THE THEORY OF A CLINE

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The intensity of natural selection, that is to say the relative fitness of several genotypes or phenotypes of the same species, can be estimated in several ways. Direct estimation is only possible in men, where, for example, 100 haemophilics or achondroplasics can be followed from birth, and their progeny compared with that of 100 normals. Similar observations in plants and animals are only possible under artificial conditions. Several indirect methods are possible. Some are dynamical. For example, the rate of spread of melanic mutants in industrial districts is roughly known, and a little is known as to the disappearance of mutants released in nature.

Others are statical. Thus on the basis of population counts Fisher (1939) showed that heterozygous dominants of *Paratettix* are fitter than the recessive type, homozygotes less so. This gives rise to balanced polymorphism. In some polymorphic species the frequency of the types is a function of the geographical situation of the populations studied. And it is sometimes found that the frequency of one type increases fairly steadily in a certain direction. Thus the Arctic skua, *Stercorarius parasiticus*, exists in two sharply distinguished types, a pale and a dark, probably genetically determined. The frequency of the pale type increases from about 25 to 75 % as the North Pole is approached (Southern, 1943). Huxley (1939, 1942) has called a gradient of this kind a cline, and cites numerous examples. It will be shown that in certain cases a cline can give quantitative information regarding the intensity of natural selection.

A cline may be due to migration from the centre of origin of a gene. The cline in the frequency of the *B* agglutinogen in our own species with a maximum in central Asia appears to be of this type. Here there is no evidence that *B* makes for greater fitness in central Asia than in Europe or China, and the situation is probably unstable. This human cline may well disappear in a few thousand years as a result of interbreeding, and will almost certainly become less intense. On the other hand, the cline of increasing human skin colour towards the tropics may well have a selective value, and is therefore more likely to persist.

But a cline may also be due to the fact that one type is favoured by selection in one part of the habitat, the other in another part. Random migration serves to keep the population mixed, either throughout its area or in a border zone. A clear case was analysed by Sumner (1929 *a*, *b*, 1932) and Blair (1944). The deer-mouse, *Peromyscus polionotus*, inhabits Florida and Alabama. On the sandy beaches of the Gulf of Mexico it is represented by the lighter coloured subspecies *leucocephalus* and *albifrons*, which are less visible than the type against a background of white sand, and more so against ordinary soils. This is believed to give them an advantage in their special habitats, and a disadvantage elsewhere. The difference is partly, but not wholly, due to a dominant gene, **Wc**, causing white cheeks in the coastal subspecies. The subspecies intergrade with the type over a belt about 40 miles wide stretching inland from the beaches. There is reason to think that the situation is fairly stable, the gene **Wc** being advantageous on the beaches and harmful far inland, and similarly for the other genes present in the coastal

subspecies. Such a situation could be due to one-way migration from a crowded to a less crowded area. Since mice of the subspecies *polionotus polionotus* seem to be rare on the beaches, this would imply that the beaches are overcrowded, or at least that mice leave them and do not enter them. However, as there is no published evidence to this effect we shall assume that migration is at random, that is to say, that a mouse is as likely to move towards the beaches as inland, regardless of its colour.

We can analyse such a case mathematically if we make the following assumptions:

(1) A species lives in an area which is supposed to be plane and infinite. Actually it must be so large that regions exist where there is no appreciable polymorphism.

(2) The density is equal through this area.

(3) An autosomal dominant **A** and its allelomorph **a** cause polymorphism.

(4) The plane is sharply divided by a straight boundary into two halves. x is the distance of any point from the boundary. In the half plane where x is positive, **aa** zygotes have a fitness $1+K$ times that of **AA** and **Aa**. In the other half plane their fitness is $1-k$. K and k are small and positive.

(5) The animals have an annual generation and one only.

(6) They migrate at random. A group of mice born at distance x breed at distances $x+t$, where t is symmetrically distributed about zero with unit standard deviation. That is to say, we take as our unit of distance the root of the mean square of the distances travelled by an animal between birth and breeding in the direction normal to the boundary. The distribution need not be normal provided it is symmetrical and has finite moments.

