

Antagonistic selection for correlated body weight traits in different mouse populations

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Introduction

Selection for growth rate in different intervals or for weight at various ages has been frequently studied in livestock and laboratory animals. Less information is available for those situations where the goal defined by a selection index is antagonistic to the genetic correlation between body weight traits; for example, in selection for an optimum growth curve with maximum growth in early stages combined with low mature weight (Dickerson 1970; Fitzhugh 1976). To evaluate the efficiency of antagonistic selection, mice were selected for high 3 to 5 week body weight gain and low body weight at 8 weeks of age over 22 generations. The selection program also involved two-way single trait selection for 3 to 5 week body weight gain and 8 week body weight in different mouse populations (von Butler and Pirchner 1983; von Butler et al. 1984).

Key words: Antagonistic selection – Body weight gain – Mouse

Materials and methods

Two foundation populations were used: a cross of four inbred lines (crossbreds) and randombred albino Swiss mice (outbreds). Two generations of random mating in each population elapsed before each was divided into two antagonistic index selection lines and three randombred control lines. The lines were reproduced from eight single pair matings in each generation. Litters were standardized within 24 h of births to eight pups in crossbreds and to ten pups in outbreds. Mice were weaned at 21 days, separated by sex and distributed into cages. Individual weights were recorded to the nearest 0.1 g at 21, 35 and 56 days of age. The mice were fed ad libitum with Altromin® Lab Chow and reared in a controlled environment at $22 \pm 2^\circ\text{C}$ and $55 \pm 5\%$ relative humidity.

Phenotypic and genetic parameters used for constructing the selection indices are given in Table 1. In the first six generations indices for antagonistic selection were constructed with phenotypic and genetic parameters estimated from full sib correlations in the two unselected base-populations (crossbreds 1,347 progenies/170 full sib families; outbreds 1,338 progenies/132 full sib families). In generation 7 index equations were recomputed using estimates of heritabilities and genetic correlations derived from response to single trait selection for low 8 week body weight and high 3 to 5 week body weight gain in the two populations (Table 1).

Table 1. Phenotypic and genetic parameters for the selected traits

	Crossbreds		Outbreds	
	8 week body weight	3–5 week body weight gain	8 week body weight	3–5 week body weight gain
\bar{X}	23.5 ± 2.0 g	9.5 ± 1.7 g	30.8 ± 2.9 g	13.3 ± 2.0 g
r_p		0.41 ± 0.02		0.40 ± 0.02
h^2	0.40 ± 0.05	0.32 ± 0.05	0.56 ± 0.06	0.65 ± 0.09
\hat{r}_g		0.29 ± 0.11		0.38 ± 0.10
$h_{\hat{r}}^2$	0.17 ± 0.01	0.13 ± 0.001	0.22 ± 0.02	0.18 ± 0.03
\bar{r}_{GR}		0.76 ± 0.03		0.81 ± 0.04
r_{GR}	0.58 ± 0.02	0.91 ± 0.04	0.75 ± 0.05	0.92 ± 0.07

\hat{r}_g , \hat{r}_g : Estimated from full sib correlations in the unselected foundation populations

$h_{\hat{r}}^2$: Heritabilities realized by single trait selection for low 8 week body weight or high 3–5 week body weight gain; 4 replicates used in each direction; empirical standard errors

\bar{r}_{GR} : Mean realized genetic correlation estimated from direct and correlated response in 8- and (5–3)+ mass selected lines after the formula given by Falconer (1981); 4 replicates used in each direction; empirical standard errors

r_{GR} : Realized genetic correlation estimated from direct and correlated response in each single trait selection line; 4 replicates used in each direction; empirical standard errors

Individuals were selected by mass selection on the basis of their index values. Realized intensity of selection averaged over the replicates was 1.3 for the outbreds and 1.2 for the crossbreds, respectively. Inbreeding coefficients, as calculated by the method given by Cruden (1949), increased at a rate of about 3.1% per generation in the lines under antagonistic selection and by 2.9% per generation in the control lines.

