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Comparison of Growth Functions Within and Between Lines of Mice Selected for Large and Small Body Weight*

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Summary. Several criteria have been suggested for comparing different nonlinear growth functions to determine which function gives the best quantitative description of a given set of observed sigmoid growth curves. These criteria were then used to compare the logistic, Gompertz and Bertalanffy functions within and among lines of mice: a control line (C_1) and lines selected for large (H_6) and small (L_6) body weight at six weeks of age.

A general comparison of the three growth functions was based on the differences in residual variances of the respective functions fitted to the growth data of individual mice. Since the three functions differ primarily in the fixed proportion of the asymptotic weight at which the inflexion point occurs, the growth function which will provide the minimum residual variance among the three considered is the one which most closely approximates the observed proportion. The results of this comparison indicated that the logistic function gave the best fit for both sexes of the H_6 and C_1 lines. While no significant differences in residual variances were evident in L_6 males, the Bertalanffy function had the smallest residual variance in L_6 females.

The four derived traits of each growth function analyzed individually were the asymptote (A), age at inflexion (t^*), rate at which a logarithmic function of body weight changes with time (k) and mean absolute growth rate with respect to body weight increase (v). The coefficient of variation among individuals within full-sib families was used to compare the relative variability of the analogous traits estimated from the three growth functions. The coefficients of variation of A, t^* and k calculated from the logistic function were significantly ($P < .01$) smaller than those from both the Gompertz and Bertalanffy functions in all three lines, while there were no significant differences in the relative variability of v among the three lines. The genetic and phenotypic correlations between the analogous traits estimated from two different growth functions were sufficiently high in most cases to conclude that the same trait was being measured by the three growth functions. Each derived trait was analyzed for variation in lines, sexes, seasons and respective interactions. The sources of variation generally exhibited similar levels of significance for the analogous traits estimated by the three functions, although a few exceptions were found. These results suggest that although the logistic function provided the best description of the growth data, the same general conclusions about differences within and among the three lines would have been reached with any of the three functions. The four derived traits of the logistic curve were used to describe quantitatively the differences in growth among the H_6, L_6 and C_1 lines.

Introduction

Growth functions have been used extensively to describe mathematically curves of limited sigmoid growth in various species. Parameter estimates of growth curves have biological meaning when their relative magnitudes may be used to assess the importance of differences in growth rate due to genetic or environmental factors. The four growth functions which have been applied most extensively to animal species are the monomolecular, logistic, Gompertz and Bertalanffy curves. 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 final weight at which the inflexion point occurs. The monomolecular function will not be discussed here since its use is limited to the description of growth subsequent to the point of inflexion (BRODY, 1945; TAYLOR, 1965). Although this study is thus restricted to the remaining three members of this family of curves, it is noted that extensive statistical methodology has been developed for the application of polynomial regression to fitting growth curves (RAO, 1958; SPRENT, 1967).

The question arises as to which of the three most widely used growth functions having an inflexion point is most appropriate for analysis of a given set of data. BERTALANFFY (1957, 1960) advocated the function he derived since it provides parameters which are interpretable in terms of rates of anabolism and catabolism. RICHARDS (1959) questioned this interpretation on grounds that it is too restrictive and thus incompatible with the growth curves of many species. LAIRD, TYLER and BARTON (1965) suggested that the Gompertz equation is the most meaningful function based on the demonstration that, over a wide age range of growth in the data they analyzed, the first derivative of the Gompertz curve gave a fit superior to the logistic.

It is apparent that objective criteria are necessary in choosing the proper growth function for specific

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data. For a set of growth points taken on an individual over a time interval, it can be shown that the growth function which will provide the "best" fit among the three considered is the one which most closely approximates the true proportion of final size at which the inflexion point occurs. This proportion is determined by the shape parameter of the function (Richards, 1959). "Best" is used in this context to denote the goodness of fit criterion of minimum error variance for the fitted curve. In addition, the usual assumptions are made regarding residuals in regression analysis (Draper and Smith, 1966). If the shape parameter is significantly different among treatment groups, or if the shape parameter is significantly different from those assumed in all of the three functions, it may be more informative to use Richards generalized curve (Richards, 1959) or the generalized logistic (Nelder, 1961).

Following this reasoning, several criteria are suggested for comparing the different growth functions. Included in these criteria are comparisons to determine if the same general conclusions concerning the data would be obtained from application of any of the growth functions. These criteria were then used to compare the estimated parameters of the logistic, Gompertz and Bertalanffy functions both within and between lines of mice selected for large and small body weight at six weeks of age.

Fitting of Growth Functions

The growth functions considered in this study and some of their important properties are presented in Table 1. The generalized growth function (Richards, 1959) for the n^{th} individual is a four parameter curve of the form

$$y_n(t) = A_n\,[1 - b_n\, e^{-k_n t}]^{1/(1-m_n)} + E_n(t)\,, \qquad (1)$$

where

$y_n(t)$ = body weight (grams) at time t (days),
b_n = time scale parameter of no specific biological significance,
k_n = rate at which a logarithmic function of weight, ln θ, changes linearly per unit of time,
A_n = asymptote or predicted final weight,
m_n = the shape parameter,
$E_n(t)$ = residual error term which is normally and independently distributed with mean zero and variance σ^2.