(7) Selection occurs at the place of breeding, not of birth. This assumption simplifies the argument but does not affect the result appreciably.

(8) Mating is at random between the different types.

(9) The population is in equilibrium. The frequency of the gene **a** in adults at a distance x from the boundary is y, the frequency of the recessive phenotype **aa** being therefore $z=y^2$.

It is to be noted that many of these assumptions can be relaxed by making suitable allowances. Thus a barrier which is difficult to pass would be the equivalent of an increased distance.

When y or z are plotted against x we must get a curve of the type shown in Fig. 1, $y \to 0$ as $x \to -\infty$, and $y \to 1$ as $x \to \infty$. When $x=0$, i.e. on the boundary, y has a definite value b which is later determined. Also dy/dx is continuous at the boundary, since any discontinuity would be smoothed out by migration. But d^2y/dx^2 changes sign abruptly at the boundary, when $x=0$.

First let us calculate the effect of migration. Since migration does not depend on genotype, we can consider the genes, not the zygotes, as migrating. Let $f(t)$ be the frequency distribution function of t, symmetrical about zero. At the point $x+t$ the gene frequency is

$$Y = y + t\frac{dy}{dx} + \frac{t^2}{2!}\frac{d^2y}{dx^2} + \dots.$$

As a result of 1 year's migration the frequency at x changes from y to

$$\int_{-\infty}^{\infty} Y f(t)\,dt = y + \frac{1}{2}\frac{d^2y}{dx^2}\int_{-\infty}^{\infty} t^2 f(t)\,dt + \frac{1}{4!}\frac{d^4y}{dx^4}\int_{-\infty}^{\infty} t^4 f(t)\,dt + \dots$$

$$= y + \frac{\overline{t^2}}{2!}\frac{d^2y}{dx^2} + \frac{\overline{t^4}}{4!}\frac{d^4y}{dx^4} + \dots.$$

For a normal distribution this is

$$y + \frac{\sigma^2}{2!}\frac{d^2y}{dx^2} + \frac{3\sigma^4}{4!}\frac{d^4y}{dx^4} + \frac{15\sigma^6}{6!}\frac{d^6y}{dx^6} + \dots.$$

Provided K and k are sufficiently small and the distribution is not too leptokurtic, we can neglect terms after the second, and we have already assumed $\sigma^2 = 1$, so we have the familiar diffusion expression

$$Y = y + \frac{1}{2}\frac{d^2y}{dx^2}.$$

As a result of selection the ratios of the genotypes are altered, when $x > 0$, from

$$(1-y)^2 \mathbf{AA} : 2y(1-y)\,\mathbf{Aa} : y^2\mathbf{aa}$$

to

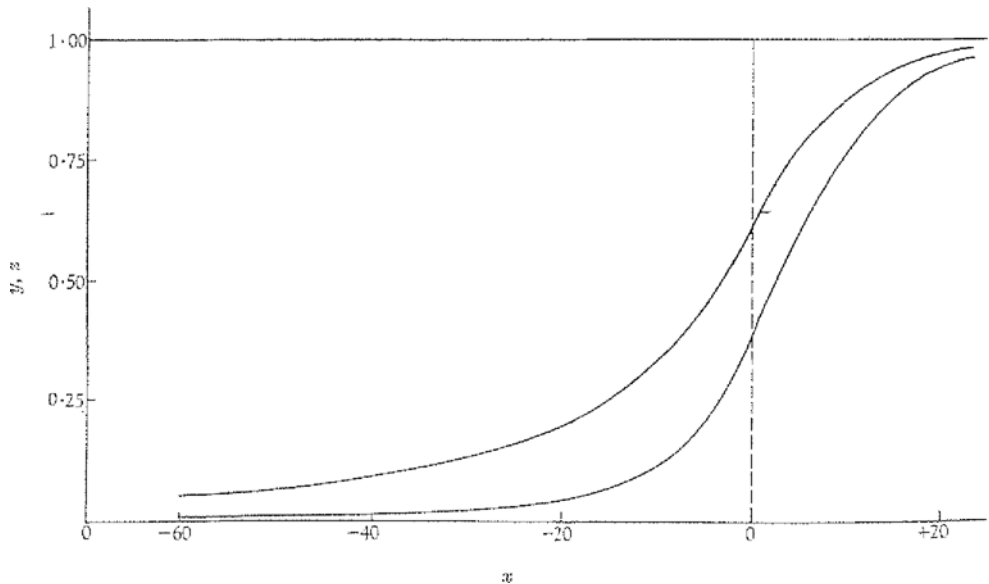$$(1-y)^2 \mathbf{AA} : 2y(1-y)\,\mathbf{Aa} : (1+K)\,y^2\mathbf{aa}.$$