Results

Direct selection responses

Direct selection responses were measured as deviations of selected line generation means from the mean of the contemporary control generation. Figures 1 and 2 show the observed standardized responses for body weight traits for antagonistic and single trait selection over the first 22 generations. Table 2 gives the direct responses estimated by linear regression on generation number of deviation of selected line means from control.

In both populations antagonistic selection showed no response in the desired direction over the first six generations (Figs. 1 and 2), which was mainly due to 'incorrect' genetic parameter values used for the index equations (Table 1). From generation 7 onwards, mean realized parameters from single trait selection were used for the index equations. In the selection lines

derived from the crossbreds, antagonistic selection reduced 8 week body weight from generation 7 to 22 (Fig. 1 and Table 2) but showed no response for 3 to 5 week body weight gain. In fact, in both lines the gain was restricted during selection. As evident from Table 2 and Fig. 2, in the lines derived from the outbred population antagonistic selection caused a response in the desired direction. Eight week body weight was significantly reduced in both lines, while 3 to 5 week gain increased significantly in replicate 2 and insignificantly in replicate 1 (Table 2).

Growth curves analysis

In generation 22, individual body weights measured to the nearest 0.1 g were taken from birth to 56 days of age at weekly intervals from the (5-3)+, 8-, control and antagonistic selection lines. The lines were reproduced from 14 single-pair matings. On the average, weights from 140 individuals were available per line. The Richards (1959) function was used to describe the growth curves (Table 3). Relative to the control line, age and weight at inflexion point were significantly reduced in the low 8 and antagonistic selection lines and increased in the (5-3)+ line derived from the crossbred population. In the outbred population, however, growth curve analysis indicated increased age,

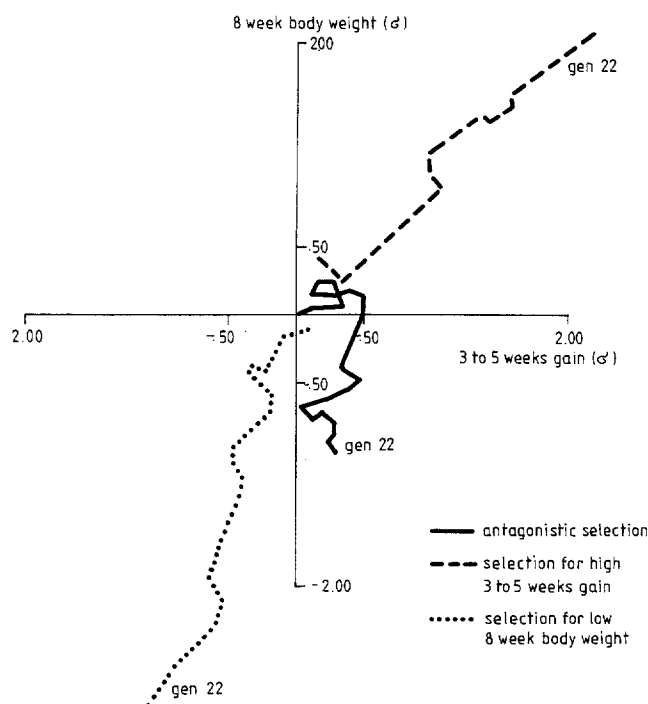


Fig. 1. Crossbred population-standardized response for single trait and antagonistic selection (generation 1-22, pooled over replicates)