It is evident from Table 1 that $m = 2$ yields the logistic curve and $m = 2/3$ yields the Bertalanffy curve. As m approaches unity in the limit, equation (1) reduces to the Gompertz (Bhattacharya, 1966). Thus, the *a priori* selection of one of these three curves fixes the inflexion point relative to the final weight. In contrast, if m is variable among genetic groups or environmental treatments, then Richards curve should be used. From this standpoint the choice of an appropriate growth function may be crucial since the inflexion point, being the age at which the absolute growth rate is a maximum, may be closely associated with important biological events such as the onset of sexual maturity (Monteiro and Falconer, 1966).

Another parameter of the growth equation investigated was the weighted mean absolute growth rate with respect to body weight increase (Richards, 1959), which is given by

$$\frac{1}{A_n}\int_0^{A_n}\left(\frac{dy}{dt}\right)dy = \frac{A_n\,k_n}{2\,(m_n+1)} = v_n\,. \qquad (2)$$

Part of the difficulty in comparing growth equations fitted to data is the rather special solutions which have been employed for each curve (Riffenburgh, 1960; Fabens, 1965), although advances in obtaining generalized least-squares solutions have been accomplished (Bhattacharya, 1966). It is therefore desirable to fit all functions using a completely generalized least-squares nonlinear estimation procedure. The maximum neighborhood method (Marquardt, 1963) was used in the present study since it performs an optimum procedural interpolation between the linearization method and the steepest descent method (Draper and Smith, 1966). A single computer program (Marquardt, 1965) which employs the maximum neighborhood method was adapted to fit all growth functions.

It was found that the three-parameter functions (e.g., logistic) generally converged rapidly, whereas the four-parameter function (Richards) converged very slowly in most cases. This was due, in part, to the high correlations between some of the parameters in the parameter correlation matrix of the four-parameter curves, which suggested that a three-parameter fit might be adequate (Marquardt, 1965). In addition, Timon and Eisen (1969) have compared the logistic (which was generally the best fitting curve in the present study) and Richards functions in lines of mice, completely unrelated to those in the present study, selected and unselected

Table 1. *Growth functions and some of their important properties*

Growth Function	Body Weight $y(t)$	Absolute Growth Rate dy/dt	Inflexion Point (y^*, t^*)	Prop. of Final Wt. at Inflexion Point $m^1/(1-m)$
Bertalanffy	$A\,(1 - b\,e^{-kt})^3$	$3\,k\,y\,[(A/y)^{1/3} - 1]$	$\left(\frac{8}{27}A, \frac{ln\,3\,b}{k}\right)$	8/27
Gompertz	$A\,e^{-be^{-kt}}$	$k\,y\,ln\,(A/y)$	$\left(e^{-1}A, \frac{ln\,b}{k}\right)$	e^{-1}
Logistic	$A/(1 + b\,e^{-kt})$	$k\,y\,(1 - y/A)$	$\left(\frac{A}{2}, \frac{ln\,b}{k}\right)$	1/2
Richards	$A\,[1 - b\,e^{-kt}]^{1/(1-m)}$	$ky[(A/y)^{1-m} - 1]/(1-m)$	$\left[m^{1/(1-m)}A\,, \frac{ln\,(b/(1-m))}{k}\right]$	Variable

for high postweaning weight gain. The mean estimates of the shape parameter, *m*, were not significantly different from two in any line-sex subclass. A second comparison showed that the residual variances of the logistic curves were not significantly greater than those of the Richards curves within line-sex subclasses. Thus, although Richards curve was considered and examined it was not included in the comparisons of the present study because of the reasons stated.

Source of Data

Rates of growth of three lines of mice, one selected for large body weight at six weeks of age (H_6), one selected for small body weight at six weeks of age (L_6) and a randomly selected control line (C_1) have been described by LANG and LEGATES (1969). Within each of four mating seasons (summer, fall, winter and spring) individual body weights measured to the nearest one-tenth of a gram were taken from birth (day zero) to 30 days of age at three-day intervals and at six-day intervals from 30 to 54 days. Data from the winter season were minimal in number and were deleted from the present analysis. An additional weight was available at 56 days of age in all seasons and additional three-day interval measurements were available in the summer for days 33, 39, 45 and 51. Thus, body weights at a total of 16 age periods were obtained for all individuals in the fall and spring, while weights at 20 age periods were obtained in the summer. Figure 1 shows the observed growth curves in the original data by line and sex pooled over seasons (LANG and LEGATES, 1969).

The diphasic nature of the growth curve of mice used in this study (LANG and LEGATES, 1969) suggested that more precise results might be obtained if only data were used subsequent to the end of the first phase of growth (15–21 days of age). Contrary to this expectation a comparison of the growth curves fitted from birth to 56 days with those fitted from 21 to 56 days gave essentially similar results. The reason for this is probably due to the relatively small maximum of the preweaning growth phase compared to the postweaning phase.

The logistic, Gompertz and Bertalanffy growth functions were fitted to the growth data of each individual from birth to 56 days. The frequency of mice which had to be deleted (3.3%) because the iterative least squares solution did not converge was not considered large enough to create any bias in the results. The distribution of the number of litters and number of observations by sex and line is given in Table 2.

Table 2. *Distribution of number of litters and number of mice by line and sex*

Line	Litters	Males	Females	Total
H_6	35	76	81	157
C_1	55	124	139	263
L_6	36	59	71	130
Total	126	259	291	550^+

$^+$ Twenty-three mice were deleted from analysis of Bertalanffy curve because the solutions failed to converge.