Fig. 1. Abscissa: distance from boundary, the unit being the root mean square of the distance migrated per generation. Ordinates: upper curve, frequency of recessive genes; lower curve, frequency of recessive zygotes. To the right of the boundary the fitness of aa is 1·01 that of **AA** or **Aa**, to the left it is 0·99 that of **AA** or **Aa**.

Thus the frequency of a is altered from y to $y + Ky^2/1 + Ky^2$, or if K is small, to $y + Ky^2(1-y)$ approximately. But selection and migration are in equilibrium. Hence

$$\left.\begin{aligned}
\frac{d^2y}{dx^2} &= -2Ky^2(1-y) \quad (x > 0), \\
\frac{d^2y}{dx^2} &= ky^2(1-y) \quad (x < 0).
\end{aligned}\right\} \tag{1}$$

and similarly

To solve this pair of differential equations, put $p = dy/dx$. Then, for $x > 0$,

$$p\frac{dp}{dy} = -2Ky^2(1-y),$$

so

$$\tfrac{1}{2}p^2 = \int p\,dp = -2K\int y^2\,(1-y)\,dy$$

$$= C - 2K\left(\frac{y^3}{3} - \frac{y^4}{4}\right).$$

Since when $x \to \infty$, $y \to 1$ and $p \to 0$, $C = \tfrac{1}{6}K$, whence

$$\left(\frac{dy}{dx}\right)^2 = \tfrac{1}{3}K\,(1 - 4y^3 + 3y^4)$$

$$= \tfrac{1}{3}K\,(1-y)^2\,(1 + 2y + 3y^2).$$

Similarly, when $x < 0$, $\qquad \left(\dfrac{dy}{dx}\right)^2 = 2C' + 4k\left(\dfrac{y^3}{3} - \dfrac{y^4}{4}\right).$

When $x \to -\infty$, $y \to 0$ and $p \to 0$, so $C' = 0$, and

$$\left(\frac{dy}{dx}\right)^2 = \tfrac{1}{3}ky^3\,(4 - 3y).$$

Now when $x = 0$, $y = b$, and dy/dx has the same value for both branches of the curve. Hence

$$\tfrac{1}{3}K\,(1 - 4b^3 + 3b^4) = \tfrac{1}{3}k\,(4b^3 - 3b^4),$$

or

$$3b^4 - 4b^3 + \frac{K}{K+k} = 0. \tag{2}$$

This equation, giving the value of y on the boundary, has one and only one root between 0 and 1. It is readily solved by iterating

$$b = \left[\left(1 + \frac{k}{K}\right)\left(\frac{4}{b} - 3\right)\right]^{-\frac{1}{3}}.$$

Values of b in terms of K/k are given in Table 1.

