

VARIATION AND DOMINANCE AT THE SCUTE LOCUS IN *DROSOPHILA MELANOGASTER*

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Summary

A genotypic scale, which is additive, has been worked out for variation of scutellar bristle number in *D. melanogaster*. sc^+ is shown to be partially dominant to sc^{sc} , the first substitution of sc^{sc} for sc^+ having about six times more effect on genotypic value than the second. Canalization at four bristles is responsible for complete dominance of sc^+ in stocks whose mean genotypic value gives a mean phenotype of four bristles in sc^+ flies. A function converting the phenotypic to the genotypic scale is given which could be used in heritability analysis.

I. INTRODUCTION

Selection for high scutellar bristle number in a *Drosophila melanogaster* stock segregating for sc^{sc} was found to be successful in an experiment already reported (Rendel 1959). Matings were between sc^{sc} males, chosen for high bristle number, and heterozygous females taken at random, all of which had four bristles in the early part of the experiment. Selection eventually resulted not only in an increase of the number of bristles on scute flies but also of the number on heterozygous scute females; but whereas the phenotype in scute flies was increased by about two bristles the corresponding change in heterozygous females was only a fraction of a bristle. It was shown by a method of analysis described below, that the estimated gene dose required to produce a given phenotypic change was much greater for some levels of phenotype than others. In Waddington's (1957) terminology, the four-bristle phenotype was strongly canalized and gene doses which produced large changes of phenotype at other levels of expression had no effect on phenotype at the level of four bristles. It was possible to map out a scale relating genotypic value to phenotypic change at different levels of expression over much of the phenotypic scale from 0 to 5 bristles; but the actual width of the four-bristle zone could be only approximately estimated. In the experiment now reported the gaps have been filled in from 0 to 7 bristles and it is possible to show the relative phenotypic effect of changes in genotypic value over this scale; the effect of a gene substitution of sc^+ for sc^{sc} in males and one or two sc^+ genes for sc^{sc} in females can also be demonstrated. Thus the dominance of sc^+ over sc^{sc} can be subdivided into the effect of gene substitution on genotypic value and the effect of changes in genotypic value on phenotype.

II. TREATMENT OF THE DATA

Bristle number has been plotted against frequency of flies with a given bristle number in Figure 1. Frequencies have been converted to percentages. Three distributions are shown; these depict typical populations of sc^{sc} males from a line selected

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for low bristle number, sc^{sc}/sc^{sc} females from a line selected for high bristle number, and sc^{+}/sc^{+} females from the same line. These distributions of phenotype give an incomplete picture of the underlying genotypic variation. sc^{sc}/sc^{sc} females of the high line cover the one-, two-, and three-bristle classes quite well, but the four class is a threshold beyond which no further change in phenotype can be seen. The four class therefore contains all flies with a sufficiently high genotypic value to have at least four bristles; but, as no flies with five bristles appear in these sc^{sc}/sc^{sc} females, it is not possible to see directly from the graph of phenotypes how

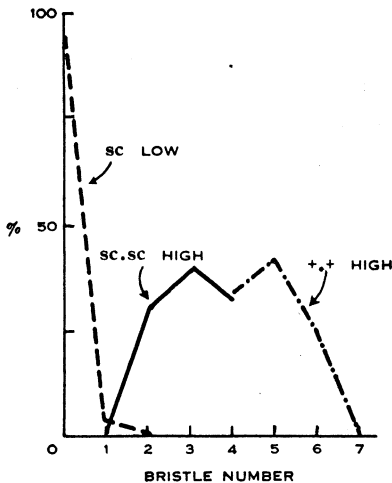


Fig. 1

Fig. 1.—Distribution of bristle number in sc^{sc} (low), sc^{sc}/sc^{sc} (high), and sc^{+}/sc^{+} (high). Subscripts to genotypes omitted for simplicity.

