

AN ABSTRACT OF THE THESIS OF

RONALD EGNARD LIND for the DOCTOR OF PHILOSOPHY  
(Name of student) (Degree)

in GENETICS presented on 28 September 1972  
(Major) (Date)

Title: ACTUAL AND PREDICTED RESPONSE TO SELECTION  
ON MATERNALLY INFLUENCED TRAITS IN THE MOUSE

Abstract approved: Redacted for privacy  
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An experiment was conducted to determine if selection from standardized litters would be effective in separating lines of mice selected for increased and decreased litter weight at 14 days of age, and if response to selection on this maternally influenced trait could be accurately predicted.

Data were collected on litter size at birth and weight at birth, 14 days, and weaning over four selected generations.

Results of the analyses indicated that, at best, genetic improvement for litter size, weights at birth, 14-days and weaning would be slow. The heritability estimates from pooled data on selected lines were  $0.11 \pm 0.23$ ,  $0.37 \pm 0.27$ ,  $0.05 \pm 0.05$  and  $0.43 \pm 0.24$  for litter size and weight at birth, 14 days and weaning, respectively. Heritability estimates in the control lines for litter size and weight at birth, 14 days and weaning were  $0.12 \pm 0.17$ ,  $0.24 \pm 0.34$ ,  $0.29 \pm 0.12$  and  $0.06 \pm 0.02$  respectively.

The data indicate that selection for 14-day weight will have little effect on changes in litter size and litter birth weight but a slight response in weaning weight and gain from 14-days to weaning could be expected. There was a genetic correlation of  $0.59 \pm 0.35$  between 14-day weight and weaning weight.

The major portion of the variability in 14-day and weaning weights (62% and 63%, respectively) was due to maternal effects. Cross fostered progeny reared by high, control and low line dams from generation 4 averaged 6.95, 6.45 and 5.34 grams, respectively. There were no differences between high, low and control line progeny when they were reared by either a high, control or low line dam. It was concluded that selection had increased milk yield in dams from lines selected for increased 14-day weight and decreased milk yield in dams from lines selected for reduced 14-day weight.

Comparison of observed with predicted 14-day weight and weaning weight were in excellent agreement in the control line as shown by a deviation of less than 1%, between observed and predicted. Lines selected for increased 14-day weight (pooled data) showed that the observed 14-day weight was approximately 8% below the predicted 14-day weight; however, observed weaning weight was within 1% of the expected weaning weight. Data from low lines (pooled data) revealed that the observed 14-day weight was nearly 17% below the

expected 14-day weight. Also, the observed weaning weight was 17% below the expected weaning weight for progeny from dams selected for reduced 14-day weight. Comparison of observed and predicted 14-day weights and weaning weights revealed that selection tended to be less effective than expected in lines selected for increased 14-day weight but more effective than expected in lines selected for decreased 14-day weight.

Actual and Predicted Response to Selection  
on Maternally Influenced Traits in the Mouse

by

Ronald Egnard Lind

A THESIS

submitted to

Oregon State University

in partial fulfillment of  
the requirements for the  
degree of

Doctor of Philosophy

June 1973

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Date thesis is presented 28 September 1972

Typed by Ilene Anderton for Ronald Egnard Lind

## ACKNOWLEDGEMENTS

Acknowledgement is extended to the Oregon State Agricultural Experiment Station for the research assistantship that made my study possible. Also, the Department of Animal Science is gratefully acknowledged for providing funds for maintenance of the mouse population.

I am indebted to Dr. Ralph Bogart, Director of the Genetics Institute and Professor of Animal Genetics, for his continued guidance and assistance during my training and preparation for this thesis. The cooperation of Dr. J. E. Oldfield, Head, Department of Animal Science is gratefully acknowledged.

My sincere thanks are extended to Drs. Kenneth E. Rowe and Norbert A. Hartman for assistance with the statistical analyses. My thanks are also extended to Mrs. Carole Avery for computer programming.

I wish to express my gratitude to my graduate committee members, Dr. Ralph Bogart, Dr. Rodney V. Frakes, Dr. F. L. Hisaw, Dr. Roger G. Petersen, Dr. Paul A. Roberts, and Dr. Kenneth E. Rowe for their time and their competent advice.

My sincere thanks are extended to Miss Kathy Barber for key punching and Mrs. John W. Amberg for typing the first draft of the thesis. Special thanks are extended to my wife, Dorothy, and my

son, Kenneth, for their sacrifices, understanding and encouragement, without which, this study would not have been possible.

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# ACTUAL AND PREDICTED RESPONSE TO SELECTION ON MATERNALLY INFLUENCED TRAITS IN THE MOUSE

## INTRODUCTION

A vast number of selection experiments have been described in the literature. Falconer (1967) points out that surprisingly few of them have set out to compare actual with predicted selection response. How accurately genetic response to selection may be predicted depends on the accuracy of the heritability estimates for the trait measured, the selection intensity and the phenotypic variance for the trait. If adequate data are available on the base population and sufficient classes of relatives (paternal-half-sibs, maternal-half sibs, single-first-cousins, and etc) are present, the phenotypic variance can be partitioned to causal components. Estimates of the causal components of phenotypic variance can be incorporated into an equation to predict response to selection. A comparison of the actual with the predicted selection response provides a check on the effectiveness of selection on a quantitative trait.

It is often difficult to obtain accurate estimates of genetic parameters in farm animals because of limited facilities and the high cost of maintenance of the herd or flock. Proposed breeding systems for the improvement of economically important traits in farm animals may be monitored on laboratory mammals because these same traits

are common to laboratory species. More accurate estimates of genetic parameters can usually be obtained on laboratory species because larger numbers of observations can be obtained due to the short generation interval, the limited space requirement and the relatively low cost of maintenance of a large population. However, the laboratory mouse may not always be a good analog for farm animals and extrapolation of experimental results across species should be exercised with care. Roberts (1965a, 1965b), Chapman (1961), and Falconer (1967) have reviewed the contribution of the laboratory mouse to animal breeding.

The present study was designed to determine the effectiveness of selection for fourteen day growth response (a maternally influenced trait) and investigate concomitant changes in correlated traits. A discrete model was developed to predict response to selection for fourteen-day weight and actual and predicted responses were compared.

## LITERATURE REVIEW

### Selection in Two Directions

Selection in two directions from a common foundation stock has been utilized to eliminate environmental bias from estimates of selection response. However, it does not permit estimates of selection response in each direction independent of environmental trends unless the researcher has evidence that the environment has remained constant throughout the experiment. Response to selection is determined by the divergence of lines unless an unselected control population is maintained. If a control population is maintained selection response in both directions can be evaluated.

Experimental evidence from the laboratory mouse (Falconer, 1953a, 1960b, 1964) has clearly demonstrated that the selection response may be markedly asymmetrical in two way selection experiments. Falconer (1953a, 1960b) suggested several possible causes for the asymmetrical response. His main conclusions may be summarized as follows:

- (1) Directional dominance - the majority of the genes influencing a trait are dominant in one direction.
- (2) Different selection differentials for upward and downward selection.

- (3) Selection for heterozygotes.
- (4) Inbreeding.
- (5) Maternal effects (maternal size and maternal metabolic activity).

The observed asymmetry in two way selection experiments may be due to a combination of these factors.

#### Selection Experiments for Growth Response

Goodale (1938, 1941) was the first to demonstrate the feasibility of selecting for body weight in the mouse. Although his effective base population consisted of only five males and eleven females, through a combination of mass selection and progeny testing he was able to increase the average 60-day weight of male mice from 25 to 43 grams. His selection response was linear over 28 overlapping generations of selection. In his 1941 paper, Goodale suggested that the potential gain from selective breeding was enormous. Although he clearly expected to make further progress through selection for 60-day weight, when Falconer and King (1953) examined his data they found that he had nearly attained his maximum response after 28 generations of selection.

MacArthur (1944a, 1949) reported on a two-way selection experiment for 60-day weight in mice. His foundation stock consisted of the random bred  $F_2$  progeny from  $F_1$  crosses of seven



inbred strains of mice, indistinguishable for size. After 23 generations of selection the large line mice were about 3 times the size of his small line mice (38 vs. 12 gms) at 60 days of age. MacArthur noticed that by the end of 21 generations of selection response was diminishing. A subsequent study by Buttler (1952), using MacArthur's strains of mice, indicates that little if any further selection progress was made.

Falconer (1953) published the results of the first 11 generations of a long term selection study on six week growth response in mice. His base population was developed from a four-way cross of inbred strains of mice. The  $F_2$  progeny were equivalent to a single full-sib family and were designated generation zero. Within family selection (1 male and 1 female selected) was practiced and each successive generation resulted from six pair matings. In Falconer's study the inbreeding increased rapidly as the first selected generation, theoretically, was 25 percent inbred. At the end of the eleventh generation high line mice were 11 grams heavier than low line mice. Falconer's lines diverged regularly but the response was much more pronounced in the line selected for decreased six week weight. He attributed the asymmetrical response to inbreeding depression.

After the 10th generation of selection, Falconer constructed a control line from the same parental strains utilizing the same mating system that was employed in the development of the original base

population. Thus in later generations he was able to evaluate response to selection in both directions as well as measure the divergence between lines.

Falconer (1960) presents the results through 28 generations of selection for increased 6-week weight and 18 generations of selection for decreased 6-week weight. His results showed that selection for increased 6-week weight produced a linear response through the 28th generation. There was a temporary plateau in selection response for decreased 6-week weight from generation 10 to generation 12. After the twelfth generation, response continued linearly, but selection for decreased weight was discontinued after 18 generations because of infertility.

An experiment initiated by Comstock in 1957 and reported by Rahnefeld et al. (1963) supports the findings of Falconer (1953, 1960). In the study reported by Rahnefeld et al. (1963), the foundation stocks were developed by crossing inbred strains, and selection was based on post-weaning gain. They observed that response to mass selection for gain from 18 to 42 days of age was linear over the first 17 generations of selection. Comstock (1969) estimated the number of loci involved in the expression of post-weaning gain to be in excess of 300 pair. In the same paper, Comstock reported that selection response had continued linearly through 35 generations of selection. Based on the estimate of the number of loci involved in the expression of

post-weaning gain, Comstock concluded that response to selection would be attained for many more generations.

Genetic selection experiments on laboratory animals are normally conducted under uniform environmental conditions, whereas, selection experiments on large animals are often conducted under a variety of environmental conditions. Because of the wide variety of environmental conditions imposed upon large animals used in selection studies, it became evident that possible genotype by environment interactions ought to be investigated. Falconer (1952) presented the theoretical framework for studies on gene-environment interactions. Later Falconer and Latyszewski (1952), Falconer (1960), Korkman (1961) and Dalton and Bywater (1963) reported on experiments designed to investigate genotype-environment interactions. The main conclusions that can be drawn from these studies are that genotype-environment interactions may mask selection response and that in selection experiments animals should be raised and selected in the environment in which they will ultimately perform.

#### Selection Experiments on Litter Size

Because of the ease of collection of data, there are numerous reports in the literature concerning reproduction in mice. In a series of papers, Falconer (1955, 1960, 1963, 1964) presented the results of a two-way selection experiment for litter size. In addition to the

lines selected for increased litter size and decreased litter size, an unselected control line was maintained. In the 1955 paper, Falconer calculated standardized partial regression coefficients for the relationships of litter size with body weight of the dams and the size of the litter in which the dam was born. He found that litter size was affected by two pathways of equal magnitude and opposite sign which explained why the direct regression of litter size on maternal litter size was zero. As a result of this finding Falconer chose a selection scheme that would avoid the complication of maternal effects and permit more accurate evaluation of selection response for litter size. He mated families of full-sib females to a single male from a different litter and then selected one female from each full sib family based on litter size at birth. Under this scheme each family contributed equally to the next generation and the male influence was ignored. Although Falconer's mating and selection scheme was designed to avoid maternal effects, he still had a maternal effect in his experiment since he did not standardize litter size. However, the maternal effect was a constant and did not complicate selection procedures.

In his 1964 paper, Falconer presented the results of the entire experiment. He observed that selection response in the first generation was directly opposite to the direction of selection. This unexpected response was attributed to a maternal effect. Mice born

to large litters are smaller and smaller mice on the average have smaller litters.

With the exception of the first generation, both selected lines showed a linear response over the first 20 generations. For the next 11 generations selection response was stable. At the selection limit, response was symmetrical with average litter sizes of 9.2, 7.6 and 6.0 in the high, control and low lines respectively. However, when Falconer accounted for differences in selection intensities in the selected lines his results showed that the realized heritabilities for litter size, calculated on a within-family basis, were 8 percent for upward selection and about 25 percent for the downward selected line. The heritability estimate obtained from the divergence of lines was 13 percent. Calculated on an individual basis, the heritability estimates for upward selection, downward selection and line divergence were 15, 40 and 22 percent respectively. Thus selection response was markedly asymmetric with a final divergence of 3.2 mice per litter which represented 1.6 times the original phenotypic standard deviation and 3.3 times the original additive genetic standard deviation for litter size.

Falconer (1963) presented evidence which indicates that the asymmetrical response can be attributed partially to an increased ovulation rate in the high line, although the ovulation rate increased somewhat in the low line when compared to the controls. He also

observed that there was a marked increase in post implantation mortality among fetuses in the low line. Through crossing low line mice with controls he was able to show that the death loss was due to maternal effects and not the genotype of the embryos.

Bateman (1966) investigated selection response for litter size from a base population derived from Falconer's stocks. Bateman's experimental design differed from that of Falconer in that selections were made from the largest litters in the high line and the smallest litters in the low line. Thus, Bateman used an among-family selection procedure whereas Falconer selected within families. Bateman obtained a 5.6 mouse divergence between lines in 12 generations of selection. When he examined components of litter size, Bateman found that the high and low lines differed in ovulation rate, implantation rate and fetal survival. The low line had a lower number of implantations. His results showed that low line dams ovulated 20 percent fewer eggs, had 4.5 times as many preimplantation losses, and 1.6 times as many dead fetuses as the high line. In an attempt to determine the effect of genotype on embryo survival Bateman crossed high and low lines and compared embryonic survival in the reciprocal line crosses and the straight line progeny. He concluded that the line of sire had little or no effect on implantation rate or post implantation survival.

Dalton and Bywater (1963) reported heritability estimates of

size at weaning in lines of mice selected on normal and restricted diets. Neither of the selected lines deviated significantly from the control line. They obtained heritability estimates of  $0.06 \pm 0.08$  and  $0.02 \pm 0.08$  for mice raised on normal and restricted diets respectively. Bradford (1968) selected for increase litter size in lines of mice derived from crosses of 4 and 8 inbred lines. He obtained a realized heritability estimate of 25 percent at the end of eight generations of mass selection. However, the realized heritability estimates dropped to  $0.13 \pm 0.07$  and  $0.22 \pm 0.06$  for the 4-way and 8-way cross lines respectively, after two further generations of selection. Mean litter size at birth in his 8-way cross line increased from 9 to 12 young through 10 generations of selection. Bradford used a mass selection program in all but one line in which intra-litter selections were made. He found that response from mass selection was nearly twice as great as the selection response from intra-litter selection.

#### Maternal Effects on Litter Size and Body Weight

MacDowell, Allen and MacDowell (1929) noted that larger mice produce larger litters than small mice. It is now well known that there is a relationship between maternal size and litter size at birth. Large dams produce large litters and the females within the large litters in turn produce small litters and the large female progeny from small litters produce large litters. Falconer (1955) analyzed

maternal effects on litter size by calculating standardized partial regression coefficients relating litter size to dams body weight and litter size to the size of the litter in which the dam was born. He found a negative correlation ( $r = -0.34$ ) between dams weight and size of the litter in which the dam was born and a positive correlation ( $r = +0.22$ ) between dams weight and dams litter size. The regression of dams litter size on size of the litter in which the dam was born was  $-.07$ , the product of the two partial correlations. However, when body weight was held constant, the partial regression of litter size on maternal litter size was positive ( $r = +0.07$ ). Thus, Falconer showed that litter size was affected by two pathways of equal magnitude but opposite sign. His results explain why the direct regression of litter size on maternal litter size is zero. A more recent and more sophisticated analysis of maternal affects on litter size (Falconer, 1964) supports his earlier observations.

Many of the early investigations of maternal effects on body weight involved line or strain crosses. When lines or strains are crossed reciprocally, except for sex-linkage effects, both groups of progeny have the same genetic potential for growth. Thus, differences between reciprocals are a reflection of maternal differences and sex-linkage effects. Buttler (1958), Mason et al. (1960) and Carmon (1963) all present evidence of maternal differences in growth performance in reciprocals of strain crosses. Chai (1956) was able



to demonstrate marked maternal effects in strain crosses. His analysis showed that maternal effects accounted for 26.3 percent of the total variation whereas genetic effects only accounted for 23.2 percent of variance in  $F_1$  hybrids. However, the pure strains used in the crosses were markedly different in adult body size so a large maternal effect could be expected.

