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Clines in polygenic traits

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Summary

This article outlines theoretical models of clines in additive polygenic traits, which are maintained by stabilizing selection towards a spatially varying optimum. Clines in the trait mean can be accurately predicted, given knowledge of the genetic variance. However, predicting the variance is difficult, because it depends on genetic details. Changes in genetic variance arise from changes in allele frequency, and in linkage disequilibria. Allele frequency changes dominate when selection is weak relative to recombination, and when there are a moderate number of loci. With a continuum of alleles, gene flow inflates the genetic variance in the same way as a source of mutations of small effect. The variance can be approximated by assuming a Gaussian distribution of allelic effects; with a sufficiently steep cline, this is accurate even when mutation and selection alone are better described by the 'House of Cards' approximation. With just two alleles at each locus, the phenotype changes in a similar way: the mean remains close to the optimum, while the variance changes more slowly, and over a wider region. However, there may be substantial cryptic divergence at the underlying loci. With strong selection and many loci, linkage disequilibria are the main cause of changes in genetic variance. Even for strong selection, the infinitesimal model can be closely approximated by assuming a Gaussian distribution of breeding values. Linkage disequilibria can generate a substantial increase in genetic variance, which is concentrated at sharp gradients in trait means.

1. Introduction

Many issues in evolutionary biology depend on spatial population structure, and most species occupy a habitat much broader than their dispersal range. Gene flow is involved in the spread of alleles, whether they be favoured everywhere (Fisher, 1937), or in only some places (Slatkin, 1973; Nagylaki, 1975; Barton, 1987). Thus, the efficiency of adaptation by natural selection depends on the spatial distribution of selection in relation to dispersal and density; indeed, the range of a species may be limited by the conflict between selection and gene flow (Holt, 1995; Kirkpatrick & Barton, 1997). If allelic combinations can be maintained only when they become sufficiently common, then gene flow interacts with random drift and selection in Wright's (1931) 'shifting balance'. The genetic variation on which adaptation depends may be maintained by the combination of heterogeneous selection with gene flow (Haldane, 1948; Goldstein & Holsinger, 1992), and the incompatibilities which are responsible for reproductive isolation may develop through divergence across a broad geographic range (i.e. in parapatry; Endler, 1977).

Although a substantial body of theory addresses these issues, it is framed almost entirely in terms of gene frequencies: there is remarkably little work on the evolution of quantitative traits in spatially extended populations (for a review, see Barton & Turelli, 1989). This is partly because the roots of quantitative genetics lie in plant and animal breeding, where spatial structure is less relevant than in nature. However, gene flow between domesticated and natural populations is significant (Ellstrand *et al.*, 1999), and the interaction between fitness and environment is an important topic in classical quantitative genetics; in particular, Falconer's (1981) representation of genotype × environment interaction by a multivariate trait is a powerful way of analysing trait evolution in heterogeneous conditions (Via & Lande, 1985).

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A more fundamental reason for the relative neglect of spatial structure in quantitative genetics is our ignorance of the causes of polygenic variation (Falconer & Mackay, 1996). Even if one supposes that quantitative genetic variation is maintained by a balance between mutation and stabilizing selection (one of many plausible mechanisms), the theory is not straightforward: the evolution of the genetic variance depends on the effects and frequencies of the underlying alleles, and cannot be reduced to a few observable phenotypic variables (Turelli, 1984). Thus, although the evolution of trait means is straightforward if the genetic variance is given, it is hard to find a robust theoretical description of the variance itself.

The aim of this paper is to give an overview of the theory for clines in an additive polygenic trait. I concentrate on deterministic selection, because it is here that the major theoretical difficulties lie: the effects of drift and gene flow on an additive trait can be simply extrapolated from the extensive theory on neutral allele frequencies in structured populations (Felsenstein, 1986; Nagylaki, 1986; Lande, 1991; Whitlock, 1999). The analysis falls into two parts. Where selection is weak relative to recombination, populations are close to linkage equilibrium, and can be described solely in terms of allele frequencies. With strong selection or tight linkage, linkage disequilibria may be significant; these can be approximated by assuming a short-term balance between gene flow and recombination. While many of the results depend on the detailed genetic basis of the traits, some robust and testable predictions do emerge.

2. Stabilizing selection and mutation in a single population

Many of the difficulties in analysing clines in polygenic traits arise from corresponding difficulties in understanding the balance between mutation and selection in a single population. Suppose that stabilizing selection on a single trait favours an optimum phenotype, z_{opt}. The fitness of an individual is given by a Gaussian function centred on z_{opt}, and with variance $1/s$. (The variance is often written as $V_s = 1/s$; Lande, 1975.) Without loss of generality, assume no environmental variance, and a continuous distribution of allelic effects. The phenotype of a diploid individual is $\Sigma_{i=1}^{n}(Z_i + Z_i^*)$, where Z_i, Z_i^* are the contributions of the maternal and paternal copies of gene i, respectively. If selection is weak enough relative to recombination that linkage disequilibria are negligible, and if selection and mutation act equally on males and females, then the population can be described by the distributions of effects at each locus, $\psi_i[z_i]$.

Kimura (1965) used a diffusion approximation to show that when mutational effects are sufficiently small, the distribution of effects is Gaussian with variance $v_i = \surd(\mu_i v_{m,i}/s)$, where $v_{m,i}$ is the variance of mutational effects at locus i. Lande (1975) extended the continuum-of-alleles model to include linkage disequilibria, by assuming that the joint distribution of allelic effects, Z, is multivariate Gaussian. However, Turelli (1984) argued that mutation rates are likely to be too low, and mutational effects too high, to justify the Gaussian approximation. He suggested that the 'House of Cards' approximation (Kingman, 1978) is more appropriate. Here, mutational effects are assumed to be so large that new alleles have effects independent of their original value. The variance contributed by a single gene is then $\sim 2\mu_i/s$ (Turelli, 1984). Given the assumption of large allelic effects, this is a much lower value than is predicted by the Gaussian approximation.

Under both the Gaussian and the 'House of Cards' approximations, selection on allele frequencies causes the variance to change much more slowly than the mean. In the limit of very many loci, the infinitesimal model is approached, in which the variance at linkage equilibrium is constant (Fisher, 1918; Bulmer, 1985); changes in variance are then solely due to linkage disequilibria. These properties of polygenic models allow the evolution of the variance to be decoupled from the evolution of the mean, and simplify the following analysis of clines.

Models with two alleles behave in a qualitatively different way from those with a continuum of alleles, because the mean and variance at each locus are coupled through a single variable, the allele frequency, this coupling leads to multiple stable equilibria. Wright (1935) showed that under stabilizing selection alone, polymorphism could be maintained at most at a single locus. However, many different allelic combinations can give a mean which is close to the optimum; for example, with 100 loci of equal effect, and a mean at the centre of the range, any genotype with 50 '+' alleles and 50 '−' alleles can be fixed. Mutation maintains polymorphism, such that if the mean is at the optimum, a genetic variance $v_i = 2\mu_i/s$ is contributed by each of the $2n$ genes (Latter, 1960; Bulmer, 1971, 1985). The mean can now be adjusted both by changes in the number of loci near fixation for '+' alleles, and by changes in allele frequencies at each locus. This flexibility sustains many more stable states; if $\mu \ll s\alpha^2 \ll n\mu$, then there are stable equilibria in which different numbers of loci are near fixation for '+' alleles, and in which the mean deviates from the optimum to different degrees (Barton, 1986).

3. Clines with a continuum of alleles

(i) *General formulae*

Suppose that genes at locus i have a continuous distribution of allelic effects, z_i; denote the distribution at position x by $\psi_i[z_i, x]$. There is weak quadratic

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selection of strength s towards an optimum at z_{opt}. Mutations occur at a rate μ_i, and add a random increment y to the allelic effect z_i; the distribution of mutational effects is $m_i[y]$, which is assumed to have zero mean. Assuming linkage equilibrium, we have:

$$\frac{\partial \psi_i}{\partial t} = \frac{\sigma^2}{2}\frac{\partial^2 \psi_i}{\partial x^2} - \frac{s}{2}((z_i - z_{opt})^2 - v_i - (\bar{z}_i - z_{opt})^2)\psi_i + \mu_i\left(\int_{-\infty}^{\infty} m_i[y]\,\psi_i(z_i - y, x)\,\mathrm{d}y - \psi_i(z_i, x)\right), \quad (1)$$

where $\bar{z}_i$, v_i are the mean and variance of effects of locus i. Gene flow is represented by diffusion at a rate σ^2, the variance of distance between parent and offspring (Nagylaki, 1975). In all the following discrete-time models, population density is held constant.