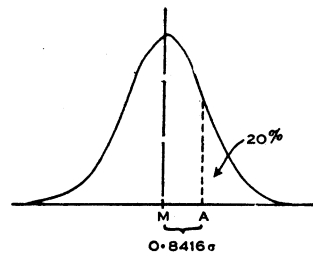


Fig. 2

Fig. 2.—Normal distribution to illustrate estimation of distance between cut-off point (A) and mean (M) by taking probits.

genotypic values above four are distributed. The sc^{+}/sc^{+} females cover the range from five to seven bristles; but again the four class is a threshold and nothing can be seen directly, from the distribution of phenotypes, about genotypic values below the four threshold. The sc^{sc} males from the low-selection line are even more extreme; this genotype only has a few representatives with one and very few with two bristles, the rest all have none so that only a small tail of the distribution is revealed above the threshold of the zero-bristle class.

It will be realized that each class has two thresholds, an upper and a lower one; the four class has one boundary between four and five bristles and one between three and four. The fact that in the high line sc^{+}/sc^{+} females never have three bristles, and in the low line never have five, indicates that a very large genotypic value separates the top of the three class from the bottom of the five class and that the four class is an extremely broad one.

Although the phenotypic distributions reveal only part of the underlying genotypic variability, it is nevertheless possible to deduce something about the

whole distribution of genotypic values from that part which is mirrored by the phenotype. If we have a distribution, some known percentage of which falls beyond a certain value as in Figure 2, conversion of the percentage into probits tells us how far the mean of the distribution is from the cut-off point in standard deviations. Thus if the point *A* cuts off 20 per cent. of the population, the distance between the mean, *M*, and *A* is 0.8416 standard deviations. This can be looked up in tables of probits (cf. Fisher and Yates 1953). As the distributions of bristle numbers of various major genotypes in the up and down lines have several cut-off points, it is possible to map the distance between the cut-off points in standard deviations of the distribution covering them. For example, in Figure 1, 95.8 per cent. of scute males in the low line have no bristles; this corresponds to a probit of 1.73; that is to say, the mean of the distribution lies 1.73 σ below the lower boundary of the one class. 99.62 per cent. of the scute males lie below the lower boundary of the two class, that is to say have 0 or 1 bristle. This puts the mean of the distribution 2.67 σ below the lower boundary of the two class. By subtraction we find that the one class spans 0.94 σ since it runs from a point 2.67 σ above the mean to a point 1.73 σ above the mean. We cannot estimate the spread of the two class from this distribution because there were no flies with three bristles and therefore no cut-off point at the top of the two class. However, different genotypes span different parts of the phenotypic scale and by putting the results together the whole phenotypic range from 0 to 4 and 4 to 7 can be filled in.

The assumption which makes this possible is that the distribution about the mean at different phenotypes is the same. This distribution is basically the distribution of genotypic values and on theoretical grounds would not be expected to change much with selection in the absence of inbreeding. The observed phenotypic distribution does contain an environmental fraction but provided a further assumption can be made, that there are no gene environmental interactions which alter the percentage of genotypic values falling beyond a given threshold, without altering the mean accordingly, values estimated at different phenotypic levels will still be comparable. The justification of these assumptions is that where distributions overlap, whether they be of males or females, scute or wild type, high- or low-selection lines, they give estimates of the distance covered by a phenotypic class which are in very close agreement.

III. EXPERIMENTAL PROCEDURE

Two lines of flies were used in this experiment. The first consisted of a stock segregating for $sc^{sc}w^w$ and sc^+w^{bl} . Matings were always made between $sc^{sc}w^w/sc^+w^{bl}$ ♀♀ and either $sc^{sc}w^w$ or sc^+w^{bl} ♂♂. Homozygous w^{bl}/w^{bl} is distinguishable from heterozygous w^{bl}/w^w which is distinguishable from w^w/w^w . In addition sc^{sc}/sc^{sc} can always be distinguished from sc^{sc}/sc^+ or sc^+/sc^+ by the number of abdominal chaetae. It is not possible to distinguish sc^{sc}/sc^+ from sc^+/sc^+ in this way except on averages. With the aid of these two scores, sc^{sc}/sc^{sc} , sc^{sc}/sc^+ , and sc^+/sc^+ genotypes can be distinguished with accuracy even when sc^{sc}/sc^{sc} flies have four scutellar bristles. Crossing over between *sc* and *w* is sufficiently rare not to introduce confusion into the scoring. This line was selected for high scutellar bristle number and when