Statistical Analyses

The first criterion considered was a general comparison of the goodness of fit among the three functions within genetic line and sex made by comparing the residual variances due to lack of fit (σ^2) of each function averaged over individuals and seasons. Examination of this statistic indicates that the smaller it is the more precise will be the predicted values of the fitted curve.

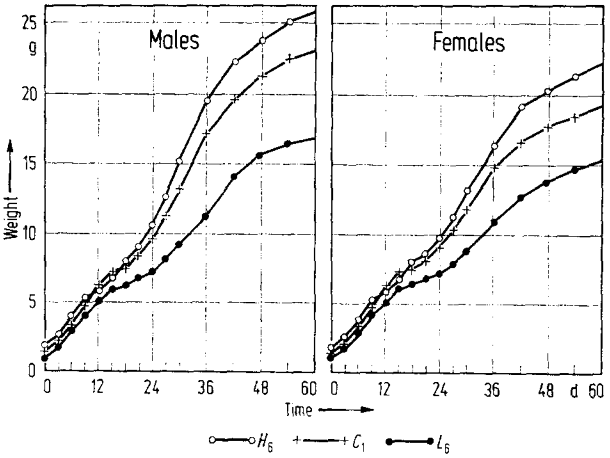

Figure 1. Observed growth curves in the original data by line and sex pooled over seasons (LANG and LEGATES, 1969)

The four derived traits of each growth function analyzed individually were the asymptote (A), age at point of inflexion (t^*), rate at which a logarithmic function of body weight changes with time (k) and mean absolute growth rate (v).

The within line analysis for each derived trait was adjusted for season, sex and season × sex interaction effects using a general least-squares procedure for unequal subclasses (HARVEY, 1960). The data were then analyzed to estimate the components of variance among and within full-sib families for each derived trait within each population. The linear model for the analysis of variance was

$$X_{ln} = \mu + f_l + e_{ln},$$

where

X_{ln} = observation (e. g., asymptote of logistic function) on the n^{th} individual from the l^{th} full-sib family litter),
μ = population mean,
f_l = effect of the l^{th} full-sib family ($l = 1, \ldots, s$),
e_{ln} = residual effect of the n^{th} progeny from the l^{th} family ($n = 1, \ldots, p_l$).

The effects in the model were assumed to be normally and independently distributed with means zero and variances σ_f^2 and σ_w^2. A preliminary analysis showed that family × sex interactions were generally unimportant and thus were pooled with the error sum of squares.

The magnitudes of the within litter variances (σ_w^2) and the coefficients of variation (C. V. = $100\,\sigma_w/\mu$) of each derived trait were utilized as a second criterion in comparing the growth functions with regard to variation among individuals within a family.

Under the assumptions of no epistasis the variance components have the following expectations (WILLHAM, 1963)

$$\sigma_f^2 = 1/2\,\sigma_a^2 + 1/4\,\sigma_d^2 + \sigma_{a_m}^2 + \sigma_{d_m}^2 + \sigma_{a a_m} + \sigma_c^2\,,$$
$$\sigma_w^2 = 1/2\,\sigma_a^2 + 3/4\,\sigma_d^2 + \sigma_e^2\,,$$

where

σ_a^2 = direct additive genetic variance,
σ_d^2 = direct dominance genetic variance,
$\sigma_{a_m}^2$ = maternal additive genetic variance,
$\sigma_{d_m}^2$ = maternal dominance genetic variance,
$\sigma_{a a_m}$ = direct-maternal additive genetic covariance,
σ_c^2 = maternal environmental variance,
σ_e^2 = random environmental variance.

It will be informative to determine if the intraclass correlations, $r_f = \sigma_f^2/(\sigma_f^2 + \sigma_w^2)$, for the same trait estimated from the three growth functions differ significantly from each other. It would have been better if data were available from paternal half-sib families which would be unencumbered by dominance and maternal influences. However, a comparison of the intraclass correlations among the three growth functions should still be valid for the specific purposes outlined.

In application to genetic selection experiments, the growth function that provides a maximum r_f for a given derived trait would be most desirable since this presumably would maximize selection response. On the other hand, if there are no significant differences among the intraclass correlations, then using information from any of the three growth functions should lead to similar responses.

Analyses of covariance between the analogous traits estimated by two different growth functions were conducted using the same linear model except that cross-product terms were obtained among and within full-sib families. From these analyses the genetic correlations (r_g) and phenotypic correlations (r_p) were obtained (FALCONER, 1960). These statistics provide a fourth criterion for comparison of the growth functions. If the genetic correlations between the analogous traits are not significantly different from unity, then the traits are assumed to be identical genetically. If only phenotypic correlations are obtainable from the data and these are close to unity, then similar conclusions are warranted on a phenotypic scale.

A useful approach for comparing the growth functions among treatments (line, sex, season and interactions in this study) would be to assign randomly the growth data of each progeny within a litter to be fitted by one of the three growth functions. The randomization procedure would assure uncorrelated errors and an analysis of variance would determine the importance of treatment × function interactions.

