The effects of population size and selection intensity in selection for a quantitative character in *Drosophila*

II. Long-term response to selection

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1. INTRODUCTION

In the past, selection theory and practice have been directed towards obtaining maximum gains in the early generations of selection. Generally, there has been reasonably good agreement between observed responses and heritability predictions during the first few generations. But in later generations, in populations of *Drosophila* (Mather & Harrison, 1949; Rasmuson, 1955; Clayton & Robertson, 1957; Sheldon, 1963), mice (Falconer & King, 1953) and poultry (Yamada, Bohren & Crittenden, 1958; Abplanalp, 1962), continued selection has led to apparent plateaux. This has directed attention to the prediction of selection limits for a particular selection programme, thus allowing the derivation of programmes to maximise total response.

Robertson (1960) developed a theory of limits to artificial selection for the simple model in which the limit is caused by loss of additive genetic variance. This work was extended by James (1962) to include selection limits caused by a decline in fitness, while the effect of linkage on selection limits has been considered by Latter (1965b) and Hill & Robertson (1966). For all these considerations, the total response could be expressed in terms of two variables, the effective population size and the selection intensity, as well as parameters of the base population.

There is little experimental evidence on the effects of these variables on selection limits. Robertson (1966) showed that an inbreeding bottleneck before selection resulted in some reduction in the limit, while Tantawy (1959) found that total selection response was drastically reduced with very small population sizes. Because of the theoretical importance of population size and selection intensity in determining selection limits, experimental evidence on their effects on long-term selection response has been obtained.

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2. MATERIALS AND METHODS

The plan of the experiment, culture and selection procedure, and details of the responses over the first 12 generations were described by Frankham, Jones & Barker (1968a). The 80 % lines were discontinued at generation 12. The experimental design (Table 1) was then an unequally replicated factorial of three population sizes (10, 20 and 40 pairs of parents) and four selection intensities (10, 20, 40 and 100 %). Selection was for the number of bristles on one abdominal sternite, fourth in males and fifth in females. In the Canberra base population at generation 0 the mean and standard deviation were $21 \cdot 7 \pm 2 \cdot 02$ in females and $17 \cdot 7 \pm 1 \cdot 93$ in males.

Table 1. *Experimental design, treatment code designation, numbers of replicates per treatment* (n) *and total number of pairs scored each generation in each replicate* (T)

Population size (pairs of parents)		Selection intensity			
		10 %	20 %	40 %	Controls
10	Code	10(10 %)	10(20 %)	10(40 %)	10(C)
	n	4	5	5	5
	T	100	50	25	20
20	Code	20(10 %)	20(20 %)	20(40 %)	20(C)
	n	2	3	3	3
	T	200	100	50	20
40	Code	40(10 %)	40(20 %)	40(40 %)	40(C)
	n	1	2	2	2
	T	400	200	100	40
40–10*	Code	X(10 %)	X(20 %)	X(40 %)	
	n	1	2	2	
	T	100	50	25	

* These lines were split from the 40-pair lines at G. 16 and selected thereafter at the same intensity with 10 pairs of parents per generation.

In each of the 40-pair selection lines at generation 16 after scoring and selection of parents, a further sample was scored and 10 pairs of parents selected, using the same selection intensity as the original line. These extracted lines (designated X(10 %), X(20 %) and X(40 %) for 10, 20 and 40 % selection intensities respectively) were maintained thereafter with 10 pairs of parents per generation.

3. RESULTS

(i) *Response to selection–treatment means*

The mean bristle number of the females at generations 0, 5, 10, ... , 50 for the various treatments are shown in Fig. 1. Plots were made only every fifth generation so the graphs would be more intelligible. Generation to generation fluctuations were similar to those over the first 12 generations (Frankham *et al.* 1968a). Males showed a similar proportional response and have not been included.

The gene *scabrous* appeared in 10(40 %)c at generation (G) 27. As this gene has a

large effect on bristle number and had been detected in other selection lines from the Canberra population (Jones, 1967*a*; Rathie, 1967), the line was terminated at G.30 after an unsuccessful attempt to eradicate *scabrous* whilst continuing selection. Clearly in plant or animal breeding programmes, the appearance of such a
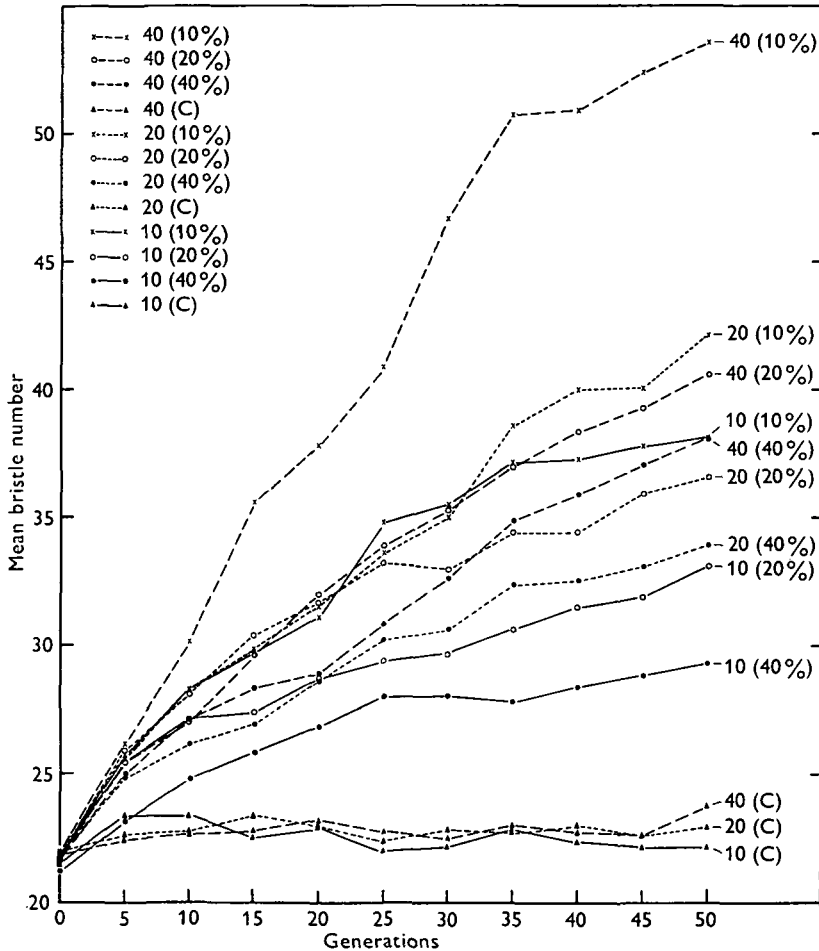