bristle number had increased sufficiently $sc^{sc}w^w/sc^+w^{bl}$ ♀♀ were mated to their $sc^{sc}w^w$ and sc^+w^{bl} sibs in pairs. These matings gave rise to cultures segregating for sc^{sc}/sc^{sc} and sc^{sc}/sc^+ on the one hand and sc^{sc}/sc^+ and sc^+/sc^+ on the other. A proportion of sc^+/sc^{sc} flies in this line had more than four bristles. A second line was similar except that w^w was in coupling with sc^+ and w^{bl} with sc^{sc} . This line was selected for low scutellar bristle number. Response to selection became very slow as selection differential fell with drop in bristle number and in order to reduce bristle number far enough for some sc^{sc}/sc^+ flies to have three bristles the final crosses were reared at 30°C instead of 25°C, high temperatures being known to reduce scutellar bristle number in scute stocks whereas low temperatures increase it. In order to test the possibility that the w^{bl} and w^w genes might differ in their effect on bristle number a small experiment was set up in which $sc^{sc}w^w$ and $sc^{sc}w^{bl}$ were segregating. There was no difference in the scutellar bristle number of w^{bl} and w^w sibs. This was felt to be important not so much when comparing the high

TABLE 1

BRISTLE NUMBER OF DIFFERENT GENOTYPES IN HIGH AND LOW LINES IN ABSOLUTE NUMBERS, CONVERTED TO PERCENTAGES AND TO PROBITS

(a) Bristle number of different genotypes

Genotype	Bristle Score	High Line		Total	Low Line		Total
		$\times sc^{sc}$	$\times sc^+$		$\times sc^{sc}$	$\times sc^+$	
sc^{sc}	0	1		1	128	125	253
	1	7	2	9	5	5	10
	2	75	53	128		1	1
	3	65	69	134			
	4	31	50	81			
sc^+	4	110	131	241	158	159	317
	5	31	58	89			
	6	6	8	14			
sc^+sc^{sc}	3				2	2	4
	4	144	141	285	162	152	314
	5	27	48	75			
	6	2	5	7			
$sc^{sc}sc^{sc}$	0					123	123
	1	1		1			
	2	38		38		7	7
	3	72		72			
	4	52		52			
sc^+sc^+	4		48	48	194		194
	5		61	61			
	6		37	37			
	7		1	1			

TABLE 1 (Continued)
(b) Bristle number converted to percentages and probits

Genotype	Bristle Score	High Line (in accumulated %)	Probits (from mean)	Low Line (in accumulated %)	Probits (from mean)
<i>sc^{sc}</i>	0	0.28	-2.77	95.8	+1.73
	1	2.83	-1.90	99.6	+2.65
	2	39.1	-0.28	100	
	3	77.1	+0.74		
	4	100			
<i>sc⁺</i>	4	70.1	+0.53	100	
	5	95.9	1.74		
	6	100			
<i>sc⁺sc^{sc}</i>	3			1.26	-2.24
	4	77.7	+0.76	100	
	5	98.1	+2.07		
	6	100			
<i>sc^{sc}sc^{sc}</i>	0			81.5	+0.90
	1	0.61	-2.50	95.4	+1.68
	2	23.9	-0.71	100	
	3	68.1	+0.47		
	4	100			
<i>sc⁺sc⁺</i>	4	32.7	-0.45	100	
	5	74.1	+0.65		
	6	99.3	+2.46		
	7	100			

and low lines as when comparing homozygous and heterozygous females of the same lines for dominance of *sc⁺* over *sc^{sc}* since the comparison is between *sc^{sc}ww/sc^{sc}ww*, *sc^{sc}ww/sc⁺w^{bl}*, and *sc⁺w^{bl}/sc⁺w^{bl}*, or vice versa depending on the genes in coupling.