The present set of data does not lend itself to this method of analysis since a sufficient number of mice were not available for sampling within litters and sex. In addition extreme heterogeneity of variances existed for the same derived trait estimated by the different functions, which would invalidate the tests of significance in the analysis of variance. Therefore, an alternative approach was considered whereby each parameter estimate within a function was analyzed separately, and a subsequent comparison made of the levels of statistical significance attained for each effect in the model. In addition, a visual appraisal of the means should reveal any obvious interactions. The statistical model for the treatment comparisons was

$$X_{ijkln} = \mu + L_i + R_j + (LR)_{ij} + f_{l(ij)} + S_k + (LS)_{ik} + (RS)_{jk} + (LRS)_{ijk} + e_{ijkln},$$

where

X_{ijkln} = observation on the n^{th} individual of the k^{th} sex within the l^{th} litter in the i^{th} genetic line and j^{th} season,
μ = population mean
L_i = effect of the i^{th} genetic line ($i = 1, 2, 3$),
R_j = effect of the j^{th} season ($j = 1, 2, 3$),
S_k = effect of the k^{th} sex ($k = 1, 2$),
$(LR)_{ij}$, $(LS)_{ik}$, $(RS)_{jk}$ and $(LRS)_{ijk}$ are respective interactions effects,
$f_{l(ij)}$ = effect of the l^{th} full-sib family within the $(ij)^{th}$ line-season subclass,
e_{ijkln} = random error.

All effects in the model were assumed fixed, except $f_{l(ij)}$ and e_{ijkln} which were random effects. In the analysis of variance, lines, seasons and line × season interactions are tested by the among litter mean square, whereas the remaining sources of variation are tested by the within litter variance.

Results and Discussion

General comparisons of growth functions: Residual variances of the logistic, Gompertz and Bertalanffy functions fitted to the growth data of individual mice and pooled over individuals and seasons are presented in Table 3. The H_6 and C_1 lines revealed a similar pattern for both sexes in that the logistic function had the smallest residual variances while the Bertalanffy function had the largest variances. This situation was exactly reversed in L_6 females, whereas essentially no differences in the residual variances were found among the functions in the L_6 males. Therefore, based on the statistical criterion of most precise prediction of a regression curve, the logistic function would be selected for the H_6 and C_1 lines while the Bertalanffy function would be favored only for females of the L_6 line.

The observed and predicted mean body weights at key ages are presented in Table 4. Body weight

Table 3. *Residual variances of the Logistic, Gompertz and Bertalanffy functions fitted to the growth data of individual mice and averaged over individuals and seasons within line-sex subgroups*$^{++}$

	H_6		C_1		L_6	
Function	Males	Females	Males	Females	Males	Females
Logistic	$0.834^{**,**}$ $(1{,}064)^{+}$	$0.585^{**,**}$ (1,173)	$0.805^{**,**}$ (1,760)	$0.628^{*,**}$ (1,999)	$0.624^{NS,NS}$ (863)	$0.626^{*,**}$ (987)
Gompertz	1.225^{**} (1,064)	0.727^{*} (1,173)	1.014^{**} (1,760)	0.688^{NS} (1,999)	0.610^{NS} (863)	0.560^{NS} (987)
Bertalanffy	1.473 (961)	0.809 (1,130)	1.151 (1.640)	0.719 (1,986)	0.613 (820)	0.517 (974)

$^{+}$ Values in parentheses are degrees of freedom obtained by multiplying the degrees of freedom for each individual curve fitted by the number of individuals

$^{++}$ Levels of significance (based on F tests) designated by a superscript attached to the residual variances are interpreted as follows: logistic superscript gives F tests of logistic versus Gompertz and logistic versus Bertalanffy respectively; Gompertz superscript gives test of Gompertz versus Bertalanffy

* $P < .05$, ** $P < .01$, ^{NS}Not significant ($P > .05$)

Table 4. *Observed and predicted mean body weights (g) at key ages within line and sex averaged over seasons*

Trait	Observed	Predicted			Observed	Predicted		
		Logistic	Gompertz	Bertalanffy		Logistic	Gompertz	Bertalanffy
	H_6 Males				H_6 Females			
Birthweight	1.59	2.05	1.51	1.20	1.50	2.17	1.68	1.43
Weaning weight	9.27	9.73	10.51	11.01	8.82	9.23	9.76	10.04
27-day weight	13.12	13.48	14.10	14.51	11.88	12.37	12.70	12.90
42-day weight	22.97	22.44	22.49	22.65	19.93	19.39	19.25	19.31
56-day weight	26.60	26.93	28.24	28.68	22.36	22.77	23.51	23.90
	C_1 Males				C_1 Females			
Birthweight	1.48	2.17	1.71	1.45	1.45	2.18	1.74	1.53
Weaning weight	8.75	9.08	9.79	10.20	8.40	8.75	9.31	9.64
27-day weight	11.61	12.27	12.87	13.23	10.80	11.46	11.85	12.14
42-day weight	20.34	19.93	20.10	20.30	17.49	17.08	17.16	17.44
56-day weight	23.45	24.01	25.17	25.63	19.15	19.62	20.38	20.97
	L_6 Males				L_6 Females			
Birthweight	1.28	2.17	1.88	1.78	1.22	2.11	1.82	1.71
Weaning weight	7.17	7.04	7.56	7.98	6.93	6.65	7.12	7.55
27-day weight	8.62	9.12	9.63	10.08	8.01	8.46	8.91	9.38
42-day weight	14.78	14.37	14.72	15.18	12.91	12.70	12.97	13.53
56-day weight	17.30	17.81	18.67	19.36	15.01	15.19	15.82	16.61

at 27 days of age is included since it approaches the average estimated weight at the point of inflexion (Table 8). The predicted means of the logistic function were closest to the observed means for weights at days 21, 27 and 56 in all line-sex subgroups with the exception of L_6 females. Although the predicted means of the logistic curve for 42-day body weight generally showed the greatest deviation from the observed means, the differences were relatively small. The predicted mean birth weights of the logistic function had the largest deviation from the observed means. Thus, even though the logistic function provided the smallest residual variance in four out of six line-sex subgroups it did not provide the best prediction of body weight at all ages.