The overall mean and variance ($\bar{z} = 2\Sigma_i \bar{z}_i$, $V = 2\Sigma_i v_i$) can be derived from (1):

$$\frac{\partial \bar{z}}{\partial t} = 2\sum_i \int_{-\infty}^{\infty} z_i\,\partial_t \psi_i\,\mathrm{d}z_i = \frac{\sigma^2}{\sigma}\frac{\partial^2 \bar{z}}{\partial x^2} - sV(\bar{z} - z_{opt}) - \frac{s}{2}\kappa_3, \quad (2)$$

$$\frac{\partial V}{\partial t} = 2\sum_i \int_{-\infty}^{\infty} (z_i - \bar{z}_i)^2\,\partial_t \psi_i\,\mathrm{d}z_i = \frac{\sigma^2}{2}\frac{\partial^2 V}{\partial x^2} + \frac{\sigma^2}{2n_e^*}\left(\frac{\partial \bar{z}}{\partial x}\right)^2 - \frac{s}{2}\left(\frac{V^2}{n_e} + \kappa_4\right) - s(\bar{z} - z_{opt})\,\kappa_3 + V_m, \quad (3)$$

where κ_3, κ_4 are the third and fourth cumulants of the distribution of breeding values, and

$$V_m = 2\sum_i \mu_i \int_{-\infty}^{\infty} y^2 m(y)\,\mathrm{d}y$$

is the increase in trait variance due to mutation. The effective numbers of loci are defined as

$$n_e \equiv \left(\sum_i v_i\right)^2 \Big/ \left(\sum_i v_i^2\right);$$

$$n_e^* \equiv \left(\sum_i \partial_x \bar{z}_i\right)^2 \Big/ \left(\sum_i (\partial_x \bar{z}_i)^2\right).$$

To the extent that the variance and gradient in mean vary across loci, these will be smaller than the actual number of loci. These equations cannot in general be solved, because they depend on the higher cumulants of the distribution of breeding values (κ_3, κ_4), and because they depend on variation across loci through n_e, n_e^*.

Slatkin (1978) derived (1), and argued (p. 215) that when selection is weak ($sV \ll 1$), the increase in variance caused by gene flow is negligible. Slatkin's argument relies on showing that the gradient in the mean is small ($\partial_x \bar{z} \sim \sqrt{(sV)}/\sigma$; p. 221), so that the variance generated by gene flow (i.e. the second term in (3) above) is also small. However, it does not follow that the effect of gene flow on the variance is small: the strength of the force returning the variance to its value outside the cline is also proportional to the small selection coefficient (third term in (3) above), and so the two forces are comparable. The analysis below shows that there can be a substantial increase in variance under weak selection. However, the increase does become small when a very large number of loci are involved.

(ii) *The Gaussian approximation*

Suppose that the distribution of allelic effects at each locus is approximately Gaussian. This is a much stronger assumption than that the overall distribution of breeding values, $2\Sigma_i z_i$, is Gaussian, and requires that there be a high rate of mutations, with effects typically small relative to the standing distribution of effects (Turelli, 1984). We must also assume that all loci have the same mean and variance, so that $n_e = n_e^* = n$; this assumption may be less restrictive, in that variation across loci might be described by taking the effective numbers of loci to be roughly constant. In the absence of gene flow, or with a uniform optimum, the equilibrium genetic variance is $V_\infty = \sqrt{(2nV_m/s)}$ (Lande, 1975; (3) above).

The simplest case is where there is an infinite linear cline, with $z_{opt} = \beta x$. Then, there is a solution where the mean is always at the optimum ($\bar{z} = \beta x$). Gene flow contributes to the variance at a constant rate $\sigma^2\beta_2/(2n)$, and has an effect equivalent to mutation, V_m. The equilibrium genetic variance is inflated by gene flow to $\sqrt{[(2nV_m + \sigma^2\beta^2)/s]}$. Felsenstein (1977) has analysed this case in the absence of mutation, but allowing for linkage disequilibrium (see below).

Next, consider a sharp change in the optimum, from $z_{opt} = -\Delta/2$ to $+\Delta/2$ at $x = 0$. Equations (2), (3) simplify to:

$$\frac{\partial \bar{z}}{\partial t} = \frac{\sigma^2}{2}\frac{\partial^2 \bar{z}}{\partial x^2} - sV(\bar{z} - z_{opt}), \quad (4)$$

where $z_{opt} = -\Delta/2$ for $x < 0$, $+\Delta/2$ for $x > 0$,

$$\frac{\partial V}{\partial t} = \frac{\sigma^2}{2}\frac{\partial^2 V}{\partial x^2} + \frac{\sigma^2}{n}\left(\frac{\partial \bar{z}}{\partial x}\right)^2 - \frac{sV^2}{2n} + V_m. \quad (5)$$

An approximate solution to (4), (5) can be found if many loci are involved ($n \gg 1$). Then, the genetic variance changes much more slowly than the mean, and hence changes over a broader spatial scale. It can therefore be taken as constant, at V_0, around the region where the mean changes sharply. The equilibrium for the mean is then:

$$\left.\begin{aligned} \bar{z} &= -\frac{\Delta}{2}\left(1 - \exp\left[+\frac{x}{\sigma}\sqrt{(2sV_0)}\right]\right) \quad \text{for } x < 0, \\ \bar{z} &= +\frac{\Delta}{2}\left(1 - \exp\left[-\frac{x}{\sigma}\sqrt{(2sV_0)}\right]\right) \quad \text{for } x > 0. \end{aligned}\right\} \quad (6)$$

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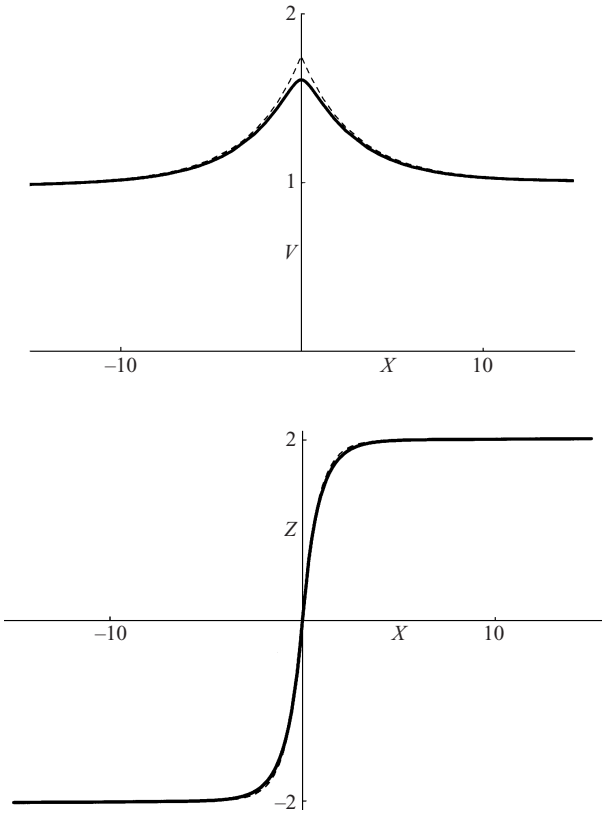

Fig. 1. The variance and mean across a cline which is maintained by a change in optimum of $\Delta = 4\sqrt{V_\infty}$ genetic standard deviations (upper and lower panels, respectively). Trait values are scaled relative to the variance outside the cline ($\bar{z}/\sqrt{V_\infty}$, V_0/V_∞), and distance relative to $\sigma/\sqrt{(2sV_\infty)}$. The dashed curves show the approximation of (8). The continuous curves show the numerical solution of (4), (5); calculations were made for $T = 30$ time units, starting from a linear cline, and over a range $-15 < X < 15$ ($T \equiv s\alpha^2 t/2$, $X \equiv x/\sigma\sqrt{s\alpha^2}$).

This is eq. 24 of Slatkin (1978). Within the region around $x = 0$, the effects of selection on the genetic variance can be neglected; gene flow is the dominant force, and causes a sharp change in the gradient of V, from $-\partial_x V_0$ to $+\partial_x V_0$. Integrating across the central region (from $x_- < 0$ to $x_+ > 0$, say), we obtain a boundary condition on the gradient at the centre:

$$\frac{\partial V}{\partial x}\Big|_{x=0} = \frac{1}{n}\int_{x_-}^{x_+}\left(\frac{\partial \bar{z}}{\partial x}\right)^2 \mathrm{d}x = \frac{\Delta^2}{2n\sigma}\sqrt{(2sV_0)}. \qquad (7)$$

Away from the centre, the change in genetic variance is given by dropping the second term on the right from (5). Integrating:

$$V = V_\infty\left(3\tanh\left[\frac{(|x|+x_0)}{2\sigma}\quad\left(\frac{2sV_\infty}{n}\right)\right]^{-2} - 2\right). \qquad (8)$$

The variance is thus increased over a region of width $\sigma\sqrt{(n/2sV_\infty)}$, a factor $\sim\sqrt{n}$ wider than the region over which the mean changes. The constant of integration x_0 is determined from the boundary condition on the gradient (i.e. equating (7) with the derivative of (8) at $x = 0$). This leads to a cubic equation for the variance V_0 at $x = 0$ which has the solution:

$$\left.\begin{aligned} V_0 = {} & \\ & V_\infty 2\sqrt{(1+9\alpha^2)}\cos[\phi] \quad \text{where } \alpha = \frac{\Delta^2}{24V_\infty\sqrt{n}}, \\ \phi = {} & \tfrac{1}{3}\arctan\{3\alpha\sqrt{[3(1+9\alpha^2+27\alpha^4)]}\} - \frac{\pi}{2}. \end{aligned}\right\} \qquad (9)$$

The increase in variance is determined by α, which is proportional to the ratio between the square of the change in optimum (Δ^2), and the genetic variance maintained by a mutation–selection balance with constant optimum (V_∞). It is also inversely proportional to the square root of the number of loci: with large numbers of loci, therefore, there will be only a small increase in variance. For a small step ($\alpha \ll 1$), $V_0 \sim 1 + (\Delta^2/8V_\infty\sqrt{n})$, whilst for a large step, $V_0 \sim \sqrt{\{3[1+(\Delta^4/64nV^2)]\}}$ (dashed curves in Fig. 2).