Table 1

K/k	0	0·0037	0·0279	0·0913	0·2183	0·4545	0·9055	1	1·5753	2·821	4·531	8·259	18·49	∞
b	0	0·1	0·2	0·3	0·4	0·5	0·6	0·6143	0·7	0·75	0·8	0·85	0·9	1

It will be seen that even when selection is much more intense in one area than another, an appreciable number of genes will diffuse into the area of intense selection against them. The value of dy/dx at the boundary is

$$\left[\frac{Kk}{3\,(K+k)}\right]^{\frac{1}{2}}.$$

When $x > 0$, $\qquad \dfrac{dy}{dx} = \sqrt{\dfrac{K}{3}}\,(1-y)\,\sqrt{(1 + 2y + 3y^2)},$

so $\qquad x = \left(\dfrac{3}{K}\right)^{\frac{1}{2}}\displaystyle\int_b^y \frac{du}{(1-u)\,\sqrt{(1 + 2u + 3u^2)}},$

or if $\qquad v = \dfrac{1}{1-u},$

$$x = (2K)^{-\frac{1}{2}}\int_{1/(1-b)}^{1/(1-y)} \frac{dv}{\sqrt{[(v - \tfrac{2}{3})^2 + \tfrac{1}{18}]}}$$

$$= (2K)^{-\frac{1}{2}}\Big[\sinh^{-1}(3\sqrt{2}v - 2\sqrt{2})\Big]_{1/(1-b)}^{1/(1-y)}$$

$$= (2K)^{-\frac{1}{2}}\left[\sinh^{-1}\left\{\frac{\sqrt{2}\,(1 + 2y)}{1-y}\right\} - \sinh^{-1}\left\{\frac{\sqrt{2}\,(1 + 2b)}{1-b}\right\}\right].$$

When $x < 0$,
$$\frac{dy}{dx} = \left(\frac{k}{3}\right)^{\frac{1}{2}} y^{\frac{3}{2}} (4 - 3y)^{\frac{1}{2}},$$

so
$$x = k^{-\frac{1}{2}} \int_y^b \frac{du}{\sqrt{[u^3 (\frac{4}{3} - u)]}},$$

or if
$$v = \sqrt{\left(\frac{1}{u} - \frac{3}{4}\right)},$$

$$x = \sqrt{3} \int_{\sqrt{(1/y - \frac{3}{4})}}^{\sqrt{(1/b - \frac{3}{4})}} dv$$
$$= \frac{1}{2}\left[\sqrt{\left(\frac{3 (4 - 3b)}{b}\right)} - \sqrt{\left(\frac{3 (4 - 3y)}{y}\right)}\right].$$

We may now suppose that m^2 is the mean square of random migration distance, so that the root mean square in the x direction is $m/\sqrt{2}$. We then have

$$\frac{2K^{\frac{1}{2}}}{m} x = \sinh^{-1}\left[\frac{\sqrt{2} (1 + 2y)}{1 - y}\right] - \sinh^{-1}\left[\frac{\sqrt{2} (1 + 2b)}{1 - b}\right] \quad \text{for } x > 0,$$

and
$$\frac{2}{m} \sqrt{\left(\frac{2k}{3}\right)} x = \sqrt{\left(\frac{4}{b} - 3\right)} - \sqrt{\left(\frac{4}{y} - 3\right)}, \qquad\qquad (3)$$

or
$$y = \frac{bm^2}{m^2 - mx \sqrt{[\frac{2}{3}k (4 - 3b)]} + \frac{2}{3}bkx^2}, \quad \text{for } x < 0,$$

where b is given by equation (2), and $y = z^2$, z being the frequency of recessives.

Fig. 1 shows the frequencies y of the recessive gene, and z that of recessive zygotes, when $K/m^2 = k/m^2 = 0.01$. The interquartile range of y is about $0.79m/\sqrt{K}$ when both quartiles are in the positive region, and $1.27m/\sqrt{k}$ when both are in the negative region. Otherwise the value is intermediate. The interquartile range of $z = y^2$, i.e. the range of x where y varies between $\frac{1}{2}$ and $\sqrt{3}/2$, is $0.811m/\sqrt{K}$, when both values of x are positive, $0.590m/\sqrt{k}$ when both values are negative, and intermediate when one falls on each side of the boundary.

