599.323.4:591.134:591.15

MEDEDELINGEN LANDBOUWHOGESCHOOL
WAGENINGEN • NEDERLAND • 74-8 (1974)

EFFECT OF SELECTION FOR RELATIVE GROWTH RATE AND BODYWEIGHT OF MICE ON RATE, COMPOSITION AND EFFICIENCY OF GROWTH

(with a summary in Dutch)

H. BAKKER

Department of Animal Husbandry, Agricultural University, Wageningen, The Netherlands

(Received 5-II-1974)

H. VEENMAN & ZONEN B.V. – WAGENINGEN – 1974

Mededelingen Landbouwhogeschool
Wageningen 74–8 (1974)
(Communications Agricultural University)
is also published as a thesis

CONTENTS

I INTRODUCTION

The value of an animal for meat production is determined by its growth rate, feed conversion and slaughter quality. Growth rate is most important for the economy of meat production because feed costs and most of the fixed costs decrease with increasing growth rate. As weight increases storage of fat must be kept to a minimum, otherwise it will negatively influence efficiency of growth and the price per kilogram product. The combination of a high growth rate and a limited fat storage can be seen in the first part of a growth curve. For instance CÖP 1971 reported that the slaughter weight in pigs (100 kg) is near the inflexion point. This is the point of the growth curve where the increasing growth rate changes over to a decrease in growth rate. The inflexion point for laboratory and farm animals occurs when about 30 percent of mature weight is reached (BRODY 1945).

The growth rate can be increased by improving the environmental influences like quantity of feed, feed composition, housing etc., and by improving the genotypic value for growth by selection and crossbreeding. In this study no special attention will be paid to environmental effects. The heterosis for post-weaning growth in pigs (FREDEEN 1957, SKÅRMAN 1965) and in beef cattle (GALL 1969) can be neglected. Thus breeding systems based on the utilisation of heterosis will not be discussed. Selection for growth rate may be successful. FALCONER 1960a reported heritabilities for growth of 0.20–0.40 in several species. An increasing mature weight is a correlated effect of selection for growth rate (BRINKS et al. 1964, TAYLOR 1968). BICHARD 1968 pointed out the following consequences of this increasing mature weight:

- an increase of the maintenance costs of the breeding stock;
- a delayed sexual maturity. The breeding stock can not be mated until later. This means an increase of the costs per breeding animal.

These points restrict the advantage of an increased growth rate. The early growth rate must be increased without or with a restricted change of mature weight. The necessity of a change in the growth curve in this way, is extensively discussed.

The limited possibilities of this change were demonstrated by TAYLOR and CRAIG 1965. BICHARD 1968 concluded: 'Genetic flexibility of the mean growth curve and the mean body proportions is not very great'. BRODY 1945 and TAYLOR 1968 also pointed this out. In contrast to these remarks are the results of ABLANALP et al. 1963 who demonstrated genetic differences in growth curves of selection lines of turkeys and those of LAIRD and HOWARD 1967 who showed similar differences in inbred lines of mice.

The aim of my study was to examine the effects of selection for early growth rate by means of the relative growth rate between 21 and 29 days and for weight at 56 days of age as an estimate of mature weight.

Relative growth rate (RG) is defined as weight gain during a given time-

interval divided by the average bodyweight in this interval (BRODY 1945). This parameter RG is an estimate for the rate of weight change and does not automatically include a high correlated change in mature weight. Besides this, RG may be seen as a parameter for maturity rate. Maturity rate at age t is defined as the percentage of mature weight that is reached at age t (FITZHUGH and TAYLOR 1971). Differences in weight at 56 days (W56D) are indications of differences in mature weight (ROBERTS 1961). Selection for W56D has the advantage over selection for mature weight, that the generation interval is strongly reduced and that only the selected animals have to be mated.

Out of one base population a control line C and four selection lines were started. In these lines, selection was made for a high and a low relative growth rate between 21 and 29 days (RGH and RGL) and for a high and a low bodyweight at 56 days (W56H and W56L). Attention was paid to:

- Direct results of the applied selection during 14 generations.
- Comparison of line and sex differences in parameters of functions which describe the growth curve in generations 6–14.
- Analysis of the composition of weight increase and energy efficiency, based on data of growth rate, feed intake and carcass composition between 3 and 15 weeks of age in generation 11 of all lines.

This report was divided according to these 3 investigations. In Chapter II only literature on general aspects of growth and development is presented. The literature directly connected to each of the three investigations is described in the relevant chapter. The consequences of the selection for RG and W56D will be discussed in Chapter VI.

II GENERAL LITERATURE ON GROWTH AND DEVELOPMENT

Growth rate and weight for age are parameters that are often estimated in animal production research. With these parameters all kinds of influences may be estimated. There have been many selection experiments for growth rate or for weight under practical and laboratory conditions (ROBINSON and BRADFORD 1969). ROBERTS 1965 stated that so much research on weight has been done with laboratory animals, because of its economic importance in animal production and the ease of bodyweight estimation.

According to DICKERSON 1970 the economic results in meat production are determined by:

- Costs of producing the slaughter animals. These are influenced by the costs of maintenance of the breeding stock and the number of offspring per animal per year.
- Costs and returns of realised weight increment of the slaughter animals. If these animals are slaughtered at fixed weight, the ratio of returns to costs per animal is determined by:

$$V \cdot P / [D \cdot I + D(B \cdot \bar{F}_m + F_p) + S]$$

in which:

V = value per unit liveweight
P = liveweight of meat animal when marketed
D = days from weaning to market weight
I = average fixed costs/animal/day
B = average post-weaning metabolic body size for individual
$\bar{F}_m$ = average maintenance feed costs/animal-day for population
F_p = average feed costs above maintenance/day for individual
S = fixed costs/slaughter animal.

From this ratio it follows, that almost all costs are directly proportional to the number of days, so inversely proportional to the growth rate.

Weight increment is quantitative and qualitative. The well-known definition by BRODY 1945, 'growth may be defined as a relatively irreversible time change in magnitude of the measured dimension or function', is only quantitative. As the proportions of the different tissues in the body change with aging (CURTIS 1969), growth is also qualitative. DOORNENBAL 1971 called this qualitative aspect development. It may defined as 'the directive coordination of diverse processes in an adult' (BRODY 1945); NEEDHAM 1964 defined this adult stage as organised heterogenity. The composition of the weight increment is of importance for the economy of meat production, because it changes with aging and determines the energy efficiency of weight increment and price per kilogram product (ROBINSON and BRADFORD 1969, DICKERSON 1970).

2.1 Description of growth rate

The growth curve may be represented in various ways. In Figure 2.1 it is presented by the absolute growth rate, the relative growth rate and the cumulative growth rate in time.

The *cumulative growth curve* is the curve of weight against time. The shape of the curve is sigmoid. After a phase of increasing growth rate, called the self-accelerating phase by Brody 1945, the weight increment per unit of time decreases (self-inhibiting phase) until the increment becomes zero and mature weight is reached. The transition point between the two phases is called inflexion point. This point has some physiological significance, because it occurs at the age of puberty (Brody 1945, Monteiro and Falconer 1966).

The *absolute growth rate* may be defined as the weight increment per unit of time:

$$(W_2-W_1)/(t_2-t_1)$$

in which (W_2-W_1) is the weight increment in time interval (t_2-t_1). This formula represents the average absolute growth rate. It is only a good representation of the real instantaneous growth rate, if it is estimated in short intervals. A mathematical representation of the instantaneous absolute growth rate at age t is dw/dt.

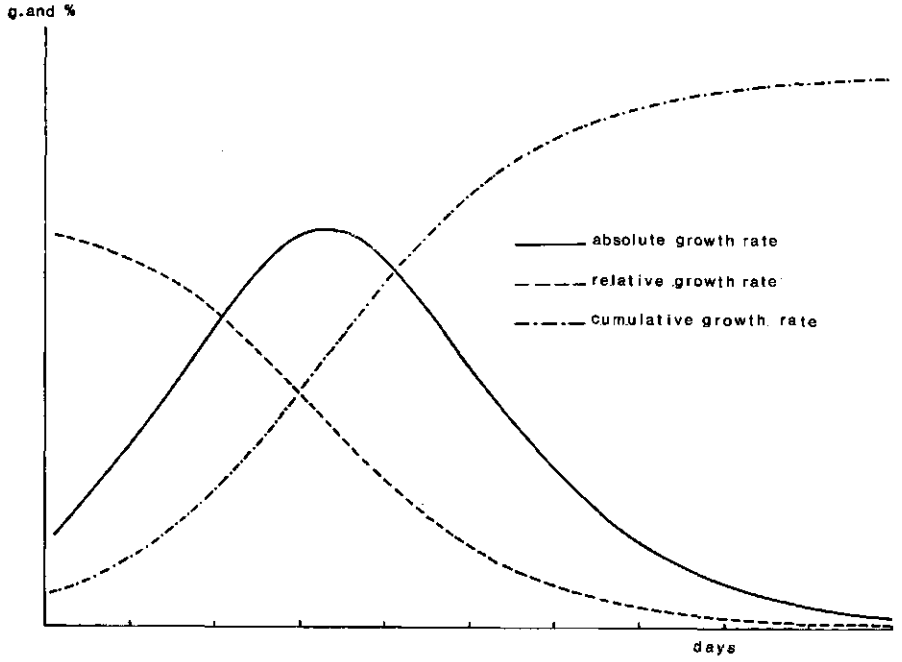

Fig. 2.1. The relation between absolute, relative and cumulative growth rate

The *relative growth rate* is defined by BRODY 1945 separately for the phase of self-accelerating and of self-inhibiting growth. Before the inflexion point it is defined as the absolute growth rate divided by the actual weight

$$k = (dw/dt)/W$$

k = relative growth rate.
The value of k may be found from

$$k = [(W_2 - W_1)/(t_2 - t_1)]/[{}^1/_2 (W_2 + W_1)]$$
$$\text{or } k = (lnW_2 - lnW_1)/(t_2 - t_1)$$

If the change in k is not linear between t_1 and t_2, this estimate gives only a poor representation of the real values of k between t_1 and t_2.

After the inflexion point, relative growth rate is defined as the absolute growth rate divided by the weight increment $(A - W)$ in which A is mature weight

$$-k = (dw/dt)/(A - W)$$

This relative growth rate past the inflexion point may be calculated as:

$$-k = [(W_2 - W_1)/(t_2 - t_1)]/[A - {}^1/_2 (W_2 + W_1)]$$

The values of k before and after the inflexion point are different and of opposite sign.

Cumulative growth curves are often described by mathematical *growth functions*. Sometimes a biological significance is given to the parameters in the function. By changes in parameters, environmental and genetic influences may be evaluated. The most well-known functions are:

- the monomolecular (WEINBACH 1941, BRODY 1945). This function gives a separate description of growth before and after the inflexion point
- the logistic function or autocatalytic. Firstly used to describe the growth of populations, but later often applied to describe growth of an organism (RHODES 1940, NAIR 1954, CARMON 1965, MONTEIRO and FALCONER 1966, TIMON 1968, TIMON and EISEN 1969, EISEN et al. 1969).
- the Bertalanffy function (BERTALANFFY 1957, 1960, FABENS 1965, GALL and KYLE 1968). This function is based on growth as the difference between anabolism and catabolism.
- the Gompertz function used by LAIRD et al. 1965, LAIRD and HOWARD 1967 and KIDWELL and HOWARD 1969.
  RICHARDS 1959 has shown that these four functions are each a special case of a general family of growth curves which differ primarily in the proportion of mature weight at which the inflection point occurs.
- the growth curve may also be described by orthogonal polynomials (WISHART 1938, RAO 1958, KIDWELL and HOWARD 1970). In these functions the parameters have no biological significance.

All these formulae describe the growth curve without taking into account the quantity of feed or energy intake.

BLAXTER 1968 and PARKS 1971, 1972 have developed formulae in which weight at a given age is also a function of feed or energy intake until that age.

2.2 Regulation of growth rate

An individual grows during postnatal life by taking in more nutrients than it requires to maintain its body mass. Gall 1969 and Parks 1972 also considered growth as a resultant of input and output of mass or energy by an individual at moment *t*. Blaxter 1968 and Parks 1972 related feed intake, growth rate and age. Blaxter 1968 supposed that the quantity of feed intake and the feed composition are the most important factors determining growth rate. Hence the regulation of growth rate has to be seen in relation to regulation of feed intake.

The regulation of feed intake in ad libitum feeding is firstly a negative feedback system of energy intake (Baumgardt 1969). Secondly specific characteristics of feed such as taste, smell, composition, temperature and the feeding system are of importance. Feed intake via energy is regulated by the amount of energy that is necessary for maintenance and production. In a young animal, weight increment is mainly an increase of skeletal and muscle tissue with some associated essential fatty tissue. If the animal has more productive energy available than can be utilized for these types of growth, then it will store the surplus as additional fatty tissue. The ratio of quantity of energy stored in muscle tissue to that in fatty tissue changes with aging in favour of fat tissue (Bichard 1968, Curtis 1969).

Only if feed is limited or its composition is suboptimum, there is a negative influence of feed on growth rate (Blaxter 1968).

2.3 Change of growth curve

Many scientists, for instance Brinks et al. 1964, Taylor and Craig 1965, Taylor 1968, have reported a high positive genetic correlation between weights of an animal at different life stages. It is often concluded from these high positive genetic correlations that weight in different stages is influenced by the same genes. This means that selection for a high growth rate involves an increase of mature weight (Taylor 1968). According to Bichard 1968, animals that are heavier when mature have a larger appetite, grow faster and more efficiently. But as has been pointed out, an increase of mature weight in the breeding stock involves an increase of costs (Bichard 1968, Dickerson 1970). Hence for breeding a high growth rate and a constant, or limited change in, mature weight and early sexual maturity are the desired characteristics (Dickerson 1970). This combination in meat production may be achieved by:

- crossing of males from a fast-growing line or breed with females of a small fertile line or breed (Smith 1964, Moav 1966a, b, c, Moav and Hill 1966, Bakker et al. 1974a). The disadvantage is that several lines or breeds have to be maintained and that the lower growth rate of the dam population will be introduced in the slaughter animals.
- changing the growth curve by means of selection (Bichard 1968, Taylor

1968, DICKERSON 1970). As the genetic correlations are high, the possibilities are restricted (BRODY 1945, TAYLOR and CRAIG 1965, BICHARD 1968, TAYLOR 1968). However the results of ABLANALP et al. 1963, with turkeys, and LAIRD and HOWARD 1967 and MCCARTHY 1971 with mice showed some genetic variance in the shape of the curve.

III SELECTION FOR PARAMETERS OF THE GROWTH CURVE

Growth curves may differ in mature weight (level) and in time taken to reach maturity (speed). This chapter describes the direct results of selection for parameters which represent level and speed of the growth curve.

Lines are started to select for high and low speed and for high and low level of the curve. Relative growth rate before the inflexion point is used as a parameter for speed, W56D is used for the level of the growth curve. The direct results are described. Attention is paid to the following correlated characters:
- fitness traits, also in connection with selection intensity;
- tail length as an estimate of changes in size of the skeleton;
- RG and W56D as correlated traits.

3.1 LITERATURE

3.1.1 *Selection criteria and selection methods*

In the many publications on selection for weight or growth rate in mice there is considerable variation in selection criteria and selection and mating methods.

In the historic selection experiments of GOODALE 1938 and MAC ARTHUR 1944, 1949, the selection goal was a high bodyweight at 60 days. In the more recent experiments selection was for weight at:

- 10 weeks (MCCARTHY 1971)
- 8 weeks (TIMON and MORE O'FERRALL 1966, MORE O'FERRALL and TIMON 1968, 1970)
- 6 weeks (FALCONER 1953, 1955, HULL 1960, LEGATES and FARTHING 1962, BAKER and COCKREM 1970)
- 5 weeks (MCCARTHY 1971)
- $4\frac{1}{2}$ weeks (HULL 1960, TIMON and MORE O'FERRALL 1966)
- 3 weeks (HULL 1960, DALTON and BYWATER 1963)

Selection for growth rate was at the time interval between
- 3–6 weeks (FALCONER 1960[b], LEGATES and FARTHING 1962, BRADFORD 1971, RAHNEFELD et al. 1963)
- 4–11 weeks (SUTHERLAND et al. 1970)
- 3–5 weeks (BATEMAN 1971)

GOODALE 1938 used a kind of progeny testing, while MAC ARTHUR 1944, 1949 applied a combination of individual and sib selection. In almost all other experiments mass or within family selection is applied. The within family selection in mice experiments was first used by FALCONER 1953. Animals are selected on their deviation from the litter mean of the same sex. Usually 1 male and 1 female are selected from each family. In a within family selection system of

full sibs, only 50 % of the genetic variance will be used. However the system has two important advantages, (ROBERTS 1965):

- It excludes maternal effects on the selection. This simplifies the interpretation of the results.
- As each family contributes equally to the production of the next generation, the effective population size will be double the number of parents (FALCONER 1960[a]). This reduces the inbreeding coefficient and the genetic drift variance.

The system of within family selection can easily be combined with a mating system of maximum avoidance of inbreeding (MAI). These MAI systems have been described by FALCONER 1967. The necessity to apply within family selection depends on maternal effects on the selected traits. From experiments of COX et al. 1959, YOUNG et al. 1965, MONTEIRO and FALCONER 1966 and EL OKSH et al. 1967, it may be concluded, that the sum of prenatal and postnatal maternal effects is about 70 % of total phenotypic variance in bodyweight between 12 and 21 days. MONTEIRO and FALCONER found that the maternal effects increased until 4 weeks of age. At this age the maternal effects are mostly postnatal. Later they are very much reduced by compensatory growth. According to MONTEIRO and FALCONER, this reduction was 60 % between 5 and 8 weeks. EL OKSH et al. found that from 6 weeks onwards the genetic influences were a larger percentage of the total variance than the maternal influences. MONTEIRO and FALCONER 1966 found the same from 7 weeks on.

3.1.2 *Estimation of genetic changes*

3.1.2.1 Separation of environmental trends

Genetic changes can only be estimated if they can be separated from environmental changes. In literature some techniques are discussed, which distinguish these changes (DICKERSON 1969, LEGATES 1971 and HILL 1972a, b). The methods mostly applied in selection experiments with mice are:

- striving for a *constant environment* in subsequent generations. To this a good climatization, constant feed composition and housing will contribute
- use of *diverging selection lines* in the same environment. A disadvantage is that changes in individual lines and the rate of asymmetry can not be estimated
- use of *constant genetic material* in subsequent generations. The control population is the most well-known example. The size of the control population has to be large enough to keep genetic change to a minimum. Also a good selection and mating system can contribute to this.

3.1.2.2 Estimation errors of the selectionresults

Selection experiments must be designed so that results can be estimated accurately. According to HILL 1972a two categories of errors may be distinguished in the estimation of genetic change: sampling error and bias.

Sampling error

Random genetic drift and random error determine the variance of estimation

in genetic change. Random genetic drift is defined by FALCONER 1960a as the changes of gene frequency resulting from sampling in small populations. The genetic drift variance is according to DICKERSON 1969:

$\sigma_d^2 = \sigma_G^2/N_e$ σ_d^2 = random genetic drift variance
σ_G^2 = genetic variance
N_e = effective population size.

So genetic drift variance can be restricted by increase of population size. The genetic drift variance is cumulative with increasing number of generations (DICKERSON 1969, HILL 1971, 1972a, b).

Random error variance is the variance of the population mean

$\sigma_r^2 = \sigma_P^2/M$ σ_r^2 = random error variance
σ_P^2 = phenotypic variance
M = number of independent values on which the generation mean is estimated.

This variance is not cumulative. HILL 1971, 1972a, b gives estimations for total variance and covariances of selection results per generation. However his approach is limited to a number of assumptions of which the most important are: 'Genetic and environmental variances and covariances remain constant in each population during the selection program. If there is much inbreeding or there are genes with a large effect on the quantitative trait under selection, changes in genetic variance are likely to occur. Therefore the results are probably of most relevance to experiments of only a few generations duration'.

Bias

Some factors have to be mentioned which cause an overestimation or an underestimation of genetic change in a given selection procedure:

- natural or unwitting selection in the control line
- change of dominance and epistatic effects; inbreeding effects on the population mean are an example of this. These effects are small in large effective populations. They can be eliminated if the inbreeding coefficient in selection lines and control line are equal. This occurs if the effective population size in selection lines and control line are equal (DICKERSON 1969)

$\Delta F = 1/2N_e$ (FALCONER 1960a)

- Genotype-environment interaction. The difference in genotype between selection and control line or between diverging lines increases if the selection is successful. Thus the genotype-environment effects may increase. If the control line is descended from a base population other than the selection line, this effect may also be of importance. The genotype-environment effect as a result of selection is non-random. It is a part of the genetic change and not of the random error. Only interactions of genotypic values with random fluctuations in environment per generation are a part of the non-cumulative random error (σ_r^2) (DICKERSON 1969).

3.1.2.3 Estimation of the realised heritability

In general the realised heritability is estimated with a method, described by FALCONER 1960a and RICHARDSON et al. 1968. An estimate is the regression of cumulative selection response on cumulative selection differential per generation. HILL 1971 has discussed the disadvantage of this method: the variance of population mean increases and the generation means are correlated by the genetic drift.

HILL 1972a compared several ways of estimating the realised heritability: regression of cumulative selection response on cumulative selection differential (b_c), regression of selection response per generation on selection differential per generation (b_f), ratio of total selection response to total selection differential (b_r), maximum likelihood estimation (*m.l.*). Estimates with b_c and *m.l.* had the smallest variance.

As the *m.l.* method could not be used for low values of h^2, HILL 1972a concluded that b_c was most advisable. FALCONER 1960a and RICHARDSON et al. 1968 used the variance of the regression coefficient as an estimate of the realised heritability.

$$\hat{s}_{b_c}{}^2 = (\sum_i R_i{}^2 - b_c \sum_i R_i S_i)/[(n-2) \sum_i S_i{}^2]$$

$\hat{s}_{b_c}{}^2$ = estimated variance of regression coefficient
n = number of generations
R_i = selection result in generation i
S_i = selection differential in generation i.

This gives an unbiased estimate of σ_{b_c} if the covariance between the R values is zero. HILL 1972a, b indicated that genetic drift may introduce covariances between the R values. These may cause an underestimation of the variance of the realised heritability. HILL gave estimations of the variance which take into account these covariances. However this method is restricted to the assumptions already mentioned. According to HILL they are usable in selection experiments of short duration only.

3.1.3 *Results of selection for bodyweight and growth rate*

3.1.3.1 Realised heritability

In Table 3.1 a survey is given of the selection experiments for bodyweight and growth rate. Mentioned are:
- selection criteria
- selection method
- efficiency of selection, expressed as the realised heritability
- number of generations.

ROBERTS 1965 concluded from a review of literature of selection experiments on weight that the 'genetic situation is primarily additive in nature and largely uncomplicated by interactions either genetic or environmental'. Large differences in weight may be brought about by selection. FALCONER 1960a reported a difference between a small and a large bodyweight line of 16 times the genetic standard deviation in the base population.

TABLE 3.1. Summary of selection experiments for body weight and growth rate.

References		Selection criterion		Selection method	h^2	generations
GOODALE WILSON et al.	1938 1971	L.[1] weight	60 d.	Progeny testing	0.32	10
MACARTHUR	1949	L. weight	60 d.	Mass + sib.	0.24	7
MORE O'FERRALL et al.	1970	L. weight	56 d.	Mass	0.12	12
FALCONER	1953	L. weight	42 d.	Within fam.	0.22	11
FALCONER	1953	S. weight	42 d.	Within fam.	0.49	11
HULL	1960	L. weight	42 d.	Within fam.	0.57	5
LEGATES et al.	1962	L. weight	42 d.	Within fam.	0.13	15
LEGATES et al.	1962	S. weight	42 d.	Within fam.	0.42	15
BAKER et al.	1970	L. weight	42 d.	Mass	0.38	4
HULL	1960	L. weight	31 d.	Within fam.	0.44	5
MORE O'FERRALL et al.	1970	L. weight	31 d.	Mass	−0.17	12
HULL	1960	L. weight	21 d.	Within fam.	0.74	5
LEGATES et al.	1962	L. litterweight	12 d.	Within fam.	0.04	15
LEGATES et al.	1962	S. litterweight	12 d.	Within fam.	0.18	15
EISEN	1972	L. litterweight	12 d.	Within fam.	0.11	10
SUTHERLAND et al.	1970	L. growth rate	28–77 d.	Mass	0.22	9
RAHNEFELD et al.	1963	L. growth rate	21–42 d.	Mass	0.24	17
DALTON	1967	L. growth rate	21–42 d.	Within fam.	0.22	13
BRADFORD	1971	L. growth rate	21–42 d.	Mass	0.24	19
FALCONER	1960b	L. growth rate	21–42 d.	Within fam.	0.26	7
FALCONER	1960b	S. growth rate	21–42 d.	Within fam.	0.42	7

[1] L = large
S = small

3.1.3.2 Asymmetrical selectionresults

The experiments of, for instance, FALCONER 1953 and LEGATES and FARTHING 1962 (Table 3.1) showed that selection for large bodyweight (large line) was less efficient than selection for small bodyweight (small line). This was also found in selection for other traits, for instance litter size (FALCONER 1960a). This asymmetrical response can be concluded from the difference in realised heritability between the large and the small line.

FALCONER 1955, 1960a discussed some reasons for this asymmetry:

- unequal selection differentials, caused by differences in natural selection, fertility or variance. If the comparison is based on realised heritabilities these effects are eliminated.
- genetical asymmetry in the base population. This concerns the degree of dominance and the gene frequencies in the base population
- selection for heterozygotes (dominance) in one of the lines. The selection results diminish if the gene frequencies approach the genetic equilibrium. If the selection is for additive genetic values in the opposite line, selection may continue until fixation occurs
- inbreeding depression. The inbreeding percentage increases during the selection experiment, especially if the effective population size is small. This con-

tributes to the asymmetry if the inbreeding depression favours one of the selection goals
- selection may change maternal effects.

Mostly it is difficult to isolate the origins of asymmetrical response (FALCONER 1960a and ROBERTS 1965). The heritability, calculated from comparison of relatives is approximately the mean of heritabilities estimated in the divergent lines (FALCONER 1960a). Thus the predicted selection response of selection for high production may be larger than the realised response, if the prediction is based on heritabilities estimated from covariance between relatives.

3.1.3.3 Results of long-term selection

The frequency of allels may increase by selection until fixation. In this situation one may expect the genetic variance to diminish to zero, and continuing or back selection to be without results, unless new variability occurs by mutation or crossbreeding (FALCONER 1960a, ROBERTS 1966a). The selection limit can be reached without the genetic variance being zero. This occurs if selection is in favour of heterozygotes or if the natural selection is in equilibrium with artificial selection (ROBERTS 1966a).

ROBERTS 1966a, b, 1967a, b gave an extensive analysis of the limits of selection for bodyweight at six weeks. He used the data of MAC ARTHUR 1949, FALCONER 1953, 1960b, FALCONER and KING 1953. ROBERTS stated the following conclusions:
- selection limits are reached in 10–30 generations
- these limits are unstable; back selection is possible
- total response in one direction is 2–6 times the phenotypic standard deviation or 3–12 times the additive genetic standard deviation.

The conclusions are in good agreement with experiments for other selection traits: LEGATES and FARTHING 1962 (bodyweight at 42 days), SUTHERLAND et al. 1970 (growth rate in 4–11 weeks), WILSON et al. 1971 (bodyweight at 60 days), BRADFORD 1971 (growth in 3–6 weeks) and EISEN 1972 (litter weight at 12 days).

The theoretical background of selection limits are discussed by ROBERTSON 1960 and HILL and ROBERTSON 1966. One of the main conclusions was that the time to reach the selection limit is related to the effective population size.

3.1.4 *Correlated effects of selection for bodyweight and growth rate*

Selection for bodyweight or growth rate will cause changes in other traits. Correlated selection results are described in a number of selection experiments. FALCONER 1953 estimated a positive genetic correlation between bodyweight at 6 weeks and taillength at this age (0.62 and 0.57). This is in agreement with the results of COCKREM 1959 and BAKER and COCKREM 1970.

MAC ARTHUR 1949 and FALCONER 1953 reported that there were more days between mating and littering in the first littering in the small line than in the large line. FALCONER suggested that this could be caused by a longer oestrus cycle and a higher percentage of matings without fertilization. LAND 1970 and BRADFORD 1971 found that selection for growth rate in 3–6 weeks increased the

number of ovulated ova. The percentage of pregnancy decreased and prenatal death increased in the later generations. This may have consequences for the realised genetic correlation between bodyweight and litter size in continuing selection for bodyweight. Also FOWLER and EDWARDS 1960 found a variation in relation between both traits in several selection lines of FALCONER 1953, 1960b. MAC ARTHUR 1949, FALCONER 1953 and RAHNEFELD et al. 1966 found an increase of litter size after selection for high growth rate and bodyweight and a decrease in litter size after selection for low growth rate and bodyweight. However ROBERTS 1961 found that in a life-time the total number of young weaned of the large line was only half that of the small line. The average number of litters in the large line was $4\frac{1}{2}$ and in the small line 11.

Dams in the large line supplied a significantly better prenatal environment for their young than dams in the small line. The maternal effect, estimated from the 12-day litter weight, increased in the large line and decreased in the small line (FALCONER 1953, YOUNG et al. 1965, WHITE et al. 1968). FALCONER as well as WHITE et al. reported a greater change in the small line. According to WHITE et al. this may be caused by inbreeding depressions on maternal influences.