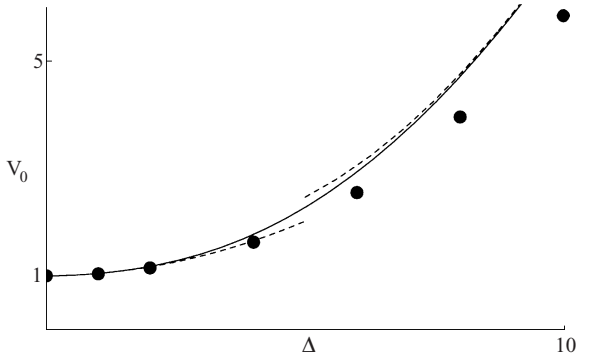

Fig. 2. The variance at the centre of a cline, V_0, plotted against the size of the change in optimum, Δ. V_0 and Δ are scaled relative to the variance outside the cline, V_∞. The continuous curve shows the approximation of (8). The dotted curves show the further approximations given below (9). The filled circles show the numerical solution of (4), (5); calculations were made for $T = 30$ time units, starting from a linear cline, and over a range $-15 < X < 15$.

Fig. 1 shows the change in mean and variance across a cline maintained by a sharp shift in optimum. The approximation of (8) agrees well with numerical solution of (4), (5) (compare dashed and continuous lines in Fig. 1). Equation (8) predicts that the genetic variance increases by 75% at the centre of the cline, whereas numerical solution of (4), (5) predicts an increase in genetic variance at the centre by 61%. Fig. 2 shows how genetic variance increases with the size of the change in optimum. The approximation of (8) is an underestimate for larger Δ; this is because the increase in variance does not rise to a sharp peak, as is assumed in deriving (8), but rather, changes

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smoothly over the narrow region in which the mean changes. Even with the moderate number of loci used in this example ($n = 10$), the approximation that the mean changes much more sharply than the variance is quite accurate (compare points and continuous curve in Fig. 2). Agreement improves with more loci.

(iii) *Accuracy of the Gaussian approximation*

Although the Gaussian approximation has been widely used to analyse the balance between mutation and stabilizing selection, it is only accurate when mutations have small effects relative to the standing variation; this implies unreasonably high mutation rates (Turelli, 1984). Here, we examine the accuracy of the Gaussian approximation in the presence of gene flow by using (1) to find the full distribution of allelic effects, $\psi_i(z_i, x)$, for an infinite linear cline. Then, there is a solution in which the mean tracks the optimum ($\bar{z} = z_{\text{opt}} = \beta x$) and the distribution of effects of each locus has a constant form: $\psi(z_i, x) = \zeta_i[z_i - \alpha_i - \beta_i x]$. For the moment, we allow the form of the distribution ζ_i to vary across loci, and allow the mean effect of each locus to vary, with the constraint that $0 = \Sigma_i \alpha_i = \Sigma_i \beta_i$. Equation (1) can then be solved numerically.

First, consider mutation–selection balance, in the absence of gene flow. If mutations have small effects, (1) can be approximated by a diffusion equation, whose solution is a Gaussian with variance $\sqrt{(\mu_i v_{\text{m},i}/s)}$, where $v_{\text{m},i}$ is the variance of mutational effects at locus i (Kimura, 1965). If all loci have equal effects, the total genetic variance is $\sqrt{(2nV_{\text{m}}/s)}$, where $V_{\text{m}} = 2n\mu v_{\text{m}}$. At the other extreme, if mutations have effects large compared with the standing distribution, they can be taken to have a distribution independent of their original (the 'House of Cards' approximation; Turelli, 1984). Replacing the last term in (1) by $\mu_i(m_i(z_i) - \zeta_i(z_i))$ gives an equilibrium

$$\zeta = \frac{\mu_i m_i(z_i)}{\mu_i + s/2(z_i^2 - v_i)}.$$

The constraint that

$$\int \zeta_i \, \mathrm{d}z_i = 1$$

determines v_i.

Now, consider the additional effect of gene flow. Because we have assumed that gene flow is sufficiently localized that it can be represented by a diffusion equation, it has an effect equivalent to mutations of small effect, and tends to produce a Gaussian distribution (Felsenstein, 1977; Slatkin, 1978). (If dispersal were highly leptokurtic, it would need to be represented by an integral of the same form as that used to represent mutation in (1). The Gaussian approximation would then fail, just as it fails when mutations have large effects). Fig. 3 shows how the variance increases as the gradient in the cline becomes steeper. With no gene flow, the variance is close to the House of Cards approximation, and fivefold smaller than the Gaussian prediction (left of Fig. 3). However, as gene flow increases, the per locus variance increases linearly, and approaches the Gaussian prediction.

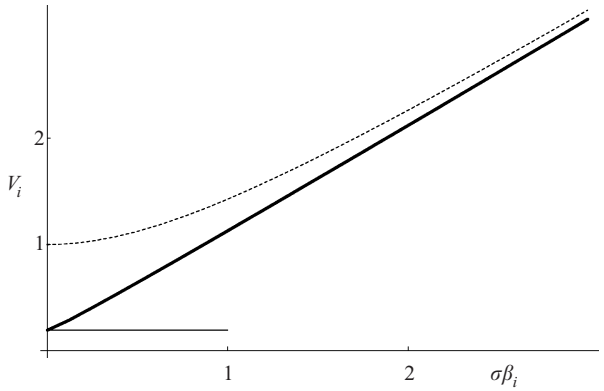

Fig. 3. The variance maintained at a single locus by gene flow and mutation, plotted against the gradient of the cline of that locus, $\sigma\beta_i$. The mutation rate is $\mu_i = 0{\cdot}1s$, and the variance of mutational effects per locus is $v_{m,i} = 10$. The continuous curve shows the numerical solution of (1); this is compared with the 'House of Cards' approximation in the absence of gene flow (lower horizontal line), and the Gaussian approximation $\sqrt{[(\mu_i v_{m,i} + \sigma^2\beta_i^2)/s]}$ (dashed curve).

4. Clines with rare alleles

(i) *Change in allele frequencies*

Suppose that we ignore linkage disequilibria, and assume weak selection; then, a cline in a trait involving n loci can be described by a set of diffusion equations for n allele frequencies. Following Barton (1986), suppose that there are equal allelic effects, α, stabilizing selection towards an optimum z_{opt}, and that variation is maintained by mutation μ:

$$\frac{\partial p_i}{\partial t} = \frac{\sigma^2}{2}\frac{\partial^2 p_i}{\partial x^2} + \frac{s\alpha^2}{2} p_i q_i (p_i - q_i - 2\delta) - \mu(p_i - q_i), \qquad (10)$$

where

$$\delta = \frac{(\bar{z} - z_{\text{opt}})}{\alpha} = \sum_i (p_i - q_i) - \frac{z_{\text{opt}}}{\alpha}.$$

The outcome depends on how the optimum changes. First, suppose that there is a step change in z_{opt}. Then, for $x \ll 0$, some loci will be near fixation for $-$alleles, and some near fixation for $+$alleles; let their numbers be m_-, M_-, respectively. We can suppose for simplicity that this combination brings the mean to the optimum. For $x \gg 0$, we have (m_+, M_+) near fixation for $-$ and $+$alleles. The set of loci that changes could be the

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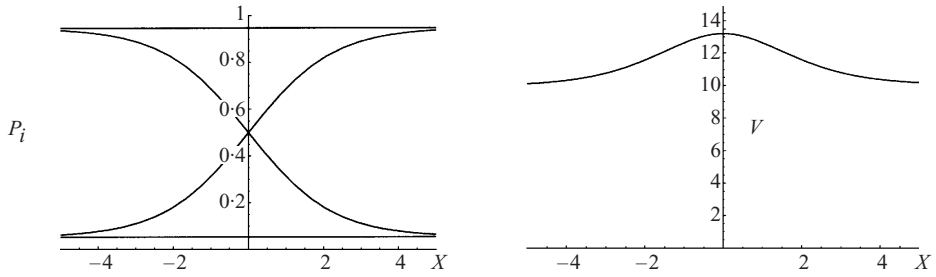

Fig. 4. Over most of the range, 50 loci are near fixation for +alleles, and 50 for −alleles; $\gamma = 0{\cdot}05$, and so $V_g = 2n\gamma\alpha^2 = 10\alpha^2$. The graph shows the allele frequencies, together with the change in genetic variance (scaled relative to α^2) across a region where four pairs of loci switch in opposite directions. The mean remains at the optimum throughout, while the variance increases from $V_g = 2n\gamma\alpha^2 = 10\alpha^2$ to $2\alpha^2(92\gamma+2) = 13{\cdot}2\alpha^2$ at its maximum.

minimal number, or could be larger; indeed, even if the optimum is constant, a set of cryptic clines may be maintained. The simplest situation, then, would be where we have four kinds of loci ($-\to-$, $-\to+$, $+\to-$, $+\to+$), each set changing in parallel: this gives four coupled equations. The outcome could be more complicated, however: it is not clear that all loci in a class will change together.