Fig. 1. Response to selection (treatment means).

gene would be gratefully accepted, and the line carefully guarded rather than discarded. However, we are aiming to compare the effects of population size and selection intensity on responses, and the inclusion of the *scabrous* line would bias comparisons. The treatment mean for 10(40%) from G.30 onwards was therefore based on only four replicates. Line 40(C)b was accidentally lost at G.31 so the 40(C) treatment mean was based on only one line after G.30.

Although some lines appeared to be plateaued at G.50, treatment means of all selection lines were still rising.

(a) Effect of population size

In general, for the same selection intensity, larger populations tended to give greater response than smaller populations. This trend was sometimes evident by G.10 and became clearer with time. 40(10%) was clearly superior to all other 10% treatments by G.10 and this superiority increased with time. There was little difference between 10(10%) and 20(10%) until G.35, after which 20(10%) was clearly superior. The high level of 10(10%) was largely due to one replicate (10(10%)b) which showed a rapid response after G.20.

With the 20% lines, 10(20%) soon fell behind the larger populations. 20(20%) was slightly higher than 40(20%) for the first 15 generations, but from G.25 the larger population maintained its rate of response while 20(20%) lagged behind.

The 40% treatments diverged quite early, 10(40%) falling behind the larger populations by G.5, and 20(40%) gradually falling behind 40(40%) from G.10 onwards.

The controls increased slightly during the first five generations so the response to selection in the other treatments over the first few generations was probably exaggerated. The controls fluctuated appreciably but from G.10 onwards showed no consistent trend, except for a slight decrease in 10(C).

(b) Effect of selection intensity

Within population sizes, higher selection intensities gave greater response in both the short and long terms. However, in some cases the trend was not clear until later generations.

For the 10-pair lines, 10(10%) soon outstripped the lower selection intensities, while 10(20%) gave more response than 10(40%). This effect was exaggerated by an exceptionally high replicate of 10(10%) and a low one of 10(40%). Two replicates of 10(10%) were only slightly higher than the 10(20%) mean by G.50.

The trend was less pronounced with the 20-pair lines. There was little difference between 20(10%) and 20(20%) to G.20 but subsequent response was greater in 20(10%). By G.10, 20(40%) had fallen behind 20(20%) but the difference changed little after G.15.

40(10%) diverged from the other 40-pair lines in the first few generations and continued to respond at a faster rate. 40(20%) and 40(40%) responded similarly for the first 10 generations, but by G.15, 40(20%) was clearly superior. The difference between these treatments changed little after G.20.

(c) Effect of experimental design in units of the same total size (T)

In most animal breeding programmes, the number of individuals which can be maintained and measured determines the total size of the population. The effect on long-term response of different selection intensities and numbers of parents per generation within a unit of given total size is therefore of interest. Three such comparisons are available in this experiment.

For 10(20%) and 20(40%), 50 pairs were scored. 10(20%) responded more

rapidly initially but by G. 20, 20(40%) had caught up. Subsequently 20(40%) was between one and two bristles higher in females and much the same in males.

In 10(10%), 20(20%) and 40(40%), 100 pairs were scored. There was little difference between 10(10%) and 20(20%) to G. 20 but subsequently 10(10%) was higher, mainly due to one replicate (10(10%)b). However, at G. 50, 20(20%) was responding faster than 10(10%). 40(40%), as expected, responded more slowly for the first 20 generations, but by G. 35 was higher than 20(20%). By G. 50, 40(40%) was about equal to 10(10%) and was responding faster.
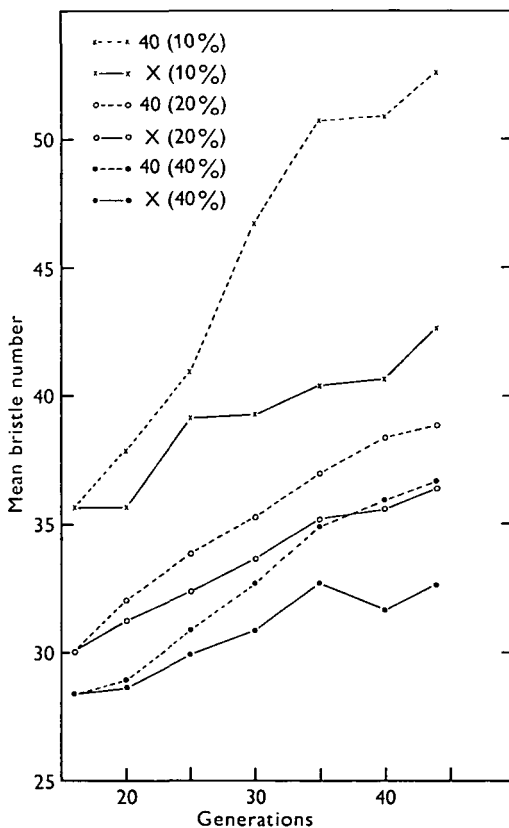

Fig. 2. Response to selection of the 40-pair lines, and of the 10-pair sublines taken from them at G. 16.