3.2 MATERIAL AND METHODS

3.2.1 *Selection criteria*

If absolute growth rate is used as a *criterion for speed of the growth curve*, a large correlated effect in mature weight has to be expected (TAYLOR 1968). However it is preferable that the covariance of the parameter of the speed of the growth curve and mature weight is low. BRODY 1945 concluded that the time to double the weight before the inflexion point is inversely proportional to the parameter for the instantaneous relative growth rate (k_1)

$$W_t = Ae^{k_1 t} \text{ (BRODY 1945)} \qquad W_t = \text{weight at age } t$$
$$ln\ W_t = ln\ A + k_1 t \qquad A = \text{weight at age 0}$$
$$t = (ln\ W_t - ln\ A)/k_1$$

Time to double the weight is:

$$(t_2 - t_1) = (ln\ 2W_1 - ln\ A)/k_1 - (ln\ W_1 - ln\ A)/k_1$$
$$(ln\ 2W_1 - ln\ W_1)/k_1 = ln\ 2/k_1 = 0.693/k_1$$

After the inflexion point, the time to halve the difference between mature weight A and actual weight W_t is inversely proportional to the instantaneous relative growth rate after the inflexion point (k_2)

$$W_t = A - Be^{-k_2 t} \text{ (BRODY 1945) } B = \text{integration constant}$$
$$A - W_t = Be^{-k_2 t}$$
$$ln\ (A - W_t) = ln\ B - k_2 t$$
$$t = [ln\ B - ln\ (A - W_t)]/k_2$$

Time to halve $(A-W_t)$ is:

$$\begin{aligned}(t_2-t_1) &= [ln\ B-\ ln\ (A-W_t)]/k_2 - [ln\ B-\ ln\ 2(A-W_t)]/k_2\\ &= [ln\ 2(A-W_t)/k_2 - [ln\ (A-W_t)]/k_2\\ &= ln\ 2/k_2 = 0.693/k_2\end{aligned}$$

The values of k_1 and k_2 are different and of opposite sign.

From these deductions it follows that the speed of the growth curve can be described by the parameters k. Hence the relative growth rate is chosen as a criterion for speed of the curve. The relative growth before the point of inflexion is chosen, as the growth in this period is of most economic importance in meat production. The relative growth rate is estimated as:

$$\begin{aligned}\text{RG} &= [(W_2-W_1)/(t_2-t_1)]/[(W_2+W_1)/2]\\ \text{of RG} &= (ln\ W_2-ln\ W_1)/(t_2-t_1)\\ W_2 &= \text{weight at age } t_2\\ W_1 &= \text{weight at age } t_1\end{aligned}$$

Preliminary investigations, with daily weight estimations in the base population, showed that the point of inflexion in this population occurred at an age of 29–30 days. This agrees with results of FOWLER 1958 and MONTEIRO and FALCONER 1966. This investigation also showed that the variation in RG was maximum between 21 and 29 days. FOWLER 1958 found the differences in relative growth rate between lines selected for bodyweight to be maximum between weaning and 30 days.

Therefore RG is determined as the average relative growth rate in the age interval of 21 and 29 days.

$$\text{RG} = [(W29D-W21D)/8]/[(W29D+W21D)/2]\cdot 100$$

So RG is expressed in percentages.

Mature weight might be the best *criterion to select for level of the growth curve*. But mature weight, defined as the weight after which no further weight increase occurs, will not be reached before 26–52 weeks (ROBERTS 1961). One of the reasons is, that after the completion of skeletal and muscle tissue, fat growth is almost linear (CURTIS 1969). So mature weight as a selection criterion has two main disadvantages:

- the breeding animals become infertile
- generation interval increases considerably.

One can select for mature weight by indirect selection for weight at a younger age, because the correlations between weights at an older age are very high (TAYLOR 1968). ROBERTS 1961 concluded that 'the proportional differences between the large and the small stocks are substantially the same at six weeks and at mature weight', and that the same genetic system controls both six weeks and mature weight.

As mating of mice, in our experiments, took place directly after the age of 8 weeks, bodyweight at 8 weeks was chosen as the selection criterion for level of the growth curve.

3.2.2 *Breeding stocks*

In 1968, the base population came from the Swiss random bred population (Cpb:SE) of the Central Institute for the Breeding of Laboratory Animals TNO (CPB) at Zeist. This population was kept under specific pathogen free (SPF) conditions. The history of this population is described in a CPB report (CPB 1967). The effective population size at CPB was about 10,000.

The base population (55 males and 55 females) was chosen from the whole stock in Zeist. Only one animal per litter was sampled. The mice were housed individually. Between 18 and 61 days of age the weight and feed intake were estimated daily (MINNAARD 1970). At an age of 61 days, 55 pairs were mated at random. From the offspring of these matings the parents of the first generation of control and selection lines were chosen at random. These lines were:

- a control line (C);
- a line selected for high RG between 21–29 days (RGH);
- a line selected for low RG between 21–29 days (RGL);
- a line selected for high W56D (W56H);
- a line selected for low W56D (W56L).

Only first litters were used.

In the control line 16 pairs were mated per generation. From each litter 1 male and 1 female were chosen at random. Also in RGH and RGL 16 pairs were mated. In these lines a system of within family selection was applied, because maternal effects on RG were expected to be of importance at 21–29 days. Per litter the male and female that showed the most deviation from the fullsib family mean per sex were selected. In W56H and W56L mass selection was applied, because it was assumed that the maternal effects on bodyweight were very much reduced at 8 weeks. This assumption is confirmed by the results of COX et al. 1959, YOUNG et al. 1965, MONTEIRO and FALCONER 1966 and EL OKSH et al. 1967. EL OKSH et al. concluded, that from 6 weeks onwards genetic effects were of more importance than the total maternal effects. MONTEIRO and FALCONER 1966 found the same from 7 weeks onwards. In these lines the 32 females and the 16 males that showed most deviation from the population mean were chosen. The only restriction was that not more than 3 mice per sex were selected from a litter.

The results of these selection methods can be predicted (FALCONER 1960a). Within family selection:

$$R_w = i \cdot \sigma_P \cdot h^2 \cdot {}^1/_2 \sqrt{(n-1)/[n(1-t)]}$$

R_w = selection response per generation
i = selection intensity
σ_P = phenotypic variation
h^2 = heritability
n = family size
t = intraclass correlation

TABLE 3.2. Mating system in lines C, RGH and RGL.

Mice in generation				
n + 1 Litternumber		n Litternumber		
		female		male
1	=	1	*	2
2	=	3	*	4
3	=	5	*	6
4	=	7	*	8
5	=	9	*	10
6	=	11	*	12
7	=	13	*	14
8	=	15	*	16
9	=	2	*	1
10	=	4	*	3
11	=	6	*	5
12	=	8	*	7
13	=	10	*	9
14	=	12	*	11
15	=	14	*	13
16	=	16	*	15

Mass selection:

$$R = i \cdot \sigma_P \cdot h^2$$

In C, RGH and RGL lines, a mating system of maximum avoidance of inbreeding was applied (FALCONER 1967). The scheme is presented in Table 3.2. Two mice extra were selected from a reciprocal mating in the scheme when a mated pair did not produce offspring or the litter died. If it was impossible to choose them in the reciprocal mating, the mice were selected from the most unrelated pair. This occurred very rarely. It is clear that this reduced selection intensity very much.

In C, RGH and RGL lines, the inbreeding coefficient could be predicted from:

$\Delta F = 1/2Ne \quad Ne = 4N/(2 + \sigma_k^2)$ (FALCONER 1960a)
ΔF = inbreeding coefficient
Ne = effective population size
N = number of parents
σ_k^2 = variance of family size

If the complete mating scheme of Table 3.2 could be realised, then

$\sigma_k^2 = 0$ and $Ne = 64$
$\Delta F = 1/128 = 0.78\%$ per generation.

In W56H and W56L the mice were mated in a harem system of 1 male and 2 females. Matings were at random with avoidance of fullsib and halfsib matings.

If it is assumed that there is a Poisson distribution of family size and all matings are fertile, then the inbreeding coefficient can be predicted:

$$\Delta F = 1/2Ne$$
$$1/Ne = 1/(4Nf) + 1/(4Nm)$$
$$\Delta F = 1/(8Nf) + 1/(8Nm)$$
$$= 1.17\% \text{ per generation}$$

Nf = number of females
Nm = number of males

ΔF is overestimated because complete random mating is assumed in the prediction.

3.2.3 *Experimental conditions*

During the 14 generations of selection the conditions were as follows:
temperature : 22 ± 1 °C,
ventilation : 10 times room volume per hour,
daylength : kept at 12 hours,
feeding : ad libitum pellets (Hope Farms RMH-B 10 mm),
tap water : ad libitum,
relative humidity: not controlled.

Mating was as soon as possible after the age of 8 weeks. As mating was always on Tuesday, not more than 10% of litters were born at the weekends. This was of much importance because the weights were always estimated at fixed ages. The males were left with the females for 17 days. As a consequence the generations in the 5 lines were synchronized. Identification was by toe-cutting. From 12 days onwards the young had the opportunity to take pellets from the bedding. After weaning at 21 days, the mice were raised in groups of four per cage of the same sex.

Housing was in Makrolon cages type Hulskamp-Komeco MAK 180, with sterilized sawdust as bedding. Management was always done by the same two persons.

3.2.4 *Data*

In 14 generations in each line, the following observations were made:
- bodyweight at 21 (W21D), 29 (W29D), 42 (W42D) and 56 (W56D) days
- tail length at 56 days
- litter size estimated within 24 hours after birth
- number of males and females weaned at 21 days
- number of days between mating and littering.

Deduced from these observations were:
- RG between 21 and 29 days
- survival percentages between 0 and 56 days.

The accuracy of weight and tail length estimations has been published elsewhere (BAKKER et al. 1974b). One of the conclusions was that the measurement error for weight and tail length was under 1% of the mean.

3.2.5 *Methods*

Firstly the mean and standard deviations of a number of traits were estimated by combining the data from the first generations of the 5 lines. The distributions of the selected traits RG and W56D were described. Sex and litter effects on these traits were quantified and the correlation coefficients between traits were estimated.

In the analysis of the selection results attention was paid to the changes in the control line. Regression coefficients of means on generation number were estimated to investigate whether a systematic change, for instance by increasing inbreeding depression or change in environment, occurred.

Changes in mean value of the selection criteria RG and W56D were evaluated in RGH, RGL, W56H and W56L. These values per generation were expressed as deviations from the control. The realised heritabilities were calculated for RG and W56D from the regression of cumulative selection response on cumulative selection differential. Calculations were made in individual selection lines with mean values expressed as deviations from the control and in diverging selection lines. The coefficients of regression were forced through the origin, as the differences between the lines in the base population were zero per definition.

The standard deviation of the realised heritability estimates were calculated as the standard deviation of the regression coefficient according to FALCONER 1960a and RICHARDSON et al. 1968. HILL 1972a, b suggested that these values might be underestimated because there was a covariance between selection responses in the subsequent generations. The method of the standard deviation of the regression coefficient was preferred, as the selection was long-term (14 generations), while the methods suggested by HILL are for short-term selection experiments only.

Finally the changes in tail length and fitness traits were estimated.

3.3 RESULTS

3.3.1 *Results in the base population*

An exact description of the base population was necessary, because the evaluation of the results of the selection was based upon the changes in the selection lines, compared to the base population.

In the first generation of the 5 lines, all data, except the data of the fertility characters, were obtained from unselected mice. Thus the data of the mice of all 5 lines could be united, so that the analysis could be based upon a large number of observations. The material consisted of data of 466 females and of 494 males, born in 99 litters.

The following data were involved in the analysis:

- the weights at 21, 29, 42 and 56 days
- the tail length at 56 days
- the relative growth rate (RG)
- the growth per day between 21–29 (P_1), 29–42 (P_2) and 42–56 (P_3) days
- the size of the litter in which the mice were born.

3.3.1.1 Means and standard deviations per sex

The averages and standard deviations of the traits are presented in Table 3.3. The sex differences were tested with Student's t-test. The sex differences in weight were not significant at 21 days. At 29, 42 and 56 days, however, significant sex differences in weight occurred. This is illustrated in Figure 3.1. The vertical lines represent plus or minus one standard deviation about the average at the age concerned. Also in the relative growth, the absolute growth and the tail length significant differences occurred.

From the significant sex effect on traits it was concluded, that the results of both sexes could not be combined. Therefore the further analysis was done separately by sex. The coefficient of variation in W56D is 10.20 % for the females and 9.09 % for the males. For the RG the coefficients of variation were 20.71 % and 13.51 %.

3.3.1.2 Frequency distributions and normality tests

To give an impression of the distribution of the traits which were selected for, the frequency distributions were made for W56D (Fig. 3.2) and for RG (Fig. 3.3). In Table 3.4, the normality tests of Fisher (De Jonge 1964), on deviations of the normal distribution, were given. In general the distributions had some skewness to the right, except for the RG of the males. This deviation by the males was caused by some extremely low RG values. These extremes were qualified by the test of Doornbos (De Jonge 1964) as outliers. Without these outliers this distribution had a skewness to the right too. Also there was a tendency towards too pointed distributions. This was small or even absent in

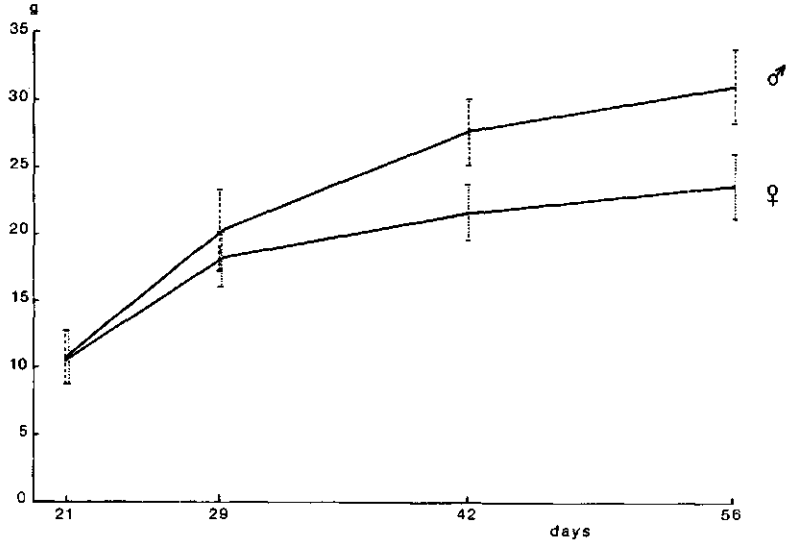

Fig. 3.1. Means and standard deviations of weights in the base population, by sex

TABLE 3.3. Means and standard deviations of traits in the first generation of each line by sex.

Character	466 ♀♀		494 ♂♂		t-test
	$\bar{x}$	s	$\bar{x}$	s	
W21D	10.49	2.04	10.59	2.00	n.s.
W29D	17.22	2.22	20.16	2.99	***
W42D	21.50	2.13	27.61	2.48	***
W56D	23.52	2.40	31.02	2.82	***
RG	6.18	1.28	7.84	1.06	***
Taillength	9.55	0.38	10.10	0.44	***
Littersize dam	10.18	2.28	10.47	2.29	n.s.
Growth P1	0.84	0.14	1.19	0.20	***
Growth P2	0.33	0.12	0.57	0.15	***
Growth P3	0.15	0.09	0.24	0.11	***
Growth total	0.37	0.06	0.58	0.07	***

n.s. = not significant
*** = $p \leqslant 0.005$

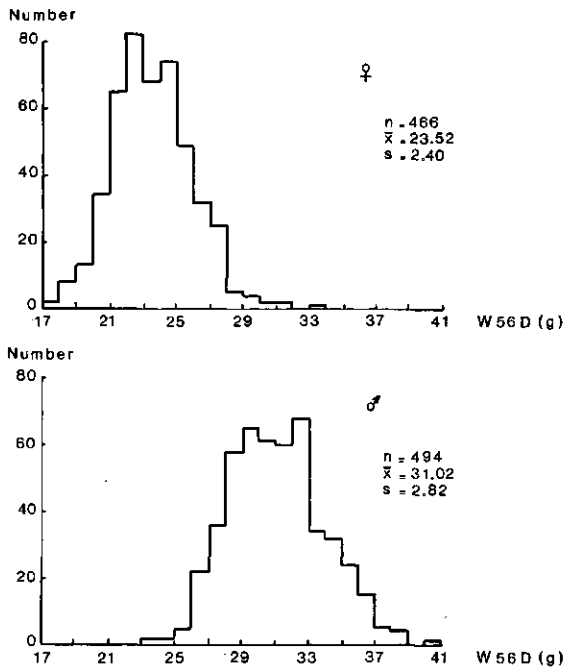

FIG. 3.2. The frequency distribution of W56D, by sex

W56D. However in RG, especially for the males, the tendency was quite clear. It was not possible to give the cause of the deviation. Natural selection against extreme small mice at an early age might have caused the skewness to the right.

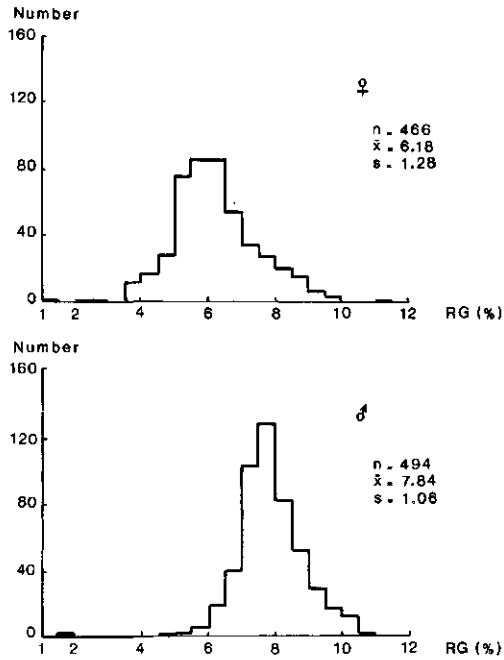

FIG. 3.3. The frequency distribution of RG, by sex

TABLE 3.4. Normality test of the distributions of RG and W56D.

	Skewness (G_1)[1]		Kurtosis (G_2)[1]	
	♀♀	♂♂	♀♀	♂♂
W56D	$G_1 = 0.43^{**}$	$G_1 = 0.21^{*}$	$G_2 = 0.57^{*}$	$G_2 = -0.32^{n.s.}$
RG	$G_1 = 0.32^{**}$	$G_1 = -0.93^{**}$	$G_2 = 0.92^{**}$	$G_2 = 6.68^{**}$

[1] Normality tests of Fisher (DE JONGE 1964)
n.s. = not significant
* = $p \leqslant 0.05$
** = $p \leqslant 0.01$

Unfavourable maternal effects could have contributed to this. To explain the cause for the deviations in RG was impractical, because of the sex differences in G_1 values. As the distributions were never very asymmetrical or had more than one point, it was not necessary to apply parameter-free methods of analysis (DE JONGE 1964).

3.3.1.3 Litter influence on the traits

To evaluate how the values of the same traits estimated on litter mates, were correlated analysis of variance was done to calculate the litter influence.

TABLE 3.5. Analysis of variance to estimate litter influence on the traits.

	Females				Males			
	Between	Within	Total	F	Between	Within	Total	F
d.f.	98	363	461	98 363	98	391	489	98 391
Characters								
W21D	16.97	0.58	4.06	29.30	16.30	0.68	3.81	24.17
W29D	17.46	1.50	4.89	11.66	34.13	2.34	8.71	14.59
W42D	13.55	2.04	4.49	6.63	18.65	2.79	5.97	6.69
W56D	15.05	3.16	5.68	4.77	22.91	3.94	7.74	5.81
RG	6.25	0.37	1.61	17.10	3.61	0.48	1.10	7.55
Taillength	0.43	0.07	0.14	6.25	0.68	0.08	0.20	8.57
Litter size dam	24.01	–	5.11	–	24.80	–	4.97	–
Growth P_1	3.81	0.63	1.31	6.04	6.99	1.18	2.34	5.93
Growth P_2	5.49	1.43	2.29	3.84	9.67	1.93	3.49	5.00
Growth P_3	2.37	1.34	1.56	1.77	4.05	1.82	2.27	2.23
Growth total	11.89	2.66	4.62	4.47	13.88	3.29	5.41	4.22

All F values: significant $p \leqslant 0.005$

This litter influence consists of:
- a deviation of the average of the additive genetic value of the parents from the population mean
- non-additive genetic effects by specific interaction (dominance and epistatic)
- maternal effects, partially determined genetically
- influences of the litter itself, for instance the litter size.

The last two points can determine most of the variance, especially in traits observed about at the age of weaning. With these data the different sources of litter influences could not be calculated. An impression could be obtained from the ratio of the between litter variance to the within litter variance. In Table 3.5, the analysis of variance of the same traits as mentioned in Table 3.3 is presented. The analyses were done per sex. All F values mentioned in Table 3.5 (except, of course, of the litter size of the mother) were significant ($p \leq 0.005$). The F values for the weights decreased with increasing age. This was true both for the females and the males. Probably because of the compensatory growth after the weaning, the variation by maternal influences and litter size was reduced. The same was true for the growth in the successive periods. If we assume that the genetic influence is a relative constant, maternal and litter size influences were decreased markedly at 56 days. In view of the age span, it might be assumed that maternal and litter size influences on RG were of importance too.

3.3.1.4 Correlations between the traits

Maternal and litter effects may have an important influence on the phenotypic correlations, especially between traits, observed before or immediately after weaning. By calculating the correlations within litters, these systematic environmental effects were excluded. However by doing this the genetic co-

TABLE 3.6. The correlations between traits estimated within litters, by sex.

Trait		W21D	W29D	W42D	W56D	RG	Tail length	Litter[1] size dam	Growth P_1	Growth P_2	Growth P_3	Growth total period
	♀		0.78	0.46	0.40	−0.42	0.31	−0.53	0.24	−0.24	0.04	−0.03
W21D	♂		0.73	0.52	0.41	−0.41	0.18	−0.49	0.27	−0.18	−0.04	−0.01
	♀			0.60	0.50	0.23	0.38	−0.39	0.80	−0.30	0.03	0.19
W29D	♂			0.63	0.43	0.31	0.23	−0.41	0.86	−0.35	−0.15	0.14
	♀				0.76	0.16	0.37	−0.34	0.49	0.58	−0.07	0.16
W42D	♂				0.74	0.11	0.30	−0.31	0.49	0.51	−0.51	0.58
	♀					0.12	0.37	−0.30	0.39	0.39	0.60	0.90
W56D	♂					0.01	0.31	−0.30	0.29	0.42	0.56	0.91
	♀						0.08	0.43	0.76	−0.04	−0.02	0.32
RG	♂						0.03	0.31	0.75	−0.21	−0.13	0.19
	♀							−0.01	0.30	0.05	0.12	0.27
Taillength	♂							−0.03	0.18	0.11	0.09	0.26
Littersize[1]	♀								0.18	0.09	0.01	0.16
dam	♂								−0.17	0.25	−0.05	0.06
Growth	♀									−0.23	0.00	0.32
P_1	♂									−0.35	−0.17	0.20
Growth	♀										−0.11	0.54
P_2	♂										−0.02	0.54
Growth	♀											0.63
P_3	♂											0.63

[1] Total correlation

Significance:	$p \leqslant 0.05$	$p \leqslant 0.01$
d.f. females 363	$r \geqslant 0.104$	$r \geqslant 0.136$
males 391	$r \geqslant 0.100$	$r \geqslant 0.130$

TABLE 3.7. The total correlations between traits, by sex.

Trait		W21D	W29D	W42D	W56D	RG	Tail length	Litter size dam	Growth P_1	Growth P_2	Growth P_3	Growth total period
	♀		0.86	0.65	0.53	−0.80	0.26	−0.53	−0.11	−0.34	−0.09	−0.35
W21D	♂		0.88	0.68	0.57	−0.63	0.24	−0.49	0.43	−0.51	−0.06	−0.16
	♀			0.75	0.65	−0.39	0.37	−0.39	0.42	−0.40	−0.05	−0.09
W29D	♂			0.78	0.61	−0.20	0.31	−0.41	0.80	−0.57	−0.13	−0.01
	♀				0.85	−0.28	0.34	−0.34	0.31	0.30	−0.07	0.33
W42D	♂				0.84	−0.15	0.43	−0.31	0.63	0.08	−0.07	0.44
	♀					−0.19	0.37	−0.30	0.31	0.25	0.46	0.61
W56D	♂					−0.18	0.41	−0.30	0.46	0.14	0.48	0.72
	♀						−0.05	0.43	0.65	0.18	0.11	0.53
RG	♂						−0.01	0.31	0.41	0.13	−0.09	0.32
	♀							−0.01	0.28	−0.08	0.15	0.17
Taillength	♂							−0.03	0.30	0.07	0.07	0.29
Littersize	♀								0.18	0.09	0.01	0.16
dam	♂								−0.17	0.25	−0.05	0.06
Growth	♀									−0.18	0.07	0.45
P_1	♂									−0.44	−0.18	0.19
Growth	♀										−0.03	0.59
P_2	♂										0.12	0.59
Growth	♀											0.60
P_3	♂											0.62

Significance:	$p \leqslant 0.05$	$p \leqslant 0.01$
d.f. females 461	$r \geqslant 0.092$	$r \geqslant 0.120$
males 489	$r \geqslant 0.089$	$r \geqslant 0.117$

variance between the litter means of the traits were eliminated too. The correlations calculated within litters and the total correlations were estimated per sex. The within litter correlations are presented in Table 3.6. Table 3.7 gives the total correlations per sex. The correlations were tested for significance with $p \leq 0.05$ and $p \leq 0.01$. From Table 3.6 it follows that in general there were only small sex differences in the correlations. The same was true for the total correlations between most traits (Table 3.7). However there were striking sex differences in the correlations of the growth between 21 and 29 days with the other traits. A possible explanation might be that compensatory growth began later in the males. Correlations between the weights at different ages were significantly positive ($p \leq 0.01$). The correlations increased with decreasing time-intervals. Total correlations between weights and RG were all significantly negative ($p \leq 0.01$). The within litter correlation, calculated between RG and W21D were significantly positive ($p \leq 0.01$) and between RG and W29D significantly negative ($p \leq 0.01$). In both cases there was auto-correlation. The correlations of RG with W42D and W56D were positive, but low. In the last case the correlation was not significant in the males; in the females significant for $p \leq 0.05$. The correlation between the tail length and the weights was significantly positive ($p \leq 0.01$). There was no significant correlation between tail length and RG. The total correlations of the litter size of the mother were all significantly negative with the weight and positive with the RG ($p \leq 0.01$). As mentioned before non-genetic correlations are of importance in this. The correlation between the growth in the succeeding periods was mostly negative and low.

3.3.2 *Selection response*

The results of the selection can be estimated from the modifications in population means in the succeeding generations of selection. The generation means of RG in the C, RGH and RGL lines are presented in Table 3.8. Table 3.9 shows the generation means of W56D in C, W56H and W56L lines. In these tables, the standard deviations and the numbers of observations are mentioned too. The averages were calculated as unweighted means of the means per sex. The standard deviation was calculated from the within sex variance:

$$s_d = \frac{(n_1-1)s_1^2 + (n_2-1)s_2^2}{(n_1 + n_2 - 2)}$$

n_1 = number of females $\qquad s_1^2$ = variance in the females

n_2 = number of males $\qquad s_2^2$ = variance in the males.

In figures 3.4 and 3.5, the average RG and average W56D per generation in the control line C are presented graphically. The regression coefficient of the average on the generation number was negative both for the relative growth and the weight. This tendency was significant ($p \leq 0.05$) for the relative growth, while the regression coefficient for the weight was not significant. The graph of the average relative growth per generation in RGH and RGL is given in Figure 3.6.

TABLE 3.8. Means and standard deviations of relative growth by generation in C, RGH and RGL.

	Control			RGH			RGL		
Generation	n	$\bar{x}$	s	n	$\bar{x}$	s	n	$\bar{x}$	s
0	140	7.62	0.95	140	7.62	0.95	140	7.62	0.95
1	144	6.90	1.10	140	7.57	1.36	140	6.92	1.32
2	138	6.58	1.08	126	6.50	1.47	134	6.44	0.98
3	122	6.35	1.24	123	6.21	0.65	141	6.86	0.80
4	133	6.48	1.63	84	6.26	1.45	137	6.19	1.20
5	91	6.36	1.30	78	6.37	1.15	74	6.20	1.06
6	127	7.27	0.82	121	6.56	0.90	96	6.43	1.07
7	114	6.43	0.92	88	7.11	1.20	101	6.48	1.00
8	73	6.25	1.09	75	6.35	1.12	91	6.18	1.34
9	98	6.73	1.38	107	6.69	1.12	92	6.11	1.26
10	125	6.60	1.50	69	6.57	0.94	102	5.94	1.12
11	129	6.00	1.15	126	6.52	1.37	113	5.32	0.98
12	93	5.40	1.70	86	6.08	0.87	132	5.14	1.08
13	107	5.78	0.87	110	6.71	1.15	119	5.35	1.29
14	110	6.37	0.97	130	6.59	1.27	117	4.86	1.04

TABLE 3.9. Means and standard deviations of bodyweight at 56 days by generation in C, W56H and W56L.

