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Recurrent selection. II. An experimental study with mice and *Drosophila*

By J. C. BOWMAN*

Institute of Animal Genetics, Edinburgh, 9

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INTRODUCTION

The development of recurrent selection in corn breeding and its application to animal breeding problems has been summarized by Bowman (1959). To date, *Drosophila* and *Tribolium* are the only organisms on which results of a recurrent selection programme have been published (Bell *et al.*, 1955; Rasmuson, 1956; Bell & Moore, 1958). This paper presents the results of two further experiments on recurrent selection, one with mice and the other with *Drosophila*.

Recurrent selection is a term commonly used in animal breeding. The technique as applied to plant breeding is the method suggested by Jenkins (1940). However, in animal breeding a modification of the method of Hull (1945) of recurrent selection for specific combining ability to a tester stock is usually applied. The design of Hull's modified technique would be briefly as follows: Males and females of an outbred strain are mated to females and males of an inbred tester stock. The hybrid progeny are reared and measured for the character under selection. On the basis of the hybrid's performance, selection is made in the outbred strain and only selected individuals are used to maintain the strain. The strain progeny are used in a further cycle of testing to inbred individuals and so on. A further modification is to test and select in only one sex of the outbred strain.

The theoretical rates of progress and other aspects of recurrent selection have been discussed by Dickerson (1952).

Hybrid vigour has been defined in a number of ways but the definition used in this paper refers to deviations in cross performance above mid-parent performance. Recurrent selection is designed to exploit hybrid vigour attributable to overdominance. Theoretically it has no advantage over individual or family selection techniques if applied to characters for which there is no overdominance.

RECURRENT SELECTION FOR LARGE LITTER SIZE IN THE HOUSE MOUSE

Materials and methods

The inbred line used in this selection experiment was the established *JU* inbred. For this experiment it was designated *I* and its origin is more fully described by Bowman & Falconer (1960). It was the only line to survive from 10 inbred lines

* Present address: Research Division, Thornber Bros. Ltd., Mytholmroyd, Yorks.

originally started from a heterogeneous base population by one generation of double first-cousin mating, followed thereafter by full sib mating. Natural selection eliminated the other nine lines because of infertility. At the time this experiment was started, the *I* line was in its 16th generation, when the dams should, theoretically, be 96·0% inbred.

The outbred stock was designated *M* and was derived from the control strain (*JC*) of the high and low litter-size selection experiment of Falconer (1955). The control strain, which was started from the same base population as the *I* inbred line, has been maintained by approximately 10 pair matings per generation. When the *M* animals were obtained, the *JC* strain was in generation 16, and the computed coefficient of inbreeding was 20%. There had been no decline in litter size over this period.

The experiment was a sire selection programme in which sires were each assessed on the mean litter size of a half-sib group of testcross daughters. The half-sib groups were produced by mating each of the sires to a number of dams of the *I* inbred strain.

As the inbred (*I*) females, when mated to *I* males, were known to have good fertility and maternal performance, they were used for crosstesting the outbred *M* males. Twenty-one *M* males were each mated to 5 *I* females in harems. The number of *I* females to be mated was fixed arbitrarily because the data necessary to decide on the optimum design were not available at the beginning. The progeny resulting from $M \times I$ matings were designated *X*. The *X* progeny were reared and 6 females were taken at random from each sire family for testing for litter size. They were intermated with *X* males, but half and full sib matings were avoided.

On the basis of the litter size of the *X* hybrid females the best 7 *M* males were selected to produce the next *M* generation. All the *M* males were each mated to three of their own strain females at the same time as the *X* offspring test matings. This design cuts down on the space available for testing, but, at the same time, reduces the length of the selection cycle. All half and full sib matings were again avoided in the *M* strain to minimize inbreeding. On the results of the *X* test matings 14 of the 21 males' *M* families were discarded and from the remaining seven, 3 males and 9 females were taken at random from each family. The 21 males so obtained were tested against another set of 105 *I* females and then mated to 63 *M* females. In this way the *M* strain was maintained by 7 males and 21 females per generation, which gives a rate of inbreeding of 2·4% per generation.

The *I* line was maintained by approximately 50 full sib matings per generation. The offspring used for *X* test matings were taken from first and second litters.

Results and analysis

The selection programme was stopped after only four cycles for two reasons. Firstly, it proved to be extremely difficult to rear the crossbred progeny on the *I* females. In each generation all *X* progeny from a few sires failed to survive and this reduced the selection intensity which could be applied. Secondly, the initial mean level of crossbred (*X*) performance was very low and showed no evidence of hybrid vigour.

The mean litter sizes of various matings made in the experiment are given in Table 1 and shown in Fig. 1. The mean litter size of *X* females (hybrid dams with hybrid progeny) was lower than the mean litter size of either parent except in

Table 1. *Mean litter size of all stocks*

Mating		Selection cycle			
♂	♀	1	2	3	4
M	*M*	8·18 ± 0·31	8·18 ± 0·32	8·19 ± 0·31	8·10 ± 0·32
X	*X*	6·85 ± 0·19	7·26 ± 0·24	6·66 ± 0·23	7·76 ± 0·22
I	*I*	7·56 ± 0·26	8·60 ± 0·35	7·73 ± 0·37	7·65 ± 0·36
M	*I*	7·75 ± 0·28	7·17 ± 0·29	7·63 ± 0·28	7·18 ± 0·35