For 20(10%) and 40(20%), 200 pairs were scored. These treatments had similar rates of response, except for more rapid response in 20(10%) between G. 30 and G. 35. Both treatments were still responding rapidly at G. 50 with 20(10%) retaining the superiority gained between G. 30 and G. 35.

(d) *Effect of restricting population size during selection*

The responses of X(10%), X(20%) and X(40%) as well as 40(10%), 40(20%) and 40(40%) between G. 16, when the X lines were split from the 40-pair lines, and

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G. 44 are shown in Fig. 2. The 10-pair lines immediately fell behind their parent lines and continued to fall further behind as selection progressed.

(ii) *Response of the individual lines*

The mean bristle number of the females for the individual lines at generations 0, 5, 10, ..., 50 is shown in Fig. 3a–c, and 4 for the 10, 20 and 40% lines and the controls. Generation-to-generation fluctuations were similar to those over the first 12 generations (Frankham *et al.* 1968a), so plots were made at 5-generation intervals to make the graphs clearer.

Table 2. *Regression coefficients of mean female bristle number on generations during 10-generation intervals*

Line	G. 0–G. 10	G. 10–G. 20	G. 20–G. 30	G. 30–G. 40	G. 40–G. 50
10(10%)a	0·75	0·21	0·50	0·05*	0·17
b	0·59	0·32	0·94	0·54	0·08*
c	0·54	0·14	0·27	−0·01*	0·09
d	0·57	0·14	0·11*	0·19	0·02*
10(20%)a	0·67	0·18	0·13	0·42	0·35
b	0·57	0·14	0·14	0·08*	0·20
c	0·41	0·09	0·21	0·06*	0·04*
d	0·33	0·23	−0·01*	0·14	0·14
e	0·61	0·28	0·05*	−0·01*	0·06*
10(40%)a	0·38	0·19	0·10	0·01*	0·08*
b	0·24	0·26	0·11	0·20	0·03*
c	0·37	0·30	0·39		
d	0·20	0·05*	0·01*	0·21	0·08*
e	0·41	0·07*	0·18	0·11*	0·11*
20(10%)a	0·72	0·27	0·20	0·75	0·19
b	0·48	0·35	0·50	0·24	0·14*
20(20%)a	0·68	0·43	0·17	0·16	0·11*
b	0·59	0·36	0·25	−0·01*	0·24
c	0·67	0·29	0·04*	0·13	0·21
20(40%)a	0·51	0·40	0·31	0·39	0·08*
b	0·25	0·25	0·16	0·05*	0·13
c	0·48	0·22	0·24	0·14	0·12
40(10%)	0·79	0·81	0·89	0·47	0·24
40(20%)a	0·57	0·43	0·40	0·25	0·20
b	0·54	0·48	0·38	0·26	0·26
40(40%)a	0·52	0·20	0·38	0·32	0·21
b	0·56	0·19	0·30	0·30	0·17
Means					
10(10%)	0·61	0·20	0·46	0·19	0·09
10(20%)	0·52	0·18	0·10	0·14	0·16
10(40%)	0·32	0·17	0·16	0·13	0·08
20(10%)	0·60	0·31	0·35	0·50	0·16
20(20%)	0·65	0·36	0·15	0·09	0·19
20(40%)	0·41	0·29	0·24	0·19	0·11
40(10%)	0·79	0·81	0·89	0·47	0·24
40(20%)	0·56	0·45	0·39	0·26	0·23
40(40%)	0·54	0·19	0·34	0·31	0·19

* Not significantly different from zero.

The regression coefficients of female bristle number on generations for each line during 10-generation intervals are given in Table 2. The coefficients for males are given elsewhere (Frankham, 1967; Jones, 1967b) and are referred to only when the responses of the two sexes were proportionately different.
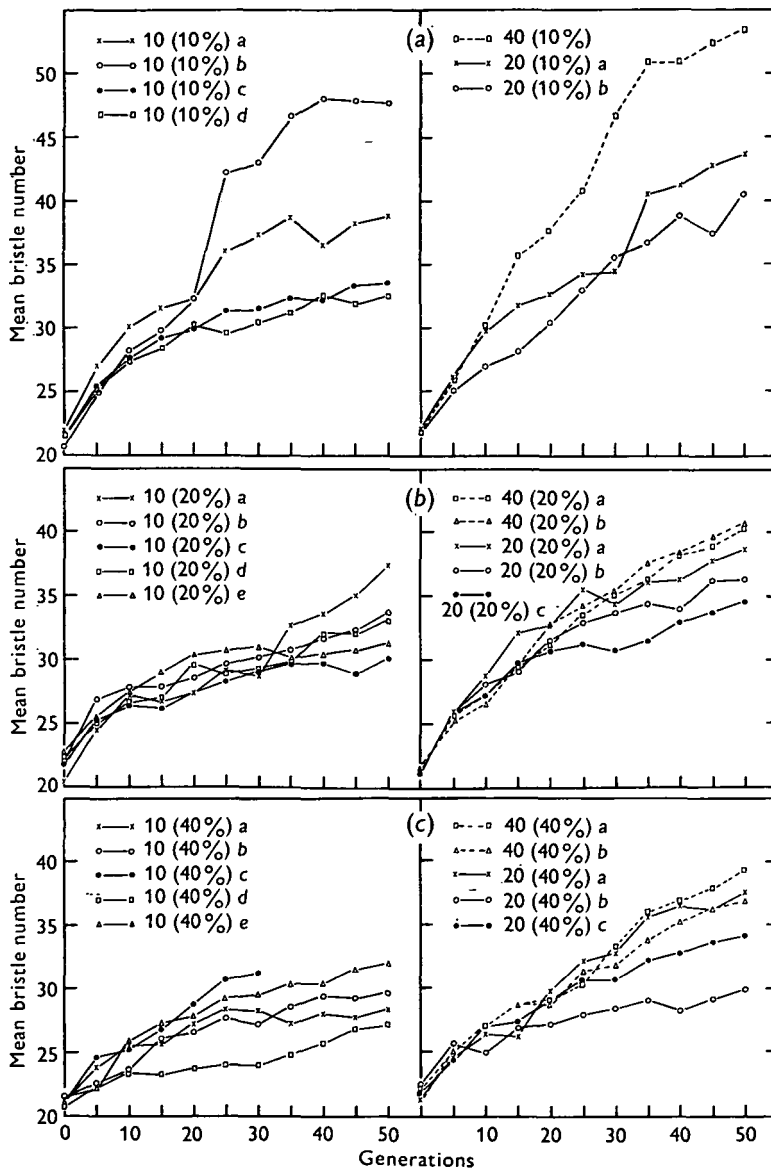