	Control			W56H			W56L		
Generation	n	$\bar{x}$	s	n	$\bar{x}$	s	n	$\bar{x}$	s
0	140	26.53	2.76	140	26.53	2.76	140	26.53	2.76
1	144	27.61	2.25	322	27.25	2.74	214	27.27	2.65
2	138	27.03	3.08	239	29.85	2.91	247	25.90	2.51
3	122	26.40	3.35	261	29.14	2.63	184	24.61	2.21
4	133	27.46	2.54	239	30.56	2.91	236	23.46	2.36
5	91	27.47	2.70	217	32.15	3.21	155	21.15	2.60
6	127	26.93	2.34	179	33.74	3.30	169	21.15	2.54
7	114	27.54	2.58	167	34.58	3.45	141	20.22	2.26
8	73	26.63	3.07	137	35.78	3.59	95	18.33	2.45
9	98	28.16	2.93	140	37.02	3.68	141	18.31	2.49
10	125	26.42	2.25	188	37.38	3.90	86	16.97	2.41
11	129	27.47	2.42	211	38.22	3.63	121	17.80	2.44
12	93	26.57	2.41	232	37.28	4.64	151	15.48	2.35
13	107	25.85	2.36	115	41.44	3.92	64	15.18	1.93
14	110	24.64	2.47	223	37.52	3.38	114	15.92	2.77

The averages were expressed as deviations from the control line, to exclude systematic environmental influences. The regression coefficient of the average RG on the generation number was in RGH 0.03 ± 0.01 ($p \leq 0.05$). In RGL the regression coefficient was -0.06 ± 0.01 ($p \leq 0.01$).

Figure 3.7 shows average bodyweights at 56 days in W56H and W56L. The values were also expressed as deviations from the control line. The regression coefficient of the average on the generation number was 0.99 ± 0.05 in W56H and -0.88 ± 0.05 in W56L (both significant $p \leq 0.01$).

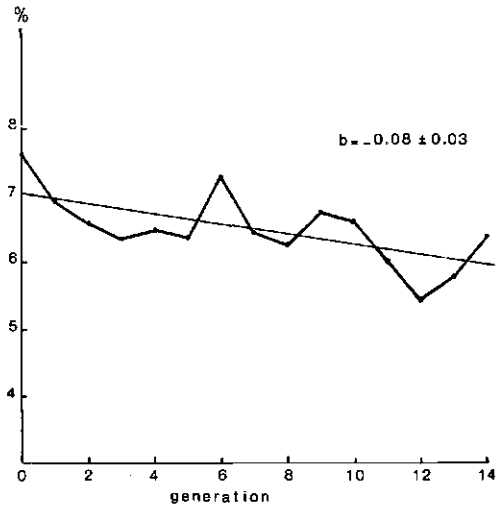

FIG. 3.4. Average relative growth in the control line

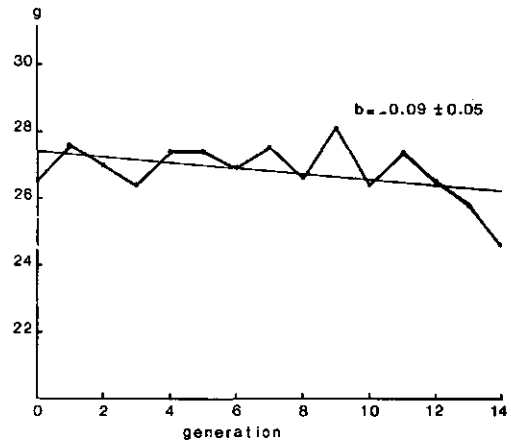

FIG. 3.5. Average bodyweight at 56 days in the control line

In the Tables 3.10 and 3.11 the changes in means and standard deviations for generations are given. There was no significant trend in the variation of the RG in C, RGH and RGL lines. The variation in W56D did not change significantly in C and W56L, but there was a significant increase of the variation ($p \leq 0.01$) in the W56H.

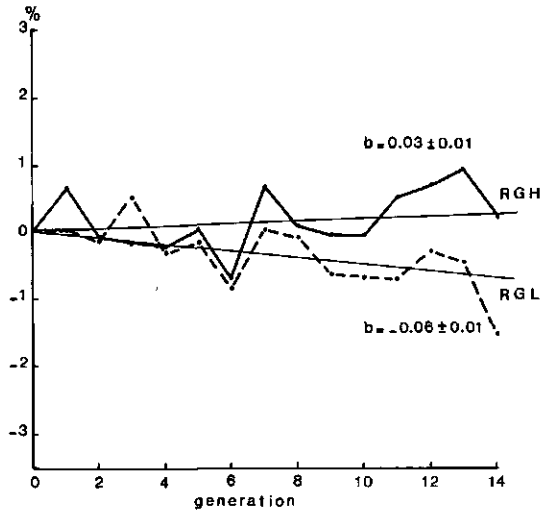

FIG. 3.6. Average relative growth in RGH and RGL as deviations from the control line

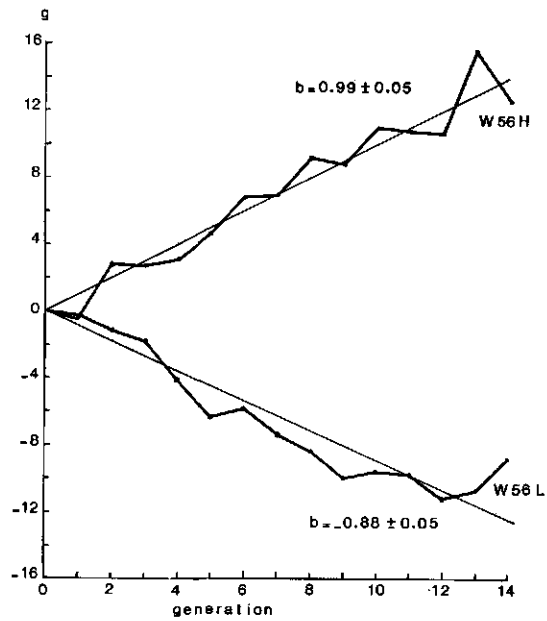

FIG. 3.7. Average bodyweight at 56 days in W56H and W56L as deviations from the control line

TABLE 3.10. Regression coefficients of relative growth generation means and variations on generation number.

	Mean (%)	Variation (%)
Control	$-0.08^{**} \pm 0.03$	$0.01^{n.s} \pm 0.02$
RGH[1]	$0.03^{*} \pm 0.01$	$-0.00^{n.s} \pm 0.01$
RGL[1]	$-0.06^{**} \pm 0.01$	$0.01^{n.s} \pm 0.01$

[1] Means corrected for deviations in control
n.s = not significant
* = $p \leqslant 0.05$
** = $p \leqslant 0.01$

TABLE 3.11. Regression coefficients of means and variations of body weight at 56 days on generation number.

	Mean (g)	Variation (g)
Control	$-0.09^{n.s} \pm 0.05$	$-0.03^{n.s} \pm 0.02$
W56H[1]	$0.99^{**} \pm 0.05$	$0.10^{**} \pm 0.02$
W56L[1]	$-0.88^{**} \pm 0.05$	$-0.02^{n.s} \pm 0.04$

[1] Means corrected for deviations in control
n.s = not significant
* = $p \leqslant 0.05$
** = $p \leqslant 0.01$

3.3.3 *Selection differential*

Tables 3.12 and 3.13 summarize the selection differential for RG (C, RGH and RGL) and W56D (C, W56H and W56L). Unwittingly there was some selection in the control line both for the relative growth and the weight. This might be explained by deviations in the random choice. On an average the selection

TABLE 3.12. Selection differential in relative growth by generation in C, RGH and RGL.

Generation	C	RGH	RGL
1	−0.09%	0.43%	−0.77%
2	0.22	0.42	−0.69
3	−0.25	0.41	−0.68
4	−0.41	0.35	−0.93
5	0.02	0.52	−0.58
6	0.02	0.34	−0.69
7	−0.22	0.51	−0.53
8	−0.16	0.49	−0.95
9	−0.18	0.30	−0.51
10	−0.11	0.33	−0.47
11	0.08	0.27	−0.74
12	−0.56	0.19	−0.86
13	0.46	0.21	−0.79
Average	−0.09	0.37	−0.71

TABLE 3.13. Selection differential in bodyweight at 56 days by generation in C, W56H and W56L.

Generation	C	W56H	W56L
1	0.41 g.	4.34 g.	−3.07 g.
2	0.23	3.97	−3.13
3	0.34	3.55	−2.60
4	0.29	3.99	−3.02
5	0.34	4.11	−2.83
6	−0.34	4.36	−3.10
7	0.15	4.08	−2.47
8	−0.16	4.06	−1.56
9	−0.20	3.70	−2.41
10	0.35	5.16	−1.91
11	0.07	5.01	−2.21
12	−0.53	6.30	−2.51
13	0.22	3.44	−0.82
Average	0.09	4.31	−2.43

differential was −0.09 % for RG and +0.09 gram for W56D. Comparison of the selection differentials in RGH and RGL showed strikingly that the selection differential in RGH was on an average nearly half of that in RGL.

The selection differential in RGH declined. However the within litter variation per sex was in RGH not much smaller than in RGL (females 0.79 and 0.80 respectively and males 0.64 and 0.66 respectively). The selection differential was in W56H higher than in W56L (4.31 against 2.43). In the estimates of the realised heritabilities of RG and of W56D, the selection differentials in the selection lines were corrected for the selection differential in the control line.

3.3.4 *The realised heritabilities*

The realised heritability was estimated from the regression coefficient of cumulative selection response on cumulative selection differential

$$h_e^2 = b_{R_{cum}\, S_{cum}} = \sum_i R_{cum\,i}\ S_{cum\,i} / \sum_i S_{cum\,i}^2$$

Corrections for environmental influences on the selection differential and the selection results were made in two ways:

- expressing the means as deviations from the mean in the control line
- basing the estimations on the difference between the divergent lines.

The cumulative selection differentials and results were calculated per generation by adding the values in the divergent lines.

Both methods were used to estimate the realised heritability for RG and for W56D.

Figure 3.8 shows the difference in total selection differential between RGH and RGL. There was a large variation in selection differential per generation. In the last generation the selection differential was even negative in RGH. This was caused by a combination of a small uncorrected differential in RGH and a large correction factor in the control. An estimate of the heritability gave for

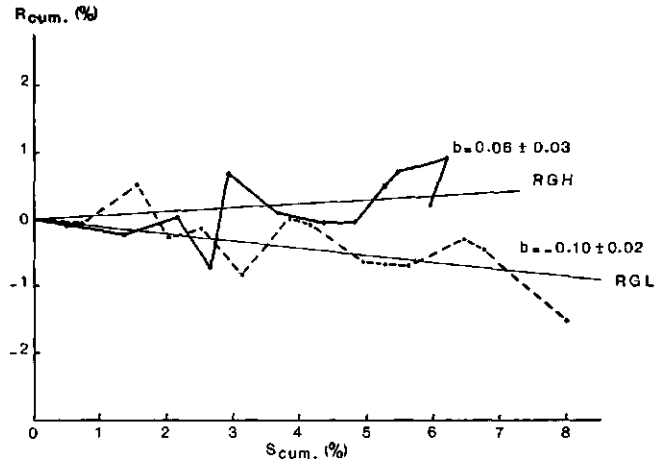

FIG. 3.8. Cumulative selection response and cumulative selection differential of relative growth in RGH and RGL

RGH a value of 0.06 $\pm$ 0.03 ($p \leq 0.05$). For RGL the realised heritability was 0.10 $\pm$ 0.02 ($p \leq 0.01$). The realised heritability estimated from the divergent lines was 0.08 $\pm$ 0.01 ($p \leq 0.01$). Figure 3.9 shows that correction for environmental influences in this situation gave a much more regular course of R_{cum} and S_{cum}. This followed also from the standard deviation of h^2, which was substantially lower in the estimation from the divergent lines.

The estimation of the realised heritability for W56D in W56H and W56L is given in Figure 3.10. The total selection differential was in W56H almost twice that in W56L. The realised heritability was 0.28 $\pm$ 0.01 ($p \leq 0.01$) for W56H and 0.35 $\pm$ 0.02 ($p \leq 0.01$) for W56L. The selection for a low weight was more effective than for a high weight. An estimation of h^2 from the divergent lines W56H and W56L (Figure 3.11) gave 0.31 $\pm$ 0.01 ($p \leq 0.01$).

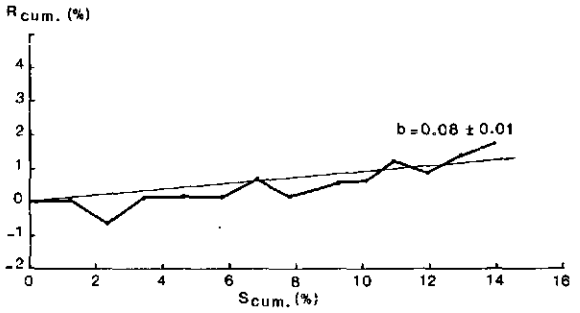

FIG. 3.9. Cumulative selection response and cumulative selection differential in relative growth estimated from the divergence of RGH and RGL

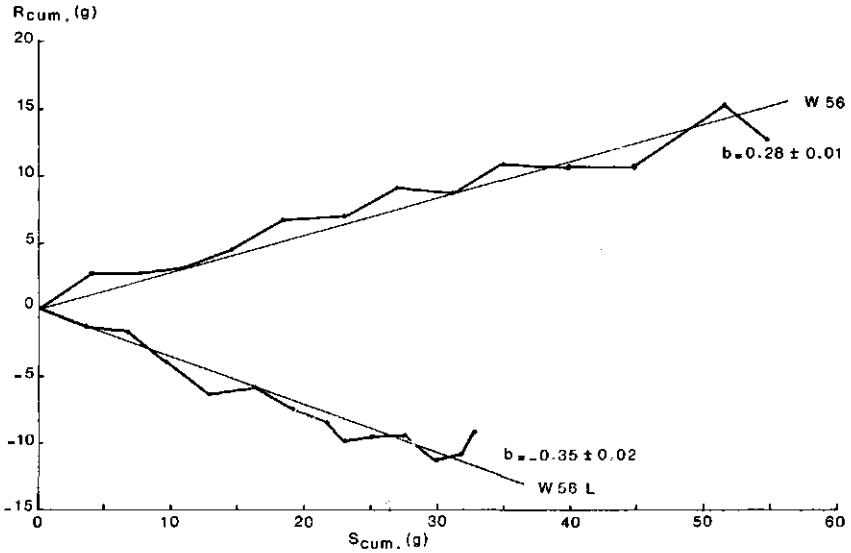

FIG. 3.10. Selection response and selection differential of weight at 56 days in W56H and W56L

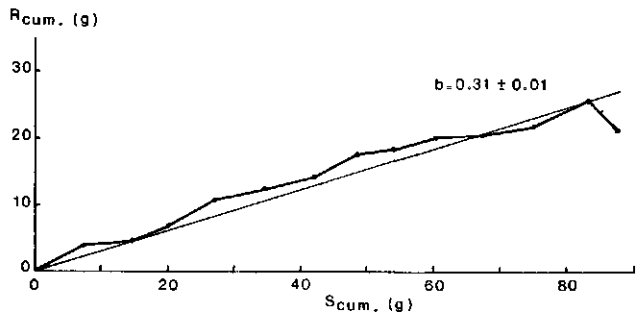

FIG. 3.11. Cumulative selection response and cumulative selection differential in weight at 56 days estimated from the divergence of W56H and W56L

3.3.5 *Correlated effects*

Selection for RG and for W56D had consequences for a number of other traits. The weights at – or the growth rate between – different ages may change, the fertility may alter, while the body composition and the growth pattern of the body components may differ between selection lines.

In this section the changes in W56D, RG, tail length, fertility and survival percentage are examined.

3.3.5.1. RG and W56D as correlated traits

Figure 3.12 shows, that the selection for W56D resulted in rather definite changes in RG, both in W56H and in W56L. Selection for high RG resulted in

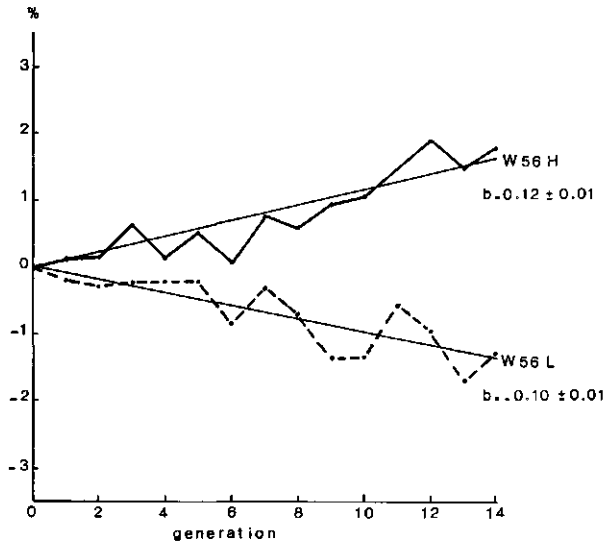

FIG. 3.12. Average relative growth in W56H and W56L as deviations from the control line

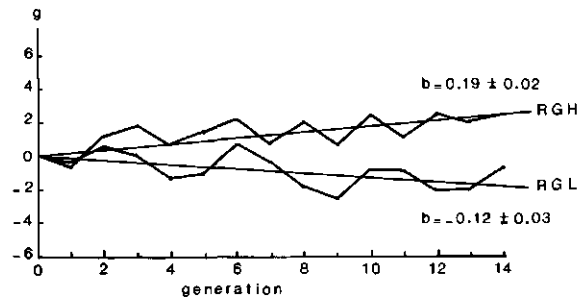

FIG. 3.13. Average weight at 56 days in RGH and RGL as deviations from the control line

an increase of W56D, while selection for low RG gave a decrease in W56D (Figure 3.13). However the changes (expressed as deviations from the average in the control line) were rather small. In Table 3.14, the changes in RG and W56D are given by means of the regression coefficients. In all four selection lines there were significant changes ($p \leq 0.01$).

With the direct (R) and correlated (CR) selection results in RG and W56D the genetic correlation could be estimated.

$$r_A^2 = \frac{CR_{RG}CR_{W56D}}{R_{RG}R_{W56D}} \quad \text{(FALCONER 1960a).}$$

If the direct and correlated results were estimated from the differences between divergent lines in generation 14, this gave:

$r_A^2 = 0.24$ and $r_A = 0.49$.

TABLE 3.14. Regression coefficients of relative growth and body weight at 56 days on generation number after selection for bodyweight and relative growth.

	Correlated response[1] in	
	Relative growth	Body weight
RGH	—	0.19** ± 0.02
RGL		−0.12** ± 0.03
W56H	0.12** ± 0.01	
W56L	−0.10** ± 0.01	—

[1] Corrected for deviations in control
** $p \leq 0.01$

Because the correlated result of RG (CR_{RG}) was strongly determined by the large differences in maternal performance and litter size between W56H and W56L, r_A was probably strongly overestimated.

3.3.5.2 The effect of selection on other traits

Besides the changes in W56D and RG as correlated effects, the changes in other traits have been observed. Attention was paid to the tail length and a number of traits, bearing upon fertility and survival of the mice. Table 3.15 shows the changes that occurred between the divergent lines. These changes were expressed as regression coefficients of the difference between divergent lines per generation on the generation number. For tail length the regression coefficients were significant ($p \leq 0.01$). The only other significantly different regression coefficients were between W56H and W56L in litter size at birth.

The Figures 3.14–3.19 give an indication of the absolute changes in the mentioned traits. Rather large differences in litter size between W56H and W56L occurred. In both lines the number of days between mating and littering increased, while the total percentage successful matings declined, sometimes under 50 percent. This all resulted in a limitation of the total number of mice to select from. The differences between RGH and RGL were small for all these traits.

TABLE 3.15. Regression coefficients of divergence in several correlated characters on generation number.

Character	Divergence of	
	RGH and RGL	W56H and W56L
Taillength	0.03** ± 0.01	0.19** ± 0.01
Days between mating and littering	$0.02^{n.s}$ ± 0.05	$0.02^{n.s}$ ± 0.09
Number of litters	$-0.12^{n.s}$ ± 0.07	$0.32^{n.s}$ ± 0.28
Littersize at birth	$0.08^{n.s}$ ± 0.07	0.29** ± 0.05
Survival percentage between 0–56 days	$0.09^{n.s}$ ± 0.51	$-0.08^{n.s}$ ± 0.28
Number of mice at 56 days	$0.04^{n.s}$ ± 1.39	$4.00^{n.s}$ ± 2.43

n.s = not significant
** $p \leq 0.01$

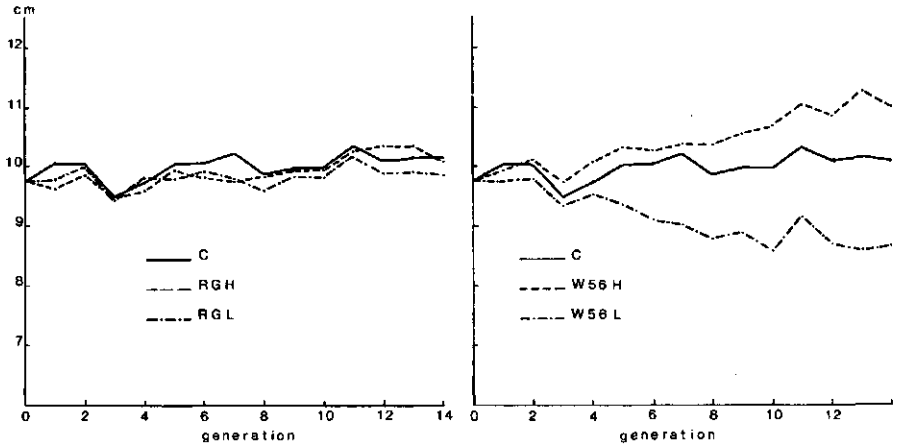

FIG. 3.14. Average tail length at 56 days, by line

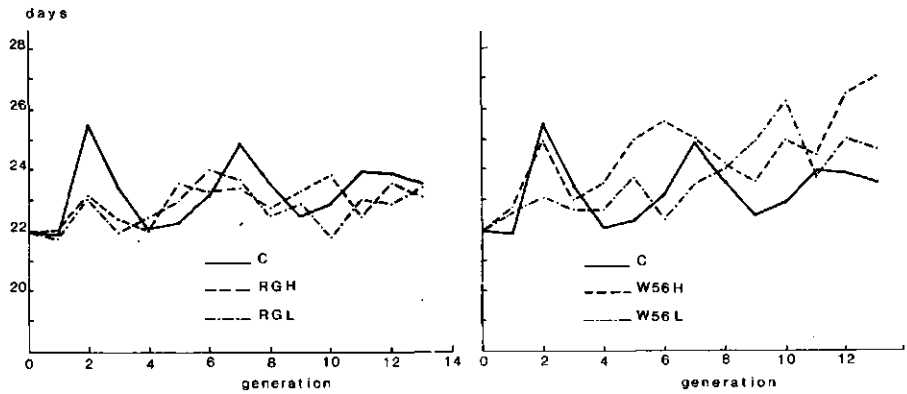

FIG. 3.15. Average number of days between mating and littering, by line

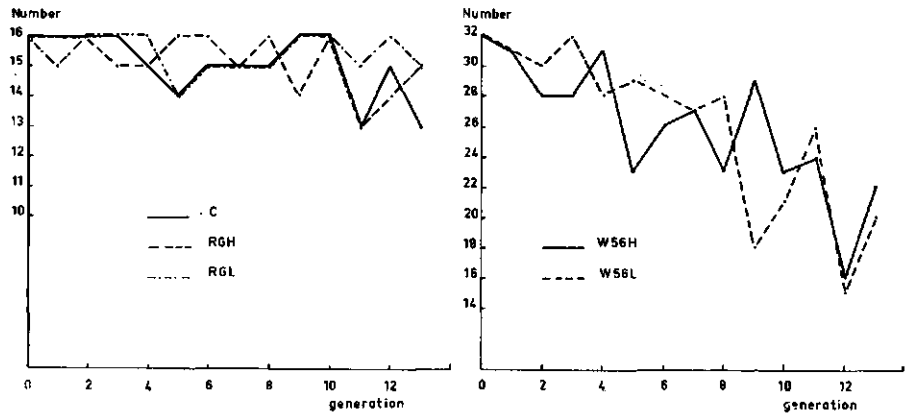

FIG. 3.16. Number of litters born, by line

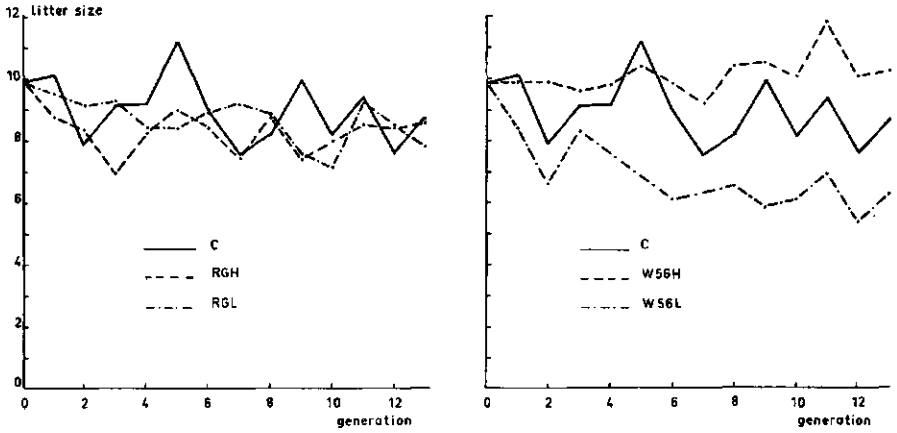

FIG. 3.17. Average littersize at birth, by line

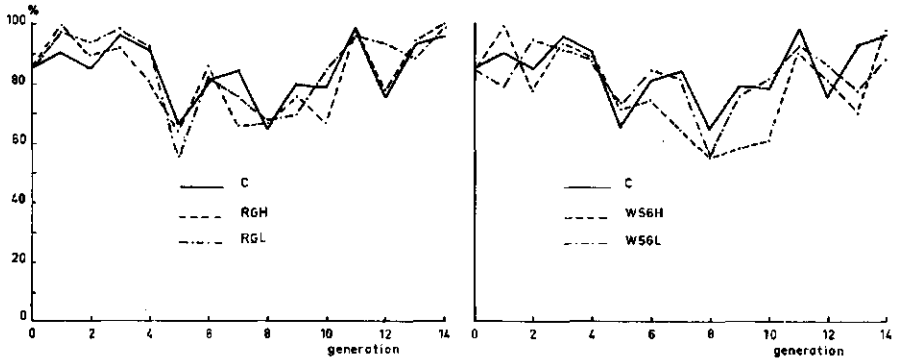

FIG. 3.18. Survival rate between 0 and 56 days, by line

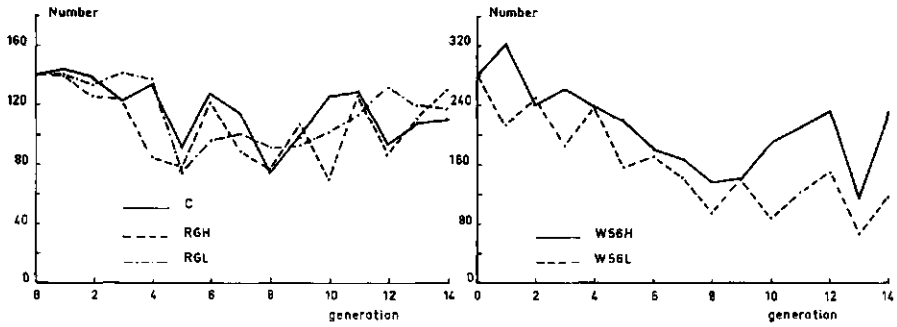

FIG. 3.19. Number of mice at 56 days, by line

IV COMPARISON OF GROWTH CURVES WITH THE LOGISTIC FUNCTION

An impression of the differences in the growth curve between sex and between lines can be read directly from a graph. As an example growth curves are given for C, RGH, RGL, W56H and W56L in generation 14, in Figure 4.1. A comparison of sexes and of lines by these graphs has limitations. Comparison is always made on the basis of time. However during selection large differences could have occurred during the time taken to reach mature weight. A comparison of the weights at the same absolute age would then be at quite different relative ages. This can be seen clearly from the difference between W56H and W56L. A comparison based on weights for age may be also biased by differences in mature weight. Therefore it is advisable to describe the growth curve by a mathematical function. A comparison of the growth curves in various lines can be based on the parameters in this function.