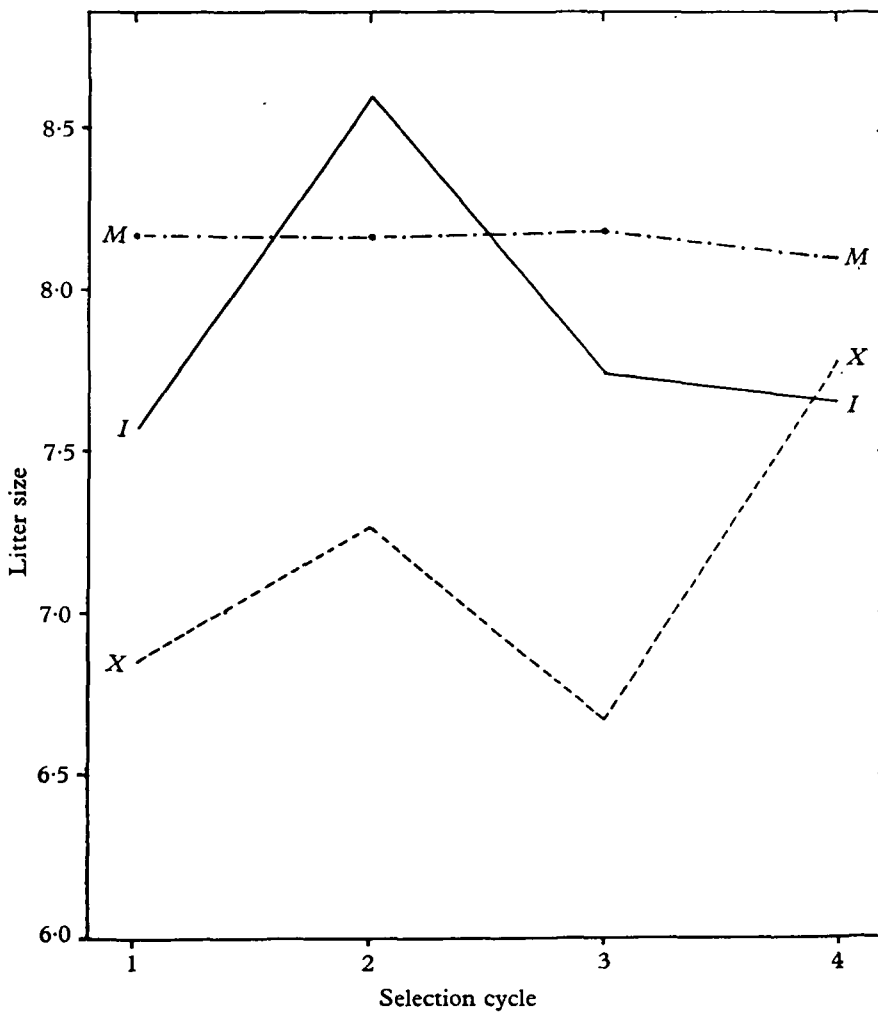

FIG. 1. Mean litter size of all matings plotted against selection cycles.

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cycle 4, when it was intermediate. This was not to be expected (Roberts, 1960; Bowman & Falconer, 1960), and only one previous report of such an occurrence is known (Mason *et al.*, 1960). Apart from this low overall *X* litter size, none of the *M* sire *X* progeny groups taken separately had a mean litter size superior to the mean litter size of the best *M* sire, as judged from the average litter size of this sire's full sisters. There was little chance, therefore, even after selection, of the *X* litter size exceeding that of either parent. The mean litter size of *M* females was extremely

Table 2. *Coefficient of variation* (%) *for litter size in* I, M *and* X *matings*

Mating		Selection cycle			
♂	♀	1	2	3	4
M	*M*	28·8	28·1	26·5	28·0
X	*X*	27·4	29·2	34·5	27·4
I	*I*	22·4	22·2	31·4	27·3

constant with the exception of cycle 4. The mean litter size of *X* females fluctuates in accord with the mean litter size of *I* females, for cycles 1, 2 and 3. Only in cycle 4 does *X* litter size show any marked increase. It can be seen from Table 2 that the percentage coefficient of variation is similar for inbred, outbred or crossbred litters. The environment provided was considered to be similar for all matings, but it appears that the litter size of the inbred dams and their crossbred daughters may be more susceptible to change from minor environmental variations than the litter size of outbred dams.

It is interesting to note that the mean litter size of *I* females mated to *M* males (inbred dams with hybrid progeny) was lower than *I* females mated to *I* males. This also was not to be expected (Roberts, 1960) and this peculiarity of the *I* line will be discussed in more detail elsewhere.

It is difficult (because of the wide fluctuations in mean litter size between cycles and because of the brevity of the selection programme), to measure the progress, if any, in mean litter size in *X* females achieved as a result of the recurrent selection. An estimate of progress can be made in two ways. Firstly, the absolute change in mean litter size of *X* females. This is $7{\cdot}76 - 6{\cdot}85 = 0{\cdot}9$ young per litter. This estimate, however, takes no account of any changes in performance of the parental lines. A second estimate which does take account of such variations is the deviation of *X* litter size from mid-parent value.

This estimate for each cycle is shown in Table 3. The deviation of *X* females from mid-parent value increases in cycles 2 and 3 and then decreases sharply in cycle 4. The net result of selection is $-0{\cdot}12 - (-1{\cdot}02) = +0{\cdot}90$ young.