Variation in body weight due to maternal effects can be attributed to two main components, prenatal and post-natal environment. These two components of maternal effects can be evaluated by ova transplants or cross-fostering experiments. Brumby (1960) used a combination of ova transplants and fostering of offspring to separate prenatal from postnatal effects. He transferred ova from Falconer's large and small strains to unselected control linedams and allowed the control line dams to foster the resulting offspring. His results indicated that prenatal influences were as important or more important than postnatal influences. His results are in agreement with those of Bateman (1954). From a cross fostering experiment Bateman (1954) found that post natal influences only accounted for 32 percent of the variation in 12-day body weight of mice. However, reports by Cox, Legates and Cockerham (1959), Farthing (1965), and El Oksh, Sutherland and Williams (1967) indicate that postnatal maternal environment accounts for 70-80 percent of the variance in 12 day weight of mice. In an experiment involving standardized

litters and family selection, Eisen, Legates and Robison (1970) were able to partition postnatal maternal environmental effects into genetic and non-genetic components. They found that 56.2 percent of the variation in 12-day weight was due to postnatal maternal environment, but only 6.1 percent was due to postnatal genetic maternal effects.

#### Relationships Between Litter Size and Body Weight Traits

MacArthur (1944b) observed a correlated response in litter size and birth weight when he selected for 60-day body weight. He reported that at the end of eight generations of selection for high and low 60-day weight, the large line produce 84 percent larger litters and individual birth weights were 24 percent heavier than those of the low line. The mean litter birth weight of large line litters was over twice that of low line litters. However, litter birth weights in both lines were approximately one-third of the dam's body weight.

Falconer (1953) observed correlated responses to selection for six-week weight in both litter size and weaning weight. He found concomitant increases and decreases in litter size while selecting for increased and decreased six week weight. The correlated response in weaning weight was not quite as pronounced. In his small line, weaning weight decreased whereas in the large line no consistent pattern of response was observed. When a strong correlation exists

between two traits, selection for one trait should result in a concomitant change in the other trait. However, Cockerham (1959) demonstrated, through 8 generations of selection, that although a positive correlation existed between body weight and tail length, through selection each trait could be increased while the other decreased. Thus although negative correlations exist between traits, it is possible through selection to improve both traits.

The observation that selection for increased size results in increased litter size suggests that there is a correlation between body size and ovulation rate. Fowler and Edwards (1960) obtained data from two sets of unrelated mice (Falconer's N and C stocks) that confirmed that large mice have a higher ovulation rate than small mice. In the N strain selection was for 6 week body weight and they observed that in the large line body weight averaged 30.1 grams and litter size was 7.9 young whereas in the small line average body weight was 13.3 grams with a litter size of 4.0. The C strain had been selected for weight gain from three to six weeks. They found that in the large line average body weight was 35.9 grams and average litter size 9.2 while in the small line average body weight was 17.6 grams and litter size average was 6.2 offspring. Their data showed a linear relationship between body weight and litter size. In an earlier study, Fowler (1958) found a correlation between carcass fat and body size. Falconer's large and small

strains and one of his control strains were used. Fowler (1958) found carcass fat percentages of 27.6 and 15.0 in the two large strains and 16.3 and 9.7 percent in the two small strains.

Roberts (1961) reported on lifetime production of offspring in mice selected for large and small body size. He observed that the large strain averaged 4-1/2 litters (6.6 progeny per litter) over their lifetime, whereas low line females averaged 11 litters (4.35 progeny per litter) during their lifetime. The net result was that during a lifetime low line females weaned twice as many progeny as large line females. The difference between lines in mean weight of progeny weaned was not nearly as dramatic as the difference in number weaned. High line dams weaned an average of 188 grams of progeny as compared to 236 grams for low line dams.

From a covariance analysis, Rahnfeld, Boylan and Comstock (1962) estimated the genetic correlation between litter size and post weaning growth. Although the correlation, +0.153, was not statistically significant they concluded that selection for increased growth rate from 18 to 42 days would result in increased litter size.

Singh (1965) reported genetic correlations between weaning weight and post weaning growth for Rahnfeld's (S) line and a line (S') derived from the same cross (two inbred lines) that produced the (S) line. A covariance analysis yielded correlations of 0.35 and 0.17 for the S and S' lines respectively. Singh noted that fertility was

not correlated with postweaning growth rate.

From a cross-fostering experiment, Young and Legates (1965) studied growth interrelationships in mice. They reported genetic, maternal, and phenotypic correlations between twelve day weight and gain from 21 to 42 days of 0.27, 0.02 and 0.12 respectively. Corresponding correlation coefficients for weaning weight with post weaning gain were 0.49, -0.27, and 0.07; and for preweaning gain with postweaning gain were 0.48, -0.27, and 0.06. The magnitude and sign of the maternal correlations between weights and postweaning gains led the authors to the conclusion that mice that were nursed by poor milking dams showed compensatory growth during the postweaning period and mice that were nursed by dams that milked well made slower postweaning gains.

Eisen, Legates and Robison (1970) reported correlations between prenatal performance and body weight traits. Genetic correlations between number born and 12-day weight, 6-week weight, 8-week weight and gain from 12 to 42 days were 0.69, 0.64, 0.69 and 0.57 respectively. The corresponding phenotypic correlations were 0.15, 0.24, 0.23 and 0.23. They also found genotypic and phenotypic correlations, 0.54 and 0.19 respectively, between postnatal maternal performance (12-day litter weight) and individual weights. The phenotypic and genotypic correlations between prenatal (litter size) and post natal (12-day litter weight) maternal performance

were 0.10 and 0.19 respectively. Eisen, Legates and Robison interpret the genetic correlation between 12-day weight and other weight traits as indicating a positive genetic correlation between lactation and body size. Their results are in agreement with Falconer's (1955) earlier conclusion that postnatal maternal performance and mature body weight are positively correlated genetically.

### Predicted Response to Selection

The agreement between observed and predicted response in selection experiments with laboratory species has not always been perfect. Clayton, Morris and Robertson (1957) selected drosophila for increased and decreased bristle number. Comparison of observed with predicted responses showed that in general there was good agreement but in some lines there were serious discrepancies. The most serious discrepancies were in lines selected for decreased bristle number. In a long-term selection experiment Clayton and Robertson (1957) found that observed response was not always in close agreement with the predicted response. Martin and Bell (1960) selected drosophila for mature body size, egg size, fecundity and adult emergence for 15 generations. Their data show that there was poor agreement between observed and predicted response throughout the experiment. They attribute the lack of agreement, in part, to the fact that they used the heritability of divergence rather than

the heritability of adult body size.

Kyle and Chapman (1952) selected rats for ovarian response to a standard dose of equine gonadotropic hormone. Their results show that in general the actual response agrees quite favorably with the predicted response in groups selected for increased response and groups selected for decreased response. Data from 314 litters in the high-response group covering 13 generations of selection showed a difference of -0.3 between observed and predicted response. However, there was a significant difference ( $P < .05$ ) between observed and predicted response in the low-response group. In the low-response group predictions were based on data from 270 litters.

Although Martin and Bell (1960) claimed that quantitative genetic theory was not adequate to predict selection response, authors of more recent reviews and texts, (Falconer, 1960, 1967; Lindstrum, 1968; and Pirchner, 1968) agree that current genetic theory is adequate to predict short-term selection response. In prediction equations heritability estimates from the base populations are usually held constant over all generations studied. Pirchner (1968) and Falconer (1969) point out that the heritability will change as a result of selection, thus one would not expect real close agreement between observed and predicted response when heritability is used as a constant in the prediction equation.

Magee (1965) points out that selection gain is equal to the

selection differential times the heritability only when selection is on a single trait. However, if there are no genetic or environmental correlations between several quantitative traits, response to selection for each of these traits could be predicted with reasonable accuracy.

There is currently a lack of evidence in the literature on the predictability of selection response for an early life trait that is strongly influenced by maternal factors.



## MATERIALS AND METHODS

### Breeding Population

The base population was formed by crossing stocks of Swiss-Webster mice that had been bred as closed random bred populations. Thus the coefficient of coancestry in the base population was zero. Individuals from the base population were randomly assigned to two high lines ( $H_1$  and  $H_2$ ), two low lines ( $L_1$  and  $L_2$ ) and a control line (C). Each of the lines,  $H_1$ ,  $H_2$ ,  $L_1$  and  $L_2$ , consisted of 20 females and 10 males and the control line consisted of 80 females and 80 males.

In all lines matings were made at random with the exception of no full-sib matings. Initially, matings were made during a two-week mating period after the youngest selected female reached 63 days of age. For the last two selected generations these restrictions were relaxed because many of the selected female mice in the low lines had not reached sexual maturity at 63 days of age. Progeny for generations 1 and 2 were produced by within-line within-generation matings. Generation 3 progeny for the selected lines were produced by mating generation 2 selected females to progeny tested sires of generation 1 progeny. Selected generation 3 females were mated to progeny tested sires of generation 2 progeny. For the selected lines later generations were to be produced by mating selected females to progeny tested males two generations back. However, the

experiment had to be terminated after the fourth generation because of an infant viral diarrhea epidemic in the population. Each generation of the control line was produced by random mating within generation. Full-sib matings were prevented in all lines.

During this experiment the mouse population was housed in a laboratory at 80° F and fed a commercial mouse chow ad libitum. Breeding groups were placed in 7" x 7" x 9" cages with half-inch mesh wire front and bottom. After the breeding period males were removed from the breeding cages and H<sub>1</sub>, H<sub>2</sub>, L<sub>1</sub> and L<sub>2</sub> males were saved for progeny testing. Random line males were culled. When females were obviously pregnant they were removed from the breeding cages and placed in individual 7" x 7" x 9" cages with 1/4" mesh front and bottom. Littering cans, four inches in diameter and three inches high filled approximately 1/3 full of dry sawdust, were placed in littering cages. Pregnant females were checked at the same time each day for new litters. Date littered, litter size and litter birth weight (to the nearest 0.01 gram) were recorded. On day four post partum, litters were standardized to 8 young, four males and four females whenever possible. Litters with less than 8 young were augmented to 8 by fostering young of the same age and comparable size from the same line. Individual mice grafted onto foster dams were identified by toe clip and culled at weaning. All mice within each litter were identified by dye (5 percent picramic acid in 95

percent ethyl alcohol) spots at 14 days of age. Fourteen and 21-day weights were recorded to the nearest 0.01 gram for each individual. At 21 days of age males and females were separated and mice of each sex from the same litter were placed in a 7" x 7" x 9" cage. When the youngest litter was weaned, at 21 days of age, gains from birth to 14 days of age for standardized litters were calculated and litters ranked in the high and low lines. Two females and one male from each of the ten highest ranked litters in each of the high lines and two females and one male from each of the ten lowest ranked litters in each of the low lines were selected. Eighty females and 80 males were selected from all progeny available for parents of the next generation in the control line. Selections were made at random within litters because 14-day weight of progeny is a maternally influenced trait. Thus, selection of the largest progeny from high-line litters and the smallest mice from low-line litters would be selecting for increased growth rate as well as increased maternal ability.

All mice in the high and low lines not selected to become parents of future generations were culled at weaning. In the random line, in addition to the individuals selected for line propagation, 100 females and 100 males were saved for use in the progeny test. All mice selected for future breeders were given a permanent ear notch identification as the dye spots would eventually fade. Mice selected for line propagation were reared in 7" x 7" x 9" cages with 1/2"

mesh wire front and bottoms but because of a need for available mouse racks for other experiments, the random line males and females saved for the progeny test scheme were reared in round cages (30 inches in diameter and 6 inches deep) from weaning until they were placed in breeding groups. Sawdust was used for litter in the 30-inch round cages.

As mentioned previously, the first two progeny groups were produced by within-line, within-generation matings and generation 3 and 4 progeny groups were sired by progeny tested males. Each selected male was assigned to mates at random for the production of the first two generations of progeny. Four selected females were assigned at random to each selected progeny tested male for propagation of the third and fourth generations. In the control line, random paired matings were made throughout the experiment.

The sires of generation one and two progeny groups were progeny tested and the five superior sires for each high line and the five inferior sires for each low line were used as sires of generation three and four progeny groups. Sires were progeny tested by mating each male to two random line females. Four daughters (two from each litter when possible) of each sire were then mated to random line males. Gains from birth to 14 days of age for standardized litters were used to evaluate sires.

In order to determine if selection response was due to improved

maternal ability or increased genetic potential for growth, a reciprocal cross fostering experiment (Eisen, Legates and Robinson, 1970) was conducted on generation two and generation four progeny.

Within-line matings were made between 20 surplus females and 10 surplus males from the selected litters (after mice for line propagation in the main experiment had been selected) in the selected lines. All matings were made (2 females to each male) at random in each of the selected lines. Forty surplus females were mated, two females to each male, in the random line. Mice were handled the same way as in the main experiment except that litters were standardized to six young, three males and three females, on day 4 post partum. Male and female progeny in each litter were identified by a toe clip at the time of litter standardization. Litters were recombined so that each dam was nursed by two high, (one male and one female) random and control line progeny.

#### Treatment of Data

Data were collected on litter size at birth, litter birth weight and individual 14-day and weaning weights. Because of unequal numbers of progeny surviving in different litters and unequal numbers of litters in different lines within each generation, least squares analyses were applied to the data to determine if selection was effective. After analyzing the data for each trait under the full

model, a reduced model was developed. Any effects in the full model that were not significant ( $P > .05$ ) were removed from the model. In the least squares procedure each factor in the model is adjusted for every other factor. Thus, as Harvey (1966) pointed out, the least squares estimates will be biased if they have been adjusted for an effect in the model that is non-existent in the data.

For each trait measured, each observation was corrected for environmental effects common to that observation and the corrected data were analyzed by a nested analysis of variance (lines  $H_1$ ,  $H_2$ ,  $L_1$ , and  $L_2$ ). Variance components from the nested analysis of variance were used to determine heritability estimates and estimates of phenotypic, genotypic and environmental correlations among the traits were calculated.

Data from the cross fostering experiment were subjected to a factorial analysis of variance.

The full models for the least squares analysis on each trait studied in the main selection experiment and the models for the factorial analysis of the data from the cross fostering experiment are listed below:

1. Least squares model for fourteen day weight response.

$$Y_{ilgk} = \mu + S_i + L_1 + G_g + SL_{il} + SG_{ig} + LG_{lg} + SLG_{slg} + \\ dN_1 + dN_2 + dA + dW_1 + dF_O + dF_D + E_{ilgk}$$

where:

$Y_{ilgk}$  = the fourteen-day weight of k-th individual of the  
i-th sex in the l-th line in the g-th generation.

$\mu$  = the population mean

$S_i$  = the effect common to the i-th sex

$L_l$  = the effect common to the l-th line

$G_g$  = the effect common to the g-th generation

$SL_{il}$  = the effect common to members of the i-th sex in  
the l-th line

$SG_{ig}$  = the effect common to the members of the i-th sex  
in the g-th generation

$LG_{lg}$  = the effect common to members of the l-th line in  
the g-th generation

$SLG_{ilg}$  = the effect common to members of the i-th sex in  
the l-th line and g-th generation

$dN_1$  = the partial regression of individual fourteen day  
weight on litter size at birth

$dN_2$  = the partial regression of individual fourteen-day  
weight on litter size at fourteen days post partum

$dA$  = the partial regression of progeny fourteen-day  
weight on age of dam

$dW_1$  = the partial regression of fourteen-day weight on  
weight at birth

- $dF_O$  = the partial regression of offspring fourteen-day weight on inbreeding of offspring  
 $dF_D$  = the partial regression of progeny fourteen-day weight on inbreeding of dam  
 $E_{ilgk}$  = random errors that are assumed to be independent and normally distributed with mean = 0 and common variance,  $\sigma^2$

2. Least squares equation for weaning weight.

$$Y_{ilgk} = \mu + S_i + L_l + G_g + SL_{il} + SG_{ig} + LG_{lg} + SLG_{ilg} + dN_1 + dN_2 + dN_3 + dA + dW_1 + dF_O + dF_D + E_{ilgk}$$

where:

- $Y_{ilgk}$  = the weaning weight of the k-th progeny of the i-th sex in the l-th line and g-th generation  
 $\mu$  = the population mean weaning weight  
 $S_i$  = the effect common to the i-th sex  
 $L_l$  = the effect common to the l-th line  
 $G_g$  = the effect common to the g-th generation  
 $SL_{il}$  = the effect common to the i-th sex in the l-th line  
 $SG_{ig}$  = the effect common to the i-th sex in the g-th generation  
 $LG_{lg}$  = the effect common to the l-th line in the g-th generation



- $SLG_{ilg}$  = the effect common to the i-th sex in the l-th line  
in the g-th generation
- $dN_1$  = the partial regression of weaning weight on litter  
size at birth
- $dN_2$  = the partial regression of weaning weight on litter  
size at fourteen days
- $dN_3$  = the partial regression of weaning weight on litter  
size at weaning
- $dA$  = the partial regression of weaning weight of progeny  
on age of dam
- $dW_1$  = the partial regression of weaning weight on birth  
weight
- $dW_2$  = the partial regression of weaning weight on fourteen-  
day weight
- $dF_O$  = the partial regression of offspring weaning weight  
on inbreeding of offspring
- $dF_D$  = the partial regression of offspring weaning weight  
on inbreeding of dam
- $E_{ilgk}$  = random errors assumed to be independent and  
normally distributed with mean = 0 and common  
variance,  $\sigma^2$ .