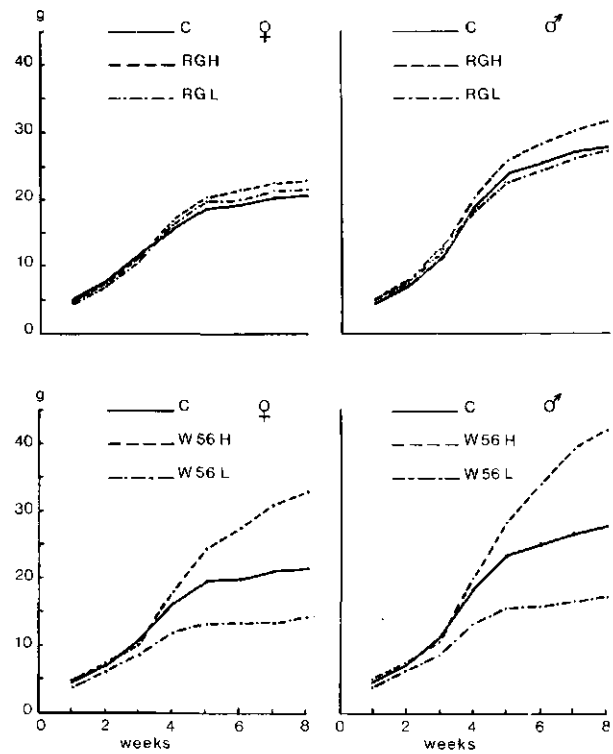

FIG. 4.1. Average weights in C, RGH, RGL, W56H and W56L by age and sex (generation 14)

This chapter reviews on the use of growth functions in mice; then a tentative choice of a function will be made. This will be tested with our own data. After a definite choice, the growth curves of the lines are compared on the basis of the parameters in this function.

4.1 Literature

Many attempts have been made to simulate growth curves by mathematical functions. Richards 1959 and Parks 1971 and 1972 distinguished functions which take into account certain fundamental postulates about the growth process (theoretical functions) and functions, which lack these theories of growth as a background. These latter functions are only used to fit the growth curve as well as possible. These are often third or fourth degree polynomials.

The choice between so-called theoretical functions and polynomials depends on the purpose of these functions. If the parameters are for physiological interpretation, only theoretical functions can be used. If maximum fit is the aim, then polynomials are often more suitable.

An important advantage of description of the growth curve with functions is, that interpolation and extrapolation become possible. Interpolation is allowed in both types of functions, while functions of the polynomial type only can be used safely within the interval of the observations, and can not be extrapolated (Parks 1971).

Rao 1958 and Kidwell and Howard 1970 used orthogonal polynomials to calculate differences in growth curves. Kidwell et al. 1969 and Kidwell and Howard 1970 found that the growth curves of 4 inbred lines and all crosses between them could be described equally satisfactorally by a theoretical function (in this case Gompertz) and a third degree polynomial. Because extrapolation is not possible and because the parameters have no biological significance, polynomials could not be used in our experiments. Hence they will not be discussed.

The four most well-known of the so-called theoretical functions are:
- Monomolecular
- Autocatalytic
- Gompertz
- Bertalanffy.

The *monomolecular function* describes the growth by two separate functions; one before and one after the inflexion point. The functions of Weinbach 1941, Brody 1945 and Taylor 1965 were deduced from the monomolecular. Mostly function after the inflexion point is used:

$W_t = A(1 - be^{-kt})$

W_t = weight at age t
A = asymptotic weight
k = rate constant, which determines the spread of the curve along the time axis
b = intergration constant

In this formula the growth rate is $k(A - W)$. As the observed weights of the mice in this experiment range over both parts of the growth curve, the monomolecular function was not used in this experiment.

The *autocatalytic* or *logistic* function is symmetrical with respect to the inflexion point t_i. The formula is

$$W = A/(1 + be^{-kt})$$

which is based on the linear decrease of relative growth rate $(dW/dt)/W$ with increasing weight. The point of inflexion is at $W_{t_i} = A/2$. The growth rate is $kW(A - W)/A$. Originally this formula was often used to describe and predict the growth of populations. It was deduced from a theoretical model (autocatalytic). Later it was much used to describe the growth of individuals.

In mice research the formula has been used by among others CARMON 1965, MONTEIRO and FALCONER 1966, TIMON 1968, TIMON and EISEN 1969 and EISEN et al. 1969. NAIR 1954 suggested that it is probably the most used function in biological research.

The *Gompertz* function is based on an exponential decay of relative growth with time. The formula is

$$W_t = Ae^{-be^{kt}}$$

The point of inflexion is at $W_{t_i} = A/e = 0.368\ A$. Growth rate is $kW\ ln\ (A/W)$. The formula was used to describe growth curves of mice by LAIRD et al. 1965, LAIRD and HOWARD 1967 and KIDWELL and HOWARD 1969.

The *Bertalanffy* function is described by BERTALANFFY 1960 and FABENS 1965. It is based on the definition of growth as the difference between anabolism and catabolism.

$$dw/dt = aW^m - cW$$

a = constant of anabolism
c = constant of catabolism
m = weight exponent.

BERTALANFFY assumed that anabolism is proportional to $W^{2/3}$. Then the growth function is.

$$W_t = A(1 - be^{-kt})^3$$

Inflexion point is at $W_{t_i} = 8/27\ A$.
The function was used by GALL and KYLE 1968 to describe growth of mice.
RICHARDS 1959 concluded that the formula is restricted to values of $m<1$.

The *Richards* function (RICHARDS 1959) is an extension of the Bertalanffy function. The function becomes empirical because A, k, b and m are estimated from the data, while m is 2/3 in the Bertalanffy function.

The Richards formulae are

$$W^{1-m} = A^{1-m}(1 - be^{-kt}) \text{ for } m<1$$

and $$W^{1-m} = A^{1-m}(1 + be^{-kt}) \text{ for } m>1$$

The four described functions can be deduced by substituting different values for m in the Richards function.

$m =$ 0 is the monomolecular function
$m =$ 2/3 is the Bertalanffy function
$m \rightarrow$ 1 is the Gompertz function ($m = 1$ gives no solution)
$m =$ 2 is the logistic function.

Increasing m gives an increasing percentage of A at the inflexion point. When m is between 0 and 1, the curves are transitional in form between monomolecular and Gompertz; between 1 and 2, the transition is between Gompertz and logistic (RICHARDS 1959). The Richards function proves that there is a strong relationship between these formulae.

Sometimes these functions are compared in literature. For the estimation of a growth function FABENS 1965 distinguished between the choice of the function and the estimation of the parameters in this function, so that the fit is as good as possible. This fit can be judged by graphical methods (subjective) as was done by BRODY 1945 and RICHARDS 1959, or by statistical techniques.

The deviations have also to be random. LAIRD et al. 1965 compared growth curves, such as the logistic and the Gompertz formula. They concluded that some asymptotic functions can be used to describe postnatal growth until early maturity. During this growth, weight increased by a factor of 2^4–2^6. They also found, that the Gompertz function gave a better description than the logistic one for longer parts of the growth curve, for instance prenatal and postnatal growth of caviae (0.062–400 grams or 10,000 fold). EISEN et al. 1969 compared the logistic, Gompertz and Bertalanffy functions for the description of growth in mice, selected for large and small bodyweight at 6 weeks and in a control line. The logistic function gave the best fit for both sexes in the large and control line. Growth curve of males in the small line was equally well described by the three functions. The growth of the females in this line was best described by the Bertalanffy function. The coefficients of variation of the parameters of the functions were significantly smallest in the logistic function. The phenotypic and genetic correlations between the same parameters in the three functions were high. So probably conclusions would be the same if another function was used. For the best fit EISEN et al. 1969 preferred the logistic function.

TIMON and EISEN 1969 compared the logistic and the Richards function to describe the growth curve of mice selected for growth rate between 3 and 6 weeks and a control. The fit of both functions was equal. Also the estimations of mature weight agreed well; however probably both were underestimated. The shape parameter m in the Richards function did not significantly differ from 2. This means, that for these data logistic and Richards functions were the same.

CARMON 1965, MONTEIRO and FALCONER 1966 and TIMON 1968 concluded that the logistic function describes postnatal growth better than other functions. CARMON 1965 found that the logistic function determined 96% of the variance of the weekly estimated weights between 0 and 56 days. TIMON 1968 estimated the weights at 1, 21, 42, 56, 70 and 84 days. The logistic function determined 98.14% of the variance in weight.

Several authors reported a systematic pattern of deviations. (CARMON 1965, LAIRD and HOWARD 1967 and TIMON 1968). These deviations were mostly related to weaning and maternal or malnutrition effects.

4.2 METHODS

4.2.1 *Choice of the growth function*

In this study the growth function was chosen in two stages:

- a tentative choice, based on comparisons of functions in the literature
- testing of the tentative chosen function with our own data. If the fit was as good as reported in literature, the function was used for the description of the growth curves of the lines.

Based on the results of comparisons of functions reported in literature the logistic function was tested with our own data. Arguments were:

- the fit of the logistic function on growth of mice between birth and 8–12 weeks is at least as good as other functions.
- parameters of this function can be used in this study:
  k = an estimation of rate of growth change
  A = an estimation of asymptotic (mature) weight
  t_i = an estimation of the inflexion point at $A/2$
- with this function there are more possibilities to compare our own results with literature than with other functions (MONTEIRO and FALCONER 1966, TIMON 1968, EISEN et al. 1969, TIMON and EISEN 1969).

4.2.2 *Estimation of parameters of the logistic function*

NAIR 1954 gave a review of methods to estimate the parameters of the logistic function.

$$W_t = A/(1 + be^{-kt})$$

One of the methods of parameter estimation is based on the relation between relative growth and weight (Fisher's method).

$$(dW/dt)/W = k(1 - W/A)$$

or $$dln\ W/dt = k(1 - W/A)$$

Fisher's method consists of an estimation of relative growth rates at ages of weight observations and the calculation of the regression coefficient of relative growth rate on weights at the diverse ages.

The $dln\ W/dt$ at age t_i is estimated from the average of $(ln\ W_i - ln\ W_{i-1})$ and $(ln\ W_{i+1} - ln\ W_i)$.

So the regression coefficient of $(ln\ W_{i+1} - ln\ W_{i-1})/2$ on W_i is calculated. This coefficient equals k/A and the constant of the regression line is k. Fisher's method assumes that the age intervals are equal.

Parameter b determines the age scale of the curve specified by A and k. NAIR 1954 cited a method of Rhodes to estimate b. The logistic function can be written in linear form after ln transformation.

$$\begin{aligned} be^{-kt} &= (A/W - 1) \\ ln\ b - kt &= ln\ (A/W - 1) \\ ln\ b &= ln\ (A/W - 1) + kt \end{aligned}$$

b can be estimated by substituting average $ln\ (A/W - 1)$ and average t values.

Average of $ln\ b = k(N-1)/2 + \Sigma_{t=0}^{N-1}\ ln\ (A/W_t - 1)\ /N$

$t = 0, 1, 2, \ldots, (N-1)$ are the moments of observations.

Estimation of the inflexion point is as follows:

$$\begin{aligned} dW/dt &= kW(1 - W/A) \\ d^2W/d^2t &= k(1 - 2W/A) \end{aligned}$$

Inflexion point is at $d^2W/d^2t = 0$
Then: $2W/A = 1$ and $W = A/2$
So age at inflexion t_i is deduced as follows:

$$\begin{aligned} A/2 &= A/(1 + be^{-kt_i}) \\ be^{-kt_i} &= 1 \\ ln\ b - kt &= 0 \\ t_i &= ln\ b/k \end{aligned}$$

Thus a relation between A and t_i and between k and t_i is introduced by the methods of estimations. The correlation between t_i and A will be positive and between t_i and k negative. The method of calculation of A and k shows that the relation between them is inpredictable. However some predictions can be made as to what happens with A and k, if a number of observations are made at the stage of compensatory growth. Then weight is relatively low and growth is relatively high, so relative growth rate will be high. This will increase the regression coefficient (k/A). Consequentially A will be underestimated and k will be overestimated. If observations are made over a long section of the growth curve, this effect will be reduced. TIMON and EISEN 1969 suggested that the mature weight is underestimated; but this depends on the section of the growth curve that is used in the estimation. From the method of estimation it follows that an underestimation of A means an underestimation of the inflexion point too.

4.2.3 *Analysis of parameters of the growth function*

The logistic function was tested in the base population. The residual variance of the correlation between calculated and observed weights was used as a

criterion for the fit. Various intervals of weight estimation were compared to evaluate the effect on the fit. Calculations were done per sex. Afterwards the selection lines were compared by means of the parameters of the logistic function.

- The regression coefficients of mean parameter values per generation on generation number were calculated to investigate how the parameters changed during selection.
- Line and sex differences of parameters were further analysed and tested in generations 13 and 14. Two generations were analysed to see whether the conclusions in both generations were the same.
- The correlation coefficients between the parameters were estimated.
- Growth curves of lines were compared after excluding differences in mature weight and time taken to mature weight.

4.3 Fitting of the logistic function to weights in the base population

In the base population, which was previously described, daily weights were observed. With these data the parameters of the logistic function were estimated per individual and calculated weights at each age could be deduced.

4.3.1 *Results*

Figure 4.2 shows the mean observed and calculated weight per sex, between 18 and 61 days. In Table 4.1 the percentages of residual variance are presented with increasing interval of weight observation. From this table, it follows that the curve fits equally well for both sexes ($p>0.05$) according to Student's t-test.

Correlations between observed and calculated weights did not change if the intervals of weight observations were varied from 1 to 7 days (test of Tukey (De Jonge 1964)).

4.3.2 *Discussion*

The frequency of observations could be decreased to once a week while residual variance did not increase. The fit of the logistic function to weights in this base population was as good as reported in literature. This could be concluded from the comparison of the correlations in Table 4.1 with the results of Carmon 1965 and Timon 1968. The higher correlation estimated by Timon might be explained by the larger section of growth curve that was described. The observation scheme could have also diminished the effect of the compensatory growth. Timon estimated weight among others at 1, 21 and 42 days. This means that the mean part of the compensatory growth is in between the observations, because at 6 weeks the phase of compensatory growth is almost over (Laird and Howard 1967).

Figure 4.2 shows systematical deviations. Weights are overestimated until 4 weeks, underestimated from 4–5 weeks, overestimated again from 5–7 weeks;

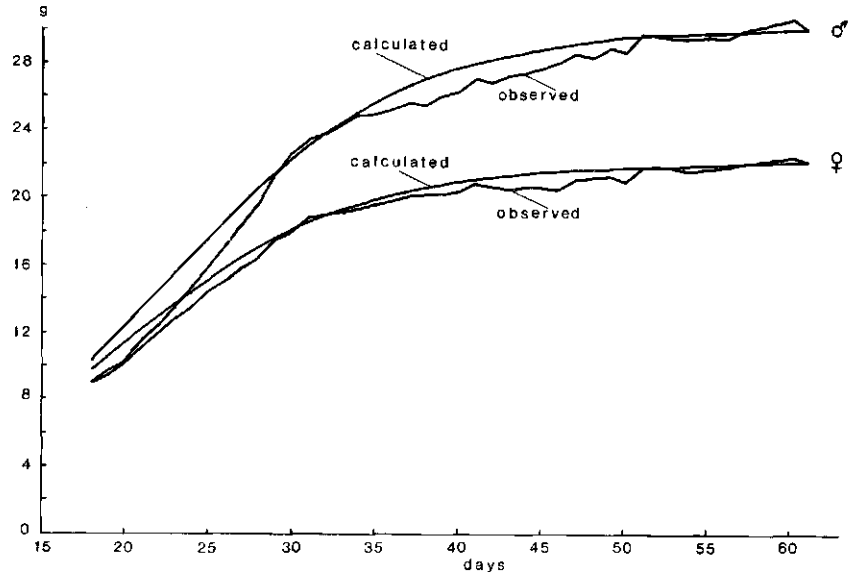

FIG. 4.2. Calculated and observed growth curves in the base population, by sex

TABLE 4.1. Fitting of the logistic function with increasing interval, by sex.

Interval length	Number of observations per sex	females		males		Sex differences
		Correlation coefficient	Residual variance	Correlation coefficient	Residual variance	
1 day	2420	0.97	5.06%	0.98	3.63%	n.s
2 days	1210	0.97	5.30	0.98	3.78	n.s
3 days	825	0.97	5.92	0.98	4.34	n.s
4 days	605	0.98	4.62	0.97	5.62	n.s
5 days	495	0.97	5.26	0.97	5.29	n.s
6 days	440	0.97	5.57	0.98	4.36	n.s
7 days	385	0.97	5.44	0.97	5.52	n.s

n.s = not significant ($p>0.05$)

weights at an older age were again underestimated. Hence mature weight will be underestimated too.

The explanation might be as follows: young mice have a shortage of feed intake at the end of the suckling period. The milk production of the dam is maximum at the end of the second week. The ability of the young to take in concentrates increases, but then a second disturbing event occurs in casu weaning. The young animals are placed in a strange environment and take time to adapt. These simultaneous events result in a phase of inhibited growth. This agrees with the results of LANG and LEGATES 1969 and of STANIER and MOUNT 1972 who

reported two growth peaks; one at about 12–14 days and one at about 30 days. As the animals become adapted, a period of increased growth rate takes place. In this period the animals catch up with their original genetically determined growth curve (LAIRD and HOWARD 1967). Of course this is only true with ad libitum feeding.

The observations in the base population started at weaning, so growth was at a relatively low level then. After that a phase of high, partly compensatory, growth followed. As a consequence k will be overestimated and A will be underestimated.

From the analysis in the base population the following conclusions could be drawn:
- the results of the fit of the logistic function to weight in the base population were in agreement with the results in literature
- there were no significant differences between sexes
- the residual variance was not increased by an increase of the interval of observation from 1–7 days
- it is advantageous to observe the weights over a large section of the growth curve
- there were systematic deviations from the observed growth curve.

4.4 PARAMETERS OF LOGISTIC FUNCTION IN SELECTION LINES

From the analysis in the base population it was concluded, that the growth curves in the selection lines could be described with the logistic function. Therefore weights from animals in the selection lines were observed weekly between 1 and 8 weeks in generation 6 until 14. The parameters of the logistic function (A, k and t_i) were estimated per individual from the observed weights.

4.4.1 *Changes in parameters during selection*

For a good comparison of the lines it is necessary that there are no differences between lines in the accuracy of description by the logistic function. The residual variances in percentages are presented per line and per sex in Table 4.2. In general the residual variances were low in comparison with the base population (Table 4.1). However some fluctuations occurred. The residual variance in females was slightly higher than in males. In C, RGH, RGL and W56H the residual variance did not increase. In RGL (females), there was even a decrease ($p \leqslant 0.05$). In W56L residual variance was increasing significantly ($p \leqslant 0.05$). In W56L residual variance was always higher than in the other lines. Table 4.3 shows the changes in parameters by the regression of parameter means on generation number. The values in the selection lines were expressed as deviations from the control.

The regression coefficients in line C showed that there were changes in the control. Mature weight decreased significantly ($p \leqslant 0.05$). The changes in k and

TABLE 4.2. Residual variances in percentages by line, sex and generation.

Generation	C		RGH		RGL		W56H		W56L	
	♀	♂	♀	♂	♀	♂	♀	♂	♀	♂
6	2.76	2.11	3.13	1.72	3.43	2.09	2.14	1.46	4.62	3.91
7	2.36	1.76	3.46	2.11	3.66	2.83	3.05	1.87	4.49	4.12
8	2.80	2.31	2.60	1.86	3.68	2.58	3.44	1.82	5.33	4.16
9	3.87	2.04	2.87	1.91	3.68	2.38	2.63	1.35	6.67	5.91
10	3.64	3.07	2.66	1.92	2.82	1.86	1.68	1.32	4.88	4.55
11	2.20	1.92	3.34	1.75	3.49	2.07	1.35	1.11	6.75	5.82
12	2.67	1.47	3.40	1.55	3.23	2.94	2.17	1.11	6.88	6.48
13	3.74	1.98	3.43	2.15	2.68	2.40	3.02	1.15	6.18	6.45
14	2.64	2.27	2.43	1.98	2.45	2.12	1.77	1.38	7.10	5.87
Average residual variances in the generations										
$\bar{x}$	2.96	2.10	3.04	1.88	3.23	2.36	2.36	1.40	5.88	5.25
s	0.62	0.44	0.40	0.19	0.47	0.37	0.71	0.28	1.05	1.05
Spearman's rank correlation coefficient										
	n.s	n.s	n.s	n.s	*	n.s	n.s	n.s	*	*
r_s =	−0.03	−0.11	−0.10	0.25	−0.70	−0.02	−0.33	−0.63	0.76	0.80

n.s = not significant
* $p \leqslant 0.05$

TABLE 4.3. Changes in k, A and t_l per generation by line as deviations from the control.

	100 k (t^{-1})	A (g)	t_l (days)
Line C	$0.00 \pm 0.07^{n.s}$	-0.30 ± 0.10*	$-0.18 \pm 0.14^{n.s}$
Line RGH	$-0.04 \pm 0.03^{n.s}$	0.16 ± 0.06*	$0.17 \pm 0.13^{n.s}$
Line RGL	$0.05 \pm 0.04^{n.s}$	$-0.19 \pm 0.10^{n.s}$	$-0.16 \pm 0.15^{n.s}$
Divergence RGH-RGL	$0.09 \pm 0.05^{n.s}$	0.36 ± 0.08***	0.33 ± 0.14*
Line W56H	-0.16 ± 0.04**	1.35 ± 0.14***	0.74 ± 0.11***
Line W56L	$0.12 \pm 0.10^{n.s}$	-0.55 ± 0.13***	-0.49 ± 0.08***
Divergence W56H-W56L	0.28 ± 0.08*	1.89 ± 0.11***	1.22 ± 0.13***

n.s = not significant ($p > 0.05$)
* = $p \leqslant 0.05$
** = $p \leqslant 0.01$
*** = $p \leqslant 0.005$

t_i were small and not significant. In RGH and RGL, the deviations of A, k and t_l from the control were almost the same size but of opposite sign. This could suggest that the same effects were of influence in RGH, RGL as in the control, for instance inbreeding depression.

The asymmetry of the results of W56H and W56L might be explained by differences in cumulative selection differentials between the lines.

The regression coefficient of the divergence in k between RGH and RGL on generation number was not significant ($p > 0.05$). Differences between t_l and A

were significant. Regression coefficients of the divergence in A, k and t_i between W56H and W56L were significant.

4.4.2 *Comparison of the parameters in generations 13 and 14*

To show what differences occurred between divergent lines, the mean parameter values per line and sex in generations 13 and 14 are presented in Tables 4.4 and 4.5. Results of both generations are given, so that the conclusions in both generations can be compared.

Differences between lines, between sexes and between generations were tested with Student's t-test. Results of the test are presented in the tables. There were significant sex differences in all lines for A and t_i in both generations. The sex

TABLE 4.4. Means and standard deviations of k, A and t_i in generation 13 by sex and line.

Line	sex	n	100 k (t^{-1})		A (g)		t_i (days)	
			$\bar{x}$	s	$\bar{x}$	s	$\bar{x}$	s
Control	♀	52	11.50	1.39	22.74	2.30	20.37	3.61
	♂	52	10.98	0.79*[1]	30.93	2.53***	23.47	2.75***
	total	104	11.24	1.13[2]	26.85	2.42	21.92	3.21
RGH	♀	58	11.29	1.19	25.17	2.26	21.85	3.75
	♂	50	10.47	0.79***	34.18	2.88***	26.03	3.31
	total	108	10.88	1.03	29.68	2.57	23.94	3.55
RGL	♀	63	11.92	1.05	21.46	1.89	19.84	3.23
	♂	55	11.12	0.94***	28.16	2.56***	23.19	2.89***
	total	128	11.52	0.96	24.81	2.14	21.56	2.95
Divergence RGH-RGL		236	−0.64***[3]		+4.87***		+2.42***	
W56H	♀	50	10.32	0.87	38.12	3.32	25.84	3.84
	♂	63	10.28	0.82[n.s]	50.48	3.90***	28.81	3.06***
	total	113	10.30	0.84	44.30	3.66	27.33	3.43
W56L	♀	31	14.63	1.85	13.82	1.57	14.12	3.14
	♂	29	13.09	1.50***	17.64	2.53***	16.39	4.26*
	total	60	13.86	1.69	15.73	2.09	15.26	3.72
Divergence W56H-W56L		173	−3.56***		+28.57***		+12.07***	

n.s = not significant
* = $p \leqslant 0.05$
** = $p \leqslant 0.01$
*** = $p \leqslant 0.001$

[1] test for sex differences
[2] within sex variation
[3] test for differences between divergent lines

TABLE 4.5. Means and standard deviations of k, A and t_i in generation 14 by sex and line.

Line	sex	n	100 k (t^{-1})		A (g)		t_i (days)	
			$\bar{x}$	s	$\bar{x}$	s	$\bar{x}$	s
Control	♀	45	10.07	1.22	23.19	1.93	22.82	3.70
	♂	64	9.84	0.97[n.s1]	30.73	2.50***	26.30	3.80***
	total	109	9.96	1.07[2]	26.96	2.28	24.56	3.76
RGH	♀	55	9.82	1.01	24.80	2.61	23.82	3.79
	♂	73	9.66	0.88[n.s]	34.85	3.33***	27.18	3.67***
	total	128	9.74	0.94	29.83	3.04	25.50	3.72
RGL	♀	68	10.87	1.36	21.47	1.89	19.62	3.01
	♂	48	9.97	1.19***	28.91	3.22***	23.67	3.99***
	total	116	10.42	1.29	25.19	2.52	21.65	3.45
Divergence RGH-RGL		244	−0.68***[3]		+4.64***		+3.85***	
W56H	♀	124	8.68	1.21	38.71	4.36	31.56	5.84
	♂	98	8.56	1.05[n.s]	53.05	7.18***	35.85	5.60***
	total	222	8.62	1.14	45.88	5.78	33.71	5.74
W56L	♀	44	11.09	1.80	14.59	1.79	16.32	3.64
	♂	59	10.16	1.22**	18.35	2.65***	19.82	4.47***
	total	103	10.63	1.49	16.47	2.33	18.07	4.14
Divergence W56H-W56L		325	−2.01***		29.41***		15.64***	

n.s = not significant
* = $p \leqslant 0.05$
** = $p \leqslant 0.01$
*** = $p \leqslant 0.001$

[1] test for sex differences
[2] within sex variation
[3] test for differences between divergent lines

differences in *k* were significant in both generations of RGH, RGL and W56L. Sex differences were small and sometimes not significant in C and W56H. This occurred in both generations 13 and 14. In both generations there were significant differences between diverging lines especially between W56H and W56L.

Generally the same conclusions could be drawn for both generations. However there were some generation effects on the parameter values. The mean values of *k* in generation 13 were significantly higher than in generation 14. The differences in mature weight were small so that the inflexion point was at an earlier age in generation 13 than in generation 14.

Point of inflexion was in general at an early age in comparison with base population and literature. This might suggest that mature weight was underestimated.

4.4.3 *Relation between parameters and RG*

In Table 4.6 the correlations between parameters of the logistic function and RG are presented. Correlations were calculated from the correlations within litters pooled in both sexes in generations 13 and 14, by z-transformation. (SNEDECOR and COCHRAN 1972). Correlations are presented per line. Correlation between RG and A was positive. Correlation between RG and k was negative or not significant. Between RG and t_i the correlation was positive, while a higher mature weight involved a later age at point of inflexion. The correlation between k and t_i was negative.

TABLE 4.6. Correlation coefficients within litters between RG, A, k and t_i pooled for both sexes and generations 13 and 14.

	line	A	k	t_i
	C	0.30**	0.00$^{n.s}$	0.39**
	RGH	0.27**	−0.19**	0.49**
RG	RGL	0.35**	0.05$^{n.s}$	0.48**
	W56H	0.22**	0.08$^{n.s}$	0.25**
	W56L	0.50**	−0.22**	0.45**
			−0.34**	0.45**
			−0.25**	0.43**
A			−0.36**	0.53**
			−0.50**	0.68**
			−0.21**	0.59**
				−0.36**
				−0.49**
k				−0.34**
				−0.65**
				−0.20*

n.s = not significant
* = $p \leq 0.05$
** = $p \leq 0.01$

Environmental covariances caused by maternal and litter influences were excluded by calculating the correlations within litters. However also part of the genetic covariance was excluded.

To investigate the influence of variation in mature weight on the correlations, calculations were made at constant mature weight. These partial correlation coefficients are given in Table 4.7. They were calculated from the correlation coefficients in Table 4.6 with the method described by SNEDECOR and COCHRAN 1972.

Correlations between RG and t_i and k and t_i decreased slightly, but remained mostly significant. As in Table 4.6, the correlations between RG and k in Table 4.7 were not very consistent. Then the significant correlations were

TABLE 4.7. Partial correlation coefficients (A constant) between RG, k and t_l, derived from Table 4.6.

	line	k	t_l
	C	0.17*	0.30**
RG	RGH	−0.13$^{n.s}$	0.35**
	RGL	0.20*	0.26**
	W56H	0.22**	0.08$^{n.s}$
	W56L	−0.13$^{n.s}$	0.23*
k			−0.24**
			−0.44**
			−0.18*
			−0.49**
			−0.09$^{n.s}$

n.s = not significant
* = $p \leqslant 0.05$
** = $p \leqslant 0.01$

positive and two nonsignificant correlations were estimated. Keeping *A* constant probably had a positive effect on the correlation between RG and *k*.