The two methods of estimating progress give similar results. The mean litter size of *X* females has increased by 0·9 young per litter. Most of this progress, however, was achieved in cycle 4.

Table 3. *Deviation of* X *mean litter size from mid-parent mean litter size*

Selection cycle			
1	2	3	4
−1·02	−1·13	−1·30	−0·12

It is possible to calculate the expected improvement in X female litter size on the assumption that the variance between M sires in X female litter size is entirely due to additive gene effects. From Lerner (1950) the genetic improvement in litter size in X progeny

$$\Delta G = \bar{\imath} r_g \sigma_s \text{ per generation}$$

where $\bar{\imath}$ = the selection differential between sire families in phenotypic standard deviations;

r_g = the correlation between the observed mean and the true mean of sire crossbred performance;

σ_s = the standard deviation of the true means of the crossbred progeny of different sires.

If r_g is converted into a term composed of the appropriate components of variance it can be shown that:

$$\Delta G = \bar{\imath} \frac{\sigma_s^2}{\sqrt{\left(\sigma_s^2 + \frac{n}{p}\sigma_b^2 + \frac{1}{k_b}\sigma_w^2\right)}} \text{ per generation}$$

where σ_s^2 = component of variance due to differences between sires;

σ_b^2 = component of variance due to differences between dams mated to the same sire;

σ_w^2 = component of variance due to differences between full sibs;

n = number of sires;

p = number of full sib groups;

k_b = number of offspring in any one full sib group.

The data have been analysed to obtain values of σ_s^2, σ_b^2 and σ_w^2 for each cycle separately and also a pooled within-cycle value. These values are presented in Table 4. The selection intensity together with the expected genetic improvement is shown in Table 5. ΔG has been calculated using the pooled within-cycle estimates of the components of variance. As mentioned previously, the number of sires which failed to leave any surviving X progeny increased each cycle, and in consequence the expected genetic improvement per cycle declined. The mean litter size of X progeny was expected to increase by 0·25, 0·24 and 0·22 for the three cycles of selection so that the net change in litter size from cycle 1 to cycle 4 was expected to be an increase of 0·71 young. This estimate agrees fairly closely with the observed comparison of 0·9 young, though the two intervening generations are not as close to expectation.

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From the signs and from the change, if any, between selection cycles in the regression of a sire's X progeny performance on his full sister performance it is possible to draw certain conclusions regarding the genetic control of a character (Bowman, 1960). Assuming no epistasis, the regression can only be negative when there is overdominance. The effect that epistasis would have on this conclusion is not known.

The regression of the mean litter size of X progeny groups for each M sire separately on the mean little size of the M sires' full sisters has been calculated for each cycle.

Table 4. *Components of variance of* X *litter size*

Components of variance due to differences between:	1	2	3	4	Pooled within cycle
Sires σ_s^2	0·18	0·46	0·18	0·52	0·36
Dams mated to the same sire σ_b^2	0·12	0*	1·51	0*	0·18
Full sibs σ_w^2	3·24	4·60	3·65	4·45	4·01

σ_s^2 = component of variance due to differences between sires;
σ_b^2 = component of variance due to differences between dams mated to the same sire;
σ_w^2 = component of variance due to differences between full sibs.

* The estimate of the component was negative.

Table 5. *Selection intensity and expected genetic improvement, for* X *litter size*

Cycle	Proportion selected	$\bar{i}$	Expected genetic improvement $\Delta G_X =$
1	7/20	1·06	0·25
2	7/19	1·02	0·24
3	7/16	0·90	0·22
		Total for 3 cycles	0·71

The regression so calculated is an estimate of both common genetic and environmental effects in the X progeny and the M full sisters. The theoretical regression values given by Bowman (1960) refer only to genetic effects. However, there is no reason to suppose that in this experiment there were any common environmental influences on the X progeny and the M full sisters of any M sire.

The regression values are shown in Table 6 together with a pooled estimate. The regressions for cycles one to three are all negative though not significantly so, whilst the regression for cycle 4 ($+0{\cdot}55 \pm 0{\cdot}15$) is positive and significant at the 1% level. It was found, Table 7, that the regressions differed significantly from each other. However, the regressions for cycles one to three are not significantly different from each other and the pooled estimate of them is $-0{\cdot}14 \pm 0{\cdot}098$. This is not significantly different from zero.

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Table 6. *Regression of* M *sires* X *progeny litter size on* M *sires' full sister litter size*

Cycle	No. of pairs	Regression coefficient ± standard error
1	20	$-0{\cdot}22 \pm 0{\cdot}113$
2	18	$-0{\cdot}01 \pm 0{\cdot}166$
3	18	$-0{\cdot}22 \pm 0{\cdot}242$
4	16	$+0{\cdot}55^{*} \pm 0{\cdot}152$

* Significant at the $P < 0{\cdot}01$ level.

Table 7. *Analysis of the heterogeneity of the regressions between cycles*

Source of variation	D.F.	Errors of estimate mean square	*F*
Deviations from individual cycle regressions	64	1·267	—
Differences between cycle regressions	3	4·733	2·74*

* Significant at the $P < 0{\cdot}05$ level.

Discussion

The main objective of this experiment, namely to test whether recurrent selection could maximize hybrid vigour due to overdominance, has not been realized. In the first cycle the litter size of the *X* females was below that of either parent strain and, even in the last cycle, the *X* females had a mean litter size below mid-parent value. Therefore, from the beginning there was no evidence that hybrid vigour was present in this particular crossmating. This fact was in such marked contrast with previous experience of crossbreeding in the mouse (Butler, 1952; Warwick & Lewis, 1954; Eaton, 1941, 1953) that a special study was necessary of the crossing performance and apparent negative heterosis in crosses of this inbred line. The results will be published elsewhere.