Fig. 3. Response to selection of individual lines, (a) 10% lines, (b) 20% lines, (c) 40% lines.

Agreement between replicates for the smaller populations was poor for long-term response. This was most evident in the 10-pair 10% treatment. 10(10%)a responded most rapidly to G.10 ($b = 0.75$), moderately between G.10 and G.20

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($b = 0.21$), and rapidly thereafter ($b = 0.50$) until it became extinct at G.37. It was reconstituted from the relaxed line taken off at G.35 but this barely regained the original level by G.50. 10(10%)b, 10(10%)c and 10(10%)d all had similar initial progress ($b = 0.59$, 0.54 and 0.57 respectively for G.0–10), after which their response slowed down ($b = 0.32$, 0.14 and 0.14 for G.10–20). Between G.20 and G.25 there was a spectacular rise of about 10 bristles in 10(10%)b. Subsequently it rose steadily until G.40 after which it was plateaued at a mean of approximately 48 bristles. 10(10%)c and 10(10%)d gave moderate further progress, rising by 3.64 and 2.44 bristles between G.20 and G.50 to levels of 33.57 and 32.55 bristles respectively.
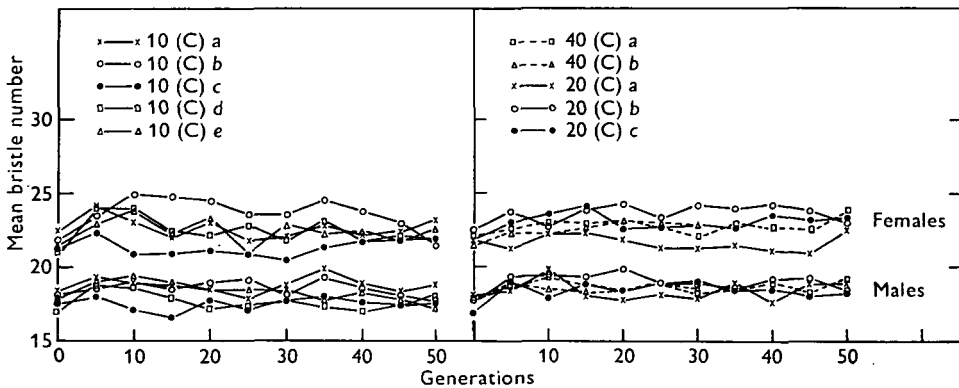

Fig. 4. Mean bristle number of the individual controls.

Table 3. *Regression coefficients of mean female bristle number on generations for X and 40-pair lines*

Line	G.20–G.30	G.30–G.40	Line	G.20–G.30	G.30–G.40
X(10%)	0.38	0.12*	40(10%)	0.89	0.47
X(20%)a	0.20	0.19	40(20%)a	0.40	0.25
b	0.38	0.07*	b	0.38	0.26
X(40%)a	0.36	0.00*	40(40%)a	0.38	0.32
b	0.22*	0.12*	b	0.30	0.30

* Not significantly different from zero.

Divergence between replicates was also large in the 10(20%) and 10(40%) treatments. At G.50, the difference between the highest replicate and the lowest was 7.50 bristles for the 20% lines (10(20%)a and 10(20%)c) and 4.96 bristles for the 40% lines (10(40%)e and 10(40%)d).

There were also considerable differences between replicates of the 20-pair treatments. 20(10%)a gave more rapid response to G.10 than 20(10%)b ($b = 0.72$ and 0.48 respectively) but they were at a similar level by G.20 in the males and by G.30 in the females. By G.50, 20(10%)a was about 3 bristles higher in the females but males were similar in the two lines. Of the 20(20%) lines at G.50, 20(20%)a was

2·36 bristles higher than 20(20%)b, and 3·99 bristles higher than 20(20%)c, while in the 20(40%) lines 20(40%)a was 7·60 and 3·58 bristles higher than 20(40%)b and 20(40%)c respectively.