4.4.4 *Comparison of the calculated growth curves*

Growth curves were also compared by graphical methods. As the systematic

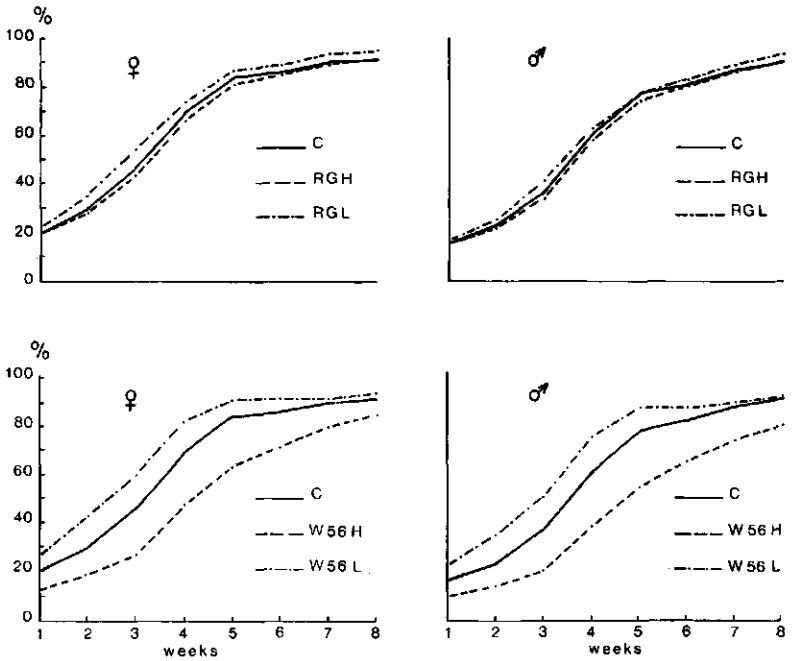

FIG. 4.3. Maturity-rate curves by line and sex (generation 14)

differences between lines were the same in generations 13 and 14, graphs were compared in generation 14 only.

In Figures 4.3 and 4.4 growth curves are presented. In Figure 4.3 weights in percentages of the calculated mature weight A are plotted against age. The advantage of this method is that differences in mature weight are excluded from the comparison. At 8 weeks, weights in percentages of the mature weight were already high. Females had mostly a higher percentage at the same age as males. Lines C, RGH, RGL and W56L were already over 90 % at 8 weeks while W56H was 80–85 %. In the part of the growth curve observed, RGL and W56L had a higher percentage than C, while RGH and W56H were at a lower percentage. However the differences between RGH and C were small.

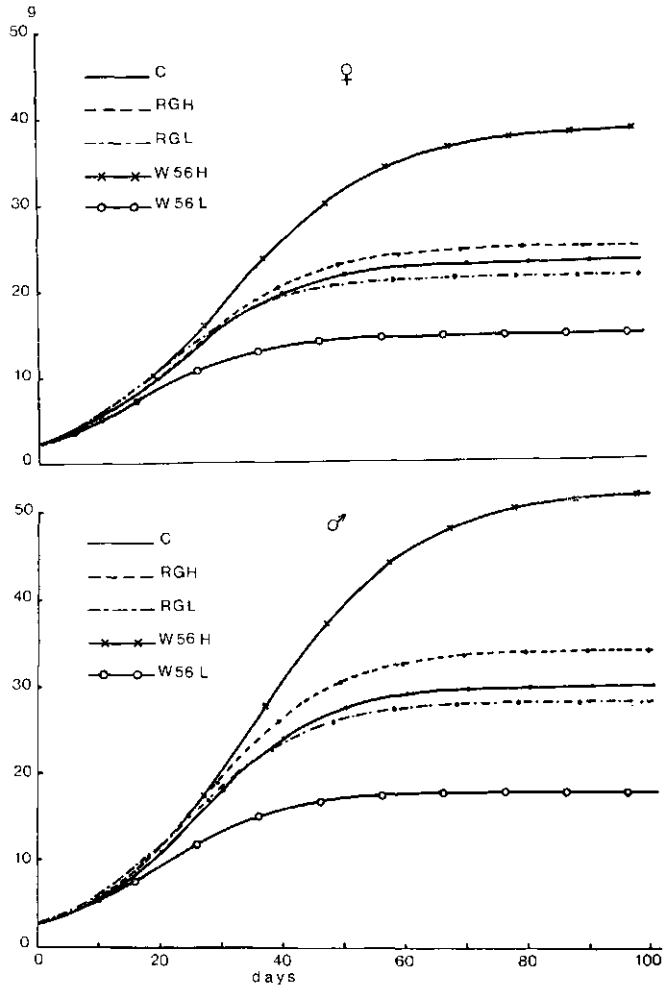

FIG. 4.4. Calculated growth curves by line and sex in generation 14

According to BRODY 1945, a comparison of growth curves is unbiased when differences in mature weight and time taken to mature are excluded. In Figure 4.5 relative bodyweight (weight in percentages of mature weight) is plotted against relative age (age in percentage of time taken to mature, or in this case to reach 0.9999 *A*). The biggest differences between the lines were observed at a relative age of about 10 percent. Females had a higher weight percentage than males at the same relative ages.

Differences between C and RGH were small. RGL deviated from C and RGH. These differences were smaller than between W56H and W56L, which diverged considerably.

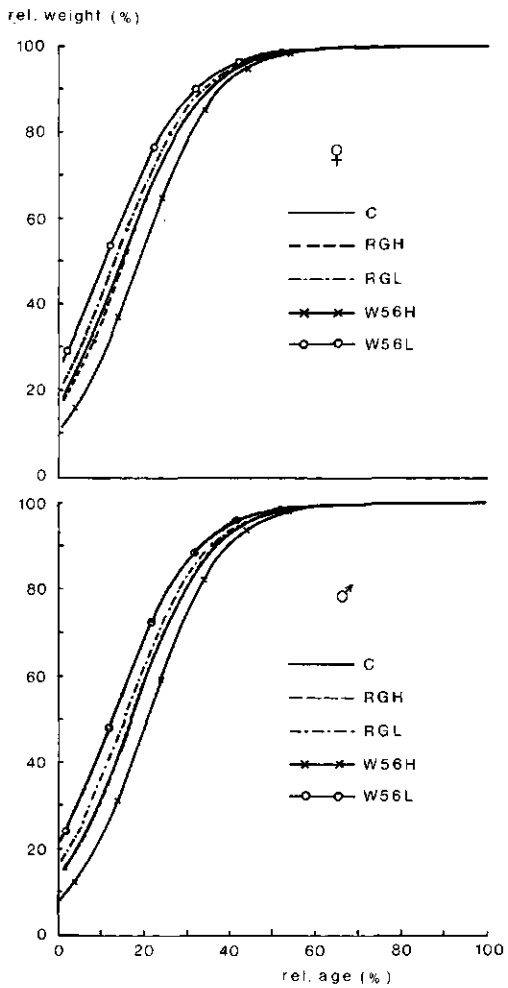

FIG. 4.5. Relative bodyweight on relative age by line and sex in generation 14

V GROWTH, EFFICIENCY OF GROWTH AND BODY COMPOSITION IN THE LINES

Growth rate, efficiency of growth and body composition are of importance in meat production. Observations on growth rate, feed intake and chemical body composition were made until 15 weeks of age to calculate line and sex differences.

5.1 LITERATURE

Literature on growth rate, feed intake, body composition and gross energy efficiency of mice is mostly related to lines selected for growth rate or bodyweight. In these publications, most of which were mentioned in Chapter II, changes in feed intake, body composition and gross energy efficiency may be considered as correlated effects. Some experiments have been described on selection for feed intake and feed efficiency (BIONDINI et al. 1968) or body composition (TIMON and MORE O'FERRALL 1966 and MORE O'FERRALL and TIMON 1968, 1970).

5.1.1 *Growth rate, feed intake and feed efficiency*

FOWLER 1962, TIMON and EISEN 1970, SUTHERLAND et al. 1970 and STANIER and MOUNT 1972 concluded from their experiments with selection lines for weight that selection for a large weight has the same effect as selection for appetite.

Differences in feed intake are strongly related to bodyweight differences but not to line or sex differences (STANIER and MOUNT 1972). TIMON and EISEN 1970 estimated a phenotypic correlation coefficient of 0.78 between feed intake and bodyweight. SUTHERLAND et al. 1970 found a genetic correlation of 0.88 between the same traits.

According to TIMON and EISEN 1970, females had a higher feed intake than males at the same weight between 10 and 30 grams. Mice from a line selected for 6 weeks weight had a higher feed intake at the same weight than control line mice. Differences in feed intake between lines and between sexes increased until an age of about 6 weeks and afterwards remained constant.

Feed efficiency is defined as the weight increase in a certain time-interval divided by the feed intake in the same interval. In this form it was used by MAGEE 1962, TIMON and EISEN 1970, SUTHERLAND et al. 1970 and STANIER and MOUNT 1972. Also the reciprocal of feed efficiency, called the feed conversion by TITUS et al. 1953, is used, for instance by SUTHERLAND 1965 and RAHNEFELD et al. 1965. TIMON and EISEN 1970 suggested that feed efficiency (growth in g./feed intake in g.) is preferable to feed conversion (feed intake in g./growth in

g.) when comparisons are made over a constant age interval, because the coefficient of variation of feed efficiency is smaller.

Selection for large bodyweight or high growth rate gave an increased feed efficiency (FALCONER 1960b, FOWLER 1962, RAHNEFELD et al. 1965, LANG and LEGATES 1969, SUTHERLAND et al. 1970 and TIMON and EISEN 1970).

However the feed efficiency of mice selected for low weight was not significantly smaller than of control line mice (FOWLER 1962, LANG and LEGATES 1969).

Initially males had a higher feed efficiency than females. These differences continued until an age of 6–8 weeks (FOWLER 1962, LANG and LEGATES 1969, TIMON and EISEN 1970). The sex differences in the small lines continued longer (FOWLER 1962, TIMON et al. 1970). According to FOWLER, this might be explained by a delayed sexual and physiological maturity in the small lines. This agrees with results of ELLIOTT et al. 1968.

Feed efficiency decreases with increasing age, because growth rate decreases and feed intake shows a slight increase. From 6–7 weeks onwards (FOWLER 1962) feed efficiency is almost constant.

There is a high genetic correlation between growth rate and feed efficiency. SUTHERLAND et al. 1970 estimated 0.91. RAHNEFELD et al. 1965 found correlations of -0.80 and -1.04 between growth rate and feed conversion. SUTHERLAND et al. 1970 found a genetic correlation of 0.52 ± 0.33. The phenotypic correlation was 0.06. Of course, these correlations are partly auto-correlations (TURNER 1959 and SUTHERLAND 1965).

SUTHERLAND et al. 1970 selected in different lines for growth rate (G), feed intake (F) and feed efficiency (E) between 4–11 weeks. The realised heritabilities were 0.23 ± 0.20, 0.20 ± 0.06 and 0.17 ± 0.04.

The lines, given in decreasing sequence for growth rate were E, F and G, for feed intake F, E and G and feed efficiency E, G and F. Mice were the fattest in the F line.

5.1.2 *Body composition*

Different methods of analysis have been used to estimate body composition. TIMON and EISEN 1970 removed head, feet, tail, skin and gut and estimated the composition of this carcass. Others, like FOWLER 1962, BIONDINI et al. 1968, LANG and LEGATES 1969 chemically analysed samples of whole mice. Mostly the mice were starved for one day to avoid differences in amounts of feed and faeces in the intestine.

Water, ash, fat and protein contents were estimated in these samples. In the description of literature on body composition, attention will be paid to line differences, sex differences and age trends; the relation between components and selection for components will also be mentioned.

Line differences

When there is selection for growth rate or bodyweight, all body components

increase in weight (BIONDINI et al. 1968, TIMON et al. 1970). The change in body composition was variable; LANG and LEGATES 1969 suggested 'the complexity of physiological events leading to the expression of bodyweight changes suggests, that there are various metabolic alternatives'. There are many examples of this. FALCONER and KING 1953 described the results of selection for bodyweight by GOODALE 1938 and MACARTHUR 1944. In the first experiment, weight increase was obtained by a substantial fat increase in mice of restricted size, while in the second experiment the mice became large but not very fat. FOWLER 1958 compared selection lines of FALCONER 1960b descending from two base populations (N and C). Both were selected for large (L) and small (S) body size. At 6 and 12 weeks, the percentage of fat was significantly higher and the mean percentage of water significantly lower in NL than in CL. At 3, 6, 8 and 12 weeks the percentages of fat and water were similar in CS and CL in spite of the large weight differences.

In the NL line the fat percentage was higher and the water percentage was lower than NS at 6, 9 and 12 weeks. Control animals had a similar carcass composition to animals in NS despite large difference in bodyweight. The difference in fat percentage in NL began at 38–40 days. LANG and LEGATES 1969 compared the body composition at 8 weeks of mice selected for high and for low weight at 6 weeks and concluded, that higher growth rate in the large line did not result from an increase in relative fat deposition. TIMON et al. 1970 compared body composition at 57 days in mice selected for high post-weaning gain and in control mice. The only difference in relative body composition was that fat percentage increased and water percentage decreased in the large line compared with the control. Composition of fat-free carcass weight was similar. BIONDINI et al. 1968 found an increased fat percentage at 112 and 150 days in two of the three replicates selected for growth rate between 4 and 11 weeks. The fat percentage in the control was decreased during selection.

Sex differences

LANG and LEGATES estimated a larger amount of fat deposition in females between 4 and 7 weeks than in males. This difference was reduced or reversed at 8 weeks of age. In the experiment of TIMON et al. 1970, male carcasses had a higher percentage of fat and a smaller percentage of ash than females. Protein and water percentages were not significantly different. The absolute quantities of all carcass components were higher in males than in females. This was in agreement with the results of BIONDINI et al. 1968.

Age effects

FOWLER 1958 estimated body composition of NL and NS lines at intervals between 13 and 107 days of age. The total amounts of body protein in NL showed a linear increase up to 40 days. Afterwards the rate of protein deposition was reduced. The increase in carcass water was closely related to carcass protein. The water: protein ratio decreased with aging. The decrease was most marked up to 46 days of age. In the large line, fat was deposited at a slow rate before

35 days. From 35 to 60 days, however, fat content of NL mice increased considerably. After 60 days the fat gain was reduced.

In the small line (NS) protein was deposited at a slower rate than in the large line. It formed a constant proportion of carcass at all carcass weights. Quantities of water were closely related to this. The water: protein ratio decreased with aging in this line too. There was no sudden increase in fat content in the small line; it showed a considerably slow but steady rate of increase. Percentage of protein decreased after 40 days of age in NL. In the small line there was almost no change. Fat percentage was similar in both lines up to 40 days. Afterwards there was a substantial increase of fat percentage in NL. In NS the increase in fat percentage was slight and gradual. In both lines the water percentages decreased with increasing age. Water percentage was similar up to 40 days in both lines. Thereafter it was less in the NL. LANG and LEGATES 1969 found decreasing water percentage, increasing fat percentage and constant protein and ash percentage with increasing age between 3 and 8 weeks of age. This agreed with the results of FOWLER 1958, 1962 and BIONDINI et al. 1968.

Relation between components

In various experiments a strongly negative correlation between fat and water content was estimated. (FOWLER 1958, LANG and LEGATES 1969, TIMON et al. 1970, STANIER and MOUNT 1972). LANG and LEGATES 1969 found a phenotypic correlation of −0.95. The increase in fat percentage of the large line was nearly the same as the water percentage decrease in the experiments of FOWLER 1962 and TIMON et al. 1970.

According to LANG and LEGATES 1969, correlations between fat and other components were negative; between water, protein and ash they were positive.

Selection for carcass components

TIMON and MORE O'FERRALL 1966 and MORE O'FERRALL and TIMON 1968, 1970 selected during 12 generations for quantity of fat and protein at 70 days of age. Realised heritability for protein weight was 0.09 ± 0.09 and for quantity of fat 0.35 ± 0.10. HULL 1960 selected for weight at 3, $4\frac{1}{2}$ and 6 weeks of age to investigate differences in quantities of fat in the lines. The quantities of fat in the lines selected for weight at a young age were not reduced as FOWLER 1958 suggested.

5.1.3 *Gross energy efficiency*

Differences in feed efficiency do not give complete information on differences in energy expenditure of the feed. The composition of the weight gain is variable and the energy content of 1 gram protein is 5.65 kcal and of 1 gram fat 9,45 kcal according to WIDDOWSON 1955. However when 1 gram protein is deposited, a quantity of water is simultaneously deposited (FOWLER 1962 suggested 3–4 gram water per gram protein). So energy content of weight gain might be variable.

If the growth rate, feed intake, energy content of feed and body composition are known, the gross energy efficiency can be estimated. Gross energy efficiency

was defined by BRODY 1945 and FOWLER 1962 as energy increase in the carcass calculated as a fraction of the gross energy consumed. Protein deposition and fat deposition can be expressed as fractions of the gross energy intake. TIMON et al. 1970 distinguished between maintenance energy, estimated from 140 $W^{3/4}$ (W = actual bodyweight) (KLEIBER 1961), and energy for growth (gross energy intake minus maintenance energy). In this calculation it is assumed, that the coefficient for maintenance is the same for the various lines and for different ages.

FOWLER 1962 found that the gross energy efficiency in the large line was higher than in the small line up to 4 weeks of age. There was no difference during the time interval of 4–6 weeks; from 6 weeks onwards the large line had a higher gross energy efficiency.

The gross energy efficiency in the large line of TIMON et al. 1970 was higher than the control between 3–8 weeks. Males were more efficient than females. Protein and fat deposition, expressed as fractions of energy for growth in the control line was similar to the large line. Males were 37% more efficient in protein deposition and 52% in fat deposition than females (differences in percentages of the mean).

FOWLER 1962 and STANIER and MOUNT 1972 did not observe a difference in caloric digestibility between large and small lines. FOWLER reported no differences in rate of activity too.

5.2 MATERIAL AND METHODS

5.2.1 *Material*

The animals for the analysis of growth rate, feed intake, feed efficiency, body composition and gross energy efficiency between 3 and 15 weeks of age in each of the five lines were produced by a large number of matings of animals in 11th generation of the lines. The number of mated animals are presented in Table 5.1.

In C, RGH, RGL and W56L all animals at 8 weeks in that generation were mated. W56H consisted at 8 weeks of 93 females and 118 males. From these, 66 females and 66 males were randomly chosen.

Matings in C, RGH and RGL were according to the MAI system. In W56H and W56L the mice were randomly mated with avoidance of fullsib and halfsib

TABLE 5.1. Number of animals mated to produce samples for analysis of growth rate, feed intake and body composition.

Line	females	males
C	64	63
RGH	64	62
RGL	54	54
W56H	66	66
W56L	67	54

TABLE 5.2. Results of matings by line.

line	n° ♀♀ mated	days mating-littering	litter-rate	litter size at birth	litter weight at birth	individual weight at birth
C	64	23.17	92.2%	9.34	13.95 g.	1.49 g.
RGH	64	22.81	98.4	8.32	12.26	1.47
RGL	54	22.42	98.2	9.74	14.38	1.48
W56H	66	23.69	83.3	11.47	17.67	1.54
W56L	67	23.66	68.7	6.89	8.98	1.30

matings. If there were more females than males in a line, some males were mated to two females. The results of the matings are presented in Table 5.2. Total litter weights were estimated at birth. All offspring were identified at 7 days of age and weighed at 7, 14 and 21 days.

The mice were weaned at 21 days. At that age two kind of groups were sampled:

- *weight groups* to estimate weekly weight increase and feed intake from 3 to 15 weeks of age. Generally this group consisted per line and per sex of 10 cages with 4 mice each. Weight increase was estimated per individual and weekly feed intake per cage
- *body composition groups* to estimate body composition at 10 ages: 3, 4, 5, 6, 7, 8, 9, 11, 13 and 15 weeks. The groups consisted per line and sex of 36 cages with 3 mice each. At the specified ages 12 mice, housed in 4 cages, were analysed in two replicates of two cages each. At 15 weeks of age, mice of the weight groups were analysed. In the body composition group, individual weights and feed intake per cage were estimated weekly.

This experimental design means that the composition of samples, analysed at different ages, was fixed at weaning. This was done because:

- mean body composition, mean feed intake and mean bodyweight could be related per sample
- individual determination of feed intake and body composition analysis was not possible, because this would have required too much labour and space.

Sampling was as follows:
Three mice were randomly sampled per sex per litter. These mice were distributed at random over separate cages, so that there were two in the body composition group and one in the weight group. If there were less than three mice per sex per litter, mice from another litter of the same age were added. In both groups all mice per cage were of the same age. In Figure 5.1 the design of this experiment is presented.

Observations

The weights were estimated weekly according to the method described previously. Weekly feed intakes were estimated per cage in the same age interval as

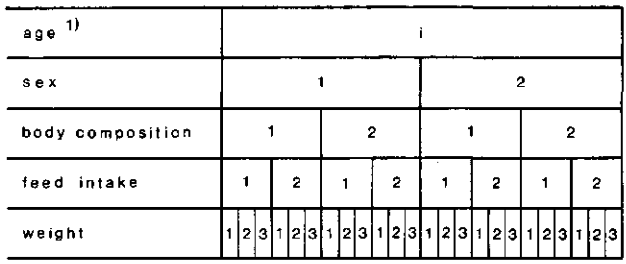

FIG. 5.1. Experimental design

weight increase observations. The amount of feed given to a cage was noted and one week later the amount left over was weighed. Dry matter contents of the fresh feed and of that left over were estimated in duplicate and feed intake per week was calculated on dry matter base.

In general analysis of body composition was done in samples of 6 mice each. At 15 weeks samples of 8 mice each were analysed. Before being killed the mice were starved for 1 day. Then they were weighed and killed with CO_2. Samples were kept deepfrozen (−28 °C) in a closed bottle and afterwards the mice were ground. From the ground sample three quantities of about 5 gram each were taken for dry matter estimation. The rest was autoclaved for 30 minutes at 125 °C after adding 100% water. Then the sample was homogenized with a Waring Blendor.

In this material, dry matter, nitrogen, ash and ether-extraction contents were estimated by the Chemical Laboratory of the Institute for Animal Husbandry Research (IVO) at Zeist.

In Table 5.3 the number of weight observations per line and sex are given.

TABLE 5.3. Number of animals at different ages.

line Age (weeks)	C		RGH		RGL		W56H		W56L	
	♀	♂	♀	♂	♀	♂	♀	♂	♀	♂
1 + 2	230	265	257	228	236	248	274	264	133	147
3	230	264	257	227	236	248	272	262	133	147
4	136	135	144	142	136	136	132	133	112	117
5	124	123	132	130	124	124	120	121	100	105
6	112	112	120	118	112	113	108	109	88	93
7	100	100	108	106	100	101	96	97	76	81
8	88	88	97	94	88	89	84	85	64	69
9	76	76	85	82	76	77	72	73	53	58
10 + 11	64	64	73	70	64	65	60	61	41	46
12 + 13	52	52	61	58	52	53	48	49	29	34
14 + 15	40	40	49	46	40	41	36	39	17	23

The number of observations on feed intake and body composition can be deduced from this table too.

5.2.2 *Methods*

With these observations the following comparisons between lines and between sexes were made:

- growth curve between birth and 15 weeks of age
- feed intake between 3 and 15 weeks of age
- feed efficiency between 3 and 15 weeks of age.

The relation between bodyweight and feed intake was studied within ages and over all ages. Differences between lines and between sexes in:

percentage of water
percentage of protein (6.25 times *N* percentage)
percentage of fat (assumed to be similar to ether-extraction)
percentage of ash

were analysed at different ages.

Comparisons were made by graphs, and by an analysis of the differences at 8 weeks. This age was chosen because most information on body composition in literature was at this age.

The gross energy intake was estimated from the feed intake multiplied by the gross energy content of 1 gram feed. It was estimated by the caloric bomb method. The gross energy was 4.1085 kcal/g. dry matter in the feed.

The total energy deposition was calculated from the deposition of protein, multiplied by 5.65 kcal and of fat multiplied by 9.45 kcal (WIDDOWSON 1955). Fat and protein deposition were always estimated at intervals starting from 3 weeks of age. Thus the energy content at the end of the interval was corrected for the energy content at 3 weeks of age. From these calculations the gross energy efficiency could be calculated for different intervals. Line and sex differences in gross energy efficiency were analysed.

The protein deposition in kcal as a fraction of gross energy intake was calculated as an estimate of efficiency of production in different lines, sexes and age intervals.

Results of VAN DER WAL and VERSTEGEN 1974 suggested that coefficients to estimate maintenance energy from metabolic weights, were quite variable in these lines. So no further separation of energy intake was made.

5.3 RESULTS

5.3.1 *Growth rate, feed intake and feed efficiency*

The growth curves between 0 and 15 weeks are presented in Figure 5.2. The mean growth rates, estimated per week are given in Figure 5.3. The maximum growth rate estimated per week was for all lines and sexes in the 4th week. From Figure 5.3 it can be seen that the inflexion point for males occurs at an older age

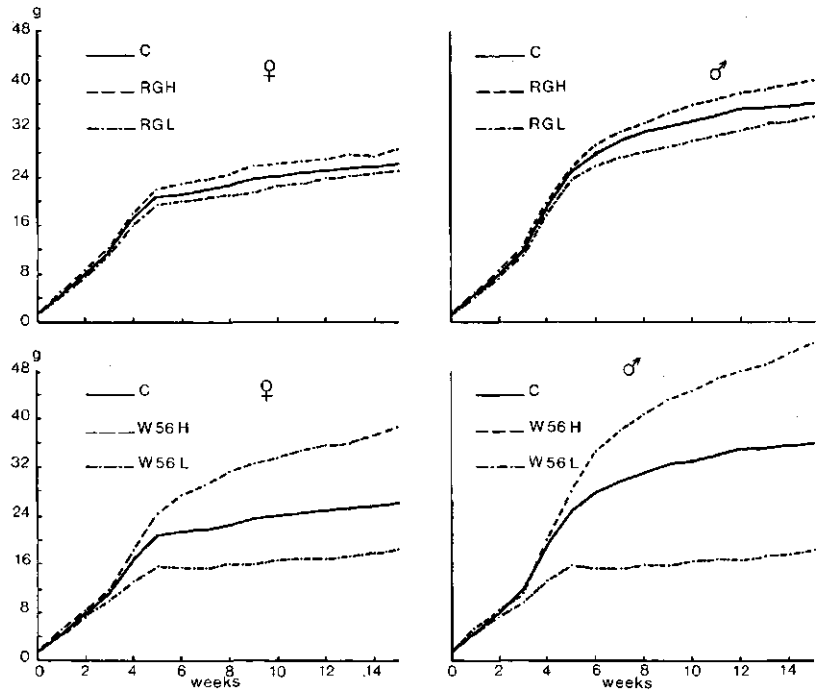

FIG. 5.2. Average weights by line, sex and age

than for females. The differences between RGH and RGL were small. Until the 10th week RGH had a higher growth rate. There were no systematic differences after that age. The difference in growth rate between W56H and W56L were substantial during the section of growth curve observed. There was a sudden decline in growth in the 5th and 6th weeks in all lines, but especially in W56L. In this line growth became zero or even negative. However afterwards there was slow but steady weight increase. Males had a higher growth rate than females, but the differences were small after about 8 weeks of age.

Cumulative feed intake is presented in Figure 5.4. The linearity of these curves shows that feed intake per line and sex must be nearly constant. This is also shown in Figure 5.5. There was an increased feed intake in all lines and sexes in the 5th week. Afterwards the feed intake had a small decrease but increased slightly at later ages. From the 6th week on, the differences between lines remained rather constant. RGH had a higher intake than RGL, while the consumption in W56H was much higher than in W56L. The feed intake of males was higher than of females. The initial increase in feed intake continued longer in males than in females.