In spite of the low cross performance, the litter size of *X* females did increase erratically as a result of the three cycles of selection applied. Measured as either an absolute change or as a change in deviation from mid-parent value, the litter size increased by about 0·9 young per litter. This increase has been shown to be in fairly close agreement with the theoretical increase if the variance between *M* sires in *X* female performance is assumed to be entirely due to additive gene effects. There is thus no reason to suppose that the recurrent selection did anything apart from utilizing the additive genetic variation in *X* litter size in the *M* sires.

This conclusion is supported by the fact that the regression of *M* sires for mean litter size of *X* progeny on *M* full sisters was not significantly different from zero for three cycles and significantly positive for the fourth cycle. Bowman (1960) has shown, theoretically, that a zero or positive regression will be found at all levels of dominance and for additive gene action. However, it is rather surprising, if there was a positive correlation between litter size for *X* progeny and *M* females, that

the mean litter size of the *M* strain did not increase at the same time as the *X* litter size. In fact the *M* strain litter size remained remarkably constant, which suggests that recurrent selection for *X* litter size was acting on genes in the *M* strain independently of the genes controlling *M* strain litter size.

A minor feature of interest in this experiment is the negative response to selection in cycle 3 and in cycle 2 if response is measured relative to mid-parent value. Such a negative response to litter size selection in the early generations has been previously reported by Falconer (1955, 1960), and explained in terms of inter-generation maternal effects. It seems reasonable to conclude that a similar explanation could apply in the present case.

Finally, it is concluded that this experiment proved to be no test of the ability of recurrent selection to maximize hybrid vigour based on overdominance, because no evidence of hybrid vigour was found. The selection technique probably did increase litter size. Both theoretical estimates of progress and regression analysis suggest that recurrent selection was exploiting additive genetic variation for litter size.

RECURRENT SELECTION FOR LOW BRISTLE NUMBERS IN *DROSOPHILA*

Materials and methods

The outbred stock of *Drosophila* used in this experiment was a sample, designated *R*, taken from the Kaduna stock cage. The Kaduna stock, derived from a capture in Kaduna, West Africa, in 1949, has been kept with an average population size of about 5000, in a population cage in a constant temperature room at $25 \pm 0{\cdot}50°$. The cage population has been sampled many times and the mean bristle number has shown no change.

The inbred tester line used was designated *L5/1*. The *L5* low abdominal bristle number line of Clayton *et al.* (1957*a*) was one of five replicate lines, derived, from a sample of Kaduna stock, by selection with an intensity of 20 individuals in 100 for low bristle number. *L5* line was analysed (Clayton *et al.*, 1957*b*) at generation 33 and was found to be carrying a lethal on chromosome 3 and to be heterozygous for small inversions in 3R. At generation 33 selection ceased when the mean bristle number was 3·7. The *L5* line was then maintained without selection for several generations before being full sib mated. After 15 generations of inbreeding, the mean bristle number reached a plateau at about 9·0, and this inbred material was designated *L5/1* and used in the current experiment. During the course of the experiment the *L5/1* line was maintained without inbreeding by mass mating in eight to ten bottles per generation. Throughout the experiment the standard agar food of the laboratory was used and all cultures were kept in a constant temperature room maintained at $25 \pm 0{\cdot}5°$ C.

Recurrent selection in the *R* strain was for low bristle number and the aim was to make a strain that was complementary to the *L5/1* line. The design of the experiment was as follows: Twelve *R*-strain males were mated in separate vials each to 10 virgin *L5/1* inbred females. After 2 days, the mates of each male were divided into two groups of 5 females and put into bottles to lay. These were known as *T*

crossbred matings. The bristles on abdominal sternites 4 and 5 of 5 female offspring from each bottle were counted. Data on females only were collected throughout the experiment. The bristle counts of 10 *T* crossbred female offspring from each *R* strain male were thus a measure of the males' crossing performance to inbred *L5/1*.

After mating with 10 *L5/1* females the same *R* males were then each mated to 10 virgin *R* females which, after a further 2 days, were also split into groups of five and allowed to lay in bottles. The bristle numbers of 5 female offspring from each bottle were counted. The bristle counts of 10 *R* female offspring from each *R* male were a measure of the sire's own strain performance.

On the basis of crossbred *T* performance the *R*-strain progeny from 3 of the 12 *R*-strain males were used in the next generation of selection, i.e. *R*-strain progeny from the 3 males having the lowest *T* crossbred bristle performance. Each selected *R*-strain male had progeny in two bottles and from each bottle 2 male and 20 virgin female offspring were collected to repeat the selection process. Thus, 12 *R* males and 120 virgin females were obtained for the next generation. One hundred and twenty virgin *L5/1* females were also collected from the *L5/1* culture bottles to repeat the measure of cross performance of the next set of *R* males.

The 120 *R* female offspring from the three selected males were mixed together and allotted at random to the 12 *R* males on test. This means that no effort was made, by planned mating of females, to reduce the rate of inbreeding of the *R* population to a minimum. A rough estimate of the rate of inbreeding can be made by assuming that in each generation the population size was 3 males and 30 females. This leads to inbreeding at 4·6% per generation (Li, 1955).