Agreement between replicates for the 40-pair lines was good but we had only two lines each for 40(20%) and 40(40%) and only one for 40(10%). 40(20%)a and 40(20%)b showed very similar response throughout with regression coefficients falling gradually from 0·57 and 0·54 to 0·20 and 0·26 respectively. 40(40%)a and 40(40%)b both continued to respond rapidly throughout (b = 0·20–0·52 and 0·17–0·56 respectively) with 40(40%)a at a slightly faster rate after G.25. In comparison with their sister 40-pair lines, X(10%), X(20%)a and X(40%)b all showed reduced regressions over G.20–30 and G.30–40, while X(20%)b and X(40%)a showed reductions only in G.30–40 (Table 3).

The responses of lines from most treatments overlapped, the extreme being 10(10%) which overlapped lines of all treatments except 40(10%) and 10(40%).

After a rise of approximately 1 bristle during the first few generations, the controls subsequently remained fairly steady at this level. By G.10 replicates of the controls had diverged considerably, but the spread and ranking remained essentially the same thereafter. The notable exception was 10(C)b which declined from being the highest control at G.35 to become the lowest at G.50.

Waves of response were shown by many of the lines. The accelerated response of 10(10%)b, and to a lesser extent 10(10%)a, after G.20 has already been noted. 10(20%)a, 10(20%)b, 20(10%)a, 20(40%)a, 40(40%)a, and 40(40%)b also showed periods of accelerated response while 10(10%)c, 10(10%)d, 10(20%)d, 10(40%)d, 20(20%)b, 20(20%)c and 20(40%)b showed periods of renewed response following apparent plateaux.

A number of lines were at or near plateau at G.50, 10(20%)c, 10(20%)e, and 10(40%)a responded only slightly after G.30, and 10(10%)b, 10(10%)d, 10(40%)b and 10(40%)d after G.40. 10(20%)c was of special interest as it showed very small response in the females over the last 20 generations (b = 0·06 and 0·04), but was still rising steadily in the males (b = 0·13 and 0·10). Some lines showed different relative responses in the sexes but this was not sufficient to influence the interpretation here and is considered in detail by Frankham (1967).

(iii) *Variance of individual lines*

As male and female variances were fairly similar, their mean value for the individual lines is shown in Fig. 5 for G.0, 2, 6, then every fifth generation to G.36 and for G.46, plotted with a squared scale on the ordinate axis. Variance was used in preference to coefficient of variation, as no relationship between mean and variance was evident.

Most lines including controls showed little change in variance. However, 40(10%) showed a spectacular increase, 10(10%)a, 10(10%)b, 20(10%)b, 20(20%)a, 20(40%)a, 40(40%)a and 40(40%)b showed appreciable increases, and 40(20%)a and 40(20%)b slight increases. 10(20%)c was notable for its low variance and most controls showed a slight decrease in variance.
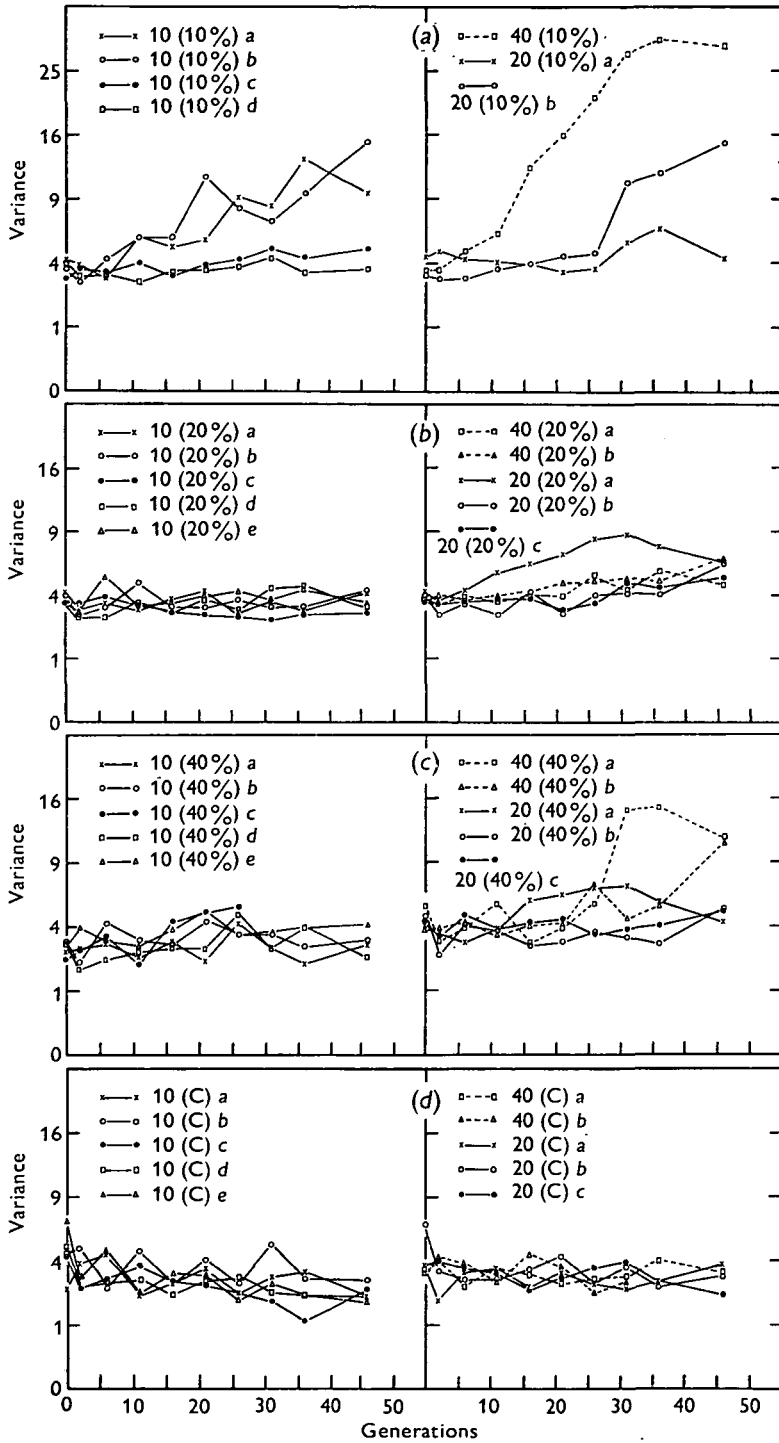
Fig. 5. Variances of individual lines. (a) 10 % lines, (b) 20 % lines, (c) 40 % lines, (d) controls.