The correlation coefficients between feed intake and bodyweight and metabolic bodyweight ($W^{3/4}$) were estimated. The correlation coefficients per line and per sex were pooled by the z-tranformation. The correlation coefficients be-

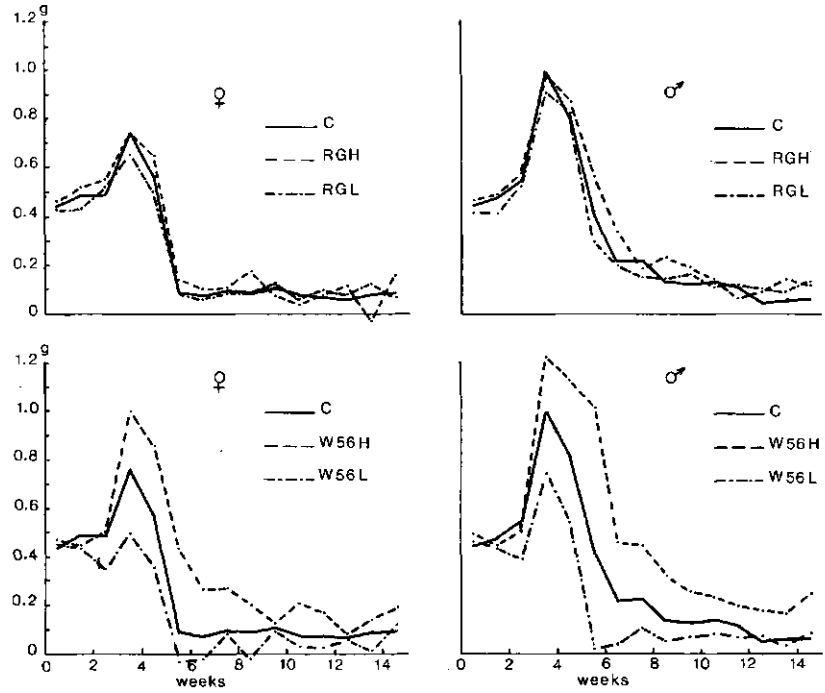

FIG. 5.3. Average growth rate by line, sex and age

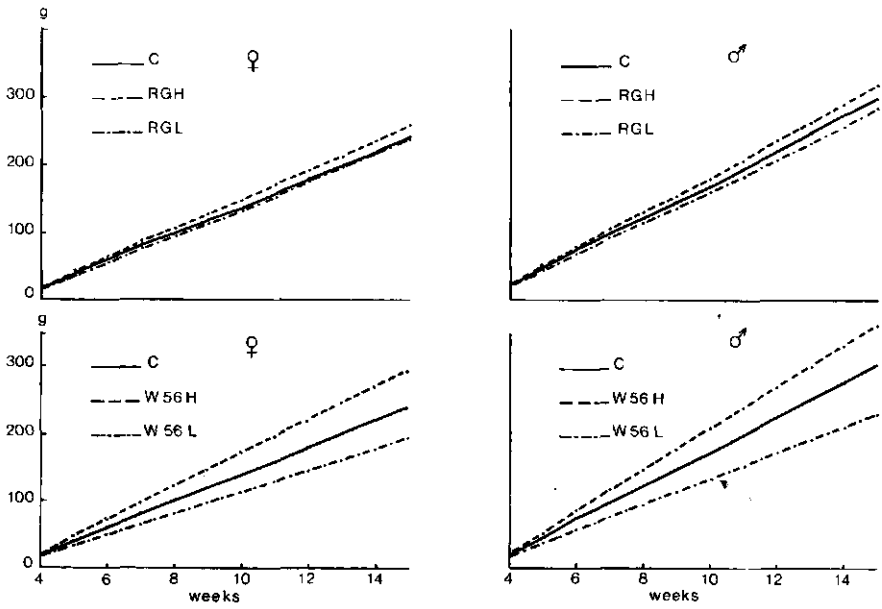

FIG. 5.4. Average cumulative feed intake by line, sex and age

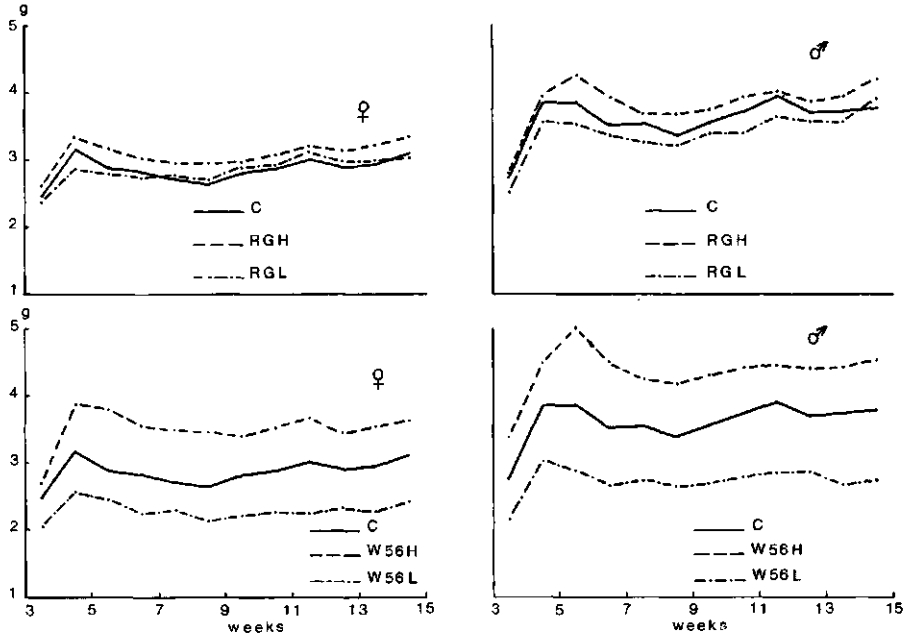

FIG. 5.5. Average feed intake per week by line, sex and age

tween feed intake and bodyweight estimated within age classes was 0.79 and between feed intake and metabolic weight 0.86. An estimation of these correlation coefficients over all ages gave 0.91 and 1.00. All these values were significant ($p \leqslant 0.01$). There were no systematic differences in coefficients between lines and sexes.

Figure 5.6 shows the feed efficiencies by line and sex. There was a considerable decrease from the 4th until the 6th or 7th week. Afterwards feed efficiency remained rather constant. Differences between RGH and RGL were small and not systematic. W56H had a much higher efficiency than W56L. But, of course, these differences became smaller with aging. Males had a higher efficiency than females until about 8 weeks. After this age, there were no systematic differences between sexes.

5.3.2 *Body composition*

Body composition curves by line and sex are presented in Figures 5.7, 5.8, 5.9, and 5.10. *Ash percentage* was rather constant (Figure 5.7). There was a slight but steady increase with aging in all lines and sexes. There were no important differences between sexes; females seemed to have a slightly higher ash percentage than males. Differences between RGH and RGL were not systematic. Mostly W56L had a higher ash percentage than W56H. Ash percentage in males of C was high in comparison with other lines at 8, 9, 11 and 13 weeks.

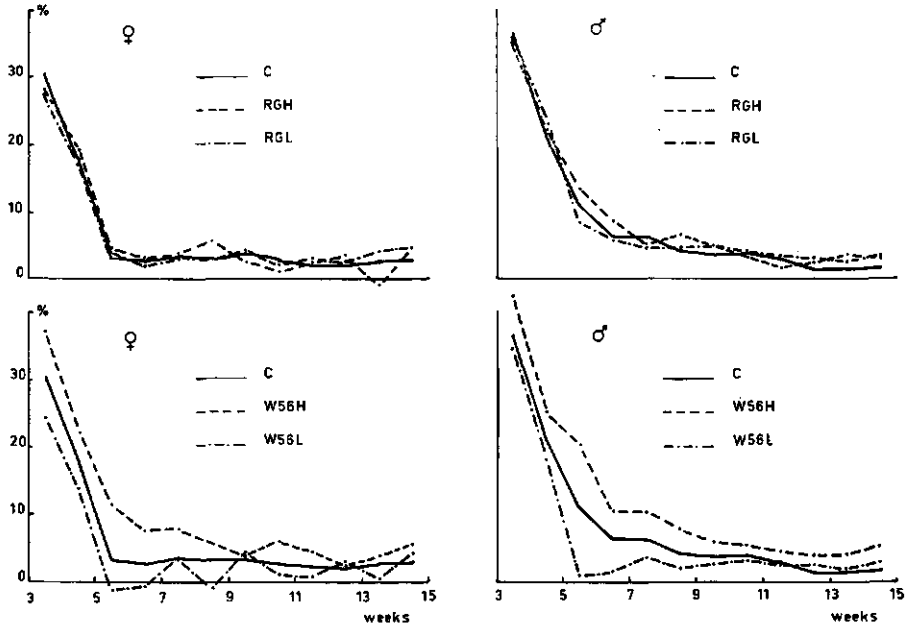

FIG. 5.6. Average feed efficiency by line, sex and age

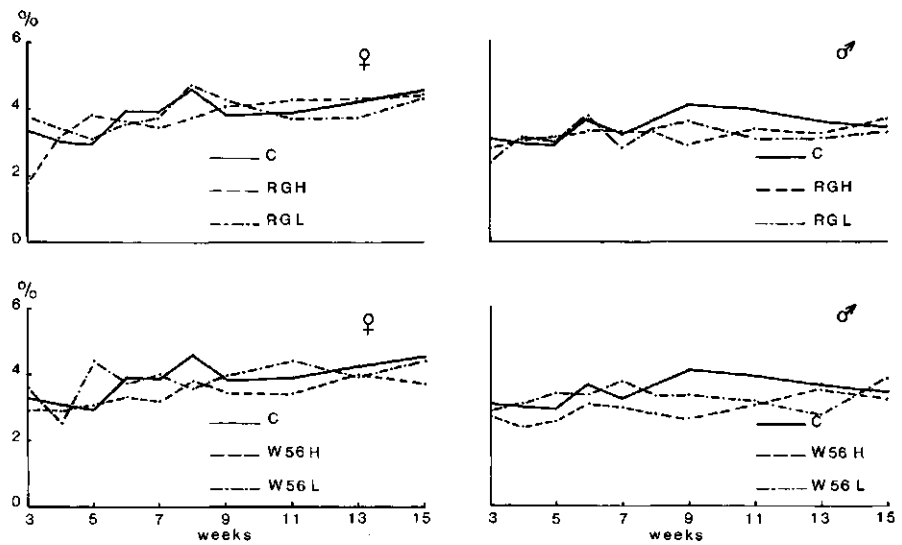

FIG. 5.7. Average ash percentage by line, sex and age

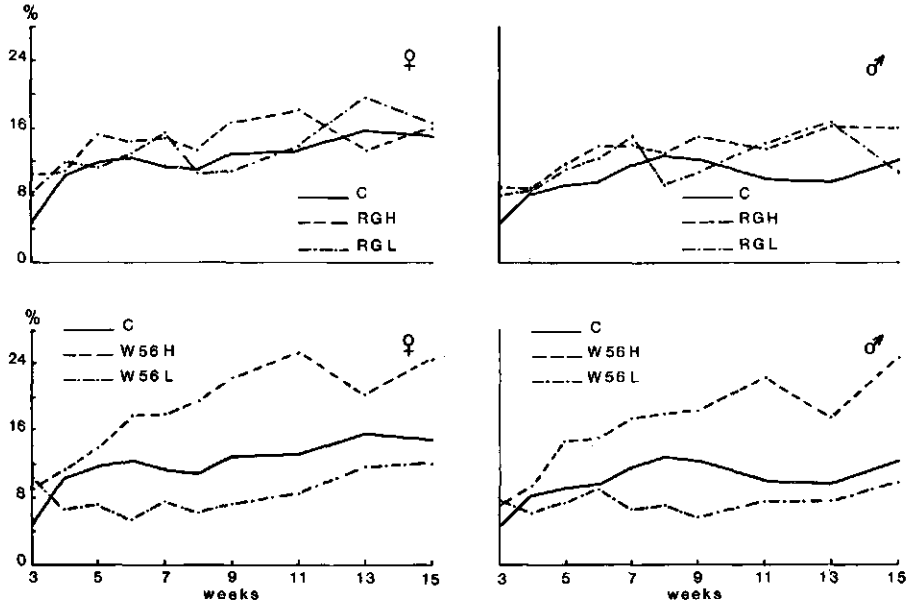

FIG. 5.8. Average fat percentage by line, sex and age

Fat percentage was more variable (Figure 5.8). There was an increase with aging. This increase was very large in W56H and small in males of W56L. In general females had a higher fat percentage than males. Fat percentage in females of W56L was very low, especially from 4–8 weeks. Until 11 weeks RGH was fatter than RGL, except at 7 weeks. The differences between W56H and W56L were very large. In W56L the fat percentage remained very low, while fat percentage in W56H increased until about 1/4 of total bodyweight.

Protein content was rather constant in time (Figure 5.9). However there were two striking exceptions. Protein percentage in RGL increased (except at 7 weeks) until 8 or 9 weeks and decreased until the level of C and RGH after that age. These trends were similar in males and females. Protein percentage in W56L was high at young ages and decreased slightly at later ages. Protein percentage in RGL was higher than in RGH at most ages, while W56L was higher than W56H.

Naturally there was a substantial interaction between the proportional body components. Especially the large variation in fat content determined differences in other components. This was also shown in the *water percentages*. The fact that water is partly substituted by fat, with aging follows from Figure 5.10. Usually females had a lower water content than males. Differences in water content between RGH and RGL were small, but RGH tended to have a lower content than RGL, except again at 7 weeks of age. Water content of W56H was much lower than of W56L.

Table 5.4 summarizes ash, fat and protein contents and ash, fat and protein

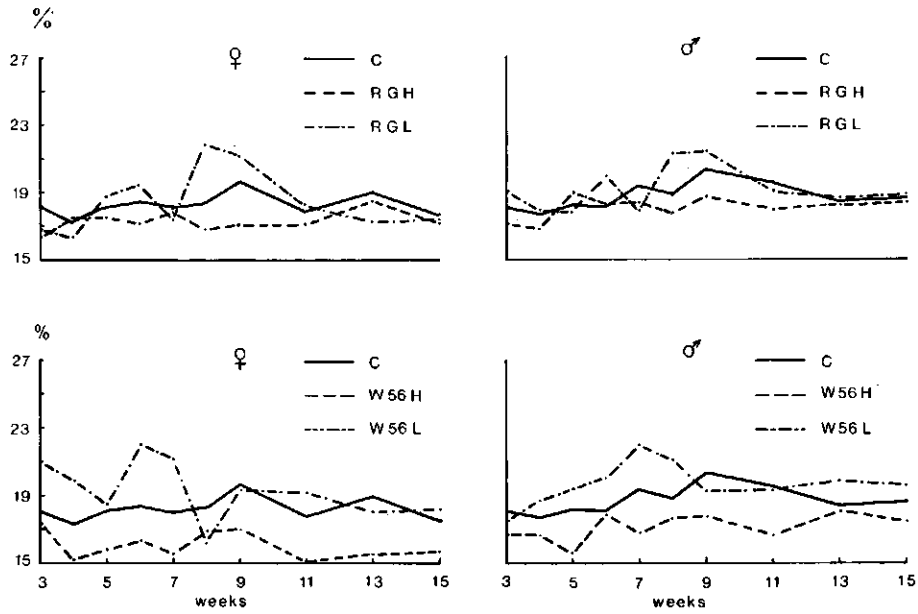

FIG. 5.9. Average protein percentage by line, sex and age

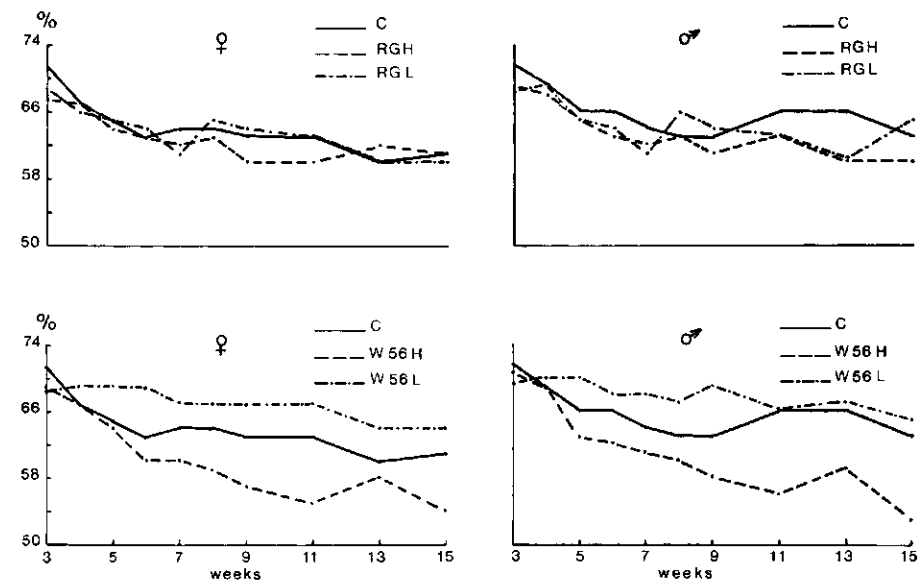

FIG. 5.10. Average water percentage by line, sex and age

TABLE 5.4. Quantities of ash, fat and protein in the carcass at 8 weeks by line and sex.

Line	sex	% ash $\bar{x}$	% ash s	% fat $\bar{x}$	% fat s	% protein $\bar{x}$	% protein s	g. ash $\bar{x}$	g. ash s	g. fat $\bar{x}$	g. fat s	g. protein $\bar{x}$	g. protein s
C	♀	4.60	± 0.13	10.97	± 4.53	18.39	± 1.23	0.90	± 0.02	2.16	± 0.99	3.59	± 0.06
	♂	3.65	± 1.03	12.81	± 0.81	18.82	± 0.37	1.00	± 0.19	3.57	± 0.56	5.22	± 0.39
	total	4.13	± 0.73[1]	11.89	± 3.25	18.61	± 0.91	0.95	± 0.14	2.87	± 0.80	4.41	± 0.28
RGH	♀	3.68	± 0.31	13.36	± 0.08	16.95	± 0.10	0.81	± 0.08	2.92	± 0.01	3.71	± 0.01
	♂	3.30	± 0.04	12.97	± 0.16	17.82	± 0.04	0.95	± 0.03	3.74	± 0.11	5.14	± 0.08
	total	3.49	± 0.22	13.17	± 0.13	17.39	± 0.07	0.88	± 0.06	3.33	± 0.08	4.43	± 0.06
RGL	♀	4.74	± 0.54	10.80	± 1.65	21.92	± 2.16	0.89	± 0.14	2.02	± 0.40	4.07	± 0.21
	♂	3.32	± 0.11	9.23	± 2.99	21.29	± 1.09	0.83	± 0.03	2.31	± 0.74	5.32	± 0.29
	total	4.03	± 0.39	10.02	± 2.41	21.61	± 1.71	0.86	± 0.10	2.17	± 0.59	4.70	± 0.25
Divergence RGH-RGL		−0.54[n.s](14.4)[2]		3.15[n.s](27.2)		−4.22[n.s](21.6)		0.02[n.s](2.3)		1.16[n.s](42.2)		−0.27[n.s](5.9)	
W56H	♀	3.87	± 0.09	19.63	± 0.08	17.00	± 0.83	1.08	± 0.02	5.45	± 0.04	4.72	± 0.22
	♂	2.78	± 0.08	18.00	± 0.88	17.56	± 0.16	1.03	± 0.02	6.69	± 0.24	6.54	± 0.15
	total	3.33	± 0.09	18.82	± 0.62	17.28	± 0.60	1.06	± 0.02	6.07	± 0.17	5.63	± 0.19
W56L	♀	3.58	± 1.22	6.43	± 0.83	16.29	± 3.44	0.47	± 0.15	0.86	± 0.08	2.16	± 0.39
	♂	3.33	± 0.23	7.06	± 0.50	21.17	± 0.13	0.57	± 0.01	1.22	± 0.16	3.64	± 0.19
	total	3.46	± 0.89	6.75	± 0.69	18.73	± 2.43	0.52	± 0.11	1.04	± 0.13	2.90	± 0.31
Divergence W56H-W56L		−0.13[n.s](3.8)		12.07**(94.4)		−1.45[n.s](8.1)		0.54*(68.4)		5.03**(141.3)		2.73**(64.0)	
Divergence Males-females		−0.82*(22.5)		−0.23[n.s](1.9)		1.22[n.s](6.5)		0.05[n.s](5.8)		0.83*(26.8)		1.52**(34.5)	

[1] within sex variation
[2] in parentheses: difference in percentage of average

n.s = not significant
* = $p \leqslant 0.05$
** = $p \leqslant 0.01$

quantities by line and sex at 8 weeks of age. Line and sex differences were tested with Student's t-test. However degrees of freedom were small.

Fat content of RGH was higher than of RGL, but ash and protein percentages were higher in RGL. As the mice in RGH were heavier, they deposited more fat, although slightly less protein. Differences between W56H and W56L in ash and protein contents were small. W56H had a much higher fat content. As the weight differences were very large W56H deposited much more fat, ash and protein. Females had a higher ash percentage than males. Fat percentage and protein percentage were similar in both sexes. Together with the weight differences this resulted in small differences in amount of ash and more fat and protein in males.

In Table 5.5 the correlation coefficients between percentages of body components are presented. These coefficients were estimated within lines, sexes and age classes. Correlations of fat percentage with water, protein and ash percentage were all significantly negative. Correlations between water and protein percentage was significantly positive. The correlations of protein and water percentage with ash were not significant.

5.3.3 *Gross energy efficiency*

The cumulative feed intake during different age intervals was substituted for energy intake by multiplying feed intake on dry matter base by the gross energy content of the feed (4.1085 kcal/g. dry matter of feed). The cumulative feed intake of mice in body composition analysis agreed well with cumulative feed intake of all mice in weight and body composition groups at the different age intervals. So Figure 5.4 gives a good indication of differences in gross energy intake between lines and between sexes.

Energy deposition in the body at different intervals was calculated from the difference in energy content of mice at 3 weeks and at the end of the actual intervals (5.65 times protein deposition plus 9.45 times fat deposition in that interval (WIDDOWSON 1955)).

Table 5.6 shows the quantities of fat and protein by line and sex at 3 weeks. The energy contents are shown too. Differences between lines were small. Fat amount in C was slightly less so energy content at 3 weeks was lower. Energy content of males was mostly smaller than that of females at 3 weeks of age.

TABLE 5.5. Phenotypic correlations between percentages of carcass components.

	water	fat	protein
fat	−0.91**		
protein	0.32**	−0.36**	
ash	$0.14^{n.s}$	−0.19*	$0.14^{n.s}$

n.s = not significant ($p>0.05$) d.f. = 176
* = $p\leq 0.05$
** = $p\leq 0.01$

TABLE 5.6. Quantities of fat, protein and energy at 3 weeks by line and sex.

line	sex	g protein	kcal	g fat	kcal	sum kcal
C	♀	1.60	9.04	0.42	3.97	13.01
	♂	1.64	9.27	0.43	4.06	13.33
RGH	♀	1.81	10.23	1.17	11.06	21.29
	♂	1.74	9.83	0.93	8.79	18.62
RGL	♀	1.59	8.98	0.79	7.47	16.45
	♂	1.85	10.45	0.78	7.37	17.82
W56H	♀	1.88	10.62	0.98	9.26	19.88
	♂	1.77	10.00	0.77	7.28	17.28
W56L	♀	1.92	10.85	0.96	9.07	19.92
	♂	1.70	9.61	0.71	6.71	16.32

The gross energy efficiency by line and sex are presented in Figure 5.11. In this figure, the points represent gross energy efficiency with increasing interval, always beginning at 3 weeks. In all lines and sexes, except females in W56L, gross energy efficiency is decreasing with increasing interval. Females in W56L were at a very low efficiency from the beginning. Differences between RGH and RGL were small. Mostly RGH had a slightly higher efficiency than RGL. The

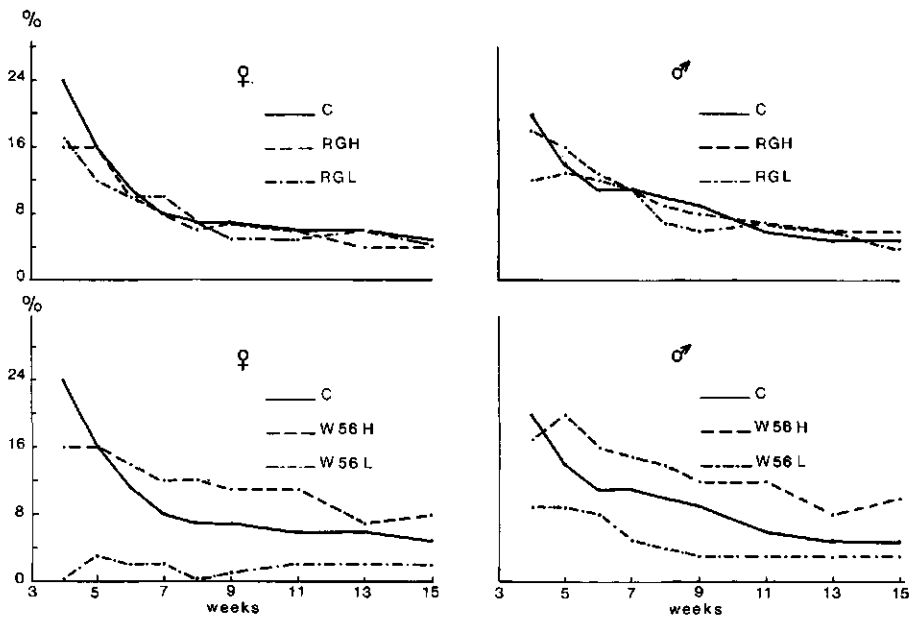

FIG. 5.11. Gross energy efficiency by line, sex and age

gross energy efficiency of W56H was much higher than of W56L. Males were more efficient than females.

The fractions of gross energy intake deposited in protein are shown in Figure 5.12. The fractions were decreasing with increasing interval. Differences between RGH and RGL were small. Initially RGH was higher but with increasing interval RGL became slightly better. W56H was better than W56L, but the difference between W56H and C were very small. Males were better than females.

Table 5.7 gives the gross energy intake, gross energy efficiency and amount of protein per gross energy intake by line and sex during 3–8 weeks. Differences between diverging lines and between sexes were tested. Degrees of freedom were small. Differences were expressed in percentages of the mean. RGH had 9% higher gross energy intake; gross energy efficiency was 10% higher in RGH. However RGL deposited 23% more protein per gross energy consumed. Energy intake, efficiency and protein deposition of energy consumed were all much higher in W56H than in W56L. Per unit of gross energy intake W56H deposited the same amount of protein as RGL. So the high gross energy efficiency in W56H was to a large extent based on fat deposition.

Males consumed 20% more gross energy than females. Gross energy efficiency of males was 32% higher. Per unit of gross energy consumed, males deposited 40% more protein than females.

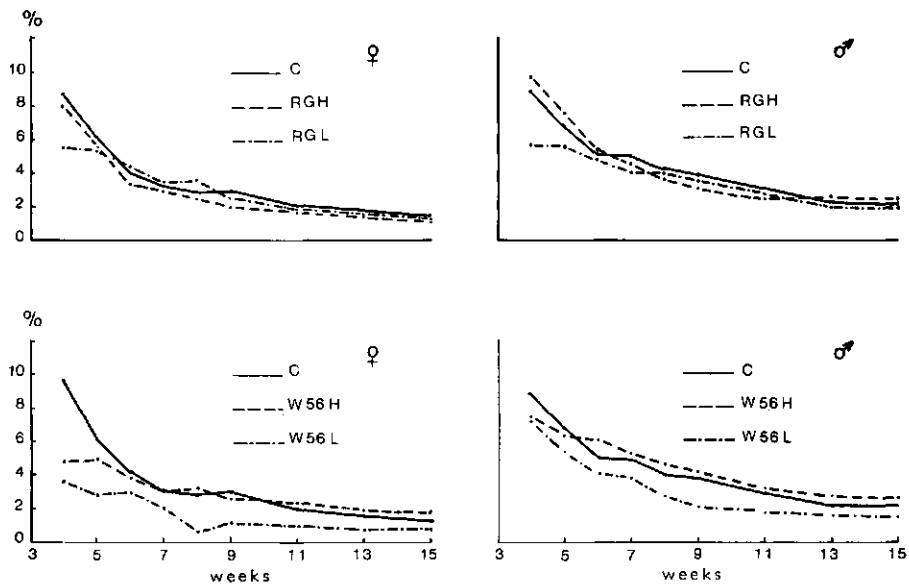

FIG. 5.12. Energy in protein as percentage of gross energy intake by line, sex and age

TABLE 5.7. Gross energy intake, gross energy efficiency and fraction of gross energy intake deposited in protein between 3 and 8 weeks by line and sex.

Line	sex	Gross energy intake (kcal)	Gross energy efficiency (%)	Protein deposited from energy intake (0.01 g/kcal)
		$\bar{x}$ s	$\bar{x}$ s	$\bar{x}$ s
C	♀	401.61 ± 13.65	6.89 ± 1.85	0.50 ± 0.03
	♂	496.72 ± 32.54	10.03 ± 1.13	0.72 ± 0.03
	total	449.17 ± 24.95[1]	8.46 ± 1.53	0.61 ± 0.03
RGH	♀	427.90 ± 1.45	6.38 ± 0.44	0.44 ± 0.00
	♂	529.59 ± 8.13	8.68 ± 0.37	0.64 ± 0.00
	total	478.75 ± 5.84	7.53 ± 0.41	0.54 ± 0.00
RGL	♀	390.31 ± 15.11	6.56 ± 0.49	0.64 ± 0.08
	♂	483.16 ± 8.13	7.05 ± 1.01	0.72 ± 0.05
	total	436.74 ± 12.13	6.81 ± 0.79	0.68 ± 0.07
RGH-RGL		42.01*(9.2)[2]	0.72[n.s](10.0)	−0.14[n.s](23.0)
W56H	♀	501.44 ± 9.01	11.62 ± 0.36	0.57 ± 0.05
	♂	599.43 ± 1.16	13.84 ± 0.25	0.80 ± 0.02
	total	550.44 ± 6.42	12.73 ± 0.31	0.69 ± 0.04
W56L	♀	331.15 ± 20.34	0.14 ± 1.11	0.08 ± 0.12
	♂	399.35 ± 5.81	3.94 ± 0.97	0.48 ± 0.04
	total	365.25 ± 14.96	2.04 ± 1.04	0.28 ± 0.09
W56H-W56L		185.19**(40.4)	10.69**(144.8)	0.41*(84.5)
Males-Females		91.17**(20.0)	2.39**(31.8)	0.22**(40.0)

[1] within sex variation
[2] in parentheses: differences in percentage of average
n.s = not significant
* = $p \leqslant 0.05$
** = $p \leqslant 0.01$

VI DISCUSSION

Selection for growth rate in different intervals or for weight at various ages have been frequently studied in livestock and laboratory animals (ROBERTS 1965), because of the economic importance of these traits. Less information is available on the results of selection for changes of the growth curve, eventually resulting in selection for an optimum growth curve. This optimum growth curve may be described as a maximum growth in early stages, while changes in mature weight are none or very restricted. There is a lack of information on selection for an optimum growth curve. This is probably because expectation for result is low as have been stated by TAYLOR and CRAIG 1965 and TAYLOR 1968. However growth curves of turkeys have been changed by index selection (ABLANALP et al. 1963). MCCARTHY 1971 reported tentative results of selection experiments with mice, from which possibilities of growth curve changes by selection were suggested too.