(ii) *Uniform optimum*

First, suppose that a pair of loci switch in opposite directions. The mean remains at the optimum throughout, and so this pair of clines will have no effect on other such pairs: we have a simple two-locus problem. Integrating (10) leads to a cline of width

$$\frac{4}{1-4\gamma}\quad\frac{\overline{\sigma^2}}{2s\alpha^2},$$

$$p-q = \sqrt{(1-4\gamma)}\tanh\left[\frac{x}{2}\quad\left(\frac{s\alpha^2}{\sigma^2}\right)\sqrt{(1-4\gamma)}\right]. \qquad (11)$$

The increase in genetic variance due to each pair of clines is $(\alpha^2-8\mu/s)$, which compares with an equilibrium variance of $4n\mu/s$. The increase may be fairly small, and restricted to a small region (Fig. 4). In principle, there could be any number of such pairs. However, adjacent clines would tend to annihilate each other, and some mechanism is needed to generate cryptic divergence. Spatially and temporally fluctuating optima could generate divergence (cf. Kondrashov & Yampolsky, 1996; Phillips, 1996), but this may be a weak effect (cf. Lythgoe, 1997).

(iii) *Step change in optimum*

Now, suppose that the optimum changes from $-\Delta/2$ to $\Delta/2$ at $x = 0$. Consider a solution where $m_{0,0}$ loci are near fixation for −alleles, at both $x \ll 0, x \gg 0$; $m_{0,1}$ are near fixation for −alleles for $x \ll 0$, and for +alleles for $x \gg 0$, etc. The simplest solution would be one where the population is at the optimal equilibrium for large x, and where the minimum number of loci change, and change in parallel (i.e. $m_{1,0} = 0$). A more complicated possibility is that some loci might change from + to −, and some larger number in the opposite direction (i.e. $m_{0,1} > m_{1,0} > 0$). If all loci in each of the four classes change in parallel, the solution can be found by following four coupled diffusion equations, with the form of (10).

Fig. 5 shows an example in which the optimum changes abruptly from -4α to $+4\alpha$ at $x = 0$. To the left, 52 loci are near fixation for −alleles, and 48 for +; the mean is at the optimum. To the right, 48 loci are near fixation for −, and 52 for +; thus, four loci change from − to + across the cline. The upper right panel shows that these four loci change in a set of clines with scaled width $w = 2{\cdot}64$. However, the cline in the mean is much narrower ($w = 0{\cdot}59$; upper left of Fig. 5). This is because the allele frequencies at the 96 loci that remain near fixation change slightly in response to the change in optimum. Since these 96 loci contribute most of the genetic variance (upper dashed line in lower left of Fig. 5), they are collectively responsible for most of the selection response. In contrast, most of the *increase* in genetic variance is due to the four loci that shift allele frequencies from low to high (lower dashed line in lower left of Fig. 5). Since the clines at these loci are wider than the clines in the mean, the increase in genetic variance is spread over a broader region than the change in mean. This is a consequence of the inherently weaker response to selection on the variance, compared with selection on the mean.

Because the genetic variance stays approximately constant across the cline, quantitative genetics can be used to make a simple prediction for the change in mean, as for the Gaussian approximation (6). This was derived by neglecting selection on the variance, which is mediated by the skew, κ_3, in (2). This corresponds to neglecting the term (p_i-q_i) relative to the term -2δ in the second term on the right of (10); it should be a good approximation when the mean deviates from the optimum by much more than the effect of a single locus. Including the effect of selection on the variance will steepen the cline. Indeed, if pairs of loci switch over in opposite directions, with the

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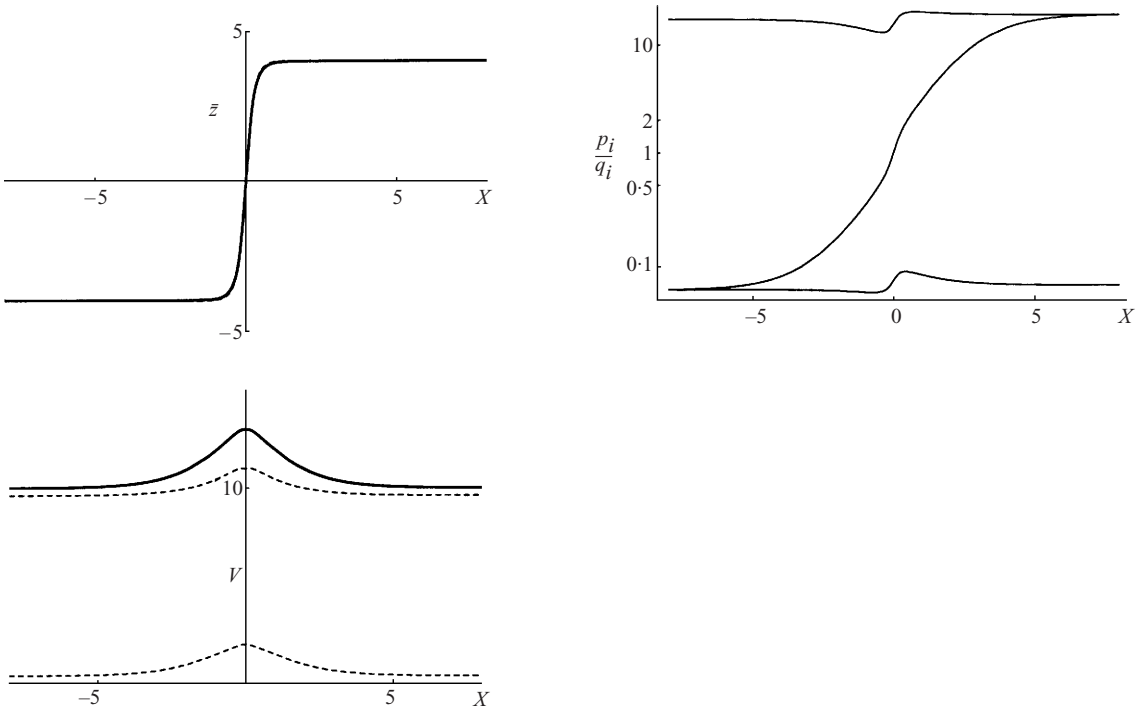

Fig. 5. The cline maintained by a step change in optimum from −4 to +4 (i.e. $\Delta = 8$). For $X \ll 0$, 52 loci are near fixation for −alleles, and 48 for +alleles; the mean is at the optimum. For $X \gg 0$, 48 loci are near fixation for −alleles, and 52 for +alleles; the mean is again at the optimum. Thus, four loci change from − to + around $X = 0$. The top right panel shows the change in allele frequency ratio, p/q, at each of the three kinds of loci. (The ratio is plotted on a logarithmic scale to show changes near to fixation more clearly.) The top left panel shows the abrupt change in mean near $X = 0$. The continuous line in the lower panel shows the change in genetic variance; the dashed lines show the contributions of the 96 loci that remain near fixation (upper dashed line) and of the four loci that change over (lower dashed line). Diffusion equations were solved numerically using the algorithm NDSolve of *Mathematica* 3.0 (Wolfram, 1996). The starting step size was set to 0·2 scaled distance units, to increase the accuracy where selection changes abruptly at $x = 0$. Reducing the step size further, to 0·1, made no appreciable difference, and was much slower.

mean remaining at the optimum (as in the previous section), clines are maintained entirely by selection on the variance.