Increased variances in 10(10%)a, 10(10%)b, 20(10%)a, 20(10%)b, 20(40%)a, 40(10%) and 40(40%)a corresponded with periods of rapid response. In 20(10%)a and 20(40%)a the variance later declined to the original level, but the other lines retained elevated variances.

Selection differentials were closely related to the level of variance in the lines. Occasionally, selection differentials were reduced due to insufficient progeny, but except for 20(10%)b (irregularly between G.14 and G.35) and 20(40%)a (after G.40) this was not important.

4. DISCUSSION

(i) *Total response—comparison with theoretical models*

Robertson (1960) showed for a simple additive model that the limit to selection for a quantitative character is a function of $N_e \bar{\imath}$, where N_e is the effective population size and $\bar{\imath}$ the standardized selection differential. In our experiments, most
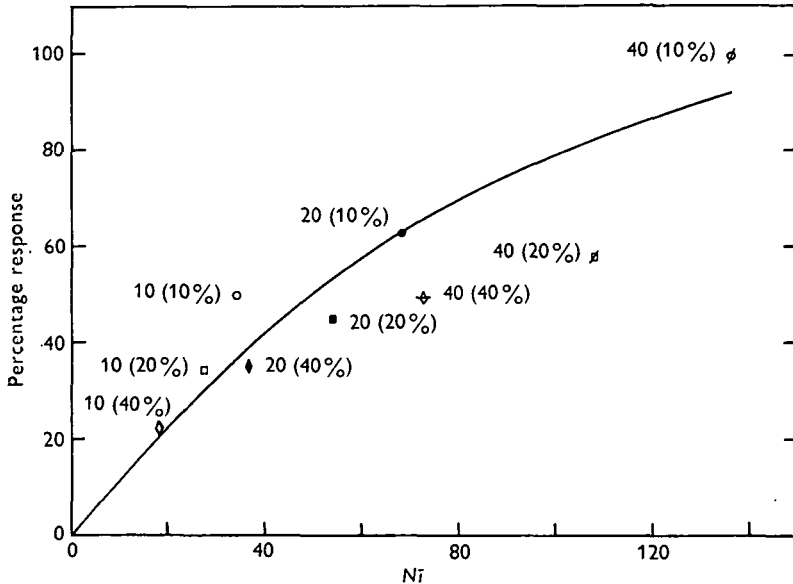

Fig. 6. Response to selection at G.50 as a percentage of the response of 40(10%).

treatments were still responding to selection at G.50, although the rate of response in the smaller populations was quite low. The approximate relationship between $N_e \bar{\imath}$ and the plateau level, however, can be got by taking the response at G.50 as a minimum estimate of the plateau level. This will, of course, underestimate the total response particularly in treatments still responding rapidly (e.g. 40(20%) and 40(40%)).

Figure 6 shows the responses at G.50 plotted against $N\bar{\imath}$. Response was computed as a deviation from the mean of the controls and is plotted as a percentage of the response made by the highest treatment (40(10%)). As the percentage response

was similar in both sexes the mean of these percentages is shown. For N_e, the number (N) of parents per generation was used. However, the effective population size would be less than this in the mass cultures used (Crow, 1954), with a further reduction due to artificial selection which would be greater at higher selection intensities (Robertson, 1961; McBride & Robertson, 1963). The values of $\bar{\imath}$ used are from Frankham *et al.* (1968*a*).

In general, response of the treatments increased with increasing $N\bar{\imath}$. Robertson (1960) predicted that the relationship between response and $N\bar{\imath}$ would be a curve approaching the limit asymptotically. To make comparison of our results with this prediction easier, a subjectively fitted curve has been drawn in Fig. 6. The points do not fit the curve closely, but the treatments deviating to the greatest extent (viz. 40(20%) and 40(40%)) were still showing appreciable responses at G.50. If allowance is made for the continuing response in 40(10%) and the greater reduction in effective population size at higher selection intensities, then one might expect the curve to be much steeper than Fig. 6 would indicate. It is not clear what value of T (total number scored) is required to gain most of the response possible in an infinite population. There has been an increase in response up to our largest T (viz. 40(10%)) but as this treatment was unreplicated there is no indication of its repeatability.

Dempster (1955) suggested that for a given T, the greatest total response is expected when half the population is selected each generation. Robertson (1960) agreed, but predicted that the curve of response against proportion selected may be very flat, particularly for large T. As a result of simulation experiments, Gill (1965*c*) doubted that selection of half the population would give maximum total response. However, he compared the efficiency of selection intensities for the same number of parents used each generation, and not for the same number of individuals scored.