3. Least squares equation for analyzing birth weight data.

$$Y_{lgk} = \mu + L_l + G_g + LG_{lg} + dN_1 + dA + dF_O + dF_D + E_{lgk}$$

where:

- $Y_{lgk}$  = the mean birth weight of progeny of the k-th litter  
of the l-th line in the g-th generation
- $\mu$  = the population mean for birth weight
- $L_l$  = the effect common to the l-th line
- $G_g$  = the effect common to the g-th generation
- $LG_{lg}$  = the effect common to the l-th line in the g-th  
generation
- $dN_l$  = the partial regression of birth weight on litter size  
at birth
- $dA$  = the partial regression of birth weight of progeny  
on age of dam
- $dF_O$  = the partial regression of progeny birth weight  
on inbreeding of progeny
- $dF_D$  = the partial regression of birth weight of progeny  
on inbreeding of dam
- $E_{lgk}$  = random errors assumed to be independent and nor-  
mally distributed with mean = 0 and common variance  
 $\sigma^2$ .

4. Least squares model for analyzing litter size data.

$$Y_{lgk} = \mu + L_l + G_g + LG_{lg} + dA + dF_O + dF_D + E_{lgk}$$

where:

$Y_{lgk}$  = the size of the k-th litter on the l-th line in the g-th generation

$\mu$  = the population mean litter size at birth

$L_l$  = the effect common to the l-th line

$G_g$  = the effect common to the g-th generation

$LG_{lg}$  = the effect common to the l-th line in the g-th generation

$dA$  = the partial regression of litter size on age of dam

$dF_O$  = the partial regression of litter size on inbreeding of progeny

$dF_D$  = the partial regression of litter size on inbreeding of dam

$E_{lgk}$  = random errors assumed to be independent and normally distributed with mean = 0 and common variance,  $\sigma^2$

5. Model for 14-day growth response for the cross-foster experiment.

$$Y_{rmlsk} = \mu + R_r + M_m + L_l + S_s + ML_{ml} + MS_{ms} + LS_{ls} + \\ MLS_{mls} + E_{rmlsk}$$

where:

$Y_{rmlsk}$  = the gain from birth to 14 days for the k-th individual

of the  $s$ -th sex and the  $l$ -th line of progeny nursing  
a dam of the  $m$ -th line in the  $r$ -th replication

- $\mu$  = the population mean individual gain from birth to  
14 days of age
- $R_r$  = the effect of replication
- $M_m$  = the effect common to all progeny nursing a dam of  
the  $m$ -th maternal level
- $L_l$  = the effect common to all members of the  $l$ -th line  
of progeny
- $S_s$  = the effect common to all members of the  $s$ -th sex
- $ML_{ml}$  = the effect common to all members of the  $l$ -th line  
of progeny nursing a dam of the  $m$ -th maternal level
- $MS_{ms}$  = the effect common to the  $s$ -th sex nursing dams  
of the  $m$ -th line
- $LS_{ls}$  = the effect common to the  $s$ -th sex of the  $l$ -th line  
of progeny
- $MLS_{mls}$  = the effect common to the  $s$ -th sex of the  $l$ -th line  
of progeny nursing dams of the  $m$ -th maternal line
- $E_{rmlsk}$  = random errors assumed to be independent and  
normally distributed

Model 5 was also used to describe the growth response from  
14 days to weaning for the mice involved in the cross fostering  
experiment. The terms in the model were redefined in terms of the

21-day growth response.

After establishing which factors in the full models were non-significant, the non-significant factors were removed from the models and the data were subjected to least squares analysis using reduced models. Also, as mentioned earlier, each observation was corrected for the significant covariates in the equation and the corrected data for lines 1, 2, 4, and 5 were subjected to a nested analysis of variance to establish heritability estimates and determine genetic, phenotypic and environmental correlations. The following formulae (Becker, 1967) were used to determine heritability estimates and genetic, phenotypic and environmental correlations between traits.

$$\text{Heritability } (h^2) = \frac{4\sigma_S^2}{\sigma_S^2 + \sigma_D^2 + \sigma_W^2}$$

where:

$\sigma_S^2$ ,  $\sigma_D^2$  and  $\sigma_W^2$  refer to the sire, dam and progeny components

of variance

$$\text{Standard error of } h^2 = \text{S. E. } h^2 = \frac{4\sqrt{\text{var}(\sigma_S^2)}}{\sigma_S^2 + \sigma_D^2 + \sigma_W^2}$$

Genetic correlation ( $r_G$ )

$$r_G = \frac{4 \text{ Cov}_{S(1,2)}}{\sqrt{4\sigma_{S(1)}^2 4\sigma_{S(2)}^2}}$$

where:

(1) = trait 1,

(2) = trait 2,

$\text{Cov}_{S(1, 2)}$  = the sire component of covariance

Environmental correlation ( $r_E$ )

$$r_E = \frac{\text{Cov}_{W(1, 2)} + \text{Cov}_{S(1, 2)} - 3\text{Cov}_{D(1, 2)}}{\sqrt{(\sigma_{W(1)}^2 + \sigma_{S(1)}^2 - 3\sigma_{D(1)}^2)(\sigma_{W(2)}^2 + \sigma_{S(2)}^2 - 3\sigma_{D(2)}^2)}}$$

where:

Cov = Covariance

$\sigma^2$  = Variance

W = Progeny component

S = Sire component

D = Dam component

Penotype correlation ( $r_P$ )

$$r_P = \frac{\text{Cov}_{W(1, 2)} + \text{Cov}_{S(1, 2)} + \text{Cov}_{D(1, 2)}}{\sqrt{(\sigma_{W(1)}^2 + \sigma_{S(1)}^2 + \sigma_{D(1)}^2)(\sigma_{W(2)}^2 + \sigma_{S(2)}^2 + \sigma_{D(2)}^2)}}$$

where:

Cov = Covariance

$\sigma^2$  = Variance

W = Progeny component

S = Sire component

D = Dam component

Heritability estimates and genetic, phenotypic and environmental correlations could not be obtained from a nested analysis of variance for the control line because a system of paired matings was utilized for line propagation. The appropriate heritability estimates and genetic correlation coefficients were obtained from a regression of offspring on mid-parent values for the control line. The formulae used are listed below.

$$\text{Heritability estimate } (h^2) = b_{\overline{OP}} = \frac{\text{Cov } XZ}{2\sigma_X^2}$$

where:

X = the mid-parent mean

and

Z = the mean of the progeny

Standard error of  $h^2$  (S. E.  $h^2$ )

$$\text{S. E. } h^2 = \sqrt{\text{Var}(b) / \Sigma x^2} \quad (\text{Dickerson, 1960 and Becker, 1967})$$

where:

$\Sigma x^2$  = the variance of mid parent values

Genetic correlation ( $r_G$ )

$$r_G = \frac{\text{Cov } X_1 Z_2 + \text{Cov } X_2 Z_1}{2\sqrt{(\text{Cov } X_1 Z_1)(\text{Cov } X_2 Z_2)}}$$



### Characterization of Traits

Falconer (1960) describes the resemblance between relatives as one of the basic phenomena exhibited for many metric traits. Data from generation one were used to characterize the traits investigated. The progeny were divided into families of individuals with the same relationship to each other such as paternal half-sibs. Theoretical biometrical relationships and assumptions as to the mode of inheritance were used to partition the observed covariance among relatives into causal components. Two nested analysis of variance computations were made on data from generation one. In the first analysis, dams were nested within sires whereas in the second analysis, sires were nested within dams. Falconer (1960) and Pirchner (1961) showed that variance and covariance components have the same theoretical expectations. The theoretical expectations of the causal components of the covariance between relatives are presented in Table 1.

The estimates of the causal components from appropriate analysis were used in the prediction equation for estimating 14-day and weaning weights.

Table 1. Expectations of the covariance between relatives.

Method of Analysis	Component of Variance	Covariance	Causal Components				
			$\sigma_A^2$	$\sigma_D^2$	$\sigma_M^2$	$\sigma_I^2$	$\sigma_E^2$
I	$\sigma_S^2$	Cov PHS	1/4	0	0	0	0
	$\sigma_D^2$	Cov FS-Cov PHS	1/4	1/4	1	1	0
	$\sigma_S^2 + \sigma_D^2$	Cov FS	1/2	1/4	1	1	0
	$\sigma_W^2$	$\sigma_T^2$ - Cov FS	1/2	3/4	0	0	1
II	$\sigma_D^2$	Cov MHS	1/4	0	1	0	0
	$\sigma_S^2$	Cov FS-Cov MSH	1/4	1/4	0	0	0
	$\sigma_D^2 + \sigma_S^2$	Cov FS	1/2	1/4	1	1	0
	$\sigma_W^2$	$\sigma_T^2$ - Cov FS	1/2	3/4	0	0	1

S = Sire, D = Dam, W = Progeny within Dams and Sires

$\sigma_A^2$  = Additive genetic variance

$\sigma_D^2$  = Variance due to dominance

$\sigma_M^2$  = Variance due to maternal effects

$\sigma_I^2$  = Variance due to epistasis

$\sigma_E^2$  = Variance due to environmental effects

Analysis I = Nested analysis of variance where dams were nested within sires.

Analysis II = Nested analysis of variance where sires were nested within dams.

### Derivation of the Prediction Equation

After characterizing the population, by use of first-generation data, a prediction equation was derived based on the multiple regression equation of Snedecor (1946).

The prediction equation was obtained by use of the path coefficient method of Wright (1921a, 1921b and 1934). Since parents of successive generations were selected on the basis of standardized litter performance, full-sibs of sires and dams and progeny provide the most meaningful information.

The information available for any parent varied from 2 to 7 full-sibs from first litters as second litters were only available for random-line dams during the first generation. The possible interrelationships of the averages of sibs of the parents and of a single litter of offspring are shown in Figure 1.

The equation for predicting the average 14-day weight of a litter of offspring from sibling averages of the parents is based on the multiple regression equation (Snedecor, 1946).

$$\hat{A}_O = \frac{\bar{A}_M + \bar{A}_F}{2} + b'_{A_O A_S \cdot A_D} (S_{A_O} / S_{A_S}) (A_S - \bar{A}_M) + b'_{A_O A_D \cdot A_S} (S_{A_O} / S_{A_D}) (A_D - \bar{A}_F) \quad (1)$$

where  $A_O$ ,  $A_S$  and  $A_D$  are as defined in conjunction with the path

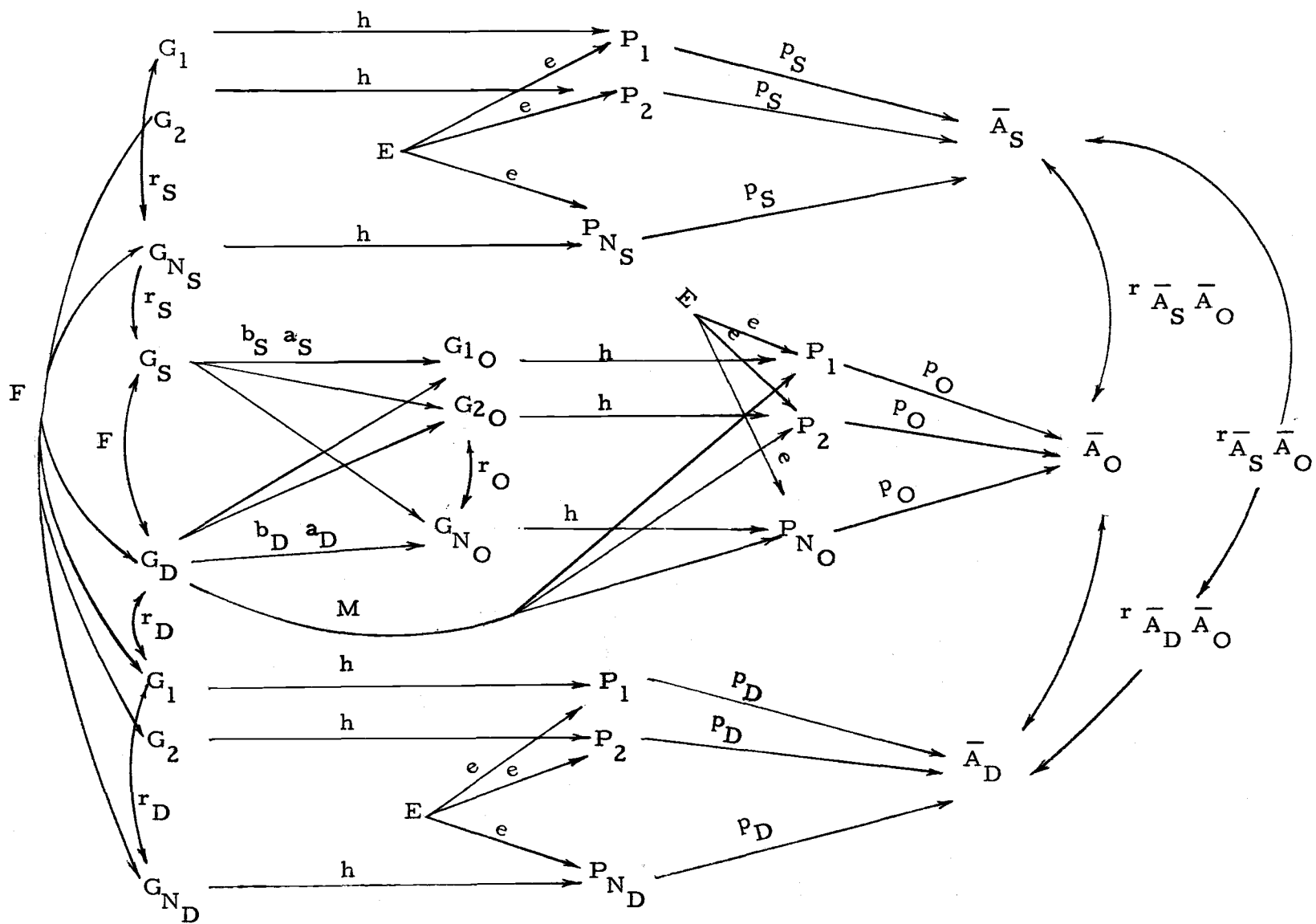


diagram and where:

$\hat{A}_O$  = predicted 14-day weight of a particular litter of offspring

$\bar{A}_M$  = the unweighted average of the siblings of all males in the  
sire generation

$\bar{A}_F$  = the unweighted average of the siblings of all females in the  
dams generation

$$b'_{A_O A_S \cdot A_D} = \frac{r_{A_O A_S} - r_{A_O A_D} r_{A_S A_D}}{1 - r_{A_S A_D}^2} = \text{the regression of} \quad (2)$$

offspring average on  
sire's sibs average  
holding dams average  
constant

$$b'_{A_O A_D \cdot A_S} = \frac{r_{A_O A_D} - r_{A_O A_S} r_{A_D A_S}}{1 - r_{A_S A_D}^2} = \text{the regression of} \quad (3)$$

offspring average on  
dams sibs average  
holding sires sibs  
average constant

$r_{A_O A_S}$ ,  $r_{A_O A_D}$ , and  $r_{A_S A_D}$  = correlations between offspring  
average and sires sibs average,  
offspring average and dams sibs  
average and between sires sibs average  
and dams sibs average, respectively.

From generation one data it was not possible to identify the genetic maternal effects and the maternal environmental effects. Therefore, it was necessary to use a composite (genetic and environmental) maternal contribution in the prediction equation.

The following equations, 4 to 13, are exact only if the path coefficients from individual phenotypes to the sib average are the same for all sibs. This will occur if  $e^2 = 0$ , if the sib average is based on a single litter or if the sister average is based on two or more litters of the same size. Otherwise, the equations are approximations based on the assumption that all path coefficients ( $p_O$ 's or  $p_D$ 's) to a particular sister average are equal.

From Figure 1,

$$r_{A_O A_S} = N_S N_O p_S p_O h^2 (r_{S S S}^b a_S + F b_{D D}^a) \quad (\text{Wright, 1934}) \quad (4)$$

$$r_{A_O A_D} = N_D N_O p_D p_O h^2 (r_{D D D}^b a_D + F b_{S S}^a) + N_D N_O p_D p_O h^2 F M \quad (5)$$

$$r_{A_S A_D} = N_S N_D p_S p_D h^2 F \quad (6)$$

where:

$N_S, N_D$  = total number of sire's sibs and dam's sibs,  
respectively in all litters.