For *Peromyscus bairdii*, Blair's (1940) data suggest that m is about half a mile, though this may be incorrect by a factor of at least 2. I have taken the same value for *P. polionotus*, though this may well be incorrect. Sumner's data show that as one goes inland the different characters of *P. polionotus albifrons* disappear at different rates. The greater length of foot and tail, of which the former at least may be an adaptation to the softness of the sand, have disappeared at a station 20 miles inland from the coast (Crystal Lake), and the foot length is even rather below the continental values. On the other hand, there has been little change in the pigmentation, whichever of several measures of it is considered. This changes rather abruptly about 40 miles inland. The zone of maximum change corresponds to the boundary between 'deep, loose, salmon-coloured sand, very similar to beach or dune sand' on a Pliocene formation, and 'red or brown loams' derived from older limestones. The boundary passes through Round Lake. Several measures of pigmentation were made, notably the coloured area, the pigmentation of the basal zone of the ventral hairs, the length of the tail stripe, and the amount of red in the dorsal hair. The first of these probably gives the best indication of the gene **Wc**. It would seem that about 40 % of the change in it occurs in about 10 miles between Round Lake and Chipley, in north-eastern Florida. We may take the interquartile range as being about 12 miles. If so, we have $m = \frac{1}{2}$, $d = 12$, and since $d = 0.7m/\sqrt{k}$ or $0.7m/\sqrt{K}$, approximately, we have

k or $K = m^2/2d^2 = 0.001$ approximately. That is to say, a selective advantage of about 0.1 % on each side of the boundary would be sufficient to account for the observed cline. Since the mean coloured area on the boundary is 46 % of the distance from that of *albifrons* to that of *polionotus*, i.e. b equals about 0.73, it would seem that K and k are not very different in magnitude. Probably the selective advantage of **Wc** on the brilliant white sand of the beaches would be much greater.

Sumner (1929 b) suggested that the beaches were not only the centre of origin of *P. polionotus albifrons*, but a centre of distribution from which it 'pressed inland, displacing and absorbing the darker form, *polionotus*, until its advance was halted by the centrifugal pressure of the latter'. If so we might expect that all the distinguishing characters of the subspecies would vary together with the distance from the coast. This is not the case. For example, the mean amount of red in the coat has reached 70 % of its inland value at Round Lake. If the characters are due to different genes subject to different intensities of selection, we should expect to find the situation actually observed. Sumner (1929 b) pointed out that 'selective elimination, on the basis of concealing coloration, is far from intense among these animals'. He added: 'The discrimination on the part of their enemies would have to be well-nigh absolute in order to maintain a condition such as we actually find here.' If the calculation made above is even roughly correct this is not so. Even if K and k were of the order of 1 %, selection could only be detected with certainty by observations on tens of thousands of animals. It might well be found that a particular predator killed say 10 % more of light than dark mice on a dark ground, but it would then have to be shown that this predator accounted for 10 % of all deaths before an intensity of selection of 1 % was established, and the possibility of a counterbalancing advantage of light colour would have to be considered.

It must be remarked that other explanations of the observed facts are possible. Thus it may be that from time to time overcrowding on the beaches causes a wave of migration, and that the populations observed by Sumner are merely the remains of the last wave. If so the frequencies in a given place should vary greatly from year to year.

THEORY OF A CLINE IN THE ABSENCE OF INTERBREEDING

Consider two species which do not interbreed, but migrate at random at the same rate. Let y be the frequency of species A at distance x from the boundary, and let the relative fitness of A be $1 + K$ in the positive area, $1 - k$ in the negative area. Then in the positive area selection would increase y to $[(1+k) y]/[1+ky]$ or $y + ky(1-y) + O(k^2)$. Thus equations (1) are replaced by

$$\left.\begin{array}{l} \dfrac{d^2y}{dx^2} = -2Ky(1-y) \quad (x>0), \\[2mm] \dfrac{d^2y}{dx^2} = 2ky(1-y) \quad (x<0). \end{array}\right\} \tag{4}$$