A plot of the residuals for all of the functions being fitted revealed a systematic non-random trend for all line-sex-season subgroups. This result was probably due to the early postweaning growth depression characteristic of the three lines (LANG and LEGATES, 1969) and indicates the difficulty which can be encountered in *a priori* fitting of growth functions.

Comparison of variability among individuals: The second statistical criterion suggested is a comparison of the variability among individuals for the analogous trait estimated from the three growth functions. This was done separately for the H_6, C_1 and L_6 lines. The within litter variances and coefficients of variation presented in Table 5 were considered appropriate measures of variability. Within litter variance measures absolute variability within families and may be subject to scaling effects (e.g., correlation between mean and variance) as well as functional variability. Therefore, the coefficient of variation was used as a measure of relative variability to eliminate scaling effects. The ratio of the variances on a logarithmic scale (approximated by squaring the ratio of the coefficients of variation) has an F distribution (LEWONTIN, 1966), and this statistic was used to test the null hypothesis of no difference in relative variability between the same trait estimated from two growth functions.

The coefficients of variation of the asymptote, age at inflexion and rate obtained from the logistic function were significantly ($P < .01$) smaller than those from both the Gompertz and Bertalanffy functions in all three populations (Table 5). For these traits the coefficients of variation computed from the Gompertz function were generally less than those of the Bertalanffy curve, but the level of significance varied. Absolute mean growth rate revealed no significant differences in relative variability among the three growth curves.

It would appear from these results together with the information on the residual variances of the nonlinear regression curves that for these growth data, the logistic function provides the best prediction of growth with a minimum of extraneous variation. As noted previously, TIMON and EISEN (1969) found that the Richards function, when compared with the logistic function, did not significantly increase the prediction of the growth curve in two other lines of mice.

Within population genetic and phenotypic comparisons: Intraclass correlations among full-sib families (r_f) and their standard errors are listed in Table 6. The comparison of chief interest is differences in r_f for the same trait computed from the three functions. Differences between functions observed for the intraclass correlation of all four traits were within the limits of the sampling errors of this experiment. This result

Table 5. *Comparison of within litter variances (σ_w^2) and coefficients of variation (C. V.) calculated within lines for the four derived traits of the three growth functions*

Trait	Function	H_6 σ_w^2	H_6 C. $V.^{++}$	C_1 σ_w^2	C_1 C. V.	L_6 σ_w^2	L_6 C. V.
Asymptote (A)	Logistic	$4.36(119)^{+}$	$7.73^{**,**}$	4.86(205)	$9.30^{**,**}$	4.37(91)	$11.03^{**,**}$
	Gompertz	20.54(119)	13.69^{NS}	20.56(205)	15.77^{NS}	20.19(91)	18.73^{**}
	Bertalanffy	28.75(109)	14.10	33.43(196)	17.52	51.03(87)	24.62
Age at Inflexion Point (t^*)	Logistic	5.38	$8.37^{**,**}$	8.16	$10.67^{**,**}$	12.35	$12.17^{**,**}$
	Gompertz	16.58	16.18^{NS}	24.44	20.71^{*}	38.24	23.36^{*}
	Bertalanffy	14.45	14.57	26.79	23.65	58.17	29.89
Rate (k)	Logistic	5.56×10^{-5}	$8.47^{**,**}$	8.75×10^{-5}	$10.84^{**,**}$	5.54×10^{-5}	$10.38^{**,**}$
	Gompertz	3.24×10^{-5}	12.50^{*}	4.79×10^{-5}	15.16^{*}	3.82×10^{-5}	16.67^{**}
	Bertalanffy	2.21×10^{-5}	14.73	3.57×10^{-5}	18.40	3.48×10^{-5}	22.61
Mean Absolute Growth Rate (v)	Logistic	1.38×10^{-3}	$9.25^{NS, NS}$	2.04×10^{-3}	$13.41^{NS, NS}$	0.81×10^{-3}	$12.74^{NS, NS}$
	Gompertz	1.02×10^{-3}	8.60^{NS}	1.55×10^{-3}	12.47^{NS}	0.65×10^{-3}	11.87^{NS}
	Bertalanffy	0.94×10^{-3}	8.65	1.40×10^{-3}	12.26	0.62×10^{-3}	11.91

[+] Values in parentheses are degrees of freedom for the four traits within a genetic line

[++] Levels of significance (based on F tests) designated by a superscript attached to the coefficients of variation are interpreted as follows: logistic superscript gives tests of logistic versus Gompertz and logistic versus Bertalanffy, respectively; Gompertz superscript gives test of Gompertz versus Bertalanffy

* $P < .05$, ** $P < .01$, ^{NS} Not significant ($P > .05$)

Table 6. *Intraclass correlations (r_f) and their standard errors computed within lines for the four derived traits of the three growth curves*