$N_O$  = number of offspring in a particular litter.

$$b'_{A_O A_S \cdot A_D} = \frac{N_O N_S p_O p_S h^2 (r_{S S S} b_{S S S}^a + F b_{D D D}^a) + N_O N_S p_O p_S h F M}{1 - N_S^2 N_D^2 p_S^2 p_D^2 h^4 F^2}$$

$$\frac{[N_O N_D p_O p_D h^2 (r_{D D D}^b + F b_{S S S}^a) + N_O N_D p_O p_D h r_D^M [N_S N_D p_S p_D h^2 F]]}{1 - N_S^2 N_D^2 p_S^2 p_D^2 h^4 F^2} \quad (7)$$

Similarly, substituting (4), (5) and (6) into (3) results in the following partial regression equation:

$$b'_{A_O A_D \cdot A_S} = \frac{N_O N_S p_O p_S h^2 (r_{S S S} b_{S S S}^a + F b_{D D D}^a) + N_O N_S p_O p_S h F M}{1 - N_S^2 N_D^2 p_S^2 p_D^2 h^4 F^2}$$

$$\frac{[N_O N_S p_O p_S h^2 (r_{S S S}^b + F b_{D D D}^a) + N_D N_S p_D p_S h M][N_S N_D p_S p_D h^2 F]}{1 - N_S^2 N_D^2 p_S^2 p_D^2 h^4 F^2} \quad (8)$$

Because  $A_O$  is the mean of the  $P_O$ 's,  $p_O$ , the path coefficient from  $P_O$  to  $A_O$  is equal to  $S_O/N_O S_{A_O}$  or  $S_{A_O} = S_O/N_O p_O$  where  $S_O$  = the standard deviation of individual progeny. Similarly,  $S_{A_S} = S_S/N_S p_S$  and  $S_{A_D} = S_D/N_D p_D$ , where  $S_S$  and  $S_D$  are standard deviations of individual sibs of sires and dams, respectively. The equations for  $S_{A_O}$ ,  $S_{A_S}$  and  $S_{A_D}$  are based on the fact that the standard deviation of average values is equal to the standard deviation of individual component values times the correlations between the individual value and the average. If the sib average was based on more

than one litter, the equation for the standard deviation would be obtained by averaging the  $N$  correlations between individual values and the family average. Because little change in variation was expected from one generation of selection it was assumed that  $S_O = S_D = S_s$ . Therefore,

$$S_{A_O}/S_{A_S} = N_{s^p_s}/N_{O^p_O} \text{ and } S_{A_O}/S_{A_D} = N_{D^p_D}/N_{O^p_O} \quad (9)$$

Substituting (7), (8) and (9) into (1) results in the following prediction equation:

$$\begin{aligned} \hat{A}_O = & \frac{\bar{A}_M + \bar{A}_F}{2} + \frac{N_{S^p_S}^2 N_{S^h}^2 [h(r_{S^b_S}^a + F b_{O^a_D}) + F_M - N_{D^p_D}^2 N_{D^h}^2 F]}{1 - N_{S^p_S}^2 N_{S^h}^2 N_{D^p_D}^2 N_{D^h}^2 F^2} \\ & \frac{(r_{D^b_D}^a + F b_{S^a_S}) - N_{D^p_D}^2 N_{D^h}^2 r_{D^M}}{1 - N_{S^p_S}^2 N_{S^h}^2 N_{D^p_D}^2 N_{D^h}^2 F^2} (A_S - \bar{A}_M) + \\ & \frac{N_{D^p_D}^2 N_{D^h}^2 [h(r_{D^b_D}^a + F b_{S^a_S}) + r_{D^M} - N_{S^p_S}^2 N_{S^h}^2 F(r_{S^b_S}^a + F b_{D^a_D}) -]}{1 - N_{S^p_S}^2 N_{S^h}^2 N_{D^p_D}^2 N_{D^h}^2 F^2} \\ & N_{S^p_S}^2 N_{S^h}^2 F M] (A_D - \bar{A}_F) \quad (10) \end{aligned}$$

In using the above equation the values of  $h$ ,  $r_S$ ,  $r_D$ ,  $b_{S^a_S}$ ,  $b_{D^a_D}$ ,  $p_S$ ,  $p_D$  and  $F$  are needed. The quantities  $r_S$  and  $r_D$  are the ordinary coefficients of relationship of siblings within the family of the sire and of the dam, respectively, and  $h^2$  is the heritability



estimate. From Wright (1921b),

$$b_{S^a S} = \frac{1}{2} \sqrt{\frac{1 + F_{X_S}}{1 + F_{X_O}}}, \quad b_{D^a D} = \frac{1}{2} \sqrt{\frac{1 + F_{X_D}}{1 + F_{X_O}}},$$

and  $F = \frac{2F_{X_O}}{\sqrt{(1 + F_{X_S})(1 + F_{X_D})}}$ . The quantities  $p_S$  and  $p_D$  can be

evaluated from the equations for the complete determination of  $A_S$  and  $A_D$ , respectively. From Figure 1 the equation for the complete determination of  $A_S$  is:

$$N_S^2 p_S^2 + \frac{2N_S(N_S - 1)}{2} p_S^2 r_S + 2 \sum_1^K \frac{N_i(N_i - 1)}{2} p_S^2 e^2 = 1$$

where:

$K$  = the number of litters

$N_i$  = the number of offspring in the  $i$ -th litter

$e$  = the path coefficient for environment common to littermates.

So,

$$p_S^2 = \frac{1}{N_S[1 + (N_S - 1)r_S^2] + e^2 \sum_1^K N_i(N_i - 1)} \quad (11)$$

likewise

$$p_S^2 = \frac{1}{N_D[1 + (N_D - 1)r_D h^2] + e^2 \sum_1^K N_i(N_i - 1)} \quad (12)$$

Since the mating system used minimizes inbreeding, a special case of the prediction equation is of interest. For non-inbred litters  $F = 0$ ,

$$b_S^a S = \frac{1}{2} \sqrt{1 + F_{X_S}}, \text{ and } b_D^a D = \frac{1}{2} \sqrt{1 + F_{X_D}}$$

Therefore

$$\begin{aligned} A_O = \frac{A_M + \bar{A}_F}{2} + \frac{N_S^2 h^2 r_S \sqrt{1 + F_{X_S}}}{2 N_S[1 + (N_S - 1)r_S h^2] + e^2 \sum_1^K N_i(N_i - 1)} (A_S - \bar{A}_M) \\ + \frac{N_D^2 h^2 r_D \sqrt{1 + F_{X_D}} + r_D^M}{2 N_D[1 + (N_D - 1)r_D h^2] + e^2 \sum_1^K N_i(N_i - 1)} (A_D - \bar{A}_F) \end{aligned} \quad (13)$$

Also when sires and dams are non-inbred the prediction equation further simplifies to:

$$\hat{A}_O = \frac{\bar{A}_M + \bar{A}_F}{2} + \frac{N_S^2 h^2 r_S}{2 N_S [1 + (N_S - 1) r_S h^2] + e^2 \sum_1^K N_i (N_i - 1)}$$

$$(A_S - \bar{A}_M) + \frac{N_D^2 h^2 r_D + r_D^M}{2 N_D [1 + (N_D - 1) r_D h^2] + e^2 \sum_1^K N_i (N_i - 1)}$$

$$(A_O - \bar{A}_F)$$

If one assumes that the environment did indeed remain constant throughout the experiment ( $e^2 = 0$ ) then the prediction equation simplified to:

$$\hat{A}_O = \frac{\bar{A}_M + \bar{A}_F}{2} + \frac{N_S h^2 r_S \sqrt{1 + F_{X_S}}}{2[1 + (N_S - 1) r_S h^2]} (A_S - \bar{A}_M) +$$

$$\frac{N_D h^2 r_D \sqrt{1 + F_{X_D}} + r_D^M}{2[1 + (N_D - 1) r_D h^2]} (A_D - \bar{A}_F) \quad (15)$$

## RESULTS AND DISCUSSION

Least squares analysis of 14-day weight, weaning weight, birth weight and litter size data, using the full models, are presented in Tables 2, 3, 4 and 5 respectively. From Table 2 it can be observed that inbreeding of dam, sex effect, and interactions involving sex did not exert a significant influence on 14-day weight. These factors were removed from the model and the reduced model was used to analyze the data.

The observation that the sex of the progeny had no effect on 14-day weight could be expected because at 14 days of age it is doubtful that the level of circulating sex hormones could be sufficient to afford a growth impetus.

The results of the analysis of 14-day weight data, using the reduced model:

$$Y_{lgk} = \mu + L_1 + G_g + LG_{lg} + dN_1 + dN_2 + dA + dW_1 + dF_O + E_{lgk}$$

where:

$Y_{lgk}$  = Fourteen-day weight of the k-th progeny of the l-th line in the g-th generation,

$E_{lgk}$  = Random errors that are assumed to independent and normally distributed with mean = 0 and common variance,  $\sigma^2$ .

Table 2. Least squares analysis of variance of data on 14-day weight.

Source of Variation	d. f.	Mean Squares	F
Total	2721	---.---	---.---
Sex	1	1.86	1.87 NS
Line	4	38.45	38.47***
Generation	3	58.89	58.91***
Sex x Line	4	.23	.23 NS
Sex x Generation	3	.12	.12 NS
Line x Generation	12	12.81	12.82***
Sex x Line x Generation	12	.63	.63 NS
Litter Size at Birth	1	86.34	86.37***
Litter Size at 14-Days	1	75.15	75.19***
Age of Dam	1	16.17	16.18***
Birth Weight	1	294.80	294.93***
Inbreeding of Offspring	1	5.56	5.56*+
Inbreeding of Dam	1	3.27	3.27 NS
Error	2676	.99	---.---

\*\*\* Significant at the 0.5% level of probability.

\*+ Significant at the 2.5% level of probability.

Table 3. Least squares analysis of variance on weaning weight data.

Source of Variation	d. f.	Mean Square	F
Total	2610	---.---	---.---
Sex	1	6.02	5.16 <sup>*+</sup>
Line	4	19.54	16.73 <sup>***</sup>
Generation	3	39.79	34.06 <sup>***</sup>
Sex x Line	4	.68	.58 NS
Sex x Generation	3	.83	.71 NS
Line x Generation	12	5.45	4.67 <sup>*</sup>
Sex x Line x Generation	12	.55	.47 NS
Litter Size at Birth	1	2.85	2.45 NS
Litter Size at 14 days	1	5.34	4.57 <sup>*</sup>
Litter Size at Weaning	1	5.45	4.67 <sup>*</sup>
Age of Dam	1	72.29	61.88 <sup>***</sup>
Weight at Birth	1	45.07	38.58 <sup>***</sup>
Weight at 14 Days	1	6149.42	5264.05 <sup>***</sup>
Inbreeding of Offspring	1	.37	.32 NS
Inbreeding of Dam	1	11.01	9.43 <sup>***</sup>
Error	2563	1.17	---.---

\* Significant at the 5% level of probability.

\*+ Significant at the 2.5% level of probability.

\*\*\* Significant at the 0.5% level of probability.

Table 4. Least squares analysis of variance of birth weight data.

Source	d. f.	Mean Square	F
Total	384	---.---	---.---
Line	4	0.078	4.00 ***
Generation	3	1.066	54.94 ***
Line x Generation	12	0.247	12.77 ***
Number at Birth	1	6.626	341.40 ***
Age of Dam	1	0.502	25.87 ***
Inbreeding of Offspring	1	0.001	0.06 NS
Inbreeding of Dam	1	0.108	5.60 ***
Error	361	0.019	---.---

\*\*\* Statistically significant at the 0.5% level of probability.

Table 5. Least squares analysis of variance of litter size data.

Source	d. f.	Mean Square	F
Total	384	---.---	---.---
Line	4	14.307	2.39 *
Generation	3	6.048	1.01 NS
Line x Generation	12	14.699	2.46 ***
Age of Dam	1	35.024	5.85 *+
Inbreeding of Dam	1	1.492	.25 NS
Inbreeding of Offspring	1	0.635	.11 NS
Error	362	5.987	---.---

\* Statistically significant at the 5% level of probability.

\*+ Statistically significant at the 2.5% level of probability.

\*\*\* Statistically significant at the 0.5% level of probability.

and where all other terms in the equation are defined as  
for the full model,  
are presented in Table 6. The effects of the main factors, line effects and generation effects as well as the line x generation interaction were significant at the 0.5% level of probability. Least squares means for line, generation and line within generation are presented in Table 10. From Table 10 and Figure 4 it can be observed that the line means fluctuated considerably from generation to generation. Genetic gain in selected lines should be evaluated relative to an unselected control line, as the control line reflects environmental fluctuations from generation to generation. Although control line parents were selected at random, sizeable selection differentials existed in the control line in different generations. Because the means of the sibs of parents did differ substantially from the mean of the parent generation, it was decided to plot means for the different lines as deviations from the overall least squares mean for the respective generations. The overall line means for 14-day weight 6.82, 6.68, 6.43, 6.10 and 5.82 grams for lines  $H_1$ ,  $H_2$ , C,  $L_1$  and  $L_2$ , respectively, show that the control line mean was intermediate between high and low line means. A comparison of least squares means by t-test showed that the means of lines selected up or down differed ( $P < .01$ ) from the mean of the control line. Overall means between the two high lines did not differ but there was a significant difference ( $P < .01$ ) between the two low line means.

The least squares means for generations 1, 2, 3 and 4 were



Table 6. Least squares analysis of variance on fourteen-day weight data utilizing the reduced model.

Source of Variation	d. f.	Mean Squares	F
Total	2721	---.---	---.---
Line Effect	4	45.066	47.45 ***
Generation Effect	3	39.527	41.62 ***
Line x Generation	12	9.868	10.39 ***
Litter Size at Birth	1	66.920	70.46 ***
Litter Size at 14-days	1	89.163	93.89 ***
Age of Dam	1	77.602	81.71 ***
Weight at Birth	1	244.195	257.13 ***
Inbreeding of Offspring	1	0.262	0.28 NS
Error	2697	0.949	---.---

\*\*\* Significant at the 0.5% level of probability.

Table 7. Least squares analysis of variance of weaning weight data utilizing the reduced model.

Source of Variation	d. f.	Mean Squares	F
Total	2610	----	----
Sex Effect	1	23.285	7.79**
Line Effect	4	294.483	98.60***
Generation Effect	3	147.725	49.46***
Line x Generation	12	59.923	20.06***
Litter Size at 14-Days	1	12.514	4.19*
Litter Size at Weaning	1	65.109	21.80***
Age of Dam	1	533.732	178.71***
Birth Weight	1	477.288	159.81***
14-Day Weight	1	1998.242	669.07***
Inbreeding of Dam	1	21.443	7.18**
Error	2584	2.987	----

\* Significant at the 5% level of probability.

\*\* Significant at the 1% level of probability.

\*\*\* Significant at the 0.5% level of probability.

Table 8. Least squares analysis of variance of data on litter size at birth (reduced model).

Source of Variation	d. f.	Mean Squares	F
Total	384	-.----	-----
Line Effect	4	3.004	29.74***
Generation Effect	3	0.862	8.53***
Line x Generation	12	1.940	19.21***
Age of Dam	1	0.101	---.--

\*\*\* Significant at the 0.5% level of probability.

Table 9. Least squares analysis of variance of data on birth weight (reduced model).

Source of Variation	d. f.	Mean Squares	F
Total	384	-.----	-----
Line Effect	4	0.0010	2.50*
Generation Effect	3	0.0204	49.03***
Line x Generation	12	0.0051	12.19***
Litter Size at Birth	1	0.1480	355.57***
Age of Dam	1	0.0105	25.23***
Inbreeding of Offspring	1	0.0302	72.44***
Error	362	0.004	-----

\* Significant at the 5.0% level of probability.

\*\*\* Significant at the 0.5% level of probability.

6.81, 6.09, 6.29 and 2.29 grams, respectively. The mean for generation 1, pooled over lines was considerably higher than the means for the next three generations. This might be explained on the basis that the parents of generation one progeny were randomly selected from the base ( $F_1$ ) population. Consequently, the difference between generation one and generation two means may have been a reflection of a heterotic effect on maternal performance.

The significant line-by-generation interaction would be expected because lines  $H_1$  and  $H_2$  were selected for increased 14-day weight and lines  $L_1$  and  $L_2$  were selected for decreased 14-day weight. In addition to line divergence, the change in rank of replicate high line means from generation 3 to generation 4 and the marked decrease in 14-day weight of low line 2 progeny contributed additionally to the significant line-by-generation interaction. Differences between means of replicate lines in the different generations can be explained in part, by differences in selection pressure applied to the different lines. Data presented in Table 14 show that there was considerable variation among lines in progeny surviving to 14-days of age.

From the comparison of means of lines (Table 10) and from Figure 4 it appears that selection was more effective in lines selected for decreased 14-day weight than for lines selected for increased 14-day weight. Previous research (Falconer 1953; 1960) has demonstrated an asymmetrical response due to directional selection for 6-week weight in mice. Falconer's (1960) study showed response to selection was greater in lines selected for decreased 6-week body weight.

The least squares analysis of weaning weight data for the full model (Table 3) showed that interactions involving sex, inbreeding of progeny and litter size at birth did not exert a significant influence on weaning weight. These factors were removed from the full model and the reduced model:

$$Y_{ilgk} = \mu + S_i + L_l + G_g + LG_{lg} + dN_3 + dA + dW_1 + dW_2 + dF_D + E_{ilgk}$$

where:

$Y_{ilgk}$  = The weaning weight of the k-th progeny of the i-th sex in the l-th line and g-th generation, and all other factors remaining in the model are defined as in the full model,

was used to analyze the data. From Table 7 it can be observed that each factor in the model exerted a significant influence on weaning weight.

The effect of sex on weaning weight was significant ( $P < .01$ ) and the least squares constant associated with sex indicated that at weaning male progeny are 0.095 grams heavier than female litter mates. The sex affect on progeny weaning weight was common in all lines and all generations.

Least squares means for lines, generations and lines-within-generations for weaning weight of the progeny are presented in Table 11. From Table 11 it can be observed that the mean of the control (8.77 grams) was lower than the overall mean for all progeny (8.92 grams) but it was intermediate between the means for replicate high and replicate low lines. T-tests between line means revealed that means for lines  $H_1$ ,  $H_2$  and  $L_1$  differed ( $P < .01$ ) from the mean

Table 10. Least squares means for lines, generations, and lines within generation for 14-day weight (grams).