These investigations arose from the need to get more information on results of selection for speed of the growth without altering mature weight automatically. This would have happened if selection would have been for absolute growth rate. It was deduced that relative growth rate (RG) was a suitable criterion. We selected for weight at 56 days to bring about differences in the level of the growth curve. This selection was not primarily done to get information on the direct results, because there are many publications on these. These lines were started mainly to contrast with lines selected for speed of the growth curves. In the indirect selection results, interest has mainly been paid to essential differences in shape of the growth curve, analysed by descriptive functions, and to differences in composition and efficiency of growth until 15 weeks of age.

The many advantages and restrictions of research with laboratory animals for the benefit of livestock improvement have been discussed by ROBERTSON 1959, CHAPMAN 1961, ROBERTS 1965 and FALCONER 1966. The advantages of low costs, large numbers and short generation interval have to be mentioned. Especially in this study as expectation for results was low. On the other hand the authors mentioned, have suggested that one has to be careful with direct application of the results to livestock improvement. The results of this study should been seen as an addition to the information on genetic aspects of growth curves and composition and efficiency of growth.

Maternal effects disturb the analysis of growth of mice. Therefore selection for RGH and RGL was done within litters.

Direct results

All values of the selection results and realised heritabilities were expressed as deviations from the control, to exclude the effects of environmental trends.

During the generations there was a significant decrease in RG in the control as was shown in Figure 3.4.
Several reasons are possible:
- Although there were no indications for changes in environment they might have occurred.
- There was some negative selection in the control (Table 3.12) in spite of chosing the animals for breeding at random.
- Population mean might have changed by random genetic drift. However no replicates were maintained so an estimation is impossible.
- Inbreeding coefficient increased in spite of the mating system of maximum avoidance of inbreeding.

This might have influenced RG directly, but also indirectly via decreased maternal effects or litter size.

The inbreeding coefficient of animals in the 14th generation was estimated with the formula of FALCONER (1960a):

$$F_t = 1 - [1 - 1/(2N_e)]^t$$
F_t = inbreeding coefficient in generation t
N_e = harmonic mean of effective population size in the generations
$$1/N_e = (1/N_1 + 1/N_2 + \ldots\ldots + 1/N_t)\,/t$$

This resulted in inbreeding coefficients in C, RGH and RGL, of about 10.5% in generation 14 which was in a good agreement with the prediction. It is not surprising that the inbreeding coefficients were similar in the three lines. Selection and mating system were the same and also the number of parents, producing the next generation, was in general similar (Figure 3.16).

Mostly inbreeding coefficients of this size cause only a slight percentual inbreeding depression (FALCONER 1960a). Correction of mean values in RGH and RGL for changes in C will also exclude most inbreeding depression effects, because proportional depression is the same in the lines and absolute differences between lines were not very large.

In Figure 3.8 the influence of correcting S_{cum} and R_{cum} of RGH and RGL for changes in C is recognizable. Changes per generation in RGL were larger than in RGH. Figure 3.8 and Table 3.12 show that the selection differential in RGH was much smaller than in RGL. This is striking, as the mean within-litter variation per sex in all generations was almost the same in RGH and RGL (females 0.786% and 0.798% and males 0.643% and 0.659% respectively). Also the numbers of litters born (Figure 3.16), the litter size (Figure 3.17) and the survival rate (Figure 3.18) were not systematically lower in RGH. The explanation for smaller selection differential in RGH will be the larger variability of litter size and more deviating sex ratios in RGH. This had important consequences for the selection differential in the within-family selection system.

The estimated realised heritabilities were low in both lines. A combined estimation of h^2 in the divergent lines gave an estimated $h^2 = 0.08$ (Figure 3.9).

Figure 3.9 shows a much more regular relation between S_{cum} and R_{cum} than after correction for mean values in C.

Forcing the regression lines through the origin decreased the realised heritability substantially. If the regression lines were forced through the average S_{cum} and R_{cum} values, the realised heritability in RGH became 0.12 ± 0.05; in RGL 0.14 ± 0.04 and from divergent lines 0.13 ± 0.02. Hence the effectivity of selection in the early generations was less than in the later ones. No results of selection for RG are known from literature. From the figures 3.8 and 3.9 it could be concluded that selection limits were not approached during these 14 generations.

The results of the selection were asymmetrical. The changes in RGL were larger than in RGH. Not only the cumulative selection differential was larger in RGL, but also the realised heritability was higher.

The regression coefficient of mean W56D values on generation number in the control did not significantly differ from zero, in spite of some low values in the last generations. It is impossible to conclude from these data in how far this decrease is systematic.

The inbreeding coefficient of animals in the 14th generation was 18.4% in W56H and 18.9% in W56L. This inbreeding coefficients were higher than in C, RGH and RGL in spite of the larger number of animals mated (32 females and 16 males). These may be caused by the random mating system (however with avoidance of fullsib and halfsib matings) and a decrease of the effective number of parents (Figure 3.16). The selection differential in W56H was much more than in W56L (Table 3.13). The main reason must be the significant increase of the variation in W56H (Table 3.11). It follows from Figure 3.19 that the number of animals at 56 days of age was mostly higher in W56H than in W56L. As a result the selection intensity was higher in W56H. Differences in cumulative selection differential were shown in Figure 3.10. The estimations of realised heritabilities were 0.28 ± 0.01 in W56H, 0.35 ± 0.02 in W56L and 0.31 ± 0.01 in the divergent lines. Forcing the regression lines through the mean of S_{cum} and of R_{cum} had almost no influence on the estimations. The estimated realised heritabilities were in good agreement with values reported in literature (Table 3.1). From the differences in heritability it might be concluded that downward selection was more effective than upward. This is in agreement with literature too. However the selection differential in W56H was much higher. So an analysis by the method of HANRAHAN et al. 1973 gave an asymmetry in favour of W56H. The change in mean bodyweight decreased in the last generations of W56L so that the selection limit seemed to be approached. The number of animals at 56 days of age decreased substantially, so selection intensity became very small. It may be expected that there will be no further large changes in this line.

Correlated traits

The comparison of the results of selection for RG and W56D showed that selection for W56D gave much larger changes. The realised heritabilities of W56D were higher than of RG and the selection differentials were substantially

more too. This is also a result of the differences in selection method. In within-family selection only 50 percent of the additive genetic variance is used, if the families are fullsibs. Correlated selection results are directly proportional to the direct selection results. Therefore no comparisons were made of correlated results in RG and W56D lines.

Tail length was measured to get an impression of the differences in skeletal size. Differences between RGH and RGL were small. This is in agreement with the phenotypic correlations between RG and tail length in the base population (Table 3.6). There were large differences between W56H and W56L in tail length and consequently in skeletal size. This agreed with the results of FALCONER 1953, COCKREM 1959 and BAKER and COCKREM 1970.

Of the differences in fertility traits between W56H and W56L (Table 3.15) litter size was the only one that was significant. The wide variation in fertility traits per generation was probably because of a smaller number of observations than the individual weight traits. There were no systematic differences in fertility traits between RGH and RGL, but there were between W56H and W56L (Figures 3.15–3.19). Number of days between mating and littering increased. Litter size increased in W56H and decreased in W56L. Pregnancy percentage decreased in both W56D lines. These results agreed with those of MAC ARTHUR 1949, FALCONER 1953, RAHNEFELD et al. 1966 and BRADFORD 1971.

There were no systematic differences in survival rates. This, in combination with the litter size, explains differences between W56H and W56L in the numbers of mice at 56 days. However in both lines the number at 56 days decreased. The number of mice at 56 days in C, RGH and RGL was nearly constant.

Growth curves

The differences in growth curves have been assessed by the parameters of the logistic function. A description of the observed growth curves in the base population gave a residual variance similar to values in literature. That the residual variance in the selection lines was lower, might be explained by the larger variation in weight that was described. This could explain the very low residual variances in W56H and the higher values in W56L too. In the W56L line the residual variance was increasing during the generations.

The parameters of the logistic function were estimated on weekly weights between 1 and 8 weeks of age. It appeared that the mature weights were underestimated. This followed from a comparison of predicted weights, based on weekly observed weights between 1 and 8 weeks of the 'weight group' in Chapter V and the observed weight at 15 weeks of the same group. The values are given in Table 6.1. The real differences will be larger, because after 15 weeks of age a further weight increase takes place (Figure 5.2). Mostly the differences between lines in predicted mature weight and observed weights at 15 weeks were proportional to weights at 15 weeks of the lines. The difference in RGL seemed to be somewhat larger. This underestimation means that the value of the description by the logistic function is relative. It might be even more valuable than the real estimated mature weight if the main interest is the description of muscle growth,

TABLE 6.1. Predicted mature weights and observed weights at 15 weeks of age in the "weight group".

Line	Females		Males	
	Predicted	Observed	Predicted	Observed
C	24.07 g.	26.24 g.	34.24 g.	36.05 g.
RGH	26.38	28.67	37.94	39.79
RGL	21.88	25.02	31.00	33.96
W56H	35.93	38.66	48.13	52.60
W56L	16.99	18.42	21.76	23.23

because almost the whole weight increase at later ages is fat growth (CURTIS 1969). So differences in the latter might disturb the description of the section of the growth curve one is interested in.

Underestimation of mature weight also means an underestimation of the time taken to mature, of the calculated weight at inflexion point and of the calculated age at inflexion point. TIMON and EISEN 1969 also found that mature weights predicted by the logistic function were underestimated. As the inflexion point in the logistic function is estimated at 50 percent of calculated mature weight, the real percentage will be lower. This agrees with the values of BRODY 1945 and TAYLOR 1965, who gave a percentage of 30 of mature weight.

The observed weights were expressed as fractions of calculated mature weight to compare the maturity rates of the lines (Figure 4.3). RGL had a higher maturity rate than RGH, while W56L was higher than W56H. Also the positive correlation between maturity rate and time taken to mature could be concluded from Figure 4.3. This was also found by EISEN et al. 1969, TIMON and EISEN 1969 and TAYLOR and FITZHUGH 1971.

A comparison of the lines on relative age and relative time scales (BRODY 1945) showed substantial differences in percentual weight at the same percentual age (Figure 4.5) especially between W56H and W56L. RGL deviated from C and RGH, which were similar. In generation 13 the same picture was observed. This seems to indicate that there were differences in the growth curve between the lines.

In these calculations birth rather than conception was taken as the zero point of the relative age scale. This choice might have influence on a comparison of the lines if there are substantial differences in time taken to mature. Calculation with conception as zero point gave the same order of lines. However the differences between lines decreased slightly.

Females had a lower mature weight A, a higher k and the calculated inflexion point at an earlier age than males. This was found in generations 13 and 14 of all lines. These sex differences were also observed by EISEN et al. 1969 and TIMON and EISEN 1969.

RGL had a higher k value, a lower mature weight and an earlier inflexion point than RGH. No comparable information was at hand in literature. Mature

weight in W56H was more than twice that in W56L. Inflexion point was earlier in W56L while k was higher in this line than in W56H. TIMON and EISEN 1969 found a higher k value in the large line than in the control. EISEN et al. 1969 found the lowest mean k value per line in the small line and the highest in the large line. However the growth curve in their small line was different from the small line in this experiment, because in the experiment of EISEN et al. growth continued for longer. In my experiment growth almost ceased in the small line after 6 weeks of age. In both reported experiments weight differences were much smaller than in my experiment. And in both experiments a negative correlation between A and k was observed.

The regression coefficients of the mean value of the parameters per line on generation number agreed with the differences between lines estimated in generations 13 and 14.

Table 4.6 showed that the correlation between the age at inflexion point and mature weight was positive. This was introduced by the definition of inflexion point at weight $A/2$ and the positive correlation between mature weight and time taken to mature. The correlation between A and k was negative. So animals with a higher mature weight took more time to approach this mature weight. Consequently the correlation between k and t_i was also negative. The correlation between A and RG was positive and between RG and t_i too. Correlations between RG and k were negative or not significant. These correlations might be influenced by the positive correlations between RG and A and a negative correlation between k and A. If A was kept constant (Table 4.7) the correlations between RG and k tended to be more positive. This agreed with the deduction of BRODY 1945, that doubling time of weight before inflexion point is inversely proportional to relative growth in this part of the growth curve. So changing RG might directly change k according to a low positive correlation, but it also changed mature weight by the positive correlation between RG and A, while the relation between A and k was negative. So indirectly via A the relation between RG and k might be negative. According to the selection results, this indirect influence seemed to be stronger as can be seen in Tables 4.3, 4.4 and 4.5. Selection for low RG, for instance, increased k and decreased A.

The correlations between A, k and t_i were similar in the lines. These correlations agreed well with the correlations given by TIMON and EISEN 1969 and EISEN et al. 1969.

From this analysis of the growth curves it might be concluded that there were substantial differences in mature weight between the lines. These changes were accompanied by differences in the parameter k and the inflexion point.

There were differences between the lines and sexes in maturity rates too. However these might be caused by differences in mature weight. Animals with a high maturity rate at any age had a low mature weight.

As a result of a high maturity rate there is a relative increase of weight at young ages. As a result of a decreased mature weight there is a decrease in weight at young ages. This conclusion comes from the high correlations between weights at different ages. In spite of the differences in maturity rate, growth

curves did not cross systematically. This was observed in preceding generations too.

Some indications for essential changes in growth curve are given in Figure 4.7 where relative weights were plotted against relative ages.

McCarthy 1971 reported tentative results of selection for shape of the growth curve by an independent culling system and index selection. The crossing of growth curves occurred, but was not systematic in the generations presented. Ablanalp et al. 1963 selected turkeys at a high weight at 8 weeks and a restricted weight at 24 weeks by means of a restricted selection index. This gave positive results so it might be concluded that the growth curve changed. However in this publication no further information on the growth curves was given.

Timon 1968 reported an estimated heritability of 0.07 ± 0.18 for the parameter k of the logistic function. The value was not significant. This agrees with the conclusion of Kidwell and Howard 1969, that a general combining ability of parameters of the Gompertz growth curve were small and not significant. To a certain extent this was also true in this experiment for RG, because heritability was only about 10%.

Growth curves, feed intake, efficiency of growth and body compositions of the lines

The data for this analysis were observed in offspring of animals from the 11th generation. These parents were unselected and consequently this material represented the mean genetic values of generation 11 of different lines.

Selection for growth rate or bodyweight is similar to selection for appetite, according to Fowler 1962, Timon and Eisen 1970, Sutherland et al. 1970 and Stanier and Mount 1972.

There were large differences in feed intake between W56H and W56L and to a smaller extent between RGH and RGL (Figures 5.4 and 5.5). From 6 weeks onwards feed intake was rather constant. Directly after weaning feed intake increased. This might be related to compensatory growth after reduced growth by change of milk intake to concentrates-intake and by weaning. Probably this was of much importance in W56H. In the second part of the suckling period, dams might be not able to supply their offspring with sufficient feed. This was indicated in experiments of Lang and Legates 1969 and Stanier and Mount 1972. This explains the relative low weights of the mice in W56H at 3 weeks of age (Figures 5.2 and 5.3).

Sexual maturity is attained at about 30 days (Monteiro and Falconer 1966). Then activity becomes greater (Fowler 1962) and thus feed intake is higher after weaning.

Correlations between bodyweight and feed intake were high. This agreed with results of Timon and Eisen 1969 and Sutherland et al. 1970.

The feed efficiency curves (Figure 5.6) agreed rather well with literature. Selection for large weight increased efficiency substantially (Falconer 1960b, Fowler 1962, Rahnefeld et al. 1965, Lang and Legates 1969, Sutherland et al. 1970 and Timon and Eisen 1970). Fowler 1962 and Lang and Legates 1969 found the same feed efficiency in the small line as in the control. In my

experiment the feed efficiency is smaller than in the control; the growth rate after 6–7 weeks is also very small compared with small lines in other experiments. It was not possible to compare RGH and RGL with literature. Males had a higher feed efficiency than females until about 8 weeks of age. The age trends were similar to the ones in literature; after 8 weeks there was no further decrease.

From the literature it was known that there were alternatives for the body composition of lines selected for large weight. In this case the large line W56H became very fat during selection and consequently the water percentage decreased. The W56L line had a low fat percentage, so water and protein percentages were high. Most surprising were the differences between RGH and RGL in protein content and fat content until 11 weeks. These seem to indicate that fat growth started at an older age in RGL than in RGH and explain the relativily larger difference between predicted mature weight and observed weights at 15 weeks in RGL in Table 6.1.

Sex differences agreed quite well with literature: females had slightly higher ash and fat percentages than males. Protein contents were not very different in males and females. The same was true for water percentage. As in literature ash percentage was rather constant in time, fat percentage increased, water percentage decreased. Protein percentage was in general constant too, except for protein percentages in RGL and W56L.

The energy deposition in the carcass during different intervals was calculated from the amount of fat and protein at 3 weeks and at the end of the intervals. Random errors in the observations at 3 weeks are of most influence in short intervals.

From the gross energy intake and the energy deposition the gross energy efficiency was estimated. The efficiencies were low. Determining factors are caloric digestibility, maintenance requirements, energy for activity etc. FOWLER 1962 estimated a caloric digestibility of about 67 percent in the large and small line. STANIER and MOUNT 1972 also found similar values for digestibility in large and small lines, but these were slightly higher. Results of VAN DER WAL and VERSTEGEN 1974 suggested that coefficients to estimate maintenance requirement were not similar in W56H and W56L. Mice in W56L seemed to be more active and agressive than mice in W56H, but these were subjective observations. FOWLER 1962 estimated no greater activity in the small line in her experiments.

From Figure 5.11 it follows that gross energy efficiency was decreasing with increasing interval. Females were less efficient than males. This was observed by TIMON et al. 1970 too. Gross energy efficiency in W56H was much higher than in W56L. FOWLER 1962 found this after 6 weeks, while TIMON et al. 1970 observed a larger efficiency in the large line between 3 and 8 weeks of age. No information was available in literature on gross energy efficiency in RG lines.

Differences between lines and between sexes in gross energy efficiency and in fraction of gross energy intake deposited in protein were summarized in Table 5.7. The choice of the interval 3–8 weeks was arbitrary, but the advantage was that a comparison could be made with the limited literature available.

Differences were tested, but the number of degrees of freedom was small. Therefore differences which were not significant are mentioned too. RGH had a significantly higher gross energy intake and a higher gross energy efficiency than RGL. However RGL deposited 23% more protein per unit gross energy intake. So the relative higher weights at an earlier age in RGL, that follow from the maturity rates, came about through a larger deposition of protein and water added; the fat deposition was smaller in this period.

Differences between W56H and W56L were large and all significant. W56H had a higher gross energy intake, gross energy efficiency and fraction of gross energy intake deposited in protein. W56L was very inefficient. Males had a significantly higher gross energy efficiency (32%) than females. Per unit gross energy intake males deposited 40% more protein than females. These sex differences were in good agreement with the results of TIMON et al. 1970.

If the amount of deposited protein per gross energy intake was used as a criterion for meat production ability, W56H and RGL were similar and the best. Protein production in males is much more efficient than in females.

VII SUMMARY

To evaluate the effect of selection for parameters of a growth curve, four selection lines and a control line were started from one base population. In the selection lines is selected for a large and a small relative growth rate between 21 and 29 days (RGH and RGL) and for a large and small bodyweight at 56 days (W56H and W56L). Besides the direct results of selection, attention was paid to the consequences for some fertility traits, the growth curve, the efficiency and composition of the growth.

Selection in RGH and RGL lines was within litter to exclude maternal effects, which are of importance at 21 and 29 days. One male and one female were chosen per litter. In the C, RGH and RGL lines 16 pairs per generation were mated, according to a system of maximum avoidance of inbreeding. In W56H and W56L mass selection was applied. Per generation 32 females and 16 males were selected and randomly mated. The material consisted of data from the first 14 generations of these lines.

Inbreeding coefficient in generation 14 was 10.5% in C, RGH and RGL lines and 18.4% and 18.9% in W56H and W56L. Relative growth rate (RG) decreased in C during generations. There was no significant change of weight at 56 days (W56D) in C.

Realised heritability of selection for RG was 0.06 ± 0.03 in RGH and 0.10 ± 0.02 in RGL. A combined estimation from divergent lines gave 0.08 ± 0.01. It followed from further analysis that the effectivity of selection was low in first generations. Cumulative selection differential in RG was small, mainly as a consequence of within family selection. There were large differences between W56H and W56L. In the last generations, mice in W56H were over twice as heavy as in W56L at 56 days. Realised heritability for W56D was 0.28 ± 0.01 in W56H and 0.35 ± 0.02 in W56L. A combined estimation from divergent lines gave 0.31 ± 0.01.

There were only small differences in tail length between C, RGH and RGL. The same applied to conception rate, timespan between mating and littering, litter size and survival rate between 0 and 56 days. Tail length increased in W56H and decreased in W56L. These changes in tail length indicate differences in size between the lines. Days between mating and littering increased in W56H and W56L; number of litters decreased substantially in both lines. Litter size increased in W56H and decreased in W56L. Survival rates were similar in the lines. As a consequence the number of mice at 56 days decreased during selection in these lines. This decrease was in W56L very strong and selection differential in females became almost zero in some generations.

Rate of death was increased from generations 5 to 8 of all lines.

Growth curves of the lines were described by the logistic function.

$W_t = A/(1 + be^{-kt})$
W_t = weight at age t
A = asymptotic weight
b = integration constant
k = parameter, that determines the spread of the curve along the time axis

The tentative choice of this function followed from literature, while a definite choice was based on a test of this function in the base population. In this base population weights were estimated daily between 18 and 61 days. Correlations between observed and calculated weights were of the level (r = 0.97) as reported in literature. However there were some systematic deviations. In both sexes weights were overestimated in the first part of the growth curve and they were underestimated in the later part. Correlations between calculated and observed weights did not decrease as the interval between observations increased from 1–7 days.

Growth curves were described in generations 6–14 of the 5 lines. Weights were observed weekly between 1 and 8 weeks. Residual variances in these lines, except W56L, were smaller than in the base population, probably because variation in the observed weights in the base population was smaller. This effect of the variation in weight might also explain the higher residual variance in females rather than in males and the low values in W56H, as follows from Table 4.2. Residual variance increased significantly during generations in W56L.

The judgement of the differences in growth curve between lines was based on the comparison of parameters k and A and calculated age at inflexion point (t_i). Changes in mean parameter values were used as indications for changes in growth curves, while line differences and sex differences were estimated in generations 13 and 14. Selection for large RG decreased k and increased A and t_i. Selection for small RG had an opposite effect. Differences between RGH and RGL were significant ($p \leqslant 0.001$). In W56H k decreased, while A and t_i increased. W56L showed opposite effects. Differences between W56H and W56L were large and significant ($p \leqslant 0.001$).

Males had a smaller k and a larger A and t_i than females. Sex differences were with some exceptions significant. Within-litter correlations between RG and parameters of the logistic function were estimated (Table 4.6). Partial correlations were calculated too while A was kept constant (Table 4.7). It followed from these calculations that the direct relation between RG and k was positive, while the indirect relation via the relation of RG and k with mature weight was negative. The differences between the selection lines showed, that the indirect relation was stronger than the direct one, because the realised correlation between RG and k was negative.

A comparison of maturity rates, defined according to TAYLOR and FITZHUGH 1971, showed that selection in RGL and W56L gave an increased maturity rate, while maturity rate in RGH and W56H was decreased. However changes in

maturity rate were accompanied by opposite changes in mature weight. The lack of systematic crossing of growth curves might be explained by the strong positive effect of changes in mature weight on weights at young ages. These effects were probably stronger than the effect of a change in maturity rates. Plotting weights and ages on a relative scale showed that differences in mature weight and in time taken to mature, did not determine all differences in the growth curve. W56H and RGH had a smaller percentage of mature weight than W56L and RGL at the same percentage of time taken to mature. Females had a higher percentage of mature weight than males at the same percentage of time taken to mature (Figure 4.5).

To examine whether there were differences in composition and efficiency of growth between the selection lines, growth, feed intake and body composition were observed in samples of mice. These samples represented mean genotypic value of generation 11 of each of the lines. Weekly weights and feed intake were determined between 3 and 15 weeks. Body composition was estimated in two replicates per sex per line of 6 mice each at 3, 4, 5, 6, 7, 8, 9, 11, 13 and 15 weeks of age.

Males had a larger growth rate than females. Differences between RGH and RGL were small; RGH had a higher growth rate until 10 weeks. Growth rate in W56H was much larger than in W56L during the whole observed timespan. Mice in W56L hardly increased in weight at all after 6 weeks of age. Feed intake was rather constant after 6 weeks. Before this age it was increased, probably by compensatory growth and extra activity during puberty. Differences between RGH and RGL were small. Feed intake in W56H was much higher than in W56L. Males ate more than females.

Feed intake and bodyweights were strongly positively correlated. Feed efficiency decreased substantially in all lines until 6 weeks and remained rather constant afterwards. Males had a higher efficiency than females until 8 weeks. Differences between RGH and RGL were not systematic. Feed efficiency in W56H was much higher than in W56L.

Ash percentage increased with aging. Differences between lines and between sexes were small and not systematic. Differences in fat percentage were much larger. It increased with aging, especially in W56H. Females had a higher fat percentage than males. Initially, RGH was fatter than RGL. Differences between W56H and W56L were very large. In W56H fat content increased up to 1/4 of total bodyweight. Protein content remained rather constant with aging. However there were two exceptions; protein percentage increased substantially until 9 weeks and decreased afterwards to the level of the other lines. This indicated that weight increase in this line consisted more of protein and less of fat until 9 weeks than in the other lines. W56L had a large protein percentage at young ages. Water percentage was low. Water percentage decreased with aging. These differences between lines and between sexes appeared also in the analysis of differences in body composition at 8 weeks (Table 5.4).

Correlations, calculated within lines, sexes and ages between fat percentage and other components were all significantly negative. Correlation between water

percentage and fat percentage was −0.91. Correlation between protein percentage and water percentage was 0.32. The other correlations between components were not significant.

Efficiency of weight increase was calculated during intervals from 3 weeks onwards. Gross energy efficiency decreased with aging, except for females in W56L which had a very low efficiency from the beginning. Differences between RGH and RGL were small and mostly in favour of RGH. Efficiency in W56H was much higher than in W56L. Males grew more efficiently than females. Fraction of energy intake deposited in protein decreased with aging. In males it was higher than in females. In the first weeks RGH was slightly higher than RGL, but afterwards this was reversed. Differences between W56H and W56L were large and in favour of W56H. However W56H was only slightly different from C. So the higher feed efficiency in W56H was to a large extent based on fat deposition. From the analysis of line differences and sex differences during the interval of 3–8 weeks it followed that RGH took in 9% more gross energy, had 10% higher gross energy efficiency; however there was 23% less protein deposited per unit gross energy intake than RGL. W56H took in 40% more gross energy, had 145% higher gross energy efficiency and deposited 85% more protein per unit gross energy intake than W56L. For sex differences these numbers were 20%, 32% and 40% in favour of males.

If the amount of deposited protein per unit gross energy intake was used as a criterion for meat production ability of a line, it could be concluded that RGL and W56H were similar and the best. Thus the higher feed efficiency in W56H in comparison to RGL was determined by the larger fat deposition in W56H.

It was concluded from the same criterion that males were much more efficient for meat production than females.

VIII SAMENVATTING

Om na te gaan wat het effekt is van de selektie op parameters van een groeicurve, is uitgaande van één basispopulatie een aantal selektielijnen en een controlelijn gestart. In de selektielijnen werd geselekteerd op een hoge en een lage relatieve groeisnelheid tussen 21 en 29 dagen (RGH en RGL) en op een hoog en een laag gewicht op 56 dagen (W56H en W56L). Naast het direkte selektieresultaat werd aandacht besteed aan de gevolgen voor enkele vruchtbaarheidskenmerken, het groeiverloop, de efficiëntie en de samenstelling van de groei.

Om de invloed van maternale effekten, die voor het gewicht op 21 en 29 dagen aanzienlijk zijn, uit te sluiten werd in de RGH en RGL lijnen geselekteerd binnen worpen. Per worp werden één mannetje en één vrouwtje gekozen. In de C, RGH en RGL lijnen werden 16 paren per generatie gefokt volgens een systeem van maximale vermijding van inteelt. In W56H en W56L werd massa selektie toegepast. Per generatie werden 32 vrouwtjes en 16 mannetjes geselekteerd en volgens toeval gepaard. Het materiaal bestond uit de gegevens uit de eerste 14 generaties van deze lijnen.

De inteeltcoëfficiënt in de 14e generatie van de C, RGH en RGL lijnen was opgelopen tot 10.5% en in W56H en W56L tot 18.4 en 18.9%.

De relatieve groeisnelheid (RG) was gedaald in de controle lijn. Van een verandering in het gewicht op 56 dagen (W56D) was geen sprake.

De gerealiseerde erfelijkheidsgraad van de selektie op RG was 0.06 ± 0.03 in RGH en 0.10 ± 0.02 in RGL. Een gecombineerde schatting uit de divergerende lijnen gaf een waarde van 0.08 ± 0.01. Uit nadere analyse bleek, dat de effektiviteit van de selektie in de eerste generaties lager was dan in de latere. Door de binnen familie selektie was het cumulatieve selektieverschil in RG niet groot. Het selektieverschil in RGH was kleiner dan in RGL. Tussen W56H en W56L zijn grote verschillen ontstaan. In de laatste generaties waren de muizen in W56H op 56 dagen gemiddeld meer dan twee keer zo zwaar als in W56L. De gerealiseerde erfelijkheidsgraad voor W56D was in W56H 0.28 ± 0.01 en in W56L 0.35 ± 0.02. Een gecombineerde schatting uit de divergerende lijnen gaf een waarde van 0.31 ± 0.01.