Results

The data throughout this experiment refer to female progeny only. The mean bristle number of *T* and *R* progeny for generations 1 to 14 are shown in Table 8 and Fig. 2. A sample of about 40 females from the *L5/1* line was counted in most generations and the means are included in Table 8 and Fig. 2. The range and coefficient of variation for all progeny are shown in Table 8. Though the original intention was to select 3 out of 12 families this intensity of selection could not be maintained. As the experiment progressed more and more males failed to produce progeny until finally in generation 15 all *T* and *R* cultures failed and the experiment terminated. The actual selection applied is shown in Table 9.

It will be noticed that marked response to selection was obtained in *T* performance in generations 1–8, when the mean fell from 33·5 to 28·3 bristles. Thereafter the mean fell erratically until in generation 13 it was 26·7, but rose again in the final generation to 27·2. The *R* mean fell from 41·0 in generation 1 to 34·9 in generation 8, and over the next 6 generations fell a further 2 bristles to 33·7 bristles in generation 14. The fall in mean was thus very similar in the two types of progeny. The *L5/1* progeny fluctuate, quite considerably between generations, about a mean of approximately 11 bristles.

Perhaps the most surprising observation is that the performance of *T* was not mid-way between the two parental types but much closer to the *R* performance

Table 8. *Generation means, range, standard deviation and coefficient of variation for abdominal bristles in* Drosophila

	R progeny			*T* progeny			*L5/1* progeny		
	Mean no. of abdominal bristles	Range	C. of V. (%)	Mean no. of abdominal bristles	Range	C. of V. (%)	Mean no. of abdominal bristles	Range	C. of V. (%)
1	41·0	35–50	8·4	33·5	25–40	8·7	8·1	0–23	67·9
2	39·0	31–48	9·3	32·9	19–43	11.5	—	—	—
3	37·2	31–51	9·2	32·2	4–45	13·4	12·9	6–18	24·5
4	36·5	29–47	8·7	35·0	26–48	11·5	13·9	5–24	40·4
5	36·6	29–46	8·7	31·6	22–38	9·5	11·9	2–21	36·1
6	35·8	28–44	8·9	30·0	19–38	11·6	10·8	2–21	45·6
7	35·9	30–42	7·7	29·8	21–36	9·9	—	—	—
8	34·9	27–41	7·9	28·3	7–38	25·4	8·1	0–16	42·6
9	34·9	25–42	7·7	30·2	17–37	9·9	10·9	5–21	33·1
10	34·7	28–45	8·4	29·4	13–35	11·3	10·1	0–17	41·2
11	33·7	27–42	9·1	27·0	3–34	23·7	13·5	5–27	36·2
12	34·7	25–46	10·9	28·3	13–35	13·6	—	—	—
13	33·6	26–45	9·1	26·7	4–36	27·4	12·5	3–18	28·3
14	33·7	27–39	7·5	27·2	11–36	21·1	9·6	2–21	40·6

level. This was a consistent finding throughout the experiment and suggests that there were one or more dominant alleles for high bristle number which were homozygous in the R strain. Though the means of both T and R progeny fell, the divergence between T and R performance remained fairly constant whilst the divergence