Generation	Line					Pooled Lines
	H <sub>1</sub>	H <sub>2</sub>	C	L <sub>1</sub>	L <sub>2</sub>	
1	7.27	6.77	6.63	6.84	6.54	6.81
2	6.52	6.41	6.28	5.66	5.58	6.09
3	6.80	6.49	6.03	6.10	6.03	6.29
4	6.69	7.05	6.78	5.80	5.13	6.29
1-4 <sup>+/</sup>	6.82 <sup>a/</sup>	6.68 <sup>a/</sup>	6.43 <sup>b/</sup>	6.10 <sup>c/</sup>	5.82 <sup>d/</sup>	6.37

<sup>+/</sup> Means with different superscripts differ significantly ( $P < .01$ ).

Table 11. Least squares means for lines, generations and line within generation for weaning weight (grams).

Generation	Line					Pooled Lines
	H <sub>1</sub>	H <sub>2</sub>	C	L <sub>1</sub>	L <sub>2</sub>	
1	10.35	8.04	9.08	6.21	9.52	8.64
2	9.39	8.90	8.46	7.15	7.25	8.23
3	9.63	9.65	7.76	6.96	7.95	8.39
4	10.99	11.77	10.18	8.76	10.16	10.42
1-4 <sup>+/</sup>	10.09 <sup>a/</sup>	9.59 <sup>b/</sup>	8.87 <sup>c/</sup>	7.27 <sup>d/</sup>	8.78 <sup>c/e/</sup>	8.92

<sup>+/</sup> Means with different superscripts differ significantly ( $P < .01$ ).

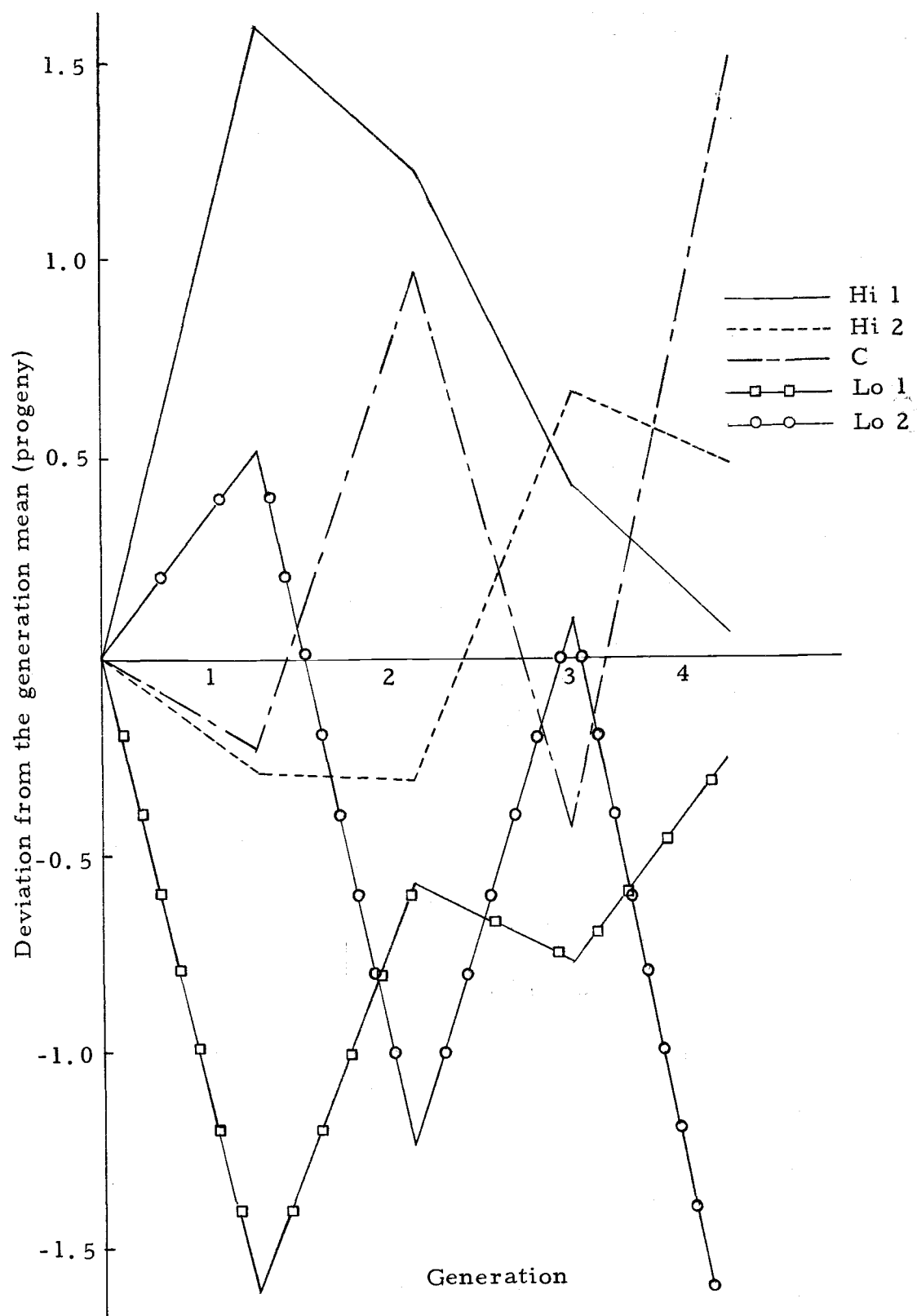


Figure 2. Response in litter size to selection for 14-day weight.

of the control line. There was no significant difference ( $P > 0.4$ ) between means for the control line and the  $L_2$  line. Also, the replicate high and replicate low lines differed ( $P < .01$ ) from each other.

Weaning weight data were adjusted to a constant-weight basis at 14 days of age. The least squares constant indicated that a deviation of 0.1 gram in 14-day weight from the mean 14-day weight caused a corresponding deviation of 0.65 gram in weaning weight.

It was observed (Table 10) that the mean 14-day weight of line  $L_1$  progeny was higher than the mean 14-day weight of line  $L_2$  progeny in each generation. The corresponding means for weaning weight (Table 11) show that in each generation line  $L_1$  progeny were lighter than the  $L_2$  line progeny. The fact that  $L_1$  line progeny were heavier at 14 days of age but lighter at weaning than  $L_2$  line progeny suggests that the  $L_1$  dams produced shorter or less persistent lactations.

A significant line-by-generation interaction was observed for weaning weight. This interaction was at least partly attributable to line divergence. Results of the analysis of birth weight data (Table 4) using the full model indicated that inbreeding of dam did not have a significant effect ( $P > .05$ ) on birth weight. Removal of inbreeding of dam from the full model resulted in the reduced model,

$$Y_{lgk} = \mu + L_1 + G_g + LG_{lg} + dN_1 + dA + dF_O + E_{lgk}$$

for birth weight. Terms remaining in the reduced model were defined in the full model.



A least squares analysis of variance on birth weight data (Table 9) revealed that all factors in the reduced model exerted a significant effect on mean birth weight. Line, generation and line-within-generation means determined by least squares analysis are presented in Table 13. A comparison of line means by t-tests revealed that line  $L_2$  was the only line that differed significantly ( $P < .05$ ) from the control line. Since the mean for the  $L_2$  was higher than the corresponding means for the control line and the replicate high lines and no differences existed between other lines it was concluded that selection of mice on the basis of weight gain from birth to 14 days of age was ineffective in changing the overall mean birth weight in the selected lines. A plot of the line means within generation, Figure 3, as deviations from the generation means revealed that there was no consistent pattern of response. Effects of sex were not considered in the analysis of birth weight data as the mean birth weight for the litter was recorded and litters were standardized to 8 progeny, four males and four females where possible.

Data presented in Table 5 indicate that the effects of inbreeding of dam and of progeny had no effect on litter size. A study reported by Falconer and Roberts (1960) showed that inbreeding of dam does affect litter size through a reduction in number of embryos that implant or in reduced embryonic survival. The low levels of

Table 12. Least squares means for lines, generations and line within generation for litter size.

Generation	Line					Pooled
	H <sub>1</sub>	H <sub>2</sub>	C	L <sub>1</sub>	L <sub>2</sub>	
1	11.30	9.42	9.48	8.11	10.24	9.71
2	11.63	10.08	11.36	9.82	9.06	10.39
3	10.22	10.46	9.36	9.02	9.89	9.79
4	9.69	10.12	11.16	9.37	7.81	9.63
1-4 <sup>+/</sup>	10.71 <sup>a/</sup>	10.02 <sup>b/</sup>	10.34 <sup>c/</sup>	9.08 <sup>d/</sup>	9.25 <sup>d/e/</sup>	9.88

<sup>-/</sup> Means with different superscripts differ significantly ( $P < .01$ ).

Table 13. Least squares means for lines, generations and lines within generation for birth weight (grams).

Generation	Line					Pooled
	H <sub>1</sub>	H <sub>2</sub>	C	L <sub>1</sub>	L <sub>2</sub>	
1	1.49	1.52	1.49	1.43	1.52	1.49
2	1.61	1.52	1.49	1.55	1.58	1.55
3	1.36	1.43	1.50	1.45	1.46	1.44
4	1.46	1.49	1.40	1.41	1.44	1.44
1-4 <sup>+/</sup>	1.48 <sup>a/</sup>	1.49 <sup>a/</sup>	1.47 <sup>a/</sup>	1.46 <sup>a/b/</sup>	1.50 <sup>a/b/c/</sup>	1.48

<sup>+/</sup> Means with different superscripts differ significantly ( $P < .01$ ).

Table 14. Number of progeny available for selection at weaning.

Generation	Line				
	H <sub>1</sub>	H <sub>2</sub>	C	L <sub>1</sub>	L <sub>2</sub>
1	107	113	390	91	96
2	103	91	353	109	69
3	58	112	243	90	115
4	56	109	201	62	42

inbreeding of progeny and dams would explain the lack of an effect of inbreeding on litter size in this study.

From Table 5 it can be observed that there was no effect of generation on litter size but a highly significant ( $P < .005$ ) line by generation interaction. Generation effect was retained in the reduced model because it was a main factor and it was involved in a significant interaction with line effect. The reduced model used for further analysis of litter size data was:

$$Y_{lgk} = \mu + L_l + G_g + LG_{lg} + dA + E_{lgk}.$$

All terms in the reduced equation are defined in the full model.

All factors remaining in the reduced model exerted a significant effect ( $P < .005$ ) on litter size at birth (Table 8). Line, generation and line-within-generation means obtained by least squares analyses are presented in Table 12. Although t-tests indicated that the overall mean for each selected line differed from the mean of the control line, a comparison of line-within-generation means indicates that there is no consistent pattern of response. A plot of the least squares line means as deviations from their respective generation means (Figure 2) also demonstrate the marked fluctuations in litter size from generation to generation. The data indicate that selection for preweaning gain had little or no effect on litter size at birth.

### Environmental Effects on Prewaning Gain

Data presented in Tables 2 through 9 showed that environmental influences common to members of particular litters exerted significant effects on litter performance.

Litter size data were analyzed as an independent trait; however, when differences exist within or between lines, litter size must be considered as an environmental effect because it exerts an influence on other traits. Litter size at birth was observed to have a significant effect on birth weight and fourteen-day weight. Least squares constants revealed that an increase of one progeny over the mean litter size resulted in decreases of -0.024 and 0.081 gram in birth weight and 14-day weight of litter mates from standardized litters. The effect of litter size at birth on 14-day weight would probably have been much greater if litters had not been standardized since standardization of litters removed competition for the limited milk supply. Litter size at birth did not appear to affect weaning weight. This might be attributed to the fact that weaning weight data were adjusted for 14-day weight and litter size at 14 days of age and at weaning. Since litter size at birth affects 14-day weight, the adjustment of weaning weight for 14-day weight probably removed the effects of litter size at birth on weaning weight.

With regard to 14-day weight and weaning weight, litter size at

14 days of age was considered an environmental effect. The least squares constant effect of litter size at 14 days of age revealed that the loss of a single progeny from the standardized litter resulted in an increase of 0.171 and 0.163 gram in individual weight at 14 days and at weaning, respectively. This was probably the result of more milk available for the surviving litter mates. Previous research by Eisen and Legates (1965) has shown that loss of a litter mate after day five post partum had no effect on 12-day weight of survivors. However, in their experiment litters were standardized to a smaller size (six progeny) which may have completely removed competition for the available milk.

Litter size at weaning has a direct influence on weaning weight. The constant effect of litter size at weaning after adjusting for litter size at 14 days of age showed that the loss of a litter mate between 14 days of age and weaning results in an increase of 0.349 gram in weaning weight of the surviving litter mates. Again this was probably the result of more milk available for the survivors.

Age of dam was shown to significantly affect litter size at birth, birth weight, 14-day weight and weaning weight of progeny. Least squares constants showed that an increase of one day in age of dam over the mean age of dam resulted in an increase of 0.029 progeny at birth and increases of 0.002, 0.003 and 0.005 gram in weight at birth, 14 days of age and at weaning, respectively. Although the

constant effects appear very small, an increase of 10 days in age of dam would result in a 0.40 gram increase in weaning weight of a litter of 8 progeny. Age of dam has been reported to influence litter size in swine (Self, Grummer and Casida, 1955; Robertson, Grummer, Casida and Chapman, 1951) and weaning weight in swine (Dickerson and Hazel, 1944) and beef calves (Koch and Clark, 1955; Eftakhari, 1971). The effect of age of dam on progeny performance in the above studies has been attributed, in part, to higher milk yield of older dams. In the present study, the increased weights at 14 days of age and at weaning of progeny born to older dams may also be attributed to a greater lactation yield from older dams.

Birth weight was observed to exert a very dramatic effect on weight at 14 days and at weaning of progeny in litters standardized to eight young. A deviation of 0.1 gram in birth weight resulted in a corresponding deviation of 2.21 and 2.95 grams in 14-day weight and weaning weight, respectively. This might be attributed to larger progeny at birth being stronger and less susceptible to stress of postnatal environmental fluctuations. It may be that large young at birth stimulate the dam to produce a greater amount of milk. Also, inherited growth rate differences may have been expressed both prenatally and postnatally.

Fourteen-day weight of progeny is a function of inheritance for growth rate and a function of pre- and post-natal maternal

environment. Consequently the effect of 14-day weight on weaning weight is also partially environmental. A deviation of 0.1 gram from the mean 14-day weight of progeny resulted in a corresponding deviation of 0.65 gram in weaning weight. Larger mice at 14 days of age were probably more aggressive and better able to compete for available milk at the time the milk supply of the dam was declining. At 14 days of age, young mice are just beginning to consume dry food and the larger progeny probably consume more dry food and make more efficient use of the dry food consumed. Eftakhari (1971) contends that during the early preweaning period, at a constant age, heavier beef calves are less susceptible to digestive disturbances and consume more of the available forage.

The overall average percentage of inbreeding of dam and progeny groups was very low, less than 1.0% for dams and 1.5% for progeny. However, the inbreeding of some litters in the fourth generation reached 25%.

Inbreeding of dam had no effect on litter size, birth weight or 14-day weight of progeny, but it did exert a significant effect on weaning weight of progeny. A 10% increase in inbreeding of dam caused a 0.51 gram reduction in weaning weight of each young. Previous research, Bowman and Falconer (1960) and Roberts (1960), has shown that inbreeding of dam influences litter size. In a later paper Falconer and Roberts (1960) presented evidence that showed

the reduced litter size to be the result of pre-implantation losses.

Falconer (1960) and Bogart (1959) point out that inbreeding depression exerts its greatest influence on maternal traits. Since 14-day weight is a maternally influenced trait, inbreeding of dam would be expected to have a negative effect on weight at 14 days of age. The negative effect of inbreeding of dam on weaning weight could have been due to shorter or less persistent lactations of inbred dams.

Inbreeding of progeny has been shown to influence litter size and 60-day weight in mice (Falconer, 1960). In the present study inbreeding had no effect on litter size or weaning weight but it did exert an effect on birth weight and weight at fourteen days of age. The least squares constants associated with birth weight and 14-day weight showed that an increase of 10% in inbreeding of progeny resulted in a 0.24 gram reduction in individual birth weight and a 0.55 gram reduction in 14-day weight. The depressing effect of inbreeding of progeny on birth weight is difficult to explain because birth weight is primarily dependent upon pre-natal maternal environment. Although the genotype of the neonate can influence birth weight, it seems unreasonable to assume that a 10% increase in inbreeding would reduce the efficiency of utilization of nutrients supplied through the maternal uterine environment to the extent of reducing birth weight by 0.24 grams. The reduced size of inbred young at



14 days of age may be attributed to inbred progeny being less well buffered against temporary environmental deviations early in life.

### Heritability Estimates

The sire components of variance from nested analyses of variance were used to estimate the heritability for birth weight, 14-day weight, weaning weight, and litter size for each of the selected lines and for pooled data from the selected lines. Heritability estimates for the four traits were calculated for the control line by the regression of offspring on the mid-parent mean. The heritability estimates (Table 15) for birth weight differ markedly for different lines. Except in the  $H_2$  line the heritability estimates for litter size are in reasonable agreement with previous estimates (Falconer, 1960; 1964; Dalton and Bywater, 1963) for mice. The estimates of heritability of 14-day weight and weaning weight (except for the  $H_2$  line) are in reasonable agreement with the literature (Eisen, Legates and Robinson, 1970; Eisen and Legates, 1966; Rahnefeld et al., 1963).

The low heritability estimates for 14-day weight, weaning weight and litter size indicate that improvement of these traits, through selection, will be slow. Genetic improvement of lowly heritable traits can be enhanced through the use of progeny tested sires. In the present study progeny tested males were used as sires of generation 3 and 4 progeny groups in the selected lines. However,

several of the progeny tested males either died or failed to sire progeny after they had been progeny tested. If all progeny tested sires had sired equal numbers of litters more accurate heritability estimates, with smaller standard errors associated with the estimates, may have been obtained.