Hence

$$\left(\frac{dy}{dx}\right)^2 = \tfrac{2}{3}K(1-3y^2+2y^3) \quad (x>0),$$

$$\left(\frac{dy}{dx}\right)^2 = \tfrac{2}{3}k(3y^2-2y^3) \quad (x<0).$$

Hence the boundary value of x is given by

$$2b^3 - 3b^2 + \frac{K}{K+k} = 0, \tag{5}$$

and equations (3) are replaced by

$$\begin{aligned}
\frac{\sqrt{K}\,x}{m} &= \tanh^{-1}\sqrt{\left(\frac{1+2y}{3}\right)} - \tanh^{-1}\sqrt{\left(\frac{1+2b}{3}\right)} \quad (x>0), \\
\frac{\sqrt{k}\,x}{m} &= \tanh^{-1}\sqrt{\left(1-\frac{2b}{3}\right)} - \tanh^{-1}\sqrt{\left(1-\frac{2y}{3}\right)} \quad (x<0).
\end{aligned} \tag{6}$$

Hence the interquartile ranges of y in the positive and negative regions are $0{\cdot}664m/\sqrt{K}$ and $0{\cdot}441m/\sqrt{k}$ respectively. It is noteworthy that these are only slightly less than the ranges found with interbreeding and dominance. In all four cases, if m is the root mean square range per generation, and d the interquartile distance, the coefficient of selection ranges between $0{\cdot}657m^2/d^2$ and $0{\cdot}195m^2/d^2$. This is a rather small range in practice.

DISCUSSION

The example given is at best approximate, and may be wholly fallacious. The method would, however, be reliable if adequate data were available, and it is hoped that the possibility of using them may stimulate their collection. An ideal set of data would include the following:

(1) Data on the frequency of different phenotypes over the area covered by the cline, especially near any conspicuous boundary.

(2) Data on the genetics of the character concerned. It is however to be noted that if a clear-cut difference is due to a single gene substitution, it makes very little difference whether this gene is dominant or recessive, since for a given intensity of selection the interquartile range is only 37 % longer in the region where recessives are favoured than in that where dominants are favoured.

(3) Evidence that mating is at random, or an estimate of the homogamy. This again is unimportant, since complete homogamy will only slightly increase the intensity of the cline, bringing it to the level characteristic for two different species.

(4) Data on migration, designed to give the mean square distance m^2 migrated per generation, and evidence that migration is random in direction, and independent of phenotype.

(5) Data over a number of years, to test whether the frequencies and migration rates are fairly stable.

The intensity of selection in the region including the quartiles, i.e. where the frequencies of one phenotype are 25 and 75 %, is then about $m^2/2d^2$, where d is the interquartile distance.

I have only made the calculation for a sharp boundary. In many cases there is no sharp boundary. Conditions change quite gradually, and the appropriate equation is something like

$$\frac{d^2y}{dx^2} = 2kx\,y^2\,(1-y),$$

which does not appear to be simply soluble. However, a comparison of the interquartile and migration ranges should give the order of magnitude of the selection needed to keep

the cline in being, and this is all that can be expected until extensive data are available, particularly on the difficult subject of random migration, which may be expected to vary very greatly in different years.

It should nevertheless be possible, without very extensive work, to say whether a given cline suggests selective intensities of the order of 10 or 0·01 %.

It is perhaps worth commenting on the low values of K and k which are found. They imply that in a mixed population it would take about 16,000 generations to change the percentage of white-cheeked mice from 1 to 99 % or conversely. Hence it is probable that the light varieties were formed under the action of much more intense selection on the beaches.

SUMMARY·

Where one phenotype is favoured in one area and another phenotype in a neighbouring area, the character in question may be expected to show a cline in the neighbourhood of the boundary. On certain assumptions the relation between the intensity of selection, the mean distance migrated per generation, and the slope of the cline can be calculated. The relation is used for a provisional calculation of intensities of selection in a population of *Peromyscus polionotus*. These have the very low value of about 0·1 %.

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