The genetic variance in mutation–selection balance, with the mean at the optimum, is

$$V_g = \frac{4n\mu}{s} = 2n\gamma\alpha^2.$$

The width, calculated by substituting this predicted V_g into (6), is

$$\frac{2\sigma}{\sqrt{(2sV_g)}} = \frac{\sigma}{\sqrt{(2n\mu)}}.$$

Remarkably, this is independent of the strength of stabilizing selection, s: the direct effect of increased selection is counterbalanced by a reduced genetic variance. In scaled units ($X = x\sqrt{[s\alpha^2/\sigma^2]}$), the predicted cline width is $w = \sqrt{(1/n\gamma)}$, which is 0·45 for the parameters of Fig. 5. The discrepancy between this and the numerical solution, $w = 0{\cdot}59$, arises in part because selection changes abruptly at $x = 0$. However, numerical errors are restricted to a small region around $x = 0$: the difference from the approximation of (6) is less than 1·6% for $|X| > 0{\cdot}2$.

Fig. 5 shows the most straightforward case, where the mean is at the optimum on either side of the cline, and where the minimal number of loci change their predominant allele. Fig. 6 shows an example with the same parameters but where, throughout, 50 loci are near fixation for −alleles and 50 for +alleles. The response to selection is thus entirely due to changes in the frequency of rare alleles. Away from the central step, the mean now deviates slightly from the optimum ($\bar{z} = 3{\cdot}87\alpha$, rather than 4α), and the genetic variance is slightly inflated ($V_g = 11{\cdot}17\alpha^2$ rather than $10\alpha^2$ for $|X| \gg 1$). However, the change in mean and variance across the cline are qualitatively the same: the simple approximation of (6) still fits closely, with a discrepancy of less than 2·5% for $|X| > 0{\cdot}2$.

Fig. 7 shows an example where the mean is at the optimum away from the cline but where more loci change their predominant allele: eight loci shift from − to +, and four loci from + to −. There is now a large increase in variance, from $V_g = 10\alpha^2$ at the edges to $V_g = 15{\cdot}6\alpha^2$ at the centre. The agreement with (6) is less close, though still surprisingly good: the error is less than 8% for $|X| > 0{\cdot}2$.

In principle, loci could change over at different places. This possibility can be investigated by fol-

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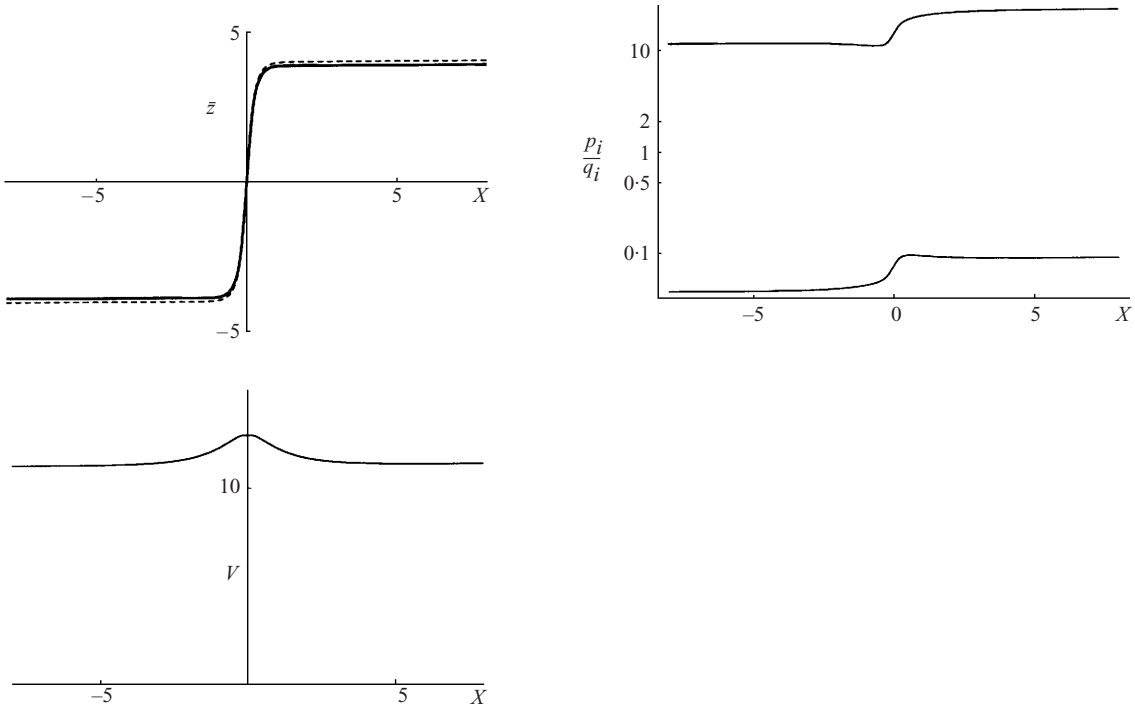

Fig. 6. The cline maintained by a step change in optimum from −4 to +4 (i.e. $\Delta = 8$). Throughout, 50 loci are near fixation for −alleles, and 50 for +alleles. Otherwise, details are as for Fig. 5.

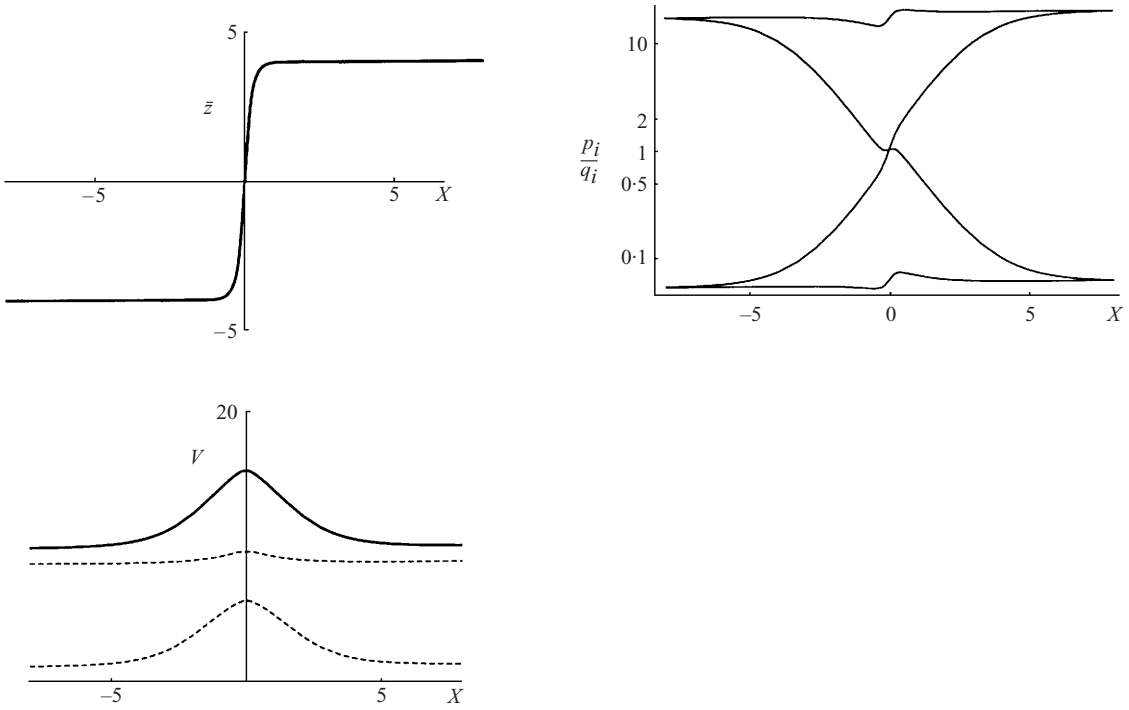

Fig. 7. The cline maintained by a step change in optimum from −4 to +4 (i.e. $\Delta = 98$). For $X \ll 0$, 52 loci are near fixation for −alleles, and 48 for +alleles; the mean is at the optimum. For $X \gg 0$, 48 loci are near fixation for −alleles, and 52 for +alleles; the mean is again at the optimum. However, in contrast to Fig. 5, more loci change their predominant allele: eight loci change from − to + around $X = 0$, and four loci from + to 0. Otherwise, details are as for Fig. 5.

lowing all n diffusion equations, and by starting these from random initial conditions to ensure that if the simple symmetric solution is unstable, it will evolve towards some asymmetric solution in which clines at different loci in the same class are scattered. This is not feasible for 100 loci, and so one cannot be sure