### Relationships Among Traits

From Figures 4 and 5 it appears that selection was effective in the separation of lines of mice for 14-day weight when they were selected for increased and decreased 14-day body weight. It also appears that selection response was greater in lines selected for decreased weight than in lines selected for increased weight. When similar plots, for colateral traits on which no selection pressure was applied, of litter size at birth (Figure 2), birth weight (Figure 3), and weaning weight (Figure 6) were compared to the plot of 14-day weight (Figure 4), there appeared to be little relationship between 14-day weight and any of the other traits. There was no consistent pattern of response between pairs of traits for the different lines of mice.

Genetic correlations for all possible pairs of traits (Table 16) were calculated from control line data. The appropriate covariances for the calculation of the genetic correlations were obtained from the regression of the progeny average on the mid-parent mean.

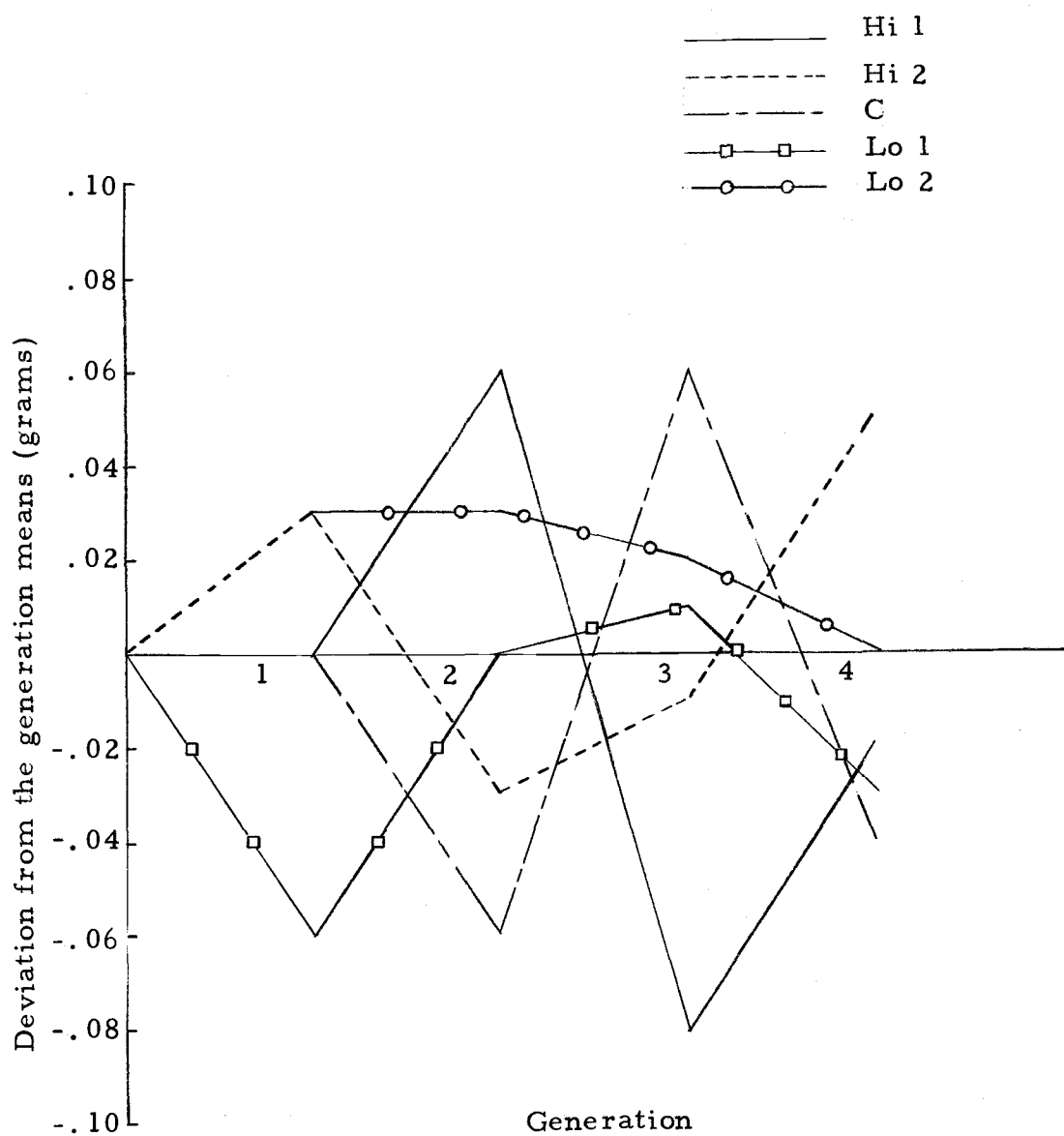


Figure 3. Response in birth weight to selection for 14-day weight.

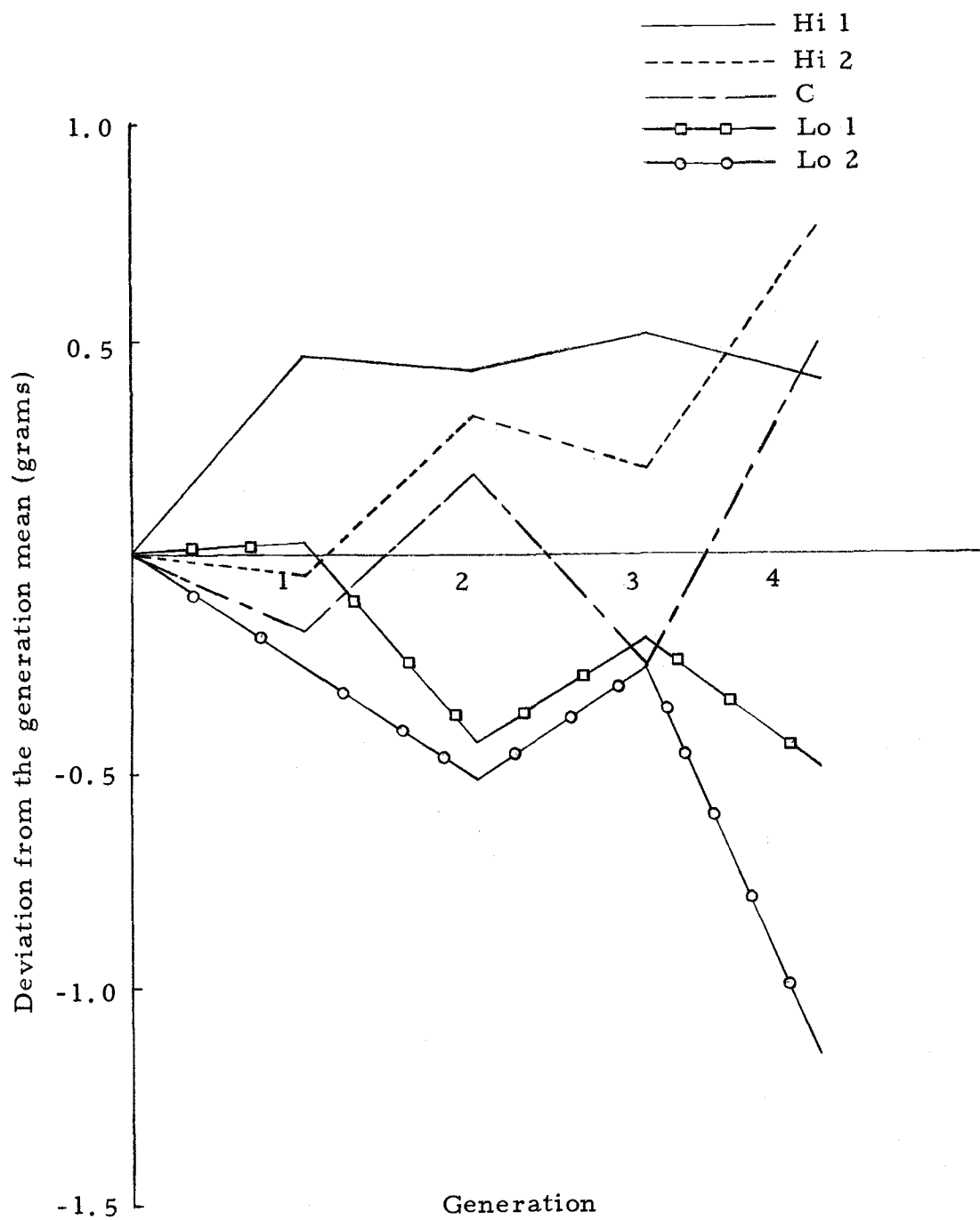


Figure 4. Response to selection for 14-day weight.

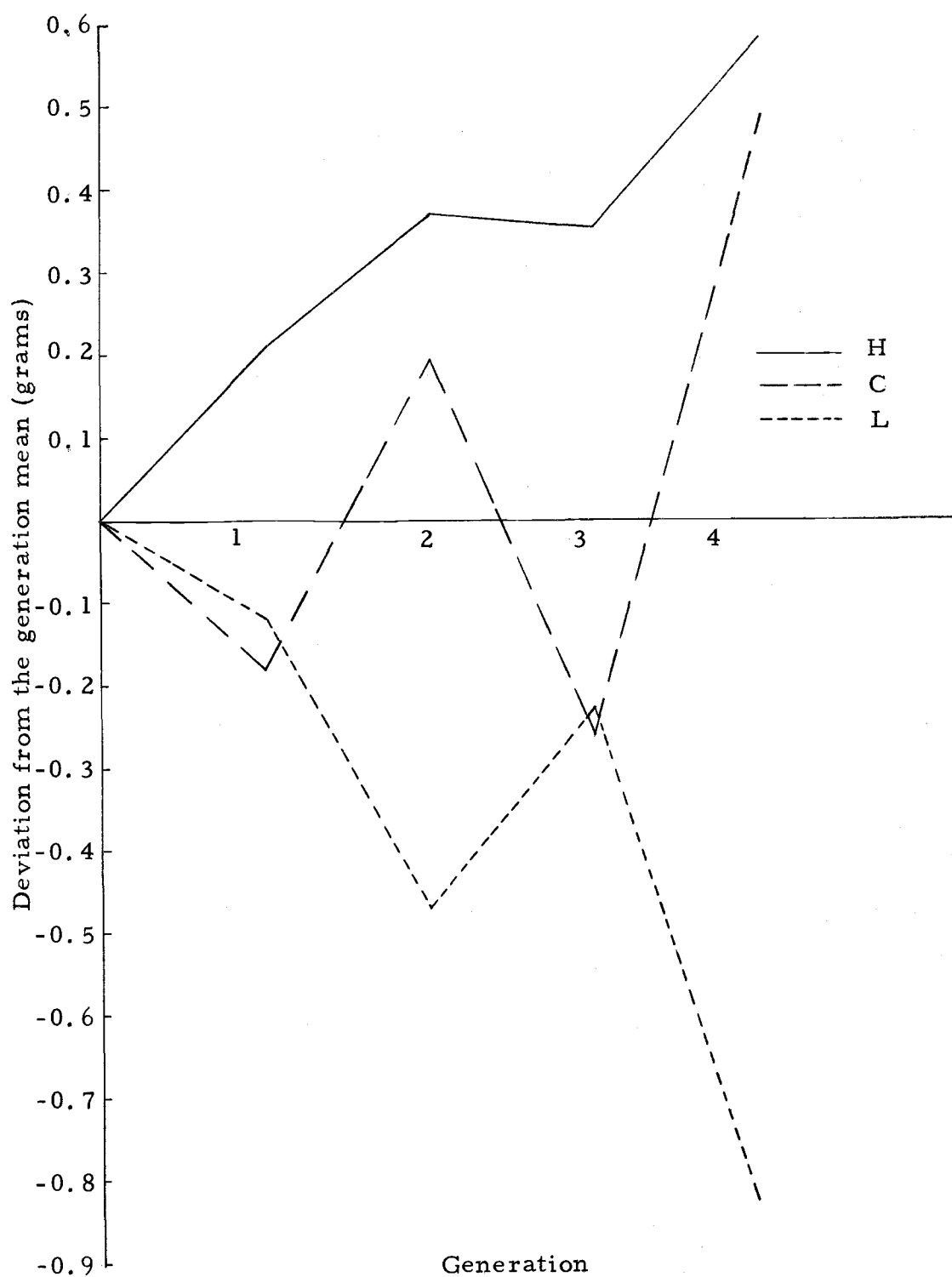


Figure 5. Response to selection for 14-day weight (response averaged for replicate lines).

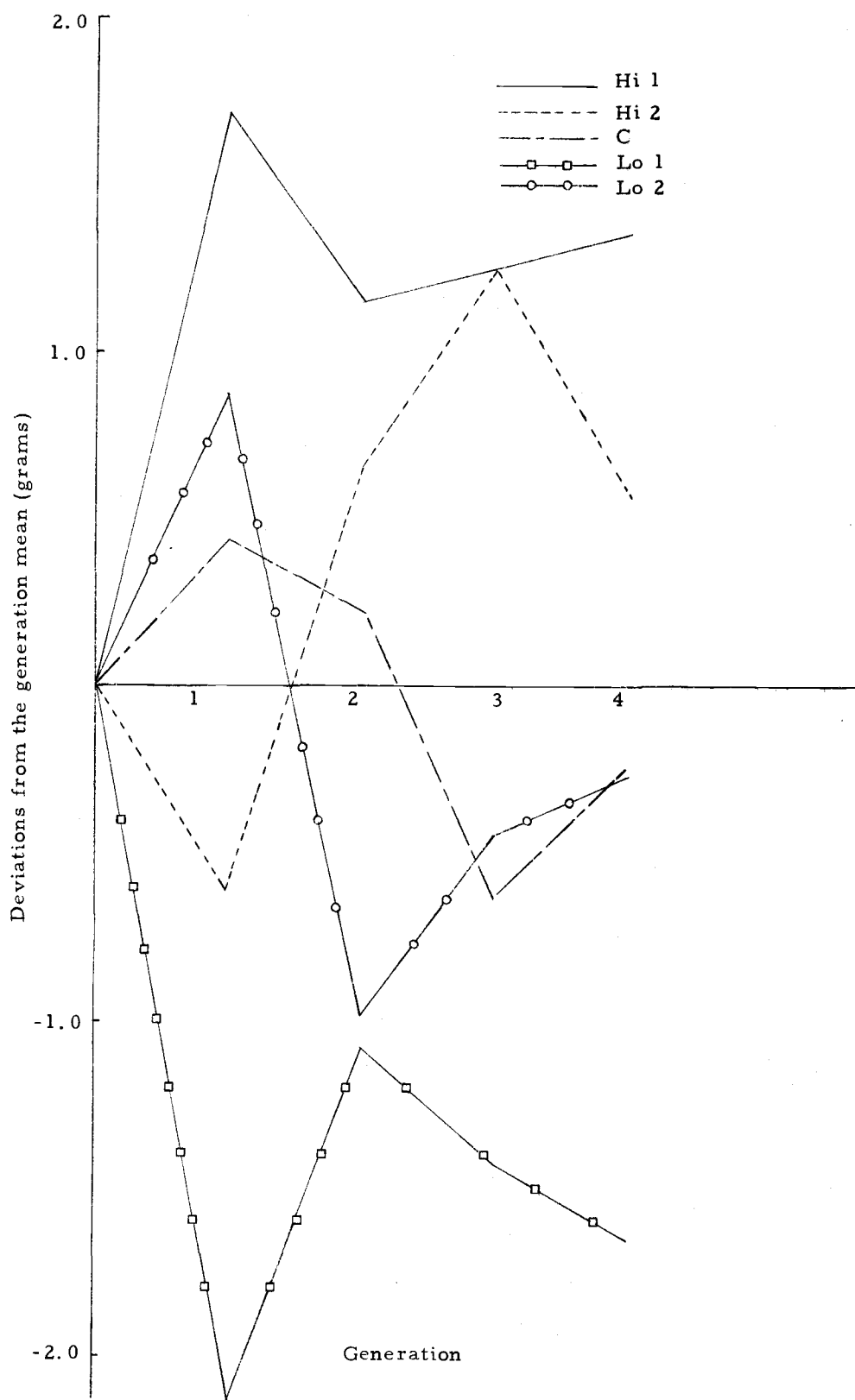


Figure 6. Response in weaning weight to selection for 14-day weight.

Table 15. Heritability estimates for birth weight, 14-day weight, weaning weight and litter size.

Line <sup>a/</sup>	Trait			
	Birth wt.	14-Day wt.	Wean wt.	Litter size
H <sub>1</sub>	0.00± --	0.23±0.17	0.22±0.37	0.00± --
H <sub>2</sub>	0.95±0.71	0.04±0.22	0.96±0.62	0.79±0.76
C	0.24±0.34	0.29±0.12	0.06±0.02	0.12±0.17
L <sub>1</sub>	1.03±0.56	0.13±0.07	0.23±0.42	0.00± --
L <sub>2</sub>	0.00± --	0.04±0.08	0.28±0.35	0.18±0.54
H <sub>1</sub> , H <sub>2</sub> , L <sub>1</sub> and L <sub>2</sub> Pooled	0.37±0.27	0.05±0.05	0.43±0.24	0.11±0.23

<sup>a/</sup> Heritability estimates were calculated from sire components of variance for lines H<sub>1</sub>, H<sub>2</sub>, L<sub>1</sub> and L<sub>2</sub> and from a regression of offspring on mid-parent means for the control line.