IV. RESULTS

The scores of flies in the two types of cross in the high line and the two types of cross in the low line are set out at the top of Table 1. The two types of cross in each case have been summed wherever they contain identical major genotypes. The totalled scores have been converted to percentages in the bottom half of the table and the probits, measured from the mean of the distributions, are shown next to the percentages. From these probit values it is possible to estimate the distance in standard deviations covered by the 1-, 2-, 3-, 5-, and 6-bristle classes. In Table 2 three estimates of the one class have been given and averaged, these come from *sc^{sc}* ♂♂ of the high and low lines and *sc^{sc}/sc^{sc}* ♀♀ of the low line; the same procedure has been followed for the remaining bristle classes. By comparing *sc^{sc}* ♂♂ and

sc^{sc}/sc^{sc} ♀♀ of the high and low lines, three estimates of the difference between the lines have been obtained and averaged. These are the distances between the 0/1 cut-off point and the 1/2 cut-off point in males of the two lines and the distance between the 1/2 cut-off point in females. The average difference between lines is 4.41σ . If we assume the two distributions of heterozygotes are separated by this distance, the distance covered by the four-bristle class is given by adding 4.41 to the distance

TABLE 2

ESTIMATION OF DISTANCES IN STANDARD DEVIATIONS OF THE DISTRIBUTION OF BRISTLE NUMBER, THIS DISTRIBUTION BEING ASSUMED CONSTANT OVER ALL PHENOTYPES

	Estimates of Distance (σ)	Sum or Average
Bristle class		
1	0.87, 0.92, 0.78	0.86
2	1.62, 1.79	1.70
3	1.02, 1.18	1.10
4	$2.24 + 4.41 + 0.76$	7.41
5	1.21, 1.31, 1.11	1.21
6		1.81
High \rightarrow low	4.50, 4.55, 4.18	4.41
High line		
$sc^{sc}/sc^{sc} \rightarrow sc^{sc}/sc^{+}$	$0.47 - 0.76 + 7.41$	7.12
$sc^{+}/sc^{sc} \rightarrow sc^{+}/sc^{+}$	$0.76 + 0.45$	1.21
$sc^{sc} \rightarrow sc^{+}$	$-0.53 + 7.41 + 0.74$	7.62
Low line		
$sc^{sc}/sc^{sc} \rightarrow sc^{sc}/sc^{+}$	$0.90 + 0.86 + 1.70 + 1.10 + 2.24$	6.80
$sc^{+}/sc^{sc} \rightarrow sc^{+}/sc^{+}$	$7.41 - 2.24 - 4.41 + 0.45$	1.21
$sc^{sc} \rightarrow sc^{+}$	$7.41 - 4.41 - 0.53 + 1.73 + 3.66$	7.86

of the mean of the low line sc^{+}/sc^{+} females from the bottom four boundary, 2.24σ , and the distance of the high line sc^{sc}/sc^{+} ♀♀ from the top four boundary, 0.76σ . The distance between sc^{sc}/sc^{sc} and sc^{+}/sc^{sc} , sc^{+}/sc^{sc} and sc^{+}/sc^{+} , and sc^{sc} and sc^{+} in the high line can be estimated directly. In the low line the position of the sc^{+} and sc^{+}/sc^{+} means must first be estimated from the position of equivalent classes in the high line by subtracting 4.41, the distance between lines. It is then possible, in addition, to estimate distances between sexes. The complete picture is shown in Table 2 and Figure 3. The genotypic values shown in Figure 3 are plotted against phenotypic means in Figure 4. The curve in Figure 4 fits, approximately, the expression

$$Y = -2.365 + 5.4196x - 2.2759x^2 + 0.05383x^3 + 0.1675x^4 - 0.021467x^5$$

up to $x = 5$. This expression was calculated from the points plotted on the University of Sydney's electronic computer, SILLIAC.