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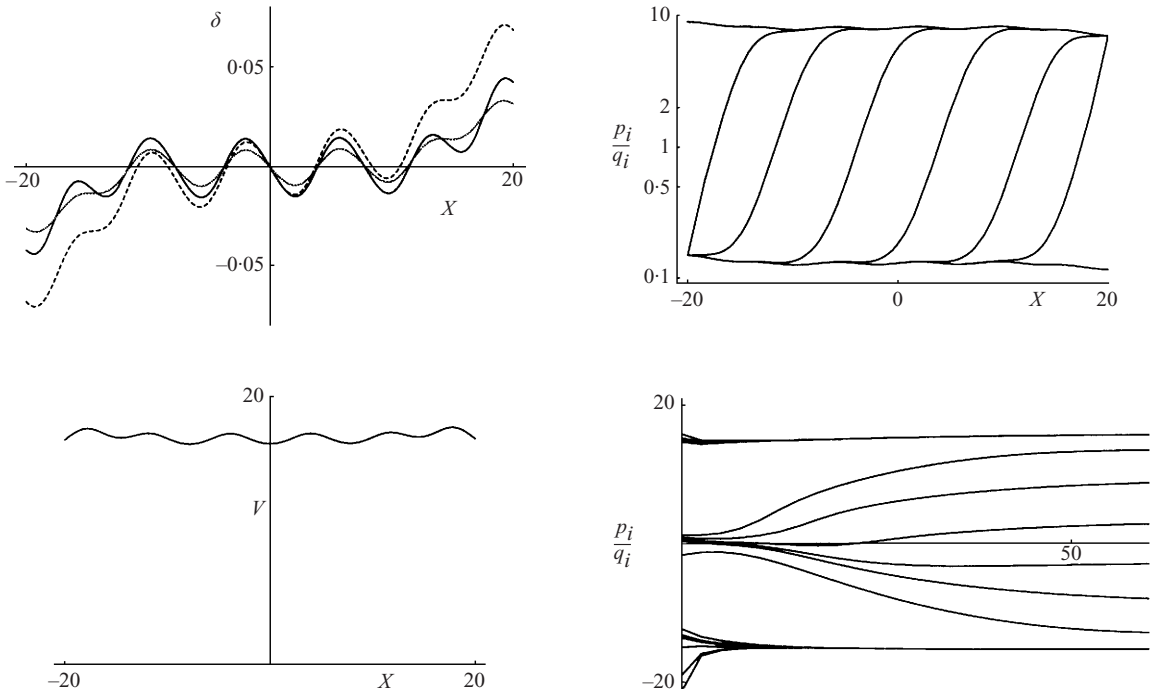

Fig. 8. The top right panel shows the allele frequency ratios, p/q, at 20 loci that determine a polygenic trait subject to stabilizing selection. The optimum changes linearly, as $z_{opt} = \beta X$, with $\hat{\beta} = 0{\cdot}2$; thus, the optimum changes from -4 at $X = -20$ to $+4$ at $X = +20$. To the left ($X = -20$), seven loci are near fixation for $+$alleles, while to the right ($X = +20$), 13 loci are near fixation for $+$alleles. Six loci change from low to high frequency of $+$alleles, in six roughly evenly spaced clines. The upper and lower lines show the allele frequencies at those loci that remain near fixation for the same allele throughout. The top left panel shows the deviation from the optimum, plotted against distance, and scaled relative to the effect of a single allele: $\delta = (\bar{z} - z_{opt})/\alpha$. The continuous line shows the numerical solution to the 20 coupled diffusion equations. The dashed line shows the prediction of (13). The dotted line shows the prediction obtained by solving $0 = pq(p-q-2\delta) - \gamma(p-q)$, instead of using the approximation of (12). The lower left panel shows the genetic variance plotted against distance. The lower right panel shows cline position plotted against time. Cline position is defined by the net frequency of the $+$allele, integrated over the whole range. The six loci that changed from low to high frequency of the $+$allele were initiated as clines scattered randomly around $X = 0$ (left of figure); the other 14 loci were started at random allele frequencies randomly scattered around their equilibrium values. Calculations were made up to $T = 100$.

that the solutions in Figs 5–7 are stable. However, runs for 20 loci show no tendency for clines to scatter; since the directional selection due to the deviation of the mean from the optimum is sharply concentrated over the central region (a region much narrower than the underlying clines) no such tendency is expected.

(iii) *A linear gradient*

Suppose now that there is a shallow linear gradient in the optimum, $z_{opt} = \beta x$. Initially, suppose that the population is everywhere in the same state, with loci near fixation for one or other allele. Where the optimum deviates sufficiently from the initial mean, this state becomes unstable, and some random locus will shift to near fixation for another allele. A set of clines will form, and will move so as to reduce the deviation of the mean from the optimum. The habitat will be divided into regions in which different numbers of loci are near fixation for $+$alleles; within these regions, allele frequencies will change smoothly, whilst between them, there will be a cline of width $\sim \sqrt{(\sigma^2/s\alpha^2)}$ at a single locus (Fig. 8). Despite abrupt changes at the underlying loci, the mean remains close to the optimum throughout ($\delta = (\bar{z} - z_{opt})/\alpha < 0{\cdot}046$; top left of Fig. 8). The genetic variance is also little affected by the sharp shifts in allele frequency (lower left of Fig 8), primarily because most variance is contributed by loci that remain near fixation: shifts at single loci make a relatively small contribution. If the mean coincides with a spatially uniform optimum, then the genetic variance is $V_g = (4n\mu/s) = 4$. The maximum genetic variance contributed by a cline at a single locus is $\alpha^2/2$, which is an order of magnitude smaller than the background contribution of mutation at the majority of loci, which are near fixation.

Some analytic results can be obtained for the limiting case of a shallow gradient. First, consider a region in which there are m loci near fixation for $-$alleles, and M for $+$alleles. Let the frequencies of the $+$allele at these loci be P, $1-Q$, respectively;

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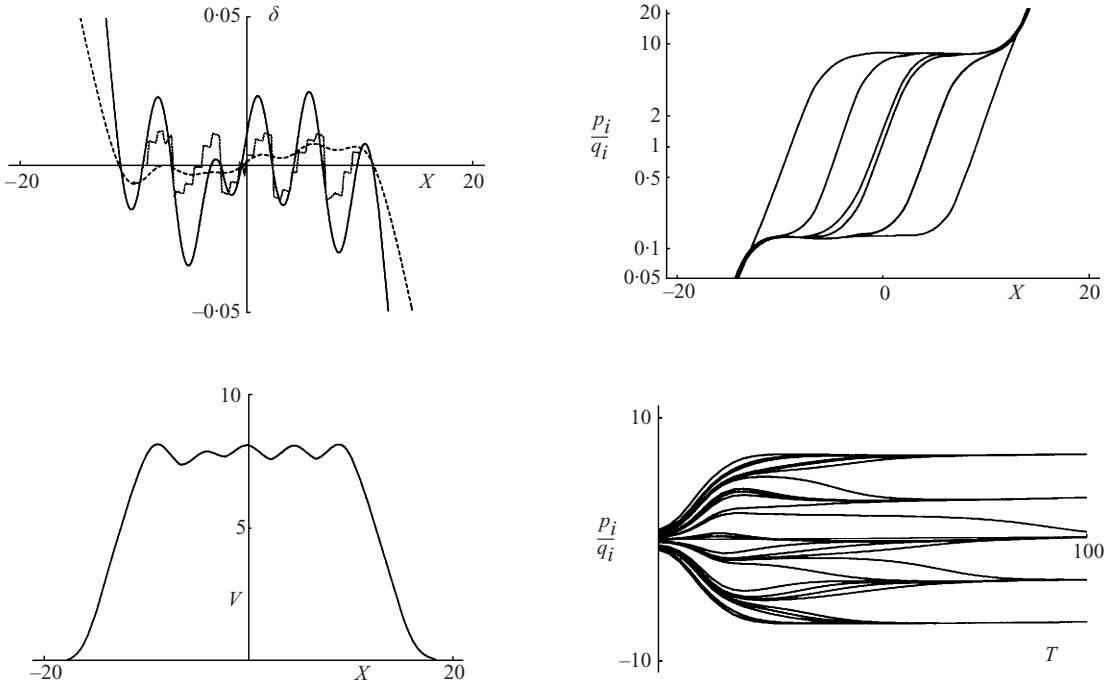

Fig. 9. The top right panel shows the allele frequency ratios, p/q, at 30 loci that determine a polygenic trait subject to stabilizing selection. Details are as for Fig. 8, but for $\hat{\beta} = 2$.

$P, Q \ll 1$. Further, assume $4ny \gg 1$. With a spatially uniform optimum, the equilibria are, from (10):

$$P = \frac{\gamma}{1+2\delta} \quad Q = \frac{\gamma}{1-2\delta},$$

where

$$\delta = \frac{(\bar{z}-z_{\text{opt}})}{\alpha} = \frac{(M-m)(1-2\gamma)-z_{\text{opt}}}{1+4n\gamma}. \tag{12}$$

If δ is indeed small, then clines at each locus have the same form as with a uniform optimum (11). Suppose that J such clines are centred at X_0, and separate a region to the left, where $\{m, M\}$ loci are near fixation for $-$, $+$alleles, from a region to the right, where $\{m-J, M+J\}$ loci are near fixation for $-$, $+$alleles. Approximating $\sqrt{(1-4\gamma)}$ by $(1-2\gamma)$, the mean in this region deviates from the optimum by

$$\delta = \frac{1}{1+4(n-J)\gamma} \left\langle \left\{ M-m+J\left[1+\tanh\left(\frac{(X-X_0)}{2}(1-2\gamma)\right)\right]\right\} (1-2\gamma)-z_{\text{opt}} \right\rangle. \tag{13}$$

In the example of Fig. 8, one locus changes at a time, and so $J = 1$. The top left panel in Fig. 8 shows that the prediction of (13) (dashed line) is reasonably close to the numerical solution of (10) (continuous line), but overestimates the deviation from the optimum towards the edges. The quantitative disagreement is not surprising since, in this example, mutation at each locus is appreciable ($\gamma = 0{\cdot}1$); the total mutation rate is not very large ($4n\gamma = 4$); and the gradient is steep enough that the clines overlap (top right of Fig. 8). Most of the error arises from approximating the solutions to $0 = pq(p-q-2\delta)-\gamma(p-q)$ by $\gamma/(1+2\delta)$, $1-\gamma/(1-2\delta)$ (12). Agreement is much closer if the exact solution to this cubic equation is used (dotted line in top left of Fig. 8).