Tussen C, RGH en RGL zijn vrijwel geen verschillen in staartlengte ontstaan. Hetzelfde geldt voor de bevruchtingsresultaten, het aantal dagen tussen paren en werpen, de worpgrootte en het overlevingspercentage tussen 0 en 56 dagen. De staartlengte nam toe in W56H en af in W56L. Deze veranderingen in staartlengte vormen een afspiegeling van de verschillen in grootte, die tussen deze lijnen zijn ontstaan. Het aantal dagen tussen paren en werpen nam in beide lijnen toe; het aantal worpen daalde sterk in beide lijnen. De worpgrootte steeg in W56H en daalde in W56L. De overlevingspercentages waren weinig verschillend in beide lijnen. Eén en ander had tot gevolg, dat het aantal dieren op 56 dagen daalde. Deze daling was in W56L zo sterk, dat het selektieverschil in de vrouwtjes in sommige generaties vrijwel nul werd.

In alle lijnen was het sterftepercentage van de 5e tot de 8e generatie verhoogd.

Het groeiverloop van de lijnen is beschreven met de logistische funktie.

$W_t = A/(1 + be^{-kt})$
W_t = gewicht op leeftijd t
A = asymptoot; een schatting voor het volwassen gewicht
b = integraal constante
k = parameter voor de snelheid van groeiverandering

Deze funktie is gekozen na literatuuronderzoek en het testen van de funktie in de uitgangspopulatie. In deze uitgangspopulatie waren de gewichten dagelijks vastgesteld tussen 18 en 61 dagen. De correlatie tussen de waargenomen en de berekende gewichten was 0.97. Deze waarde stemt overeen met in de literatuur vermelde. Wel bleken systematische afwijkingen voor te komen. In beide geslachten werden aanvankelijk de gewichten overschat, terwijl het latere groeiverloop werd onderschat. De correlaties tussen de berekende en de gevonden gewichten daalden niet als het waarnemingsinterval werd verlengd van 1 tot 7 dagen.

Het groeiverloop in de 6e tot en met de 14e generatie van de 5 lijnen werd beschreven. Daartoe werden van alle dieren de wekelijkse gewichten tussen 1 en 8 weken bepaald. De restvariantie in deze lijnen, W56L uitgezonderd, was lager dan in de basispopulatie. Dit moet waarschijnlijk worden toegeschreven aan de grotere spreiding in gewichten, waaruit de logistische funktie werd bepaald. Dit verklaart tevens waarom de restvariantie bij vrouwtjes hoger was dan bij mannetjes en in W56H het laagst en W56L het hoogst was, zoals uit Tabel 4.2 volgt. In W56L steeg de restvariantie significant.

De beoordeling van de verschillen in groeiverloop tussen de lijnen werd gebaseerd op de vergelijking van de parameters k en A en de berekende leeftijd waarop het buigpunt werd bereikt (t_i). De vergelijking van de veranderingen in groeiverloop in de lijnen is gemaakt aan de hand van de veranderingen in het gemiddelde van de parameters per generatie per lijn en door middel van een vergelijking van de lijnen en van de geslachten in de generaties 13 en 14. De resultaten hiervan bevestigen elkaar. Selektie op een hoge RG verlaagde het tempo en verhoogde het volwassen gewicht. Het buigpunt werd later bereikt. Selektie op een lage RG had een tegengesteld effekt. De verschillen tussen RGH en RGL waren zowel in generatie 13 als in generatie 14 significant ($p \leqslant 0.001$). In W56H was k gedaald; A en t_i waren gestegen. In W56L werd het tegengestelde gevonden. Voor alle drie criteria werden tussen W56H en W56L grote verschillen gevonden ($p \leqslant 0.001$).

Mannetjes hadden een lagere k, een hoger volwassen gewicht en het buigpunt op een latere leeftijd dan vrouwtjes. Deze verschillen waren op enkele uitzonderingen na significant. Schattingen van de binnen worp correlaties tussen RG en de parameters van de logistische funktie werden verricht (Tabel 4.6). Bovendien werden partiële correlaties berekend, waarbij A constant werd gehouden (Table 4.7). Uit deze berekeningen volgde o.a. dat de direkte relatie

tussen RG en *k* positief is, terwijl de indirekte relatie via het volwassen gewicht negatief is. Uit de veranderingen in de selektielijnen bleek, dat het effekt van dit indirekte verband sterker is geweest, omdat het gerealiseerde verband tussen *k* en RG negatief was.

Een vergelijking van de mate van vroegrijpheid, gedefiniëerd volgens TAYLOR en FITZHUGH 1971, liet zien dat de selektie in RGL en W56L een grotere mate van vroegrijpheid tot gevolg had, terwijl in RGH en W56H de mate van vroegrijpheid daalde. De veranderingen in vroegrijpheid gingen echter gepaard met tegengestelde veranderingen in het volwassen gewicht. Het feit, dat kruising van de groeicurven niet systematisch optrad, moet worden verklaard uit het feit dat de veranderingen in het volwassen gewicht waarschijnlijk meer bepalend waren voor de hoogte van de gewichten op jonge leeftijd dan de verschillen in vroegrijpheid.

Door de gewichten en de leeftijden tegen elkaar uit te zetten op een relatieve schaal, bleek dat de verschillen in groeiverloop niet volledig werden bepaald door de verschillen in volwassen gewicht en de tijd die nodig is om dit te bereiken. Bij eenzelfde percentage van de tijd, die nodig is om het volwassen gewicht te bereiken hadden W56H en RGH een lager percentage van het volwassen gewicht bereikt dan W56L en RGL. Vrouwtjes hadden bij eenzelfde procentuele leeftijd een hoger percentage van het volwassen gewicht bereikt dan mannetjes (Figuur 4.5).

Om na te gaan of er door de selektie verschillen in de samenstelling en de efficiëntie van de groei zijn ontstaan, werden in groepen muizen, die een afspiegeling vormden van de gemiddelde genotypische waarden in de 11e generatie van elk der selektielijnen, groei, voeropname en lichaamssamenstelling bepaald tussen 3 en 15 weken. Daartoe werden wekelijks de gewichten individueel en de voeropname per kooi bepaald, terwijl de lichaamssamenstelling in telkens twee steekproeven van elk 6 muizen werd vastgesteld op 3, 4, 5, 6, 7, 8, 9, 11, 13 en 15 weken.

Mannetjes groeiden sneller dan vrouwtjes. De verschillen in groeisnelheid tussen RGH en RGL waren klein; tot ongeveer 10 weken groeide RGH sneller. W56H had gedurende het gehele waargenomen trajekt een veel hogere groeisnelheid dan W56L. In W56L groeiden de muizen na 6 weken vrijwel niet meer.

De voeropname was na 6 weken tamelijk constant. Daarvoor was de voeropname gestegen, waarschijnlijk door compensatoire groei en extra aktiviteit tijdens de puberteit. De verschillen tussen RGH en RGL waren klein; W56H had een veel grotere voeropname dan W56L. Mannetjes namen meer voer op dan vrouwtjes.

De voeropname en het gewicht waren in hoge mate gecorreleerd. De voederefficiëntie daalde in alle lijnen sterk tot ongeveer 6 weken en bleef daarna vrijwel constant. Mannetjes hadden tot 8 weken een hogere efficiëntie dan vrouwtjes. De verschillen tussen RGH en RGL waren niet systematisch. W56H had een aanzienlijk hogere voederefficiëntie dan W56L.

Het aspercentage steeg enigszins bij het ouder worden. De verschillen tussen

de lijnen en tussen de geslachten waren gering en niet systematisch. De verschillen in vetpercentage waren veel groter. Het vetpercentage steeg bij het ouder worden, vooral in W56H. Vrouwtjes hadden een hoger vetpercentage dan mannetjes. RGH was aanvankelijk vetter dan RGL. De verschillen tussen W56H en W56L waren zeer groot. In W56H steeg het vetgehalte tot 1/4 van het lichaamsgewicht. Het eiwitgehalte bleef vrijwel constant bij het ouder worden. Hierop waren twee uitzonderingen; in RGL steeg het eiwitgehalte aanzienlijk tot ongeveer 9 weken en daalde daarna tot het niveau van de andere lijnen. Dit wijst erop dat de gewichtstoename in deze lijn aanvankelijk veel meer uit spierweefsel en minder uit vetaanzet bestond dan in de andere lijnen. Ook W56L had in het begin een hoger eiwitgehalte. In alle situaties van een hoog vetgehalte was het watergehalte laag. Het watergehalte daalde bij het ouder worden. Deze verschillen tussen de lijnen en tussen de geslachten bleken ook bij de analyse van de verschillen in lichaamssamenstelling op 8 weken (Tabel 5.4).

De correlaties, berekend binnen lijnen, geslachten en leeftijdsklassen, waren voor het vetgehalte met de gehaltes van de andere componenten alle significant negatief. De correlatie tussen water- en vetgehalte was hoog (−0.91). Tussen eiwit- en watergehalte was de correlatie 0.32 ($p \leqslant 0.01$). De correlaties tussen as- en water- en tussen as- en eiwitgehalte waren niet significant.

De efficiëntie van de gewichtstoename werd bij toenemende intervallengte berekend vanaf 3 weken. De bruto energetische efficiëntie daalde bij het ouder worden, behalve in de vrouwtjes van W56L, waar de waarden vanaf het begin zeer laag waren.

De verschillen tussen RGH en RGL waren klein. RGH had meestal een iets hogere bruto energetische efficiëntie dan RGL. W56H was steeds veel hoger dan W56L. Mannetjes groeien efficiënter dan vrouwtjes.

De fraktie van de opgenomen energie die in eiwit werd vastgelegd, daalde bij het ouder worden. Mannetjes hadden een hogere fraktie dan vrouwtjes. De verschillen tussen RGH en RGL waren klein. Aanvankelijk was RGH hoger, daarna RGL. De verschillen tussen W56H en W56L waren groot ten gunste van W56H. W56H week echter maar weinig van de controle af. De hogere bruto energetische efficiëntie van W56H werd dan ook grotendeels door de vetaanzet bepaald. Uit de analyse van de verschillen tussen de lijnen en tussen de geslachten in het interval tussen 3 en 8 weken bleek, dat RGH 9% meer energie opnam, 10% hogere bruto energetische efficiëntie had, maar 23% minder eiwit aangezet had per eenheid bruto opgenomen energie. W56H nam 40% meer energie op, de bruto energetische efficiëntie was 145% hoger en er werd 85% meer eiwit aangezet per eenheid opgenomen energie. De verschillen tussen geslachten waren 20%, 32% en 40% in het voordeel van de mannetjes.

Wanneer de hoeveelheid aangezet eiwit per eenheid opgenomen voer werd gehanteerd als criterium voor de vleesproduktiegeschiktheid van een lijn, dan waren RGL en W56H het gunstigst. Hieruit volgt, dat de hogere voerefficiëntie in W56H in vergelijking met RGL dus berust op hogere vetaanzet in W56H. Op grond van hetzelfde criterium kon tevens worden geconcludeerd, dat mannetjes aanzienlijk geschikter zijn dan vrouwtjes.

REFERENCES

ABLANALP, H., F. X. OGASAWARA and V. S. ASMUNDSON: Influence of selection for bodyweight at different ages on growth of turkeys. B. Poultry Sci. **4** (1963): 71–82.

BAKER, R. L. and F. R. M. COCKREM: Selection for bodyweight in the mouse at three temperatures and the correlated response in taillength. Genetics **65** (1970): 505–523.

BAKKER, H., J. OLINK and J. H. WALLINGA: Litterweight of mice after combination of lines selected for litter size and for bodyweight. Zeitschr. Tierz. u. Z. biol. (1974a). In press.

BAKKER, H., J. H. WALLINGA and W. J. KOOPS: The accuracy of the measurements of weights and taillength in mice. Zeitschr. Versuchstierk. (1974b). In press.

BATEMAN, N.: Selection of mice for growth on constant and on changing maize-milk diets. Anim. Prod. **13** (1971): 425–440.

BAUMGARDT, B. R.: Voluntary feed intake. In: Animal growth and nutrition. Lea and Febiger. Philadelphia. 1969. Chapt. 6: 164–174.

BERTALANFFY, L. von: Principles and theory of growth. In: Fundamental aspects of normal and malignant growth. Elsevier. Amsterdam. 1960.

BICHARD, M.: Genetic aspects of growth and development in the pig. In: Growth and development of mammals. Butterworths. London. 1968: 309–324.

BIONDINI, P. E., T. M. SUTHERLAND and L. H. HAVERLAND: Body composition in mice selected for rapid growth rate. J. Anim. Sci. **27** (1968): 5–12.

BLAXTER, K. L.: The effect of the dietary energy supply on growth. In: Growth and development of mammals. Butterworths. London. 1968: 329–344.

BRADFORD, G. E.: Growth and reproduction in mice selected for rapid bodyweight gain. Genetics **69** (1971): 499–512.

BRINKS, J. S., R. T. CLARCK, N. M. KIEFFER and J. J. URICK: Estimates of genetic, environmental and phenotypic parameters in range Hereford females. J. Anim. Sci. **23** (1964): 711–716.

BRODY, S.: Bio-energetics and growth. Reinhold Publ. Corp. New York. 1945.

CARMON, J. L.: The effects of radiation on growth pattern of mice. Growth **29** (1965): 85–95.

CHAPMAN, A. B.: Contributions of laboratory animals to research in livestock improvement. In: Germ. Plasm. Resources. Amer. Ass. Adv. Sci. **66** (1961): 225–238.

COCKREM, F.: Selection for relationships opposite to those predicted by the genetic correlation between two traits in the house mouse (Musculus). Nature **183** (1959): 342–343.

CÖP, W. A. G.: De groei bij varkens. (Literatuuroverzicht). Meded. Landbouwhogeschool. **71-4** (1971): 40 p.p.

COX, D. F., J. E. LEGATES and C. C. COCKERHAM: Maternal influence on bodyweight. J. Anim. Sci. **18** (1959): 519–527.

C.P.B. Mededelingen. Centraal Proefdieren Bedrijf, T.N.O. Zeist. **1**. 1967.

CURTIS, H. J.: Aging. In: Animal Growth and nutrition. Lea and Febiger. Philadelphia. 1969. Chapt. 9: 164–174.

DALTON, D. C. and T. L. BYWATER: The effect of selection for litter size and litterweight at weaning in mice maintained on two diets. Anim. Prod. **5** (1963): 317–326.

DALTON, D. C.: Selection for growth in mice on two diets. Anim. Prod. **9** (1967): 425–434.

DICKERSON, G. E.: Techniques for research in quantitative animal genetics. In: Techn. and proc. in anim. sci. research. Amer. Soc. Anim. Sci. 1969: 36–79.

DICKERSON, G. E.: Efficiency of animal production- molding the biological components. J. Anim. Sci. **30** (1970): 849–859.

DOORNENBAL, H.: Growth, development and chemical composition of the pig. I. Lean tissue and protein. Growth **35** (1971): 281–295.

EISEN, E. J., B. J. LANG and J. E. LEGATES: Comparison of growth functions within and between lines of mice selected for large and small bodyweight. Theor. Appl. Genet. **39** (1969): 251–260.

EISEN, E. J.: Long term selection response for 12-day litterweight in mice. Genetics **72** (1972): 129–142.

ELLIOTT, D. S., J. E. LEGATES and L. C. UHLBERG: Changes in reproductive processes of mice selected for large and small body size. J. Reprod. Fert. **17** (1968): 9–18.

EL OKSH, H. A., T. M. SUTHERLAND and J. S. WILLIAMS: Prenatal and postnatal maternal influence on growth in mice. Genetics **57** (1967): 79–94.

FABENS, A. J.: Properties and fitting of the Von Bertalanffy growthcurve. Growth **29** (1965): 265–289.

FALCONER, D. S.: Selection for large and small size in mice. J. Genet. **51** (1953): 470–501.

FALCONER, D. S. and J. W. B. KING: A study of selection limits in the mouse. J. Genet. **51** (1953): 561–581.

FALCONER, D. S.: Patterns of response in selection experiments with mice. Cold Spr. Harb. Symp. quant. Biol. **20** (1955): 178–196.

FALCONER, D. S.: Introduction to quantitative genetics. Oliver and Boyd, Edinburgh and London. 1960a.

FALCONER, D. S.: Selection of mice for growth on high and low planes of nutrition. Genet. Res. **1** (1960b): 91–113.

FALCONER, D. S.: The relevance of experiments with laboratory animals to the genetic improvement of farm livestock. Rep. of Proc. and Inv. Papers. 9th Int. Congr. of Anim. Prod. (1966): 235–241.

FALCONER, D. S.: Genetic aspects of breeding methods. In: The U.F.A.W. Handbook on the care and management of laboratory animals. Livingstone. Edinburgh and London. 1967. Chapt. 6.: 72–96.

FITZHUGH, H. A. and ST. C. S. TAYLOR: Genetic analysis of degree of maturity. J. Anim. Sci. **33** (1971): 717–725.

FOWLER, R. E.: The growth and carcass composition of strains of mice selected for large and small body size. J. Agric. Sci. **51** (1958): 137–148.

FOWLER, R. E. and R. G. EDWARDS: The fertility of mice selected for large or small body size. Genet. Res. **1** (1960): 393–407.

FOWLER, R. E.: The efficiency of food utilization, digestibility of foodstuffs and energy expenditure of mice selected for large and small body size. Genet. Res. **3** (1962): 51–68.

FREDEEN, H. T.: Crossbreeding and swine production. Anim. Breeding Abstr. **25** (1957): 339–347.

GALL, G. A. E. and W. H. KYLE: Growth of the laboratory mouse. Theor. Appl. Genet. **38** (1968): 304–308.

GALL, G. A. E.: Genetics of growth. In: Animal Growth and Nutrition. Lea and Febiger. Philadelphia. 1969. Chapt. 3: 63–81.

GOODALE, H. D.: A study of inheritance of body weight in the albino mouse by selection. J. Hered. **29** (1938): 101–112.

HANRAHAN, J. P., A. C. HOOPER and J. C. MCCARTHY: Effects of divergent selection for bodyweight on fibre number and diameter in two mouse muscles. Anim. Prod. **16** (1973): 7–16.

HILL, W. G. and A. ROBERTSON: The effect of linkage on limits to artificial selection. Genet. Res. **8** (1966): 269–294.

HILL, W. G.: Design and efficiency of selection experiments for estimating genetic parameters. Biometrics **27** (1971): 293–311.

HILL, W. G.: Estimation of genetic change: I. General theory and design of control populations. Anim. Breed. Abstr. **40** (1972a): 1–15.

HILL, W. G.: Estimation of genetic change: II. Experimental evaluation of control populations. Anim. Breed. Abstr. **40** (1972b): 193–213.

HULL, P.: Genetic relations between carcass fat and bodyweight in mice. J. Agric. Sci. **55** (1960): 317–321.

JONGE H. DE: Inleiding tot de medische statistiek. Deel I en II. Leiden. 1964.

KIDWELL, J. F. and A. HOWARD: The inheritance of growth and form in the mouse. I: A diallel analysis of weight from birth through 10 weeks. Growth **33** (1969): 269–289.

KIDWELL, J. F., A. HOWARD and A. K. LAIRD: The inheritance of growth and form in the

mouse. II: The Gompertz growth equation. Growth **33** (1969): 339–352.
KIDWELL, J. F. and A. HOWARD: The inheritance of growth and form in the mouse. III: Orthogonal polynomials. Growth **34** (1970): 87–97.
KLEIBER, M.: The fire of life: An introduction to animal energetics. Wiley. New York. 1961.
LAIRD, A. K., S. A. TYLER and A. D. BARTON: Dynamics of normal growth. Growth **29** (1965): 233–248.
LAIRD, A. K. and A. HOWARD: Growth curves in inbred mice. Nature. London. **213** (1967): 786–788.
LAND, R. B.: Genetic and phenotypic relationships between ovulation rate and bodyweight in the mouse. Genet. Res. **15** (1970): 171–182.
LANG, B. J. and J. E. LEGATES: Rate, composition and efficiency of growth in mice selected for large and small bodyweight. Theor. Appl. Genet. **39** (1969): 306–314.
LEGATES, J. E. and B. R. FARTHING: Selection for growth and maternal performance in mice. J. Anim. Sci. **21** (1962): 974 (Abstract).
LEGATES, J. E.: Mimeographed notes. Dept. Anim. Husb. Wageningen. 1971.
MAC ARTHUR, J. W.: Genetics of body size and related characters. I: Selecting small and large races of the laboratory mouse. Amer. Nat. **78** (1944): 142–157.
MAC ARTHUR, J. W.: Selection for small and large body size in the house mouse. Genetics **34** (1949): 194–209.
MAGEE, W. T.: Relationship between daily feed consumption and feed efficiency. J. Anim. Sci. **21** (1962): 880–882.
MCCARTHY, J. C.: Effects of different methods of selection for weight on the growth curve in mice. Proc. E. A. A. P. Congr. Paris. 1971.
MINNAARD, P. R.: Genotype-milieu interaktie bij muizen bij een positieve selektie op het lichaamsgewicht op de leeftijd van 56 dagen. Scriptie Veeteelt en Erfelijkheidsleer. Wageningen. 1970.
MOAV, R.: Specialised sire and dam lines. I: Economic evaluation of crossbreds. Anim. Prod. **8** (1966a): 193–202.
MOAV, R.: Specialised sire and dam lines. II: The choice of the most profitable parental combination when component traits are genetically additive. Anim. Prod. **8** (1966b): 203–211.
MOAV, R.: Specialised sire and dam lines. III: Choice of the most profitable parental combination when component traits are genetically non-additive. Anim. Prod. **8** (1966c): 365–374.
MOAV, R. and W. G. HILL: Specialised sire and dam lines. IV: Selection within lines. Anim. Prod. **8** (1966): 375–390.
MONTEIRO, L. S. and D. S. FALCONER: Compensatory growth and sexual maturity in mice. Anim. Prod. **8** (1966): 179–192.
MORE O'FERRALL, G. J. and V. M. TIMON: Selection for bodyweight and tissue growth in mice. Proc. E.A.A.P. Dublin. 1968.
MORE O'FERRALL, G. J. and V. M. TIMON: Direct selection for tissue weight and correlated response in lines selected for weight in mice. Brit. Soc. Anim. Harrogate. 1970.
NAIR, K. R.: The fitting of growth curves. In: Statistics and mathematics in biology. Iowa State College Press. Ames. 1954.
NEEDHAM, A. E.: The growth process in animals. Pitman and sons Ltd. London. 1964.
PARKS, J. R.: Phenomenology of animal growth. N. C. State Univ. Raleigh. 1971.
PARKS, J. R.: The physiology of growth: Animals as input-output devices. Proc. Int. Summer School on computers and research in Animal Nutrition and Veterinary medicine. Elsinore. 1972: 383–403.
RAHNEFELD, G. W., W. J. BOYLAN, R. E. COMSTOCK and M. SINGH: Mass selection for post-weaning growth in mice. Genetics **48** (1963): 1567–1583.
RAHNEFELD, G. W., R. E. COMSTOCK, W. J. BOYLAN and M. SINGH: Genetic correlation between growth rate and feed per unit gain in mice. J. Anim. Sci. **24** (1965): 1061–1066.
RAHNEFELD, G. W., R. E. COMSTOCK, M. SINGH and S. R. NAPUKET: Genetic correlation between growth rate and litter size in mice. Genetics **54** (1966): 1423–1429.

RAO, C. R.: Some statistical methods for comparison of growth curves. Biometrics **14** (1958): 1–17.
RHODES, E. C.: Population mathematics III. J. Roy. Stat. Soc. **103** (1940): 362–387.
RICHARDS, F. J.: A flexible growth function for empirical use. J. exp. Botany **10** (1959): 290–300.
RICHARDSON, R. H., K. KOJIMA and H. L. LUCAS: An analysis of short term selection experiments. Heredity **23** (1968): 493–506.
ROBERTS, R. C.: The lifetime growth and reproduction of selected strains of mice. Heredity **16** (1961): 369–381.
ROBERTS, R. C.: Some contributions of laboratory mouse to animal breeding research. Anim. Breed. Abstr. **33** (1965): 339–353 and 515–526.
ROBERTS, R. C.: The limits to artificial selection for bodyweight in the mouse: I. The limits attained in earlier experiments. Genet. Res. **8** (1966a): 347–360.
ROBERTS, R. C.: The limits to artificial selection for bodyweight in the mouse: II. The genetic structure of the limits. Genet. Res. **8** (1966b): 361–375.
ROBERTS, R. C.: The limits to artificial selection for bodyweight in the mouse: III. Selection from crosses between previously selected lines. Gen. Res. **9** (1967a): 73–85.
ROBERTS, R. C.: The limits to artificial selection for bodyweight in the mouse: IV. Sources of new genetic variance – irradiation and outcrossing. Gen. Res. **9** (1967b): 87–98.
ROBERTSON, A.: Laboratory breeding experiments and animal improvement. Proc. 10th Intern. Congr. Genet. **1** (1959): 199–205.
ROBERTSON, A.: A theory of limits in artificial selection. Proc. R. Soc. B. **153** (1960): 234–249.
ROBINSON, D. W. and G. E. BRADFORD: Cellular response to selection for rapid growth in mice. Growth **33** (1969): 221–229.
SKÅRMAN, S.: Crossbreeding experiments with swine. Lantbrukshögsk. Ann. **31** (1965): 3–92.
SMITH, C.: The use of specialised sire and dam lines in selection for meat production. Anim. Prod. **6** (1964): 337–344.
SNEDECOR, G. W. and W. G. COCHRAN: Statistical methods. 6th Ed. Iowa State Univ. Press. Ames. 1972.
STANIER, M. W. and L. E. MOUNT: Growth rate, food intake and body composition before and after weaning in strains of mice selected for mature body weight. Br. J. Nutr. **28** (1972): 307–325.
SUTHERLAND, T. M.: The correlation between feed efficiency and rate of gain, a ratio and its numerator. Biometrics **21** (1965): 739–749.
SUTHERLAND, T. M., P. E. BIONDINI L. H. HAVERLAND, D. PETTUS and W. B. OWEN: Selection for rate of gain, appetite and efficiency of feed utilization in mice. J. Anim. Sci. **31** (1970): 1049–1057.
TAYLOR, ST. C. S.: A relation between mature weight and time taken to mature in mammals. Anim. Prod. **7** (1965): 203–220.
TAYLOR, ST. C. S. and J. CRAIG: Genetic correlation during growth of twin cattle. Anim. Prod. **7** (1965): 83–102.
TAYLOR, ST. C. S.: Genetic variation in growth and development of cattle. In: Growth and Development of mammals. Butterworths. London. 1968: 267–290.
TAYLOR, ST. C. S. and H. A. FITZHUGH: Genetic relationships between mature weight and time taken to mature within a breed. J. Anim. Sci. **33** (1971): 726–731.
TIMON, V. M. and G. J. MORE O'FERRALL: Studies of tissue growth in mice. Brit. Soc. of Anim. Prod. Harrogate. 1966.
TIMON, V. M.: Genetic studies of growth and carcass composition in sheep. In: Growth and Development of mammals. Butterworths. London. 1968: 400–415.
TIMON, V. M. and E. J. EISEN: Comparison of growth curves of mice selected and unselected for postweaning gain. Theor. and Appl. Genet. **39** (1969): 345–351.
TIMON, V. M. and E. J. EISEN: Comparisons of ad libitum and restricted feeding of mice selected and unselected for postweaning gain. I. Growth, feed consumption and feed efficiency. Genetics **64** (1970): 41–57.

TIMON, V. M., E. J. EISEN and J. M. LEATHERWOOD: Comparison of ad libitum and restricted feeding of mice selected and unselected for postweaning gain. II. Carcass composition and energetic efficiency. Genetics **65** (1970): 145–155.

TITUS, H. W., A. L. MEHRING and J. H. BRAMBAUGH: Variation of feed conversion. Poultry Sci. **32** (1953): 1074–1077.

TURNER, H. N.: Ratios as criteria for selection in animal or plant breeding with particular reference to efficiency of food conversion in sheep. Aust. J. Agric. Res. **10** (1959): 565–580.

WAL, H. VAN DER and M. W. A. VERSTEGEN: Personal communication. 1974.

WEINBACH, A. P.: The human growth curve. I: Prenatal growth. Growth **5** (1941a): 217–233.

WEINBACH. A. P.: The human growth curve. II: Birth to puberty. Growth **5** (1941b): 253–255.

WHITE J. M., J. E. LEGATES and E. J. EISEN: Maternal effects among lines of mice selected for bodyweight. Genetics **60** (1968): 395–408.

WIDDOWSON, E. M.: Assessment of energy value of human foods. Proc. Nutrit. Soc. **14** (1955): 142–154.

WILSON, S. P., H. D. GOODALE, W. H. KYLE and E. F. GODFREY: Longterm selection for bodyweight in mice. J. Hered. **62** (1971): 228–234.

WISHART, J.: Growth rate determination in nutritional studies with bacon pigs and their analysis. Biometrika **30** (1938): 16–28.

YOUNG, C. W., J. E. LEGATES and B. R. FARTHING: Prenatal and postnatal influences on growth, prolificacy and maternal performance in mice. Genetics **52** (1965): 553–561.