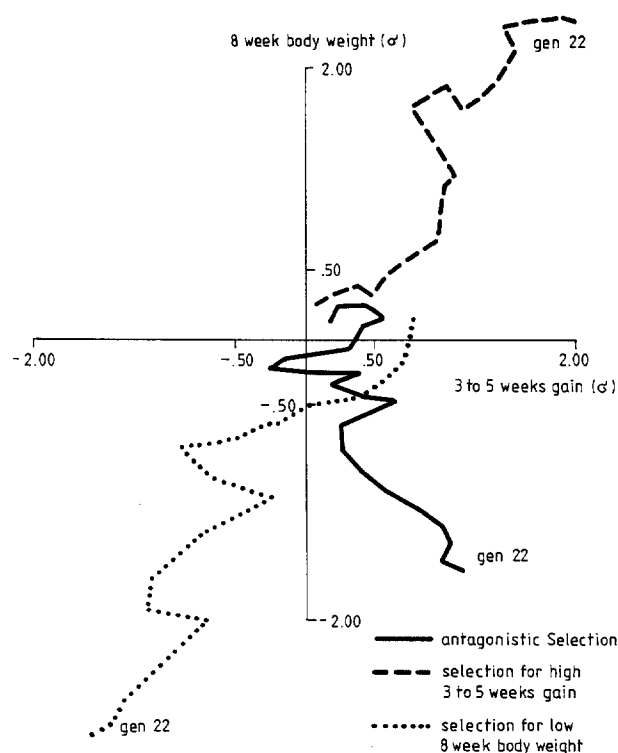


Fig. 2. Outbred population-standardized response for single trait and antagonistic selection (generation 1-22, pooled over replicates)

Table 2. Direct responses (g) – regressions on generation number of deviation of selected line mean from control (generation 1 to 22)

	Crossbreds		Outbreds	
	8 week body weight	3–5 week body weight gain	8 week body weight	3–5 week body weight gain
Antagonistic selection				
Replicate 1	–0.04*	–0.02	–0.12**	0.06
Replicate 2	–0.06*	–0.008	–0.16*	0.08*
Mean	–0.05*	–0.01	–0.14**	0.07*
Single trait selection (pooled over replicates)				
8–	–0.37**	–0.16*** ^a	–0.74**	–0.35*** ^a
(5–3)+	0.27*** ^a	0.22**	0.45*** ^a	0.30**

^a Correlated response* $P \leq 0.05$; ** $P \leq 0.01$ **Table 3a.** Growth curve analysis – crossbreds (gen 22)

Line	3–5 week gain	8 week weight	Inflexion point		
			Age	Weight	Gain
Control	8.5±1.6	22.7±2.0	15.8±0.6	8.5±0.2	0.53±0.01
Antagonistic	8.1±1.7	19.4±1.9	13.3±0.6	7.1±0.2	0.56±0.01
8–	4.8±1.6	16.4±2.1	13.0±1.0	6.8±0.3	0.43±0.02
(5–3)+	9.5±1.9	24.1±2.2	17.9±0.7	9.6±0.2	0.59±0.01

Table 3b. Growth curve analysis – outbreds (gen 22)

Line	3–5 week gain	8 week weight	Inflexion point		
			Age	Weight	Gain
Control	9.6±2.2	28.6±2.0	20.7±0.7	11.5±0.3	0.60±0.01
Antagonistic	10.3±2.2	25.7±2.2	21.9±1.1	13.1±0.5	0.71±0.04
8–	7.7±2.7	21.2±3.6	18.3±1.3	8.7±0.6	0.45±0.03
(5–3)+	13.7±1.9	33.5±3.5	23.2±1.8	16.2±0.3	0.87±0.03

weight and gain at inflexion point for the antagonistic and (5–3)+ line and reduced growth function traits in the low 8 line. This is an agreement with the analysis of direct responses, the antagonistic selection in the outbreds responded in the desired direction.

Index in retrospect and expected selection responses

To evaluate the selection actually practiced, the weights given to 8 week body weight and 3 to 5 week gain were obtained from an index in retrospect (Yamada 1977):

$$\begin{bmatrix} b_1 \\ b_2 \end{bmatrix} = i^2 \left[\begin{bmatrix} P_{1.1} & P_{1.2} \\ P_{2.1} & P_{2.2} \end{bmatrix} \begin{bmatrix} P_{1.1} & 0 \\ 0 & P_{2.2} \end{bmatrix} \right]^{-1} \begin{bmatrix} P_{1.J} \\ P_{2.J} \end{bmatrix}$$

where, 1, 2: the two selected traits; i = realized selection intensity; $P_{1.1}$, $P_{2.2}$ = direct selection differentials based on paper single trait selection for X_1 or X_2 ; $P_{1.J}$, $P_{2.J}$ = realized selection differentials in X_1 and X_2 by index selection.