At our lowest value of T (50 pairs), 20(40%) made slightly more progress than 10(20%). At the next value (100 pairs), 40(40%) had caught the treatments with more intense selection and was responding more rapidly. 10(10%) was slightly higher than 20(20%), but this was largely due to one exceptionally high replicate (10(10%)b). There was little difference between the treatments with 200 pairs scored (40(20%) and 20(10%)) at G.50 and both were still responding to selection. There was therefore rough agreement with the prediction that the total response would be greatest when half the population was selected, but as Robertson (1960) suggested the proportion selected made little difference over the range used here.

Robertson also suggested that restricting population size after a number of generations of selection would have little effect on the total response. All favourable genes are expected to be at appreciable frequencies and should not be lost by reducing population size. Contrary to expectations, 10-pair sublines taken off the 40-pair lines at G.16 and selected at the same intensity immediately fell behind their parent lines and gave considerably less progress. Thus there were desirable genes still at low frequencies.

(ii) *Duration of response*

Robertson (1960) showed that the half-life of the selection response was expected to be approximately $1\cdot4N_e$. This varied according to initial gene frequencies and was lower for high values of $N_e\bar{\imath}$. Gill (1965 a), in a simulation study, found the half-life reduced from $1\cdot4N$ for $N = 8$ to $0\cdot3N$ for $N = 32$ for the complete dominance model. Thus population size made little difference to the absolute value of half-life. In simulation studies using an additive model, Latter (1966) showed that half-life was markedly reduced by large gene effects ($0\cdot5$ versus $0\cdot1$ standard deviations), increased by low initial gene frequencies, decreased by more intense selection, and that population size had little or no effect on the absolute value of half-life. Assuming that the effective population sizes were about half the actual sizes (due to mass culturing and selection), then the expected half-lives ($1\cdot4N_e$) would be 14, 28 and 56 generations for the 10-, 20- and 40-pair lines.

Table 4. *Half-lives of selection (minimum estimates*)*

| Population size | Selection intensity | | |
(pairs of parents)	10 %	20 %	40 %
10	18·5	17·2	14·5
20	21·2	14·0	18·2
40	20·5	20·0	24·2

* These estimates are based on the number of generations required to reach half the response obtained in fifty generations of selection.

Minimum estimates of half-lives for our treatments were calculated as the average time taken to reach half the responses obtained at G.50 in males and females (Table 4). We would emphasize that these estimates are minimum and average, that many lines were still responding at G.50, and that the number of generations of further response may vary with the intensity of selection and population size. As the 10-pair lines generally gave little progress over the last ten generations (Table 2), they might be expected to give reasonably realistic estimates of half-lives, which were 18·5, 17·2 and 14·5 generations for 10(10 %), 10(20 %) and 10(40 %) respectively. Contrary to expectations, the lower selection intensity lines did not have longer half-lives. However, the 10(40 %) lines may have continued to respond for longer, although at a slow rate, while the average estimates for 10(10 %) and 10(20 %) are increased by those lines showing large, rapid responses in later generations. As few of the larger populations had stopped responding at G.50, we can only note that their half-lives were generally greater than those for the smaller populations, while for the 40-pair lines, the half-life with 40 % selection intensity would probably be greater than that with 20 % or 10 %.

(iii) *Patterns of response of individual lines*

As Robertson's (1960) model represents the simplest reason for a limit to selection, we need to consider models which allow for factors other than the exhaustion of additive genetic variance. James (1962) extended the model to allow for natural selection for an intermediate optimum opposing artificial selection. The response for this model will be somewhat less than predicted by Robertson. The response curves are of a similar form except that different parameters are used. In both cases, the mean (U_t) after t generations can be expressed in the form

$$U_t = a(1 - (1 - b)^t),$$

where a and b are constants and $b < 1$, i.e. response to selection will slow down asymptotically. James (1965) suggested that fitting exponential curves ($y = \alpha + \beta \rho^x$) to the selection response may give a true picture of the form of the response and possibly detect an approaching limit. However, he found them to be of limited value in predicting the future response in a number of selection experiments.

Gill (1965b,c) obtained response curves for populations in which one of several modes of gene action was simulated; additive, complete dominance, overdominance, and several forms of epistasis, combined with various degrees of linkage. Most of the response curves were of a similar form to those of James and Robertson, i.e. they approached limits asymptotically.

Some of our lines (e.g. 40(20%)a, 40(20%)b) had response curves of the predicted form. However, many of the lines (e.g. 10(20%)d, 20(20%)b, 20(20%)c) had periods of little or no response followed by further response. Others (e.g. 10(10%)b, 20(10%)a) had periods of very rapid response after 20 or 30 generations, when we expected them to be slowing down. It was not considered worthwhile trying to fit response curves because of these irregular patterns of response.

Another feature of our lines was the poor agreement between replicates, particularly for the 10- and 20-pair lines. Thus conclusions regarding treatments must be regarded with caution, particularly for long-term results. There was quite good agreement between replicates in 40(20%) for 50 generations and in 40(40%) for 30 generations. However, it is not clear whether 40 pairs of parents are adequate to give repeatable results, as each of these had only two replicates.

Clayton & Robertson (1957) and Sheldon (1963) also obtained poor agreement between replicates in 20 pairs, 20% lines selected for abdominal bristle number, but on different media and from different base populations. A number of Clayton & Robertson's (1957) lines stopped responding rather suddenly and in one high line and several low lines the response increased, rather than decreased, in later generations. Cessation of response was fairly sudden in Sheldon's (1963) lines and periods of increased response appeared in one line.