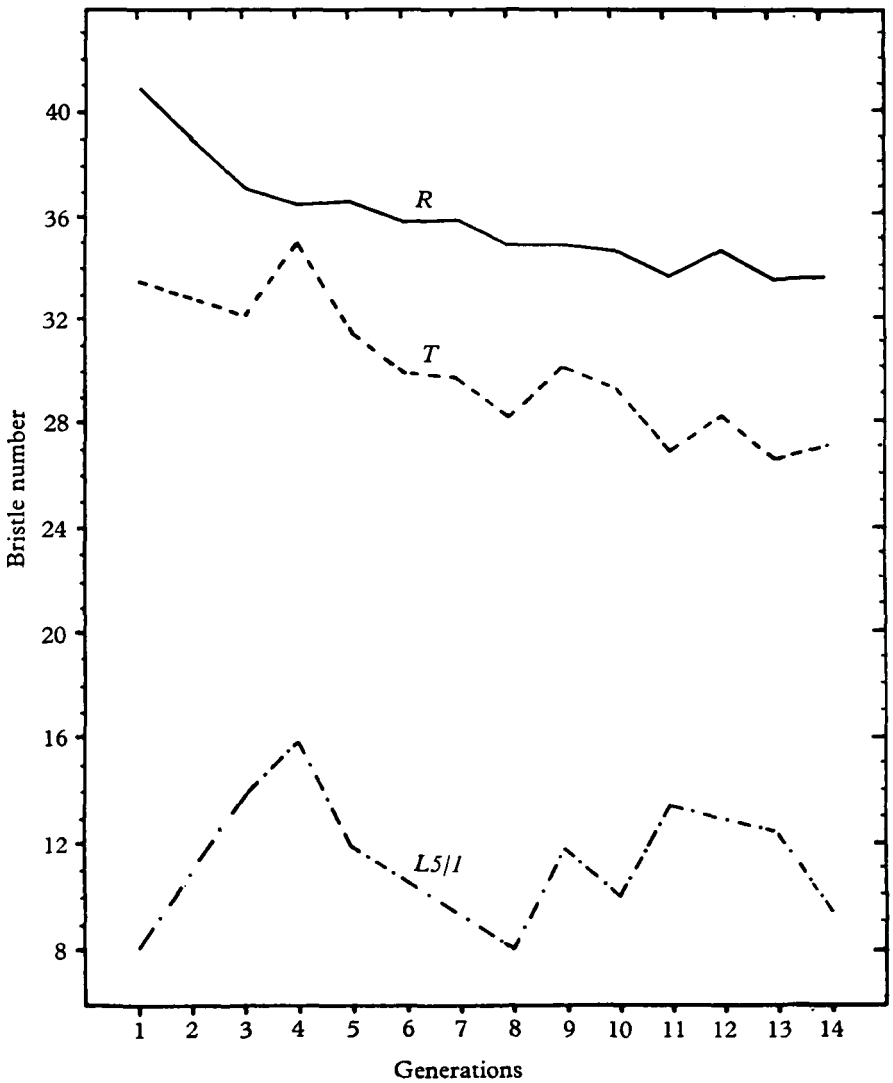

FIG. 2. Mean bristle number for R, T and $L5/1$ progeny plotted against generations.

between T and $L5/1$ was reduced. However, even by generation 14 the T performance was not at the mid-parental value. The fall in the T mean was associated with a marked rise in the range of observed bristle number. The number of T individuals with very low bristle numbers was small in generations 1 to 7 but thereafter progressively increased. As selection proceeded the range in bristle number of the T

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progeny became more characteristic of the *L5/1* line. The *T* generation means are far more erratic than for those of *R*. The coefficient of variation of the *R* progeny was fairly constant for all generations, and offspring with very low bristle numbers were not found among the *R* progeny.

The design of the experiment was such that each male was represented by a count of 10 *T* and 10 *R* female progeny, each group of progeny having come from two bottles. The data from each generation were analysed to obtain estimates of the components of variance due to differences between sire families (σ_S^2), between bottles within sire families (σ_B^2) and within bottles within sire families (σ_W^2) for *T* and *R* progeny separately. There were marked fluctuations for components from generation to generation so that within-generation pooled estimates were calculated for generations 1 to 5, 6 to 10, and 11 to 14. All estimates of the components of variance are given in Table 10. As selection proceeded, there was a marked rise in the components of variance within bottles and between bottles within families

Table 9. *The intensity of selection for* Drosophila *bristles in* R *progeny based on* T *progeny performance*

Generations	p	$\bar{i}$
1–9 inclusive	0·25	1·27
10	0·38	1·01
11	0·33	1·09
12	0·30	1·16
13	0·60	0·55

p = proportion of sire families selected;
$\bar{i}$ = selection differential in phenotypic standard deviations.

for the *T* progeny. Also, the component between sire families for *T* progeny has a positive value only in the first pooled estimate, the last two pooled estimates being negative. In contrast, the same components for the *R* progeny all remain comparatively constant.

It is realized that the use, for prediction purposes, of pooled estimates of certain population parameters is liable to error, if, as expected, the values of the parameters alter from generation to generation as a result of selection. With this qualification in mind, the observations so far lead to the prediction that response to selection should have ceased after generation 5, whereas it can be seen that the mean *T* performance fell from 30·0 at generation 6 to 27·2 at generation 14 a difference of 2·8 bristles. Using the *T* pooled estimates for generations 1 to 5 and assuming that the variation between *R* males in *T* performance was all additive genetic variation, the expected response ΔG_T can be shown to be 1·12 bristles per generation or 5·60 bristles over 5 generations. The observed response was 3·5 bristles, which is only 62·5% of the improvement expected based on the above assumption.

The phenotypic and genetic correlations between the performance of the purebred *R* and crossbred *T* progeny of the same sire were calculated from the between-family variance and covariance, mean squares and components respectively. The three

Table 10. *Components of variance for bristle number*

	T progeny			R progeny		
Generation	σ^2_{WT}	σ^2_{BT}	σ^2_{ST}	σ^2_{WR}	σ^2_{BR}	σ^2_{SR}
1	7·06	0·84	0·55	8·13	0·39	2·09
2	10·40	1·66	2·28	9·36	2·52	1·12
3	14·97	0·71	2·91	9·99	1·63	−0·20
4	10·44	3·83	1·92	7·55	−0·19	2·47
5	6·10	0·32	2·62	8·38	1·45	0·31
Pooled 1–5	9·80	1·62	1·90	8·70	1·03	1·19
6	10·36	0·25	1·40	7·52	2·09	0·61
7	8·46	−0·78	0·20	6·04	0·78	0·86
8	38·33	13·23	−5·10	7·19	0·29	0·17
9	7·28	−0·49	1·73	6·05	0·00	1·13
10	8·82	0·71	1·40	7·81	−0·86	0·73
Pooled 6–10	15·11	3·00	−0·26	7·90	0·29	0·77
11	19·91	21·32	−6·96	8·02	−0·04	1·49
12	12·21	−1·10	2·54	9·86	3·43	0·89
13	50·82	−0·02	2·78	8·44	0·27	0·69
14	10·55	22·52	−9·52	5·22	0·32	0·81
Pooled 11–14	19·33	11·57	−3·18	7·88	0·95	1·19

σ^2_S = component of variance due to differences between sire families;
σ^2_B = component of variance due to differences between bottles within sire families;
σ^2_W = component of variance due to differences within bottles within sire families.
The subscripts T and R refer to T and R progeny respectively.

within-generation pooled analyses are shown in Table 11. Apart from the phenotypic correlation for generations 11–14, which is about zero, the correlations are positive. There is a marked decline in the value of the correlations as selection proceeded. The environmental conditions of the experiment were maintained as constant as possible and the only notable change throughout the experiment was a reduction in the population density of the cultures. The decline in the correlations, therefore, suggests that as selection proceeded there was a drastic change in the frequency of genes controlling bristle number. It is not possible, however, from this information to draw any conclusions regarding the level of dominance at loci controlling bristle number, by the method suggested by Bowman (1960).