Trait	Function	H_6	C_1	L_6
Asymptote (A)	Logistic	.21 ± .09	.16 ± .06	.34 ± .10
	Gompertz	.11 ± .08	.21 ± .07	.29 ± .09
	Bertalanffy	.22 ± .09	.23 ± .07	.32 ± .10
Age at Inflexion Point (t^*)	Logistic	.44 ± .09	.42 ± .07	.34 ± .10
	Gompertz	.41 ± .08	.38 ± .07	.33 ± .10
	Bertalanffy	.49 ± .09	.39 ± .07	.39 ± .08
Rate (k)	Logistic	.21 ± .08	.24 ± .07	.30 ± .10
	Gompertz	.36 ± .09	.38 ± .07	.37 ± .09
	Bertalanffy	.42 ± .09	.41 ± .07	.38 ± .10
Mean Absolute Growth Rate (v)	Logistic	.33 ± .08	.13 ± .06	.17 ± .10
	Gompertz	.41 ± .07	.18 ± .06	.20 ± .09
	Bertalanffy	.45 ± .09	.21 ± .07	.21 ± .08

was consistent for the H_6, C_1 and L_6 lines. There was some tendency for r_f to be larger with the Bertalanffy curve for the rate and mean absolute growth rate traits, but this was not significant.

It was indicated earlier that r_f represents the proportion of phenotypic variance due to genetic and maternal factors. Therefore, no matter which curve was considered, the same general statements may be made concerning the relative magnitude of combined genetic and maternal factors influencing a specific derived trait.

The C_1 line provided estimates of the intraclass correlation which were least likely to be biased by directional selection. The combined genetic and maternal influences accounted for a larger proportion of the total variation for age at inflexion point (t^*) and rate (k) than for final weight (A) and mean absolute

Table 7. *Genetic (r_g) and phenotypic (r_p) correlations between the same derived trait estimated from two different growth functions*

Trait	Functions Correlated	H_6 r_g ± s. e.	H_6 r_p	C_1 r_g ± s. e.	C_1 r_p	L_6 r_g ± s. e.	L_6 r_p
Asymptote (A)	Logistic-Gompertz	.61 ± .50	.85**	.71 ± .48	.81	.88 ± .39	.87
	Logistic-Bertalanffy	.10 ± .48	.64	.35 ± .48	.65	.66 ± .38	.77
	Gompertz-Bertalanffy	.84 ± .66	.95	.93 ± .47	.95	.95 ± .42	.96
Age at Inflexion Point (t^*)	Logistic-Gompertz	.99 ± .32	.99	.99 ± .26	.98	.99 ± .40	.97
	Logistic-Bertalanffy	.99 ± .29	.98	.99 ± .26	.96	.96 ± .38	.94
	Gompertz-Bertalanffy	.99 ± .28	.99	.99 ± .26	.99	.99 ± .36	.99
Rate (k)	Logistic-Gompertz	.90 ± .51	.93	.94 ± .37	.94	.86 ± .40	.88
	Logistic-Bertalanffy	.75 ± .53	.83	.85 ± .36	.87	.77 ± .39	.79
	Gompertz-Bertalanffy	.99 ± .38	.99	.99 ± .29	.99	.99 ± .37	.98
Mean Absolute Growth Rate (v)	Logistic-Gompertz	.99 ± .39	.98	.97 ± .63	.98	.98 ± .69	.98
	Logistic-Bertalanffy	.98 ± .41	.97	.92 ± .63	.96	.94 ± .73	.96
	Gompertz-Bertalanffy	.99 ± .34	.99	.99 ± .53	.99	.99 ± .65	.99

** All phenotypic correlations are significant at $P < .01$

growth rate (v). Similar full-sib correlations have been reported for final weight and rate obtained by fitting the logistic function to individual growth data of mice (CARMON, 1965).

The genetic (r_g) and phenotypic (r_p) correlations between the analogous traits estimated from two different growth functions (Table 7) were sufficiently high in most cases to conclude that the same trait was being measured by the three growth functions. The only case where the genetic correlations differed significantly from unity involved the estimated asymptotes of the logistic and Bertalanffy curves in the H_6 and C_1 lines, respectively. An examination of the family means indicated that the larger variation among individuals within families for the Bertalanffy asymptotes caused changes in ranking of family means which would explain the low genetic correlations.

Comparison among populations: Means of the four derived traits for each growth function are given in Table 8 by line-sex subclasses averaged over seasons, and analyses of variance are presented in Table 9. The sources of variation generally exhibited similar levels of significance for the same trait estimated by the three functions, although a few exceptions may be noted. Seasonal effects were significant ($P < .01$) for the asymptote and age at inflexion point of the logistic function, but were not significant ($P > .05$) for the Gompertz and Bertalanffy curves. Examination of seasonal means for these traits revealed the same ranking of means for the three curves. Similar results were encountered in line differences for age at inflexion, line × sex interaction for the asymptote and season × sex interaction for rate. Failure to reach statistical significance in the cited cases was probably due to the increased residual variance in these traits derived from the Gompertz and Bertalanffy functions.

Examination of Table 8 clearly shows that although absolute means differed considerably for the analogous traits estimated by each curve, relative ranking of the means was unaltered. It should be noted that the asymptote means of the logistic are underestimated. This is simply a function of the fact that the mice in this study were weighed to 56 days only, whereas growth of mice are known to continue beyond this age. However, the criteria discussed earlier clearly favor the logistic curve.