If the gradient in the optimum is steep, the component clines overlap, and one can no longer separate the range into homogeneous regions separated by sharp clines. However, numerical solutions suggest that the outcome is qualitatively similar, in that a set of scattered clines is maintained. Fig. 9 shows an example with $\sigma\beta = 2\sqrt{(s\alpha^2)}$, and $n = 30$ loci, on a habitat which runs from $x/\sigma\sqrt{(s\alpha^2)} = -20$ to $+20$; the scaled mutation rate is $\gamma = 0{\cdot}1$. At the edges, the optimum is $\pm 40\alpha$, and so the population approaches fixation for all $-$alleles, or all $+$alleles; the mean is then at its maximum possible magnitude of $\pm 30\alpha$. Initially, clines are randomly scattered around the concordant solution. This solution is unstable, and five clusters, each of six clines, are formed (upper right of Fig. 9). At the edges, the mean necessarily deviates substantially from the optimum. However, the mean remains quite close to the optimum within the central region: for $|X| < 10$, $(\bar{z}-z_{\text{opt}}) < 0{\cdot}31\alpha$ (upper left of Fig. 9). Though small relative to the change in mean (40α), this deviation is substantially larger than seen for a shallow gradient

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($\sigma\beta = 0{\cdot}2\sqrt{(s\alpha^2)}$; top left of Fig. 8). The two approximations used in Fig. 8 now underestimate the deviation from the optimum (dashed and dotted lines in upper left of Fig. 9). In a spatially uniform population, $V_g = (4n\mu/s) = 6\alpha^2$. Each cline contributes an additional genetic variance of $\alpha^2/2$ at its centre. Thus, we expect a genetic variance of approximately $3a^2$ at the centre of a cluster of six clines, plus a contribution of $4{\cdot}8\alpha^2$ due to mutation at the remaining 24 loci. This rough prediction of $V_g = 7{\cdot}8\alpha^2$ is close to the value observed across most of the range. At the edges, however, the genetic variance tends to zero as the trait approaches its limit, and loci approach fixation (lower left of Fig. 9).

5. Linkage disequilibria

When a trait is determined by many loci, selection on each becomes small, and so allele frequencies change slowly. In the short term, the genetic variance then changes primarily because of changes in linkage disequilibrium (Bulmer, 1971, 1985). When selection or gene flow are strong, the genetic variance can change substantially, even when loci are loosely linked. The limit of very many unlinked loci is described by the 'infinitesimal model', under which offspring are normally distributed about the mean breeding value of the parents, with a constant variance independent of parental phenotype (Fisher, 1918; Bulmer, 1971). We now consider how quantitative traits respond to spatially varying selection under the infinitesimal model.

Analytical results are complicated by the need to examine strong selection and gene flow: weak forces have negligible effects on the variance under the infinitesimal model. Therefore, continuous time is used, allowing gene flow to be described by diffusion, as in the weak selection approximations above. However, note that quadratic selection does not maintain a Gaussian distribution in the absence of gene flow, as would be the case with Gaussian selection and discrete generations. Another complication is that with continuous mortality and reproduction, we cannot suppose that population density remains constant, as was assumed in the discrete-time models above.

Suppose that in some small interval of time, δt, a fraction δt of individuals produce offspring according to the infinitesimal model; these disperse with variance $\sigma^2\delta t$; and there is density- and genotype-dependent mortality at a rate $(\mu[\rho_T] + s/2\,(z - z_{\mathrm{opt}})^2)\delta t$ where $\rho_T \equiv \int\rho[z]\,\mathrm{d}z$ is the net population density. The mortality is the sum of a density-dependent mortality, and a mortality due to stabilizing selection towards an optimum z_{opt}. Time has arbitrarily been scaled relative to the rate of reproduction; reproduction may be density-dependent, but such dependence can be absorbed into the other parameters. The equation for total density is:

$$\frac{\partial\rho_T}{\partial t} = \frac{\sigma^2}{2}\frac{\partial^2\rho_T}{\partial x^2} - \mu[\rho_T]\rho_T - \frac{s}{2}(V + (\bar{z} - z_{\mathrm{opt}})^2)\rho_T + \rho_T. \tag{14}$$

The equation for the distribution of breeding values, $\psi = \rho/\rho_T$, is

$$\begin{aligned}\frac{\partial\psi}{\partial t} = {} & \frac{\sigma^2}{2}\frac{\partial^2\psi}{\partial x^2} + \sigma^2\frac{\partial\log[\rho_T]}{\partial x}\frac{\partial\psi}{\partial x} \\ & - \frac{s}{2}((z - \bar{z})^2 + 2(z - \bar{z})(\bar{z} - z_{\mathrm{opt}}) - V)\,\psi \\ & + \left(\int \frac{\psi[z^*]\,\psi[z^{**}]}{\sqrt{(\pi V_{\mathrm{LE}})}}\exp \right. \\ & \left. \left[-\frac{1}{V_{\mathrm{LE}}}\left(z - \frac{(z^* + z^{**})}{2}\right)^2\right]\mathrm{d}z^*\,\mathrm{d}z^{**}\right) - \psi.\end{aligned} \tag{15}$$

Variations in density, due to variations in mean fitness, cause asymmetric gene flow (second term on the right of (15). This can lead to a positive feedback, such that poorly adapted regions decrease in density, and so receive more locally maladapted immigrants (Kirkpatrick & Barton, 1997). For simplicity, we assume here that density is strongly regulated towards a spatially uniform carrying capacity: μ is zero below a threshold, and very high above it. Then, the population attains the threshold density provided that the mortality due to selection, $s/2(v + (\bar{z} - z_{\mathrm{opt}})^2)$, does not exceed the rate of reproduction (here set to 1).

Equation (15) can readily be solved numerically using Fourier transforms (Turelli & Barton, 1994). Fig. 10 shows an example, in which the optimum changes by $\Delta = 4\sqrt{(V_{\mathrm{LE}})}$, and stabilizing selection has strength $s = 0{\cdot}4$. This maintains a sharp cline, with width $2{\cdot}48\sigma/\sqrt{(2sV_{\mathrm{LE}})}$; the mixing of populations increases the genetic variance to $2{\cdot}17V_{\mathrm{LE}}$, over a region of similar width. This contrasts with a reduction in genetic variance outside the cline, to $0{\cdot}66V_{\mathrm{LE}}$ due to the negative linkage disequilibria generated by stabilizing selection. The selection strength was chosen as the largest value at which the genetic load does not exceed the fecundity; if s were any larger, the population would collapse at the centre, and the cline would become much steeper.

Under the Gaussian approximation, and constant density, (15) gives an equation for the mean which is identical to (4). The variance is given by

$$\frac{\partial V}{\partial t} = \frac{\sigma^2}{2}\frac{\partial^2 V}{\partial x^2} + \sigma^2\left(\frac{\partial\bar{z}}{\partial x}\right)^2 - sV^2 - \tfrac{1}{2}(V - V_{\mathrm{LE}}). \tag{16}$$

(Felsenstein (1977) has analysed this model for the case of a linear gradient, but allowing for a finite

