{\langle Z(X, T) Z(X, T) \rangle}{\bar{p}\bar{q}} \quad (\text{S11})$$

The fluctuations scale proportionally to $\frac{1}{\mathcal{N}\sqrt{s}}$, where \mathcal{N} is the neighbourhood size in one dimension, and $\frac{\sqrt{\pi/2}}{\mathcal{N}\sqrt{s}} = 4\rho l s$, which is the “ β ” of Nagylaki (1978).