The attention actually given to the body weight traits and the expected selection responses as determined from the index in retrospect are given in Table 4. Negative attention for eight week body weight and positive attention for the gain was achieved as planned in the crossbred and outbred populations. Due to infertility and failure to produce offspring in roughly equal numbers, the weights actually used for the crossbred population failed to agree with the equations. Al-

Table 4. Index in retrospect – pooled over replicates

	Crossbreds		Outbreds	
	8 week body weight	3–5 week body weight gain	8 week body weight	3–5 week body weight gain
Used weights	–0.81	1.00	–0.63	1.00
Realized weights	–0.60	1.10	–0.67	1.15
Expected responses	–0.03	0.10	–0.18	0.05
Observed responses	–0.05	–0.01	–0.14	0.07

though it is difficult to compare observed and expected selection responses, since index selection itself might have changed genetic parameters, expected response from the index in retrospect and responses observed are in fairly good agreement in the outbred population. In the crossbreds, observed and expected responses did not appear to be in agreement for 3–5 week body weight gain (Table 4). The asymmetrical genetic correlation which become apparent in this population (Table 1) could have lead to an incorrect index since the mean realized genetic correlation was used for constructing the index. Retrospectively, using a genetic correlation of $r_g \cong 0.80$ in the index should have resulted also in an antagonistic response in the crossbreds, whereas genetic correlations greater than 0.80 are expected to change both body weight traits in a positive direction, which is not the case in this population.

Discussion

A majority of experiments for the simultaneous improvement of antagonistic traits was successful and brought changes contrary to the sign of the genetic correlations (Pirchner 1980). Genetic correlations between body weight traits are high and the possibilities for antagonistic selection are restricted (Taylor 1968). However, the results of Abplanalp et al. (1963) with turkeys, Merritt (1974) and Ricard (1975), with poultry, and McCarthy and Bakker (1979) with mice, point to genetic variance in the shape of the growth curve. From the present study it is apparent that at least with index selection changes opposite in sign can be brought about for two body weight traits such as gain from 3 to 5 weeks and 8 week weight. Index selection changed weight at 8 weeks in a negative direction and the gain in the positive direction in the two replicates derived from the outbred population. In the lines derived from the crossbreds, antagonistic selection reduced 8 week weight and suppressed correlated response in the gain. One may ask the cause of this difference in the outcome of the antagonistic selection between the two popula-

tions. As shown by the index in retrospect, desired and used index weights are in satisfactory agreement for the outbred lines, but considerable discrepancy is evident between the weights used and those expected in the crossbred lines. However, the selection actually practiced should have lowered eight week weight but increased gain. While the observed response corresponded to expectation for weight, it failed in the case of gain and by a rather wide margin. The reason for this may be the strongly asymmetric genetic correlation in the crossbreds which obviously impairs the index. A further explanation could be that real incompatibility for antagonistic selection exists in this population.

Genetic progress was slow in both populations and therefore relatively long-term selection was needed to evaluate antagonistic selection. Although selection was performed under highly standardized conditions, an index in retrospect revealed some discrepancy between used and intended index weights in the crossbred lines. Index selection is important to animal improvement and an optimum response is only obtained if the index is constructed with 'correct' parameter values (Sales and Hill 1976). From our experience and as pointed out by several investigations (Nagai et al. 1978; McCarthy and Bakker 1979) realized estimates of heritability and genetic correlation from single trait selection would be most appropriate to use in an index. However, asymmetry of genetic correlation which became evident especially by single trait selection in the crossbred population, and in several experimental selection studies (Lang and Legates 1969; Nagai et al. 1978; Baker et al. 1984) may impede the construction of an optimal antagonistic selection index.

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