If the genetic correlation is taken at its theoretical maximum of 1 for generations 1–5 then the expected change in R mean can be shown to equal:

$$r_{RT}\frac{\sigma_{SR}}{\sigma_{ST}}\Delta G_T$$

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Table 11. *Mean squares and components of variance and covariance due to differences between sire families, and resulting phenotypic and genetic correlations between* T *and* R *progeny of the same* R *males*

Generations pooled	Degrees of freedom	Mean squares		
		T	R	Cov. $T \times R$
1– 5	54	38·8	25·7	20·7
6–10	48	28·0	17·9	6·9
11–14	23	51·1	30·1	−1·2
		Components		
1– 5		1·98	1·19	2·07
6–10		−ve	0·80	0·69
11–14		−ve	1·51	−0·12
		Correlations		
		Phenotypic	Genetic	
1– 5		0·66	1·35	
6–10		0·31	—	
11–14		−0·03	—	

If the theoretical change in T mean ($\Delta G_T = 5{\cdot}6$ bristles over 5 generations) is used to predict the change in R mean then

$$\Delta G_R = \frac{1{\cdot}19}{1{\cdot}90} \times 5{\cdot}6 = 4{\cdot}4 \text{ bristles over 5 generations}$$

where r_{RT} = genetic correlation for R sires between R and T performance;
σ_{SR} = standard deviation between R sires half-sib groups (R progeny);
σ_{ST} = standard deviation between R sires half-sib groups (T progeny).

If the actual change in T mean ($\Delta G_T = 3{\cdot}5$) is used then

$$\Delta G_R = \frac{1{\cdot}19}{1{\cdot}90} \times 3{\cdot}5 = 2{\cdot}8 \text{ bristles over 5 generations}$$

The observed value of ΔG_R was 5·2 bristles which is in excess of the expected values calculated from either the expected or the observed change in T mean.

The component of variance due to differences between families (σ^2_{SR}) in the R strain is equal to a quarter of the additive genetic variation. The values of the genetic and total variation, and of the heritability, together with standard errors of the pooled estimates are given in Table 12. There was no decline in heritability in the R strain during the experiment.

Table 12. *Genetic and total variation and heritability for bristle number in the* R *strain*

Generation	σ^2_{GR}	σ^2_{PR}	Heritability (h^2_R%)
1	8·36	10·22	81·8
2	4·48	13·00	34·5
3	−0·80	11·62	−0·1
4	9·88	10·02	98·6
5	1·24	10·14	12·2
1–5	4·76	10·92	43·6 ± 13·7
6	2·44	10·22	23·9
7	3·44	7·68	44·8
8	0·68	7·65	8·9
9	4·52	7·18	63·0
10	2·92	8·54	34·2
6–10	3·08	8·96	34·4 ± 12·9
11	5·96	9·51	62·7
12	3·56	14·18	25·1
13	2·76	9·40	29·4
14	3·24	6·35	51·0
11–14	4·76	10·02	47·5 ± 17·6

σ^2_{GR} = genetic variation = $4\sigma^2_{SR}$

$$h^2_R = \frac{\sigma^2_{GR}}{\sigma^2_{PR}}$$

σ^2_{PR} = total variation = $\sigma^2_{SR} + \sigma^2_{BR} + \sigma^2_{WR}$

Discussion

Throughout this study the prime interest has been to find evidence of over-dominance and, if present, to see whether it could be exploited by recurrent selection. It has already been pointed out that the *T* progeny performance was not intermediate between the *R* and *L5/1* performance and that this could be explained in terms of homozygous dominant or interacting genes for high bristle number in the *R* strain. This finding disagrees with previous work which indicated intermediacy of cross performance for bristle number (Mather & Harrison, 1949; Clayton *et al.*, 1957*b*).

The early sporadic appearance of individuals with very low bristle numbers among the *T* progeny, which were never found among the *R* progeny, can be explained in terms of a complex genetic situation rather than a simple one. If low bristle number was caused by recessive genes, then low bristle number individuals would be expected in the *R* progeny, at least in the later generations when the frequency of recessive genes had been increased by selection. This explanation does not appear to be the correct one unless such recessive germs were linked to other lethal or sterile genes or chromosome segments.

A chromosome analysis of *L5/1* (Dr A. Robertson, private communication) made by a technique similar to that of Mather & Harrison (1949, p. 22) showed that interchromosomal interactions were comparatively small. The *L5/1* line was known to be heterozygous for small inversions on 3R and to be carrying a lethal gene on chromosome 3 (Clayton *et al.*, 1957*b*), and a female-sterile gene (Dr A. Robertson, private communication). If, in the *R* strain, either or both of these genes were linked with genes or chromosome segments responsible for low bristle number then selection will tend to cause increasing sterility and lethality in the *R* and *T* individuals. Therefore, as selection continued there would be fewer individuals with very low bristle numbers and a higher *T* mean than expected. Further it would become increasingly difficult to maintain the intended selection intensity because of the decline in fertility of the *R* strain. The results reported are in agreement with this hypothesis.