Table 16. Genetic correlations with standard errors of litter size, birth weight, 14-day weight and weaning weight.

Trait	Trait		
	Birth weight	14-Day weight	Weaning weight
Litter Size	-0.17 ± 0.47	-0.46 ± 0.38	-0.42 ± 0.22
Birth Weight		0.74 ± 0.65	0.44 ± 0.43
14-Day Weight			0.59 ± 0.35 <sup>a/</sup>

<sup>a/</sup> Calculated from covariance components obtained from the regression of progeny on the mid-parent mean.

The genetic correlations between litter size and birth, 14-day and weaning weights were -0.17, -0.47 and -0.42, respectively. The negative correlations indicate that an increase in litter size will result in a concomitant decrease in individual birth weight, 14-day weight and weaning weight. Genetic correlations between birth weight and 14-day weight and between birth weight and weaning weight were 0.74 and 0.44, respectively, indicating that in general larger progeny at birth are larger at 14 days of age and at weaning. Also, the positive correlation (0.59) between 14-day weight and weaning weight indicates that selection on the basis of 14-day weight should be effective in increasing weaning weight in mice. However, based on the magnitude of the standard errors associated with the estimates of the genetic correlations, the relationships between these traits must be viewed sceptically.

Genotypic, phenotypic and environmental correlations between 14-day weight and weaning weight were calculated for the upward and downward selected lines. The original data for 14-day weight and weaning weight were adjusted for significant sources of environmental variation and then subjected to nested analyses of variance. Separate analyses of variance were performed on 14-day weight, weaning weight, and 14-day and weaning weight combined. The sire, dam and progeny-within-dam covariances were obtained by the following procedure (Pirchner 1968).



$$\sigma^2(A + B) = \sigma_A^2 + \sigma_B^2 + 2\sigma_{AB}$$

$$\sigma_{AB} = \frac{\sigma^2(A + B) - (\sigma_A^2 + \sigma_B^2)}{2}$$

where:

$$\begin{aligned}\sigma^2(A + B) &= \text{The variance of traits A and B combined.} \\ \sigma_A^2 &= \text{The variance of trait A.} \\ \sigma_B^2 &= \text{The variance of trait B.} \\ \sigma_{AB} &= \text{The covariance of trait A with trait B.}\end{aligned}$$

The genetic, phenotypic and environmental correlations between 14-day weight and weaning weight are presented in Table 17. From Table 17 it can be seen that the genetic correlation coefficients vary markedly, both for replicate high and for replicate low lines. The amount of genetic variation in weaning weight that was accounted for by genetic variation in 14-day weight was determined by squaring the genetic correlation coefficients. Genetic variation in weaning weight accounted for by genetic variation in 14-day weight was 0.98, 0.02, 0.03, 0.05 and 0.50 for lines  $H_1$ ,  $H_2$ , C,  $L_1$ , and  $L_2$ , respectively. Based on these data any conclusion about the genetic relationship between 14-day weight and weaning weight would be hazardous.

Phenotypic correlations between 14-day weight and weaning weight, for the selected lines were positive and in reasonable agreement. Phenotypic coefficients of determination ( $r_p^2$ ) indicate that

Table 17. Genotypic, phenotypic and environmental correlations of 14-day weight with weaning weight.

Line	Correlation		
	G	P	E
H 1	+.989	.672	-.718
H <sub>2</sub> 2	-.121	.529	-.623
C*	+.588	.---	.---
L 1	-.217	.580	-.731
L 2	+.707	.354	-.629

\*The genetic correlation between 14-day weight and weaning weight for the control line was calculated from covariances obtained from the regression of progeny average on the mid parent mean.

Table 18. Analysis of variance of 14-day weights of cross-fostered progeny groups reared by dams from generation two.

Source of Variation	d. f.	Mean Squares	F
Total	35	-.----	-.---
Maternal Lines	2	5.3140	7.40**
Progeny Line	2	.2502	.35 NS
Sex	1	.0155	.02 NS
Replications	1	.0542	.08 NS
Maternal Line x Progeny Line	4	.2171	.30 NS
Maternal Line x Sex	2	.0081	.01 NS
Progeny Line x Sex	2	.1626	.23 NS
Maternal Line x Progeny Line x Sex	4	.0268	.04 NS
Error	17	.7178	-.---

\*\*Significant at the 1% level of probability.

from 13 to 45% of the phenotypic variation in weaning weight could be attributed to variation in 14-day weight. These data show that 14-day weight is not a highly accurate predictor of weaning weight.

Estimates of the environmental correlation ( $r_E$ ) between 14-day weight and weaning weight were in good agreement. The moderate negative estimates of  $r_E$  indicate that an environment conducive to rapid growth from birth to 14 days of age will retard growth from 14 days to weaning. Small progeny at 14 days of age that have been raised under environmental stress (poor milking dam) will show compensatory growth between 14 days of age and weaning.

Estimates of the dam and progeny-within-dam components of variance for each trait and covariance for each pair of traits are necessary for the calculation of phenotypic and environmental correlations. Birth weight and litter size were recorded as single observations for each litter so it was impossible to obtain separate estimates of dam and progeny components of variance and covariance. Consequently, phenotypic and environmental correlations were not calculated among traits where litter size or birth weight was involved as one of the traits.

#### Results of the Cross-Foster Study

Fourteen-day weight is influenced by maternal environment and

the individual's own genotype. Consequently, any change in means of lines may have been due to selection for increased or decreased growth rate rather than selection for greater or lesser postnatal maternal environment. To determine if selection was influencing postnatal maternal environmental effects on preweaning growth of mice a cross-foster study was conducted on generation 2 and generation 4 progeny groups. The results of the cross foster study are presented in Tables 18, 19, 20 and 21. From Tables 18 and 19 it can be observed that maternal line exerted a significant effect on 14-day weight ( $P < .01$ ). From Table 22 it can be observed that the mean for progeny reared by low line dams was higher than the mean for progeny reared by control line dams in generation 2. However, in generation 4 the mean for progeny reared by low line dams was 1.055 grams lower than the mean of progeny reared by control line dams. Analysis of weight gain from 14 days of age to weaning (Tables 20 and 21) showed that there was a significant ( $P < .05$ ) interaction between maternal line and line of progeny (generation 4). Results of the analysis of cross-foster data indicate that selection on 14-day weight in standardized litters was in essence selection for maternal performance. The significant interaction of maternal line by progeny line indicated that mice nursing dams with low milking ability showed compensatory growth after they started consuming dry food.

Table 19. Analysis of variance of 14-day weights of cross-fostered groups of progeny<sup>a/</sup> reared by dams from generation four.

Source of Variation	d. f.	Mean Squares	F
Total	35	-. ----	-. --
Maternal Line	2	5.6474	7.63 *
Progeny Line	2	.3812	.51 NS
Sex	1	.0213	.03 NS
Replication	1	.1708	.23 NS
Maternal Line x Progeny Line	4	.2604	.35 NS
Maternal Line x Sex	2	.0094	.01 NS
Progeny Line x Sex	2	.2033	.27 NS
Maternal Line x Progeny Line x Sex	4	.0481	.06 NS
Error	17	.7398	-. --

\* Significant at the 1% level of probability.

<sup>a/</sup> Data for 11 litters were deleted from the analysis because of Viral diarrhea. The deletion of 11 litters may have biased the results substantially because six of the 11 litters discarded were reared by low line dams.

Table 20. Analysis of variance of gains from 14-days of age to weaning by cross-fostered groups nursing dams from generation two.

Source of Variation	d. f.	Mean Squares	F
Total	35	-. ----	-. --
Maternal Line	2	1. 2526	. 95 NS
Progeny Line	2	. 5747	. 43 NS
Sex	1	. 4070	. 31 NS
Replication	1	. 3374	. 25 NS
Maternal Line x Progeny Line	4	4. 5442	3. 43 <sup>+</sup>
Maternal Line x Sex	2	. 1500	. 11 NS
Progeny Line x Sex	2	. 0657	. 05 NS
Maternal Line x Progeny Line x Sex	4	. 2908	. 22 NS
Error	17	1. 3243	-. --

<sup>+</sup>Significant at the 10% level of probability.

Table 21. Analysis of variance of weight gains from 14 days of age to weaning by cross-fostered groups of progeny<sup>a/</sup> nursing dams from generation four.

Source of Variation	d. f.	Mean Squares	F
Total	35	-.-----	-.---
Maternal Line	2	3.7212	3.04 NS
Progeny Line	2	1.1438	.94 NS
Sex	1	.2131	.17 NS
Replication	1	.6120	.50 NS
Maternal Line x Progeny Line	4	5.7083	4.67*
Maternal Line x Sex	2	.2773	.23 NS
Progeny Line x Sex	2	.1651	.14 NS
Maternal Line x Progeny Line x Sex	4	.4331	.35 NS
Error	17	1.2211	-.---

\* Significant at the 5% level of probability.

<sup>a/</sup> Data for 11 fostered litters were deleted from the analysis because of Viral diarrhea. Six of the 11 litters discarded were reared by low line dams.

Table 22. Mean<sup>a/</sup> 14-day weights (grams) of high, control and low line progeny fostered by high, control or low line dams.

Progeny Line	Maternal Lines			Progeny Line Mean
	H	C	L	
(Dams from Generation 2)				
H	6.880	5.374	5.825	6.026
C	6.281	5.396	5.812	5.830
L	6.625	5.194	5.352	5.724
Maternal Line Mean	6.604	5.321	5.656	
(Dams from Generation 4)				
H	6.962	6.528	5.497	6.329
C	7.052	6.476	5.355	6.294
L	6.852	6.358	5.165	6.125
Maternal Line Mean	6.955	6.454	5.399	

<sup>a/</sup> Means were pooled for replicate high, control and low lines.



### Comparison of Actual and Predicted Response

Nested analyses of variance (Tables 23 through 26) were performed on data collected on generation 1 progeny. The components of variance obtained were used in the calculation of the causal components of variance used in equations 13 and 14 for predicting 14-day weight and weaning weight. In the analysis where dams were nested within sires, the sire component ( $\sigma^2_S$ ) estimates one-fourth of the additive genetic variance. The heritability ( $h^2$ ) estimates ( $4 \sigma^2_S / \sigma^2_T$ ) obtained for 14-day weight and weaning weight were 0.28 and 0.30 respectively. The difference between the covariance between maternal half sibs and the covariance of paternal half sibs estimates the maternal variance ( $M^2$ ). Maternal variance (genetic + environmental) was obtained by subtracting the percentage of variance attributed to sires in the analysis where dams were nested within sires from the percentage of variance attributed to dams in the analysis where sires were nested within dams. The estimates of  $M^2$  were 0.62 for 14-day weight and 0.63 for weaning weight.

The variance due to dominance effects and epistasis were assumed to be zero and the environmental component of variance ( $e^2$ ) was obtained by subtraction ( $e^2 = 1.0 - (h^2 + M^2)$ ). The estimates of  $e^2$  were 0.10 and 0.07 for 14-day weight and weaning weight, respectively.

Table 23. Nested<sup>a/</sup> analysis of variance of 14-day weight data.

Source of Variation	d. f.	Mean Squares	Component	% of Variation
Sires	28	10.9931341	.163577	6.99
Dams	19	1.3934961	.1812690	77.46
Progeny	314	.0363895	.0363895	15.55
Total	361	.9421343	.2340162	100.00

<sup>a/</sup> Dams were nested within sires.

Table 24. Nested<sup>a/</sup> analysis of variance of 14-day weight data.

Source of Variation	d. f.	Mean Squares	Component	% of Variation
Dams	50	3.9305572	.1393975	69.32
Sires	50	.2447752	.0303248	15.08
Progeny	641	.0313705	.0313705	15.60
Total	741	.3088733	.2010928	100.00

<sup>a/</sup> Sires were nested within dams.

Table 25. Nested<sup>a/</sup> analysis of variance of weaning weight data.

Source of Variation	d.f.	Mean Squares	Component	% of Variation
Sires	28	9.0474567	.1010170	7.46
Dams	19	7.7054974	.9947330	73.47
Progeny	314	.2582298	.2582298	19.07
Total	361	1.3319041	1.3541152	100.00

<sup>a/</sup> Dams were nested within sires.

Table 26. Nested<sup>a/</sup> analysis of variance of weaning weight data.

Source of Variation	d.f.	Mean Squares	Component	% of Variation
Dams	50	19.2463797	.7096690	70.32
Sires	50	1.1515704	.1805458	17.89
Progeny	641	.1189846	.1189846	11.79
Total	741	1.4793072	1.0091004	100.00

<sup>a/</sup> Sires were nested within dams.

The observed and predicted 14-day weights for the two high lines ( $H_1$  and  $H_2$ ), the control line (C) and the two low lines ( $L_1$  and  $L_2$ ) are presented in Tables 27, 28 and 29, respectively. From Table 27 it can be observed that the predicted 14-day weight was consistently higher than the observed. There was reasonable agreement between observed and predicted 14-day weight for the  $H_1$  line for generation 2 and for the two high lines combined for generation 2. The lack of agreement between observed and predicted 14-day weight for generation 4 was attributed to the loss of progeny tested sires and the failure of selected males to sire progeny. Also, infant viral diarrhea affected some generation 4 litters and data on affected litters were not included in analysis. Data for eight litters of high line 2 progeny from generation 4 were not included in the analysis. Three of the litters were devoured after standardization and 5 litters were discarded because of viral diarrhea. The loss of data could have biased the observed mean 14-day weight in a negative direction.

Data presented in Table 28 showed that there were considerable differences between observed and predicted 14-day weights for both lines of mice selected for decreased weight. However, the predicted 14-day weight was closer to the observed weight for both lines in generation 2 than it was in generation 4. The estimates of the causal components of variance used in the prediction equation may not have been applicable after the first generation of selection in the low lines.

Table 27. Average of factors involved in the predicted equation, averages of the observed and predicted 14-day weights and the observed and predicted 14-day weights and the differences between observed and predicted 14-day weights for unselected mice from parents selected for increased 14-day weight.

Line	Offspring generation	No. of litters	Sires	Sibs average (grams)	Population average (grams)	No. of sibs	Inbreeding coefficient	Sibs relation-ship	Sex	Selection differential (grams)	Average no. of offspring	Observed offspring average (grams)	Predicted offspring average (grams)	Observed ave. - predicted ave. <sup>a/</sup> (grams)
H <sub>1</sub>	2	16	Sires	7.543	7.345	6.333	0.000	0.500	M	0.198	6.875	7.041	7.315	-0.274
			Dams	7.515	7.200	6.625	0.000	0.500	F	0.315				
H <sub>2</sub>	2	14	Sires	7.085	6.932	6.714	0.000	0.500	M	0.153	6.786	6.419	6.920	-0.501
			Dams	7.004	6.858	7.000	0.000	0.500	F	0.146				
H <sub>1</sub>	4	7	Sires	7.327	7.345	5.000	0.000	0.500	M	-0.018	8.000	5.992	6.643	-0.651
			Dams	7.132	6.768	6.143	0.000	0.500	F	0.364				
H <sub>2</sub>	4	16	Sires	7.124	6.932	6.750	0.000	0.500	M	0.192	7.500	6.356	6.562	-0.206
			Dams	6.539	6.166	6.600	0.008	0.502	F	0.373				
H <sub>1</sub> + H <sub>2</sub>	2	30	Sires	7.336	7.140	6.500	0.000	0.500	M	0.196	6.833	6.730	7.094	-0.364
			Dams	7.317	7.025	6.778	0.000	0.500	F	0.292				
H <sub>1</sub> + H <sub>2</sub>	4	23	Sires	7.197	7.140	6.000	0.000	0.500	M	0.057	7.652	6.174	6.759	-0.585
			Dams	6.719	6.332	6.455	0.004	0.501	F	0.387				
H <sub>1</sub> + H <sub>2</sub>	2 + 4	53	Sires	7.296	7.140	6.348	0.000	0.500	M	0.156	7.189	6.453	6.967	-0.514
			Dams	7.056	6.768	6.633	0.002	0.500	F	0.288				

<sup>a/</sup> Negative numbers mean that selection was less effective than expected.

Table 28. Averages of factors involved in the prediction equation and averages of the observed and predicted 14-day weights and the differences between observed and predicted 14-day weights of unselected offspring from parents selected for decreased 14-day weight.