The three fitted growth functions for the males and females of the H_6, C_1 and L_6 lines are plotted in Figure 2. It is difficult to distinguish the three growth functions for the same line-sex subclass within the range of birth (day zero) to 56 days, while the growth rates of the three lines are clearly dis-

Table 8. *Means and standard errors of A, t^*, k and v for each growth function by line and sex averaged over seasons*

		Asymptote (g) A		Age at Inflexion Point (days) t^*	
Line	Function	Males	Females	Males	Females
H_6	Logistic	29.25 ± .25	24.58 ± .24	28.85 ± .33	27.00 ± .32
	Gompertz	36.72 ± .52	29.46 ± .50	27.12 ± .58	23.90 ± .56
	Bertalanffy	42.34 ± .72	33.66 ± .68	24.73 ± .66	21.96 ± .62
C_1	Logistic	26.42 ± .19	20.93 ± .18	28.87 ± .26	24.97 ± .24
	Gompertz	33.29 ± .41	24.36 ± .38	26.99 ± .45	21.12 ± .43
	Bertalanffy	36.68 ± .56	27.39 ± .51	24.91 ± .51	18.94 ± .47
L_6	Logistic	20.76 ± .28	17.14 ± .25	30.63 ± .37	27.05 ± .34
	Gompertz	27.19 ± .39	20.74 ± .54	29.39 ± .66	23.48 ± .60
	Bertalanffy	33.28 ± .80	24.23 ± .72	28.80 ± .73	21.69 ± .66

		Rate ($ln\ \Theta$/day) k		Mean Absolute Growth Rate (g/day) v	
Line	Function	Males	Females	Males	Females
H_6	Logistic	.0850 ± .0010	.0862 ± .0009	.440 ± .005	.358 ± .004
	Gompertz	.0446 ± .0007	.0455 ± .0007	.402 ± .004	.332 ± .004
	Bertalanffy	.0311 ± .0007	.0321 ± .0006	.386 ± .004	.318 ± .004
C_1	Logistic	.0842 ± .0008	.0867 ± .0007	.370 ± .004	.302 ± .003
	Gompertz	.0422 ± .0005	.0481 ± .0005	.343 ± .003	.288 ± .003
	Bertalanffy	.0294 ± .0005	.0354 ± .0005	.330 ± .003	.280 ± .003
L_6	Logistic	.0704 ± .0011	.0717 ± .0010	.243 ± .005	.204 ± .005
	Gompertz	.0350 ± .0008	.0392 ± .0007	.230 ± .005	.197 ± .004
	Bertalanffy	.0237 ± .0008	.0286 ± .0007	.224 ± .004	.193 ± .004

Table 9. *Analyses of variance of the four derived traits for each growth function*

		Mean Squares					
		Asymptote			Age at Inflexion Point		
Source	D. F.	Logistic	Gompertz	Bertalanffy	Logistic	Gompertz	Bertalanffy
Line (L)	2	2,172.59**	2,851.16**	2,823.79**	161.10**	262.33	449.80*
Season (R)	2	226.27**	112.84	131.60	166.95**	256.53	245.50
$L \times R$	4	18.79	65.10	165.05	103.07*	313.64*	364.05*
Among Litters/($L \times R$)	117	9.42	43.34	88.78	32.49	90.44	118.87
Sex (S)	1	2,138.04**	6.191.58**	10,282.77**	1,225.02**	3,160.94**	3,853.74**
$L \times S$	2	17.24*	37.70	62.91	53.49**	100.08*	191.99**
$R \times S$	2	9.76	0.62	26.81	6.71	17.66	0.38
$L \times R \times S$	4	2.94	21.59	29.99	12.91	25.64	21.93
Within Litters	415^+	4.61	20.47	35.96	8.27	25.21	30.27

		Mean Squares					
		Rate $\times 10^2$			Mean Absolute Growth Rate $\times 10$		
Source	D. F.	Logistic	Gompertz	Bertalanffy	Logistic	Gompertz	Bertalanffy
Line (L)	2	118.01**	30.32**	16.67**	106.74**	82.07**	69.49**
Season (R)	2	38.04**	14.82**	8.88**	23.06**	17.15**	13.58**
$L \times R$	4	9.60**	7.28**	4.86*	3.81**	2.86*	2.26**
Among Litters/($L \times R$)	117	1.67	1.46	1.21	0.32	0.29	0.28
Sex (S)	1	17.74**	20.47**	23.03**	35.60**	24.50**	18.31**
$L \times S$	2	3.70**	2.78**	2.82**	1.42**	1.07**	0.99**
$R \times S$	2	3.84**	1.17	0.95	1.26**	0.67**	0.49**
$L \times R \times S$	4	2.08*	1.42*	1.35**	0.24	0.19	0.16
Within Litters	415^+	0.71	0.41	0.32	0.16	0.12	0.11

* $P < .05$, ** $P < .01$

+ D. F. = 392 for Bertalanffy function

tinguishable based on a comparison within any of the three functions. These results were perhaps anticipated because of the high positive phenotypic correlations between the analogous traits of the three curves which were discussed previously and again suggest that any of the three functions would have described the data adequately regarding discrimination among treatments.

Correlated responses in the characteristics of the growth curve of the H_6 and L_6 lines due to divergent selection for six-week body weight have been discussed by Lang and Legates (1969). These results may be further quantified by comparison of the estimated parameters of the growth curves. The logistic function was used for this purpose since it fit the data best based on the criteria outlined earlier.