A simpler but less likely explanation of the occurrence of individuals with low bristle numbers among the *T* progeny but not among the *R* progeny is that some of the *L5/1* females were not virgins when mated to *R* males. The standard procedure for the collection of *L5/1* virgin females was to collect from *L5/1* cultures after not more than an interval of 6 hours following the previous collection. It is known that on rare occasions females will mate very shortly after emergence (Dr E. C. R. Reeve, private communication). It is possible, therefore, that *L5/1* females which had already mated with *L5/1* males, were sometimes used to produce *T* progeny. The low score individuals would be *L5/1* progeny and not crossbred progeny. This explanation is unlikely for two reasons. Firstly, the number of low score *T* individuals increased per generation as the experiment progressed. Secondly, such individuals occurred in both bottles from some of the males tested which means that more than one *L5/1* female per *R* male must have been previously inseminated by a *L5/1* male.

The whole of the response to selection for generations 1–5 in the *T* mean bristle number can be accounted for on the hypothesis that variation between *R* males in bristle number is all additive genetic variation. In fact the response was only 63% of the expected change. This agrees with the work of Morris (1954) who carried out within-strain half-sib family selection for low bristle number for seven generations, again using the same base population. For three replicates his rates of observed response to expected was 78%. Though no response to selection in the *T* mean was expected after generation 6, the mean fell by nearly 3 bristles in the next 8 generations. The three separate generation estimates of σ^2_{ST} which are negative are associated with very high between-bottle within-sire components of variance. The pooled estimates of σ^2_{ST} for generations 6–10 and 11–14 are both negative but some of the separate generation estimates are positive. It may be that, in the later generations of the experiment, the differences in the values of the variance components from generation to generation were too great for pooled estimates to predict the situation adequately.

The observed change in the *R* mean is more surprising, since it was greater than expected when the estimate was calculated from either the expected or the observed

change in the T mean. As the genetic correlation between T and R progeny performance of the same male was at a theoretical maximum, the discrepancy cannot be explained in terms of an underestimate of the genetic correlation. The heritability estimate is in fairly good agreement with the estimates made by Clayton *et al.* (1957*a*) for the same Kaduna stock. If sterility and lethality were causing the discrepancy between the expected and the observed change in T mean it is difficult to explain why these factors did not also reduce the expected change in the R mean.

The conclusions from this experiment are two-fold. Firstly, there was no evidence to suggest that overdominance was involved in the genetic control of bristle number in the crossbred progeny. Secondly, the selection response of the crossbred was more than accounted for by the additive genetic variation for bristle number in the R males on test.

CONCLUSIONS

The purpose of these experiments was to try and answer two questions. Firstly, does recurrent selection work as a method for exploiting heterosis and secondly, can anything be learnt about the genetic explanation of heterosis from this selection procedure?

In this work over a short time period it was found that in both experiments the observed response could be fairly accurately predicted by methods based on additive genetic variance alone. There was no reason to suppose that the selection applied had altered the frequency of genes at loci exhibiting overdominance or epistasis, if such loci existed at all. The level of hybrid performance did suggest the presence of dominance and other genetic interactions but in neither experiment were they favourable to the direction of selection. On the long-term view the mouse experiment was stopped when response was still being obtained and thus it gives no indication of the ultimate performance attainable by recurrent selection. The hybrid performance in the *Drosophila* experiment did not progress as far as lines selected by individual and family selection by previous workers.

The present experiments lead to two main tentative conclusions. Firstly, in terms of the selection applied, the response from recurrent selection was no greater and probably less than for individual or family selection. However, because of the longer cycle, or the greater requirement of facilities recurrent selection was inferior for exploiting additive genetic variance. Secondly, recurrent selection did not produce a hybrid with a performance more extreme than the performance of a closed population after many generations of individual selection. Therefore, it seems that either recurrent selection was for some reason not efficient at exploiting genetic interactions, or that there was no non-additive genetic variance apart from dominance in the material used in these experiments.

In view of the paucity of the experimental evidence, recurrent selection must be treated with extreme caution. However, in a field with so few published results tentative conclusions are considered to be valuable.

SUMMARY

1. An experimental study has been made of recurrent selection to an inbred tester. A suitable inbred line is used as a tester parent, and selection is made within a non-inbred population on the individuals crossing performance with the tester line.

It is concluded that there are two situations in which recurrent selection could be profitably applied. Firstly, recurrent selection should, theoretically, be successful when applied to characters closely related to fitness which have little additive genetic variance and secondly, in cases where a character has already been subjected to individual or family selection and has reached a plateau level in that population.

2. The two experiments—i.e. recurrent selection for large litter size in mice and for low bristle number in *Drosophila melanogaster*—reported here are respectively an example of each of the above situations. In each experiment selection was made between males within the closed non-inbred population on the basis of the performance of their testcross progeny resulting from matings with inbred line females.

3. Initial generation hybrid performance in both experiments was not intermediate between parental performance levels and the divergence from intermediacy was away from the direction of selection.

4. In both experiments there was no evidence to suspect the presence of overdominance.

5. Response to selection was obtained in each experiment but this was close to or less than the expected response calculated on the assumption that all the variance between sires in crossing performance was additive genetic variance.

6. From these experiments it is not possible to draw any firm conclusions about the effectiveness of recurrent selection for exploiting overdominance. It is, however, a very inefficient way of exploiting additive genetic variance. It is suggested that more success might be obtained by careful choice of base population material used in recurrent selection.

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