Line	Offspring generation	No. of litters		Sib average (grams)	Population Average (grams)	No. of sibs	Inbreeding coefficient	Sibs relation-ship	Sex	Selection differential (grams)	Average no. of offspring	Observed offspring average (grams)	Predicted offspring average (grams)	Observed ave. - predicted ave. <sup>a/</sup> (grams)
L <sub>1</sub>	2	17	Sires	6.263	6.970	6.888	0.000	0.500	M	-0.734	6.886	5.969	6.878	-0.909
			Dams	6.230	6.954	6.941	0.000	0.500	F	-0.724				
L <sub>2</sub>	2	10	Sires	6.251	6.563	6.500	0.000	0.500	M	-0.312	7.000	5.880	6.480	-0.600
			Dams	6.588	6.435	6.800	0.000	0.500	F	-0.153				
L <sub>1</sub>	4	8	Sires	6.463	6.287	7.000	0.000	0.500	M	+0.176	7.750	5.172	6.284	-1.112
			Dams	5.782	6.316	7.000	0.000	0.500	F	-0.534				
L <sub>2</sub>	4	6	Sires	6.682	6.210	6.250	0.000	0.500	M	+0.472	7.000	4.492	6.029	-1.537
			Dams	4.845	5.934	5.833	0.024	0.506	F	-1.089				
L <sub>1</sub> + L <sub>2</sub>	2	27	Sires	6.258	6.715	6.733	0.000	0.500	M	-0.457	6.925	5.925	6.650	-0.725
			Dams	6.361	6.636	6.889	0.000	0.500	F	-0.275				
L <sub>1</sub> + L <sub>2</sub>	4	14	Sires	6.582	6.715	6.571	0.000	0.500	M	-0.133	7.429	4.832	6.347	-1.515
			Dams	5.422	6.064	6.500	0.010	0.502	F	-0.642				
L <sub>1</sub> + L <sub>2</sub>	2 + 4	41	Sires	6.360	6.715	6.682	0.000	0.500	M	-0.355	7.097	5.379	6.469	-1.090
			Dams	6.052	6.298	6.756	0.001	0.500	F	-0.246				

<sup>a/</sup> Negative numbers mean that selection was more effective than expected.

Table 29. Averages of factors involved in the prediction equation, averages of the observed and predicted weights and differences between observed and predicted 14-day weights of unselected progeny from unselected control line parents.

Line	Offspring generation	No. of litters		Sib average (grams)	Population average (grams)	No. of sibs	Inbreeding coefficient	Sibs relation-ship	Sex	Selection differential (grams)	Average No. of offspring	Observed offspring average (grams)	Predicted offspring average (grams)	Observed ave. - predicted ave. <sup>a/</sup> (grams)
R	2	54	Sires	6.602	6.526	6.736	0.000	0.500	M	+0.076	7.333	6.396	6.474	-0.078
			Dams	6.416	6.416	6.679	0.000	0.500	F	+0.153				
	4	43	Sires	5.917	6.108	5.907	0.005	0.501	M	-0.191	6.977	6.289	6.286	0.003
			Dams	6.382	6.472	5.139	0.005	0.501	F	-0.053				
	2 + 4	97	Sires	6.311	6.358	6.219	0.003	0.501	M	-0.047	7.175	6.353	6.395	-0.042
			Dams	6.382	6.435	5.928	0.003	0.501	F	-0.053				

<sup>a/</sup> Negative numbers mean that selection was more effective than expected.

If the true heritability for 14-day weight was indeed smaller than the estimate used in the prediction analysis, weight would be inflated. Also, since the square root of the maternal component of variance ( $M$ ) appears in the numerator of the prediction equation, over estimation of  $M^2$  would inflate the predicted 14-day weight.

The estimates of the predicted 14-day weight for the control line were in very close agreement with the observed 14-day weights (Table 29). The close agreement between observed and predicted 14-day weight indicates that the estimates of the causal components used in the prediction equation were relatively accurate.

Predicted weaning weight for  $H_1$  mice (Table 30) was in close agreement with the observed weaning weight for generation 2 but differed considerably for generation 4. As mentioned earlier, 8 litters of line  $H_1$  for generation 4 were lost from the experiment and may have biased downward the observed mean weaning weight. The observed and predicted weaning weights for the  $H_2$  line were in poor agreement for generation 2 and in reasonable agreement for generation 4. The mean weaning weight of high line 2 was considerably lower for generation 2 than the mean for generation 1 (Figure 6). This might have been due to sampling from the base population. If the differences between lines  $H_1$  and  $H_2$  were due to sampling from the base population then the estimates of heritability, maternal variance, and non-genetic, non-maternal environmental variation



Table 30 Averages of factors involved in the prediction equation, averages of the observed and predicted weaning weights and differences between observed and predicted weaning weights of unselected progeny from dams selected for increased 14-day weight.

Line	Offspring generation	No. of litters		Sib average (grams)	Population average (grams)	No. of sibs	Inbreeding coefficient	Sibs relationship	Sex	Selection differential (grams)	Average no. of offspring	Observed offspring average (grams)	Predicted offspring average (grams)	Observed ave. - predicted ave. <sup>a/</sup> (grams)
H <sub>1</sub>	2	16	Sires	11.342	11.107	6.333	0.000	0.500	M	0.235	6.438	11.323	10.957	0.366
			Dams	11.351	10.684	6.625	0.000	0.500	F	0.667				
H <sub>2</sub>	2	14	Sires	10.424	10.190	6.714	0.000	0.500	M	0.234	6.214	9.264	10.146	-0.882
			Dams	10.568	9.949	7.000	0.000	0.500	F	0.619				
H <sub>1</sub>	4	7	Sires	10.885	9.680	5.000	0.000	0.500	M	1.205	7.857	8.308	9.988	-1.680
			Dams	10.598	9.792	6.143	0.000	0.500	F	0.806				
H <sub>2</sub>	4	16	Sires	10.073	8.774	6.750	0.000	0.500	M	1.299	7.188	9.072	8.773	0.299
			Dams	9.512	8.456	6.400	0.008	0.502	F	1.056				
H <sub>1</sub> + H <sub>2</sub>	2	30	Sires	10.870	10.653	6.524	0.000	0.500	M	0.217	6.333	10.551	10.533	0.018
			Dams	10.949	10.306	6.813	0.000	0.500	F	0.643				
H <sub>1</sub> + H <sub>2</sub>	4	23	Sires	10.419	9.054	5.875	0.000	0.500	M	1.365	7.188	9.380	9.129	0.251
			Dams	10.044	8.823	6.272	0.004	0.501	F	1.221				
H <sub>1</sub> + H <sub>2</sub>	2 + 4	53	Sires	10.641	9.964	6.199	0.000	0.500	M	0.677	6.792	9.965	9.907	0.058
			Dams	10.515	9.757	6.542	0.002	0.500	F	0.758				

<sup>a/</sup> Negative numbers mean that selection was less effective than expected.

used in the prediction equation were not applicable. The observation that the predicted weaning weight, based on pooled high line data for generations 2 and 4 combined, was in close agreement with the overall observed mean also indicates that sampling was responsible for the within-line within-generation disagreement between predicted and observed weaning weights.

Data presented in Table 31 showed that actual and predicted weaning weights differed markedly for each low line in each generation. The reduced size of low line mice at 14 days of age may have made them more susceptible to temporary stress conditions. If this was true, then the estimate of the non-genetic non-maternal environmental variation was probably an under estimate as far as the low lines were concerned. As a consequence the predicted weight for low line mice would be biased upwards.

Actual and predicted weaning weights for control line progeny (Table 32) was in excellent agreement. This again indicates that the estimates of heritability, maternal variance and environmental variance were reasonably accurate. The control line data showed that response to selection for a maternally influenced trait can be predicted with reasonable accuracy.

Table 31. Averages of factors involved in the prediction equation, averages of observed and predicted weaning weights and differences between observed and predicted weaning weights of unselected progeny from dams selected for decreased 14-day weight.

Line	Offspring generation	No. of litters		Sib average (grams)	Population average (grams)	No. of sibs	Inbreeding coefficient	Sibs relationship	Sex	Selection differential (grams)	Average no. of offspring	Observed offspring average (grams)	Predicted offspring average (grams)	Observed ave. - predicted ave. <sup>a/</sup> (grams)
L <sub>1</sub>	2	17	Sires	9.060	10.393	6.777	0.000	0.500	M	-1.333	6.882	8.676	10.166	-1.490
			Dams	8.966	10.355	6.882	0.000	0.500	F	-1.389				
L <sub>2</sub>	2	10	Sires	9.255	9.566	6.500	0.000	0.500	M	-0.311	6.100	8.241	9.403	-1.162
			Dams	9.430	9.285	6.800	0.000	0.500	F	+0.145				
L <sub>1</sub>	4	8	Sires	9.230	10.393	7.000	0.000	0.500	M	-1.308	7.750	7.229	9.363	-2.134
			Dams	8.542	8.822	6.375	0.000	0.500	F	-0.280				
L <sub>2</sub>	4	6	Sires	10.092	9.566	6.250	0.000	0.500	M	+0.526	7.000	6.316	8.522	-2.206
			Dams	5.861	7.963	5.667	0.024	0.506	F	-2.102				
L <sub>1</sub> + L <sub>2</sub>	2	27	Sires	9.155	9.875	6.639	0.000	0.500	M	-0.720	6.592	8.558	9.721	-1.163
			Dams	9.197	9.700	6.841	0.000	0.500	F	-0.503				
L <sub>1</sub> + L <sub>2</sub>	4	14	Sires	9.637	9.875	6.625	0.000	0.500	M	-0.238	7.429	6.872	8.967	-2.095
			Dams	7.280	8.255	6.021	0.012	0.503	F	-0.975				
L <sub>1</sub> + L <sub>2</sub>	2 + 4	41	Sires	9.396	9.875	6.632	0.000	0.500	M	-0.479	6.877	7.716	9.325	-1.609
			Dams	8.299	8.846	6.431	0.006	0.501	F	-0.547				

<sup>a/</sup> Negative numbers mean that selection was more effective than expected.

Table 32. Averages of factor involved in the prediction equation, averages of observed and predicted weaning weights and differences between observed and predicted weaning weights of unselected progeny from unselected parents.

Line	Offspring generation	No. of litters		Sib average (grams)	Population average (grams)	No. of sibs	Inbreeding coefficient	Sibs relationship	Sex	Selection differential (grams)	Average no. of offspring	Observed offspring average (grams)	Predicted offspring average (grams)	Observed ave. - predicted ave. (grams)
R	2	54	Sires	9.150	9.314	6.660	0.000	0.500	M	-0.164	7.148	9.128	9.170	-0.042
			Dams	9.228	9.024	6.528	0.000	0.500	F	+0.204				
	4	43	Sires	8.251	8.315	5.837	0.005	0.501	M	-0.064	6.977	8.654	8.638	0.016
			Dams	9.253	8.948	4.953	0.005	0.501	F	+0.305				
	2 + 4	97	Sires	8.768	8.913	6.156	0.003	0.501	M	-0.145	7.072	9.901	8.957	-0.056
			Dams	9.238	8.998	5.763	0.003	0.501	F	+0.240				

## GENERAL DISCUSSION

An attempt was made to determine if selection would be effective in separating lines selected for increased and decreased 14-day weight. Data were also collected on litter size at birth, birth weight and weaning weight to determine whether or not selection for 14-day weight would bring about changes in other maternally influenced traits. The generally low heritabilities for litter size, birth, 14-day, and weaning weight indicated that genetic improvement of these traits would be slow. The genetic correlations among traits were low to moderate indicating that it would require several generations to demonstrate any clear pattern of response to selection for increased or decreased 14-day weight, in such correlated traits as either size, birth weight or weaning weight for which no direct selection pressure was applied.

Least squares analysis of the data clearly showed that environmental effects significantly influenced the expression of each of the four traits. If the data had not been adjusted for significant non-contemporary environmental influences the calculations of heritability estimates and genetic correlations would have been less accurate.

It has been well established by previous researchers that large dams produce large litters of small progeny and the small

progeny in turn produce small litters of large progeny. In an attempt to avoid this reciprocating maternal effect, progeny that were to become parents of the next generation were chosen at random from the standardized litters selected to provide future parents. Parents (2 females and 1 male) for future generations were chosen from the superior ten litters for high lines and the inferior ten litters for low lines. In lines where only 10 litters survived through weaning no direct selection pressure was applied, consequently, selection may have been in the reverse direction because nature selects for an intermediate genotype. Considerably more selection pressure could have been applied if four female and 2 male progeny had been selected from the superior (inferior in the case of low lines) five litters surviving to weaning. Although this would have resulted in more inbreeding in selected lines, it would probably have resulted in a greater divergence for 14-day weight among selected lines.

Progeny testing permits a more accurate evaluation of an individual's genotype; therefore, more rapid genetic gains can be made in lowly heritable traits if progeny tested sires are used. In the present study progeny tested sires were used as parents of progeny in generation 3 and 4. Based on limited observations there appeared to be some hazards in using progeny tested males. Mice tend to be cannibalistic; consequently, males could not be housed

together after they had been progeny tested. Housing males individually required considerable cage space and increased the cost involved in care of experimental animals. The males kept in individual cages tended to become large, and to eventually lose their libido. Consequently, when these males were placed in breeding cages, some failed to sire any progeny and others only successfully impregnated one or two females. In an experiment where line size is small, the loss of a litter or the failure of a selected male to sire litters has a large effect on the results of the experiment. If data from more litters were available for the selected lines the observed and predicted 14-day and weaning weights may have compared more favorably.

The estimates of causal components of the phenotypic variance were estimated from generation 1 data. The parents of generation 1 were all  $F_1$  progeny (base population), therefore, data from all four selected lines could be pooled. In selected lines each male was mated to two females so a nested analysis of variance, where dams were nested within sires, could be performed. The random line dams were used in the progeny test so it was also possible to perform a nested analysis of variance with sires nested within dams, as random line dams had produced two litters, each sired by a different male. From the two nested analyses of variance, estimates of the covariance of paternal-half-sibs and the covariance of

maternal-half-sibs were available for estimation of the variance due to total maternal effects. The variance due to maternal effects was large, 62% for 14-day weight and 63% for weaning weight. However, the estimate of maternal variance would be biased somewhat because the effects due to parity were not removed from the data.

Selection causes change in the estimates of heritability, maternal variance, dominance effects, epistatic effects and environmental effects. Consequently, the response to selection should be predicted on the basis of estimates obtained from the prior generation. Due to line sizes it was not possible to obtain reliable parameter estimates for each line in each generation. Therefore, it was necessary to use the same estimates for predicting 14-day and weaning weights in generation 2 and generation 4. Predicted response for generations 1 and 3 was not calculated because progeny tested sires of generation 1 were used to produce generation 3 progeny. If one assumed that the parameter estimates obtained from  $F_2$  data were applicable to  $F_1$  data then response could have been predicted for generations 1 and 3 if information on the sire's sibs were available.

Response to selection for increased and decreased 14-day weight was attributed to maternal effects. Cross-fostered litters that were reared by high line dams had a heavier mean 14-day weight than cross-fostered litters reared by low line dams indicating that



selection was effective in increasing milk yield in high line dams and decreasing milk yield in low line dams.

Based on the limited number of generations and the small line sizes the results of this study must be considered only as indications. Before any strong conclusions can be drawn concerning the effect of directional selection for 14-day weight on changes in other maternally influenced traits, a study on a larger scale involving more generations of selection should be conducted.

## SUMMARY AND CONCLUSIONS

Sexually mature Swiss- Webster mice from two random bred colonies were crossed to form the base population. Twenty female and ten male progeny were randomly selected from the base population to become parents of the first generation progeny for the establishment of each of two high lines and two low lines. The first generation of the control line was propagated from 80 female and 80 male progeny randomly selected from the base population. In all lines, matings were made at random with the exception of no full-sib matings. Selection was based on 14-day weight of litters standardized to 8 progeny (4 males and 4 females).

Male parents of generations 1 and 2 were progeny tested and the superior 5 males (inferior in the case of low lines) were selected to become parents of generations 3 and 4.

Data were collected on litter size at birth, litter birth weight, and individual 14-day and weaning weights of progeny in standardized litters.

Statistical analysis of the data support the following conclusions:

1. In the present experiment genetic gains could not be measured in the selected lines relative to the control line. From Tables 29 and 32 it was observed that sizeable selection differentials were generated in the control line; consequently, in the present experiment

the control line did not measure environmental fluctuations. Genetic change was therefore evaluated in terms of the deviations of selected line means from the overall least squares generation mean.

2. Based on a within-generation comparison of the least squares line means with the least squares mean for the pooled lines, selection for 14-day weight was effective in the separation of lines. The overall least squares mean for the control line was intermediate between the means for high and low lines.

3. Selection appeared to be more effective in decreasing 14-day weight in the low lines than in increasing 14-day weight in high lines (Figure 5).

4. Selection for 14-day weight was not effective in changing litter size at birth or individual birth weights but did appear to exert a positive effect on weaning weight.

5. The overall mean weaning weight for the control line was intermediate between means for high and low lines. The positive genetic correlation between 14-day weight and weaning weight indicated that a change in mean 14-day weight produced a concomitant change in mean weaning weight.

6. The major source of variation in 14-day weight and weaning weight was that caused by maternal environment. Maternal effects (genetic + environmental) were estimated to account for 62 and 63 percent of the variation in 14-day weight and weaning weight,

respectively. Results from a cross-fostering experiment indicated that selection for decreased 14-day weight was effective in reducing milk yield in low line dams. Selection also appeared to increase milk yield in high line dams.

7. The generally low heritability estimates of litter size, 14-day weight and weaning weight indicates that genetic improvement in any one of the traits will be slow.

8. Response to selection can be predicted with reasonable accuracy for a maternally influenced trait. There was excellent agreement between predicted and observed 14-day weight and weaning weight for the control line data. Observed weights for control line data were not expected to change from generation to generation. The fact that observed and predicted weights were in good agreement indicates that the estimates of the causal components used were relatively accurate for the control line.

9. The general lack of agreement between observed and predicted 14-day weights and weaning weights in the selected lines was attributed to insufficient numbers of observations. Infant viral diarrhea affected some litters of progeny in generation 4. Deletion of affected litters from the analyses may have biased the observed 14-day and weaning weights in the selected lines.

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