V. DISCUSSION

This investigation is one illustration of the general problem of scaling data for biometrical analysis, a subject which is discussed by Mather (1949) in his book "Biometrical Genetics". In this attempt at scaling the object has been to determine directly what equal changes of genotypic value do to phenotype over the whole

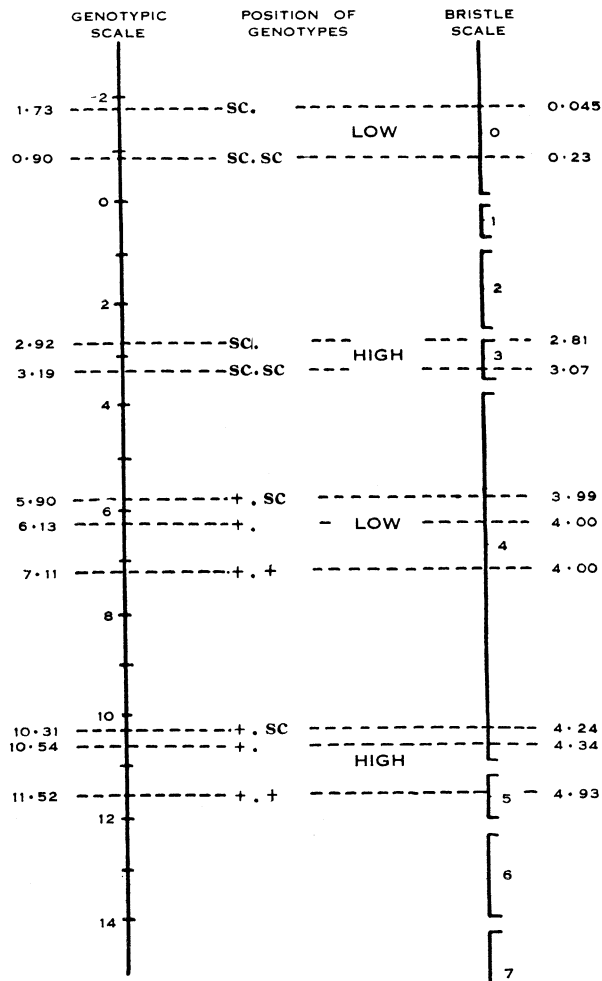


Fig. 3.—Chart showing genotypic scale on the left, phenotypic scale on the right. Position of different genotypes and lines is shown on both scales. Numbers on the extreme left are standard deviations from 0. Numbers on the extreme right are mean bristle numbers. Subscripts to genotypes omitted for simplicity.

range of phenotypes from 0 to 7 bristles, rather than find by trial and error some function which appears to reduce variance. The scale is successful insofar as substitutions of sc^+ for sc^{sc} have the same effect over the whole scale. The validity of the scaling method depends on assumptions already dealt with in Section II.

Part of the inadequacy of the bristle score as a scale might be overcome by measuring the length and diameter of bristles in addition to counting them. In the low line sc^+/sc^{sc} flies had noticeably smaller bristles than their sc^+/sc^+ sibs and in some few flies the "bristle" was only a bristle site or a thin short wisp of bristle. However, all such had been defined before the experiment as bristles and so were scored as such. Detailed examination of these, particularly at the edges of the four-bristle class is a subject for future investigation.

The final scale has a most marked broadening of the four class and smaller ones at the two and six classes. The symmetry of the scale about four is intriguing but may have no significance. The character is certainly markedly canalized.

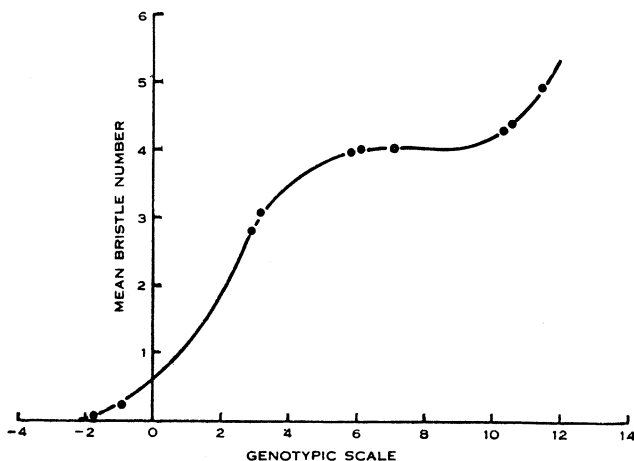


Fig. 4.—Phenotypic change plotted against change measured on the genotypic scale taken from Figure 3.