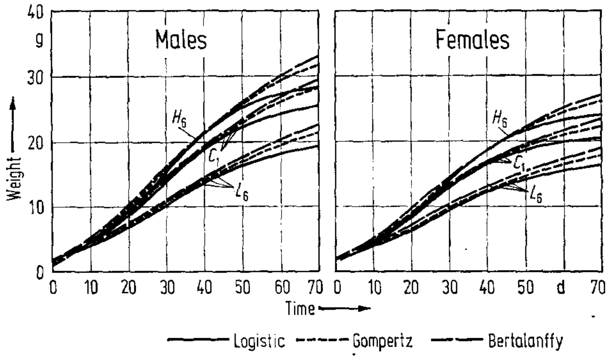

Figure 2. Fitted growth curves for H_6, C_1 and L_6 males and females averaged over seasons

Large seasonal, line and sex differences were found for the four traits (Table 9). Seasonal and season × line interaction variation in the growth curves of these populations were indicated by Lang and Legates (1969).

Laird and Howard (1967) fitted the Gompertz curve to means of several inbred lines of mice and some of their reciprocal crosses. Although significant differences were found among lines in several of the growth parameters, individual and litter variation was not taken into account in their study. It can be shown, for example, that in general the average of several Gompertz functions will not yield a Gompertz function (Merrell, 1931; Winsor, 1932).

Relative to the control line, mean absolute growth rate (v) was significantly ($P < .01$) reduced in the L_6 line and significantly ($P < .01$) increased in the H_6 line. The decreased mean absolute growth rate in the L_6 line relative to the control line was approximately twice as great as the increased v in the H_6 line. This result reflects the asymmetry of selection line divergence from the control population for six-week body weight (Legates and Farthing, 1962; Lang and Legates, 1969). The asymptote (A)

means also reflect the asymmetric response to selection for body weight which is slightly greater in males than in females. Mean absolute growth rate was consistently larger in males than in females, but the magnitude of the difference was less in the L_6 line than in the H_6 line as evidenced by the significant ($P < .01$) sex × line interaction. However, on a percentage basis the differences between males and females were similar in all three lines.

Table 10. *Phenotypic and genetic correlations among the four derived traits of the logistic function calculated within genetic line*$^+$

	Line	Asymptote (A)	Age at Inflexion Point (t^*)	Rate (k)	Mean Absolute Growth rate (v)
Asymptote (A)	H_6	—	.40 ± .37	−.28 ± .57	.77 ± .50
	C_1	—	.28 ± .31	−.47 ± .46	.26 ± .54
	L_6	—	.44 ± .37	−.76 ± .50	.58 ± .46
Age at Inflexion Point (t^*)	H_6	.31**	—	−.69 ± .47	−.69 ± .37
	C_1	.43**	—	−.79 ± .36	−.64 ± .40
	L_6	.58**	—	−.73 ± .52	−.22 ± .49
Rate (k)	H_6	−.20*	−.73**	—	.83 ± .51
	C_1	−.21*	−.77**	—	.73 ± .46
	L_6	−.43**	−.72**	—	.09 ± .56
Mean Absolute Growth Rate (v)	H_6	.57**	−.39**	.69**	—
	C_1	.51**	−.38**	.72**	—
	L_6	.57**	−.09	.48**	—

* $P < .05$, ** $P < .01$

$^+$ Genetic correlations and standard errors above the diagonal and phenotypic correlations below the diagonal

Rate of growth may be expressed as a logarithmic function of weight change with respect to time; $\ln \theta = \ln [(A - y)/y] = \ln b - k\,t$ in the logistic case. The difference between the means of k in the H_6 and C_1 lines was not significant. In contrast the rate (k) was significantly lowered in the L_6 line relative to the C_1 line. In all lines k was larger in females than in males which is in agreement with the results of LAIRD and HOWARD (1967).

Age at inflexion point (t^*) was significantly increased in both H_6 and L_6 females and in L_6 males. However, no change in age at inflexion was observed between H_6 and C_1 males. The corresponding body weights at the points of inflexion, obtained by linear interpolation of the observed means, were 14.69, 12.80 and 9.92 g for H_6, C_1 and L_6 males and 11.88, 9.93 and 8.00 g for H_6, C_1 and L_6 females, respectively. Thus, selection for six-week body weight has increased the weight at point of inflexion in both sexes of the H_6 line while decreasing it in the L_6 line. The age at point of inflexion was greater in males than in females for all three lines. TIMON (1968) reported a similar sex difference in age at inflexion in an outbred strain of mice.

These results demonstrate that selection for a single age-point (large or small six-week body weight) on the growth curve has altered its characteristics as determined by four derived traits of the fitted logistic growth function. The four traits are correlated phenotypically and genetically so that concomitant mean changes due to short-term selection could be predicted. However, in a long-term selection experiment these correlated responses might not be adequately predicted from the genetic correlations since the actual responses differed somewhat depending on the direction of selection and the sex of progeny (e.g., age at inflexion point).

Phenotypic and genetic correlations among the four derived traits of the logistic function calculated within lines are presented in Table 10. The genetic correlation estimates are of limited utility since, aside from having large standard errors, they may contain maternal and dominance effects. However, the correlations display a definite pattern. Not only are the genetic (or phenotypic) correlations between two traits of the same sign for each line, but all of the genetic and phenotypic correlations for a given pair of traits are of the same sign.

Direct single trait selection for the estimated parameters of the growth curve would be of interest in determining the amount of additive genetic variation in these traits, and the correlated responses to selection for the other parameters and for specified points on the growth curve. The extent to which the pattern of growth can be altered more efficiently than by selecting for a single trait may be studied by selecting for an index which combines genetic information on the entire set of parameters of the growth function. TALLIS (1968) has suggested an alternate procedure which could be compared experimentally.

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