Clayton & Robertson's (1957) lines reached a similar average level to our comparable 20(20%) treatment (37·5 and 36·6 respectively for one segment in females). However, the response in many of our lines persisted for much longer than those of the above authors. Probably this was because we selected on only one segment,

while they selected on the sum of two segments. This has a higher heritability and so gives more rapid initial response. Long continued response was obtained by Rasmuson (1955), a few lines continuing to respond to selection for abdominal or sternopleural bristle number for up to 70 generations. This was surprising as population size was small (two pairs of parents) and selection intensity high (2/25). Sismandis (1942) obtained response to selection for scutellar bristles for more than 20 generations in some lines with only a single pair of parents, as did Payne (1918) for 29 generations under similar conditions. Mather & Harrison (1949) obtained periods of response after 100 generations of selection in an abdominal bristle number line with two pairs of parents per generation, despite periods of no response in the meantime. 'Waves of response' have been found also by Payne (1918, 1920), and Fraser *et al.* (1965) in lines selected for scutellar bristle number, by Zeleny (1922) in bar lines selected for increased eye size, and Thoday & Boam (1961) in lines selected for increased sternopleural bristle number.

There are a number of possible causes of irregular response patterns. Mather & Harrison (1949) suggested that the irregular patterns in their lines were due to the gradual break-up of balanced polygenes. In a simulation study, Fraser & Hansche (1965) showed that for small populations this explanation was reasonable, but that similar patterns would occur either if suitable interactions were present, or if a few recessive major genes were at low initial frequencies. A particular type of interaction, which may be important, is one in which selection changes the background such that a polygene is converted to a major gene. Such interactions were suggested by Robertson & Reeve (1952), and have been found by Fraser (1963), and Scowcroft (Fraser & Hansche, 1965).

Latter (1966) showed by simulation that linkage of genes of large effect at low initial frequency could have an appreciable effect on the pattern of response, although Latter (1965*b*) and Hill & Robertson (1966) found that the effect of linkage on total responses would be small for a two-locus model unless linkage was very tight. Linkage had little effect on response during the early generations when the frequency of $+-$ and $-+$ gametes were increasing. Provided neither was lost by chance, and both reached appreciable frequencies, there was a period of little or no response with $+-$ and $-+$ segregating jointly. After recombination $++$ gametes were selected and a period of rapid response resulted. The marked responses observed by Zeleny (1922) were presumably due to duplication or deficiency products as the result of unequal crossing-over.

New mutations with large effects would also produce irregular response patterns. However, spontaneous mutations are unlikely to be important here as B. J. Hollingdale (personal communication) found no response for abdominal bristle number in 20 generations of selection in lines derived from an inbred line.

Periods of rapid response in 10(10%)a, 10(10%)b, 20(10%)a, 20(10%)b, 20(40%)a, 40(10%) and 40(40%)a coincided with large increases in variance. Latter (1965*a*) showed that a gene of large effect at low initial frequency would cause a large increase in additive genetic variance as its frequency increased. This may have occurred in the above lines. The variance later declined in 20(10%)a and

20(40%)a indicating that the gene(s) responsible became fixed. In the other lines, the variance remained at the increased level, suggesting that the gene(s) responsible were still segregating, and in all cases lethals at medium to high frequency were detected (Frankham *et al.* 1968*b*).

Therefore, much of the response in some lines was probably due to genes (or gene combinations) with large effects on bristle number. Without measuring the effects of individual genes it is difficult to assess the importance of large genes. However, the work of Wehrhahn & Allard (1965), Spickett & Thoday (1966), Robertson (1966), and Law (1966, 1967) suggests that a significant proportion of the variation of some quantitative characters may be controlled by relatively few genes with large phenotypic effects. As genes of large effect are expected to be rapidly fixed there is contradiction between the retention of genetic variation for long periods and the presence of large genes. However, fixation may be delayed with recessives at low initial frequency, linked genes at low initial frequency or where the effect of a gene is dependent on the genetic background. In these cases irregular patterns of response are expected.

Whatever the cause of the irregular response patterns, they make the long-term behaviour of any particular line more or less unpredictable. We should question whether the results are peculiar to the character selected or to *Drosophila*. Evidence on irregular patterns of response, genes of large effect on quantitative characters and variation between replicates is limited (reviewed by Frankham, 1967), but make it unlikely that our results are peculiar to abdominal bristles in *Drosophila*. Nevertheless, it is important that similar studies on other characters and other species should be done.

To the extent that we can generalize from our results, the unpredictable long-term response of a particular population is rather discouraging to the animal breeder. However, long-term response to selection will tend to increase as the size of the unit is increased and reliability of response is increased as more parents are used in each generation.

5. SUMMARY

1. An experimental evaluation of Robertson's (1960) theory of limits in artificial selection was attempted. A number of lines from the Canberra base population were selected for abdominal bristle number over 50 generations with population sizes of 10, 20, and 40 pairs of parents and selection intensities of 10, 20 and 40% as well as unselected controls.

2. In general, the total response obtained increased with an increase in $N\bar{\imath}$ (product of population size and standardized selection differential).

3. Thus, total response increased with increase in the number of individuals scored, or, for a fixed number of parents, increase in selection intensity increased both rates of response per generation and total response.

4. But for the same total number scored, the response increased as selection intensity decreased. However, the proportion selected had only a small effect as compared with that of the total number scored.

5. Sublines in which the population size was reduced after 16 generations of selection but with the selection intensity kept constant, immediately fell behind their parent lines and gave much less response.

6. Agreement between replicate lines was generally poor, particularly for the 10- and 20-pair lines.

7. Patterns of response in individual lines were frequently irregular and 'waves of response' were not uncommon.

8. The results are discussed in terms of several theoretical models of selection limits. In general, agreement with these models was poor, as much of the response appeared to be due to a few genes (or gene combinations) with large effects on bristle number.

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