There is, of course, one assumption not so far mentioned, which has been made throughout the analyses; it is assumed that the genes determining the canalization zone, or the relationship of genotypic value to phenotype, do not alter significantly throughout the experiment. It has been shown elsewhere that this relationship can be altered by appropriate selection; but in the work reported here no such selection was applied and changes in the mean expression of the character, as for example between scute and non-scute phenotypes or high- and low-selection lines, are very large compared to changes, which can be brought about by selection, in the width of a canalization zone. The idea is that genotypic values are completely additive, but changes in genotypic values have effects on phenotype depending on the level of expression of the character; this gives rise to epistatic effects near the canalization zone. Further epistatic effects would result from gene variation changing the degree of canalization.

Since on the phenotypic scale the effect of a gene substitution depends on phenotype and this is determined not only by other genes but at least by temperature and possibly crowding also, there will be both epistatic and gene environment

interactions on this scale. However, they will not be specific to particular genes and particular environments and can be removed by conversion to the genotypic scale by using the expression $Y = (F)X$. Heritabilities calculated on the genotypic scale should give valid predictions over the whole range of scutellar bristle number so far examined.

Dominance of sc^+ over sc^{sc} is shown up very clearly. In unselected stocks a single sc^+ gene puts the mean phenotype near the middle of the four zone and this is so broad that no effect is gained by adding another sc^+ gene. However, if the mean of the population is increased or decreased sufficiently, effects of a second sc^+ gene substitution can be measured. Dominance of sc^+ is largely due to the fact that the first gene substitution has a genotypic value of about 7 whereas the second has one of only 1.21. But complete dominance is brought about when the heterozygote has a mean genotypic value at least 2.5σ above the lower boundary of the four class and at least 3.5σ below the upper boundary. If it is closer to either boundary a count of sufficient flies will show some effect of the second substitution. It seems probable that selection of modifiers in at least some cases will affect dominance by creating a zone of canalization resistant to all forms of variation. On the other hand, it is hard to see how the difference in genotypic value of the first and second gene substitution can be due to anything but some form of chemical equilibrium analogous to pH buffering and other mass action equilibria. If, for example, the rate of a reaction leading to bristle formation were dependent on the rate of removal of end-product, a second sc^+ gene would have an effect only insofar as removal of end-product was determined by its rate of formation and insofar as two genes would reach equilibrium sooner than one. This is in contrast to the dominance found by Dun and Fraser for the tabby gene in mice (Dun and Fraser 1959). Heterozygotes appear to have an intermediate genotypic value and all dominance comes from canalization. Presumably the Ta^+ gene has no limit to its action other than its own efficiency.

The type of dominance for sc^+ is of particular interest in the light of Haldane's discussion of industrial melanism (Haldane 1957). Haldane shows there is not time for melanism to acquire dominance through differential survival of genes modifying specifically the dominance of a melanic gene in the heterozygote; but if melanism is of advantage and is initially variable in the homozygous as well as the heterozygous state in response to both genetic and environmental change, there will be a tendency for canalization of the character to appear as a result of differential survival in homozygotes and with this a great reinforcement to other forms of dominance.

VI. ACKNOWLEDGMENT

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VII. REFERENCES

- DUN, R. B., and FRASER, A. S. (1959).—Selection for an invariant character, vibrissa number, in the house mouse. *Aust. J. Biol. Sci.* **12**(4): 506–23.

- FISHER, R. A., and YATES, F. (1953).—"Statistical Tables for Biological, Agricultural, and Medical Research." 4th Ed. (Oliver and Boyd: Edinburgh.)
- HALDANE, J. B. (1957).—The cost of natural selection. *J. Genet.* **55**: 511-24.
- MATHER, K. (1949).—"Biometrical Genetics." (Methuen: London.)
- RENDEL, J. M. (1959).—Canalization of the scute phenotype. *Evolution* (in press).
- WADDINGTON, C. H. (1957).—"Strategy of the Genes." (Allen and Unwin: London.)