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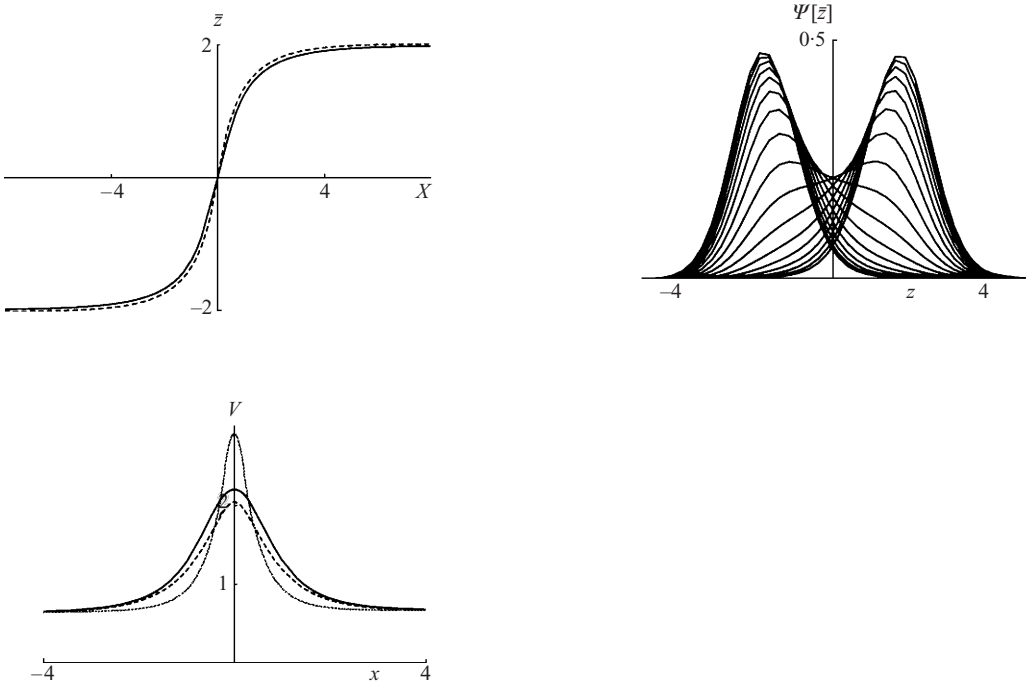

Fig. 10. A step cline in a trait determined by an infinite number of unlinked loci. The optimum changes by $\Delta = 4\sqrt{V_{LE}}$ at $x = 0$, and stabilizing selection has strength $s = 0{\cdot}4$. Distance, X, is scaled relative to $\sigma/\sqrt{(2sV_{LE})}$. The top right panel shows the distribution of breeding values, z. Distributions are superimposed for $X = -8$ to $X = +8$, in unit steps. The top left panel shows the cline in the mean. The continuous line is the numerical solution of (15), while the dashed line is the Gaussian approximation of (16). The bottom left panel shows the same for the variance; the more sharply peaked dotted line shows the quasi-linkage equilibrium approximation. Calculations were started from a sharp step, and continued to $t = 10$, by which time the population was close to equilibrium.

number of loci with a multivariate normal distribution of effects.) These equations for the mean and variance are similar to (4), (5), which describe changes in allele frequencies. However, the inflation of the variance by gradients in the mean, and the reduction by selection, are both greater by a factor equal to twice the effective number of loci (second and third terms in (16). Also, genetic variance is maintained by the rapid segregation of variation within families ($\sim V_{LE}/2$), rather than by a weaker mutation rate (V_m in (3)). The dashed lines in Fig. 10 show that this approximation is close, even when selection is so strong that the distribution in the cline is appreciably non-Gaussian (top right panel in Fig. 10).

A more drastic approximation is to assume 'quasi-linkage equilibrium' (Turelli & Barton, 1994): that is, to assume a short-term balance between the forces generating genetic variance, and recombination. Then, V is given by the solution to (16), disregarding the first diffusion term on the right. This approximation applies when selection is weak, and numerical results for allele frequency clines show that it gives an accurate approximation to linkage disequilibrium for moderately strong selection (Barton & Gale, 1993; Barton & Shpak, 1999; Kruuk *et al*., 1999). It can yield simple analytical results, by reducing the system to a single equation for the mean. However, in this example it performs poorly: gene flow and selection are so strong that the excess variance diffuses over a broad region before a quasi-equilibrium is reached (dotted line in bottom left panel of Fig. 10).

6. Discussion

Understanding the evolution of quantitative traits across clines is hindered by our ignorance of the processes which maintain polygenic variation. Unless there are very many genes, the outcome depends on genetic details of which we are usually ignorant. The models analysed here are restricted to stabilizing selection towards a spatially changing optimum, and to the separate effects of allele frequency change, and of linkage disequilibria. However, some general features do emerge, which are likely to apply more widely. First, the mean changes over $\sim \sigma/\sqrt{(2sV)}$, regardless of the genetic basis of the trait (Slatkin, 1978). Because the response to selection is proportional to the total genetic variance, summed over all loci, this scale may be just a few dispersal ranges, $\sim \sigma$, and so the mean can track the optimum closely. Second, with discrete alleles the underlying clines change over a much broader scale ($\sim \sigma/\sqrt{2s\alpha^2}$), because individual alleles are subject to much weaker selection than the trait mean. Consequently, the

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genetic variance may change over a much broader region than the change in mean. Third, in the infinitesimal limit, linkage disequilibria can generate a substantial increase in variance, which is concentrated around the region where the cline in the mean is steepest. The increased variance accelerates the response to selection, steepens the cline, and so further increases the variance. This positive feedback may lead to a sharp step at the centre of a polygenic cline, a phenomenon found in other models of multilocus clines (Barton, 1983; Baird, 1991; Kruuk *et al*., 1999).

Under stabilizing selection, the same phenotype can be maintained by many different combinations of alleles (Wright, 1935). Thus, while the trait mean may closely track the optimum, and the trait variance may stay approximately constant, there can be considerable cryptic divergence in the constituent allele frequency clines. This discordance suggests caution in interpreting clines in quantitative trait loci (QTL). In particular, the change in mean and variance may be influenced at least as much by a large number of loci which remain near fixation as by a small number which shift from low to high frequency, and which may therefore be identified as QTL. Moreover, even if a QTL is identified which accounts for a large part of the change in mean, there may be many other divergent genes which alter the mean in opposite directions, and so are not detected.

Goldstein & Holsinger (1992) suggest that gene flow between populations containing alternative allelic combinations may maintain substantial genetic variance. For the parameters illustrated in Figs. 4–9, the increase in genetic variance due to gene flow is smaller than the standing variance due to mutation. However, in these examples a rather high mutation rate is assumed. Since in general mutation rates are much lower than migration rates, this mechanism is potentially important. The key difficulty is that different allelic combinations must be established despite the gene flow which is required to maintain variation within populations. In the island model at least, random drift is unlikely to achieve this unless the number of migrants, Nm, is small (Coyne *et al*., 1997, appendix); then, m is so small that little variation is maintained. A spatially varying optimum can generate genetic variance. Linkage disequilibria maintain an excess variance equivalent to an increase in V_{LE} of $2\sigma^2\beta^2$, where $\beta = \partial\bar{z}/\partial x$ is the gradient in trait mean (16). In the continuum of alleles model, mixing along a linear cline inflates the genetic variance to $\sim \sqrt{(\sigma^2\beta^2/s)}$ for $2nV_m \ll \sigma^2\beta^2$. This is likely to be larger than the contribution of linkage disequilibria unless the genetic load due to mixing of populations approaches 1. With discrete alleles, a shift at one locus causes a change in trait mean of 2α. Therefore, a gradient in optimum of β requires loci to shift at a rate of $\beta/2\alpha$ per unit distance. The increase in variance per cline, integrated over the cline, is $\sim \sqrt{(4\sigma^2\alpha^2/s)}$ (13). Hence, the net increase in variance is $\sqrt{(\sigma^2\beta^2/s)}$, just as for a continuum of alleles model (see Barton & Turelli, 1989). Taking the strength of stabilising selection as $s = 0{\cdot}2\sqrt{V_{\mathrm{E}}}$ (cf. Turelli, 1984), we see that substantial heritability could be maintained if the optimum changes by $\sigma\beta \sim 0{\cdot}2\sqrt{V_{\mathrm{E}}}$ in one dispersal range.

There has been surprisingly little empirical work on the quantitative genetics of clines. While there are many studies of morphological change across clines or hybrid zones (e.g. Endler, 1977; Barton & Hewitt, 1985), most reduce trait variation to a discriminant function, and concentrate on changes in mean. The theory presented here suggests several ways of investigating polygenic clines in nature. First, any increase in genetic variance due to changing allele frequencies should be spread over a wider region than the cline in mean; the ratio of widths should give a measure of the number of loci involved. Secondly, even where the trait mean is uniform, there may be cryptic divergence at the underlying loci. This might be revealed by an increase in genetic variance either in nature, or in crosses between divergent populations. Finally, the increase in genetic variance due to linkage disequilibrium can be distinguished from other sources of excess variance by examining covariances between unrelated traits, or associations between Mendelian markers: all are generated in the same way by the mixing of populations. Nurnberger *et al*. (1995) found significant covariances between a variety of unrelated traits in the *Bombina* hybrid zone, but also found that these were half as strong as expected from associations between Mendelian markers. However, Kruuk (1997), using a much larger sample, found good agreement between these two measures of linkage disequilibrium, giving confidence that the variance due to linkage disequilibrium can be estimated from associations between traits and markers. Since linkage disequilibria are primarily generated by dispersal, such measures also lead to robust estimates of dispersal rates. It may be that the study of clines involving multiple traits and loci can shed light on the selection which maintains them, and on the genetic basis of divergence in quantitative traits.

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