

Usefulness of Growth Curve Parameters in early selection of pigs

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ABSTRACT

Data from 698 pigs were used to examine the potential applications of growth curve parameters as selection criteria for altering the relationship between body weight and age. A logistic growth function was found to be best fitted for modelling the growth. Estimates of asymptotic body weight (K), maximum growth rate (R) and age at point of inflection (t^*) have been obtained by nonlinear least squares. Phenotypic and genetic parameters were estimated for the estimated growth curve parameters and for body weights through 24 weeks of age. Half-sib model was used for computing genetic parameters. Estimated genetic correlations suggest that t^* may be useful in selecting pigs for increased body weights at 24th week of age which is very close to slaughtering age and simultaneously for decreased mature body weight.

Keywords: Growth curve, heritability, genetic correlation, phenotypic correlation, pig, logistic model.

1. Introduction

The relationship between body weight and age is particularly important in animals such as beef cattle, pig *etc.* Growth is the foundation on which the other forms of production such as milk, meat depend. Because this relationship is of interest throughout an animal's lifetime, it is critical to study it as a whole rather than in isolated pieces (Cartwright 1970; Dickerson 1978). Determining the genetic control of growth curves is important because they correct irregularities in the data caused by human error or random environmental effects. Fitzhugh (1976) suggested that a 'desirable' pattern of growth would be one characterized by small birth weight relative to dam size in order to reduce dystocia, rapid early growth and small mature size in the parental stocks so as to have a low maintenance cost.

The age-weight relationship could be altered through selection and a criterion is required for this. Genetic analysis of growth curves has been applied to lactation curves of dairy cows (Shanks *et al.* 1981; Rekaya *et al.* 2000), body weight-age curves in cattle (DeNise and Brinks 1985, Beltran *et al.* 1991), body weight-age curves in poultry (Barbato 1991), body weight-age curves in mice (McCarthy and Bakker 1979, Kachman *et al.* 1987, Eisen 1976), body length curves in fish (Rocchetta *et al.* 2000) and height-age curves in woody perennial species (Gwaze *et al.* 2002). But this type of studies has been completely ignored in case of pigs.

The body weight-age relationship can be described with a growth function. In these functions growth rate first increases with age and then decreases as the animal approaches the maturity which gives a sigmoid body weight-age plot (Brody 1945; Parks 1982). The nonlinear Richards' function or special cases of it are commonly used to model growth in animals (Parks

1982). Parameters describe various aspect of growth and provide potentially useful criteria for altering the age-weight relationships by genetic means. The objective of this study is to examine the possible usefulness of growth curve parameters as selection criteria to accomplish the above in pig.

2. Data Description

The growth data of 698 pigs from piggery farm of the I. V. R. I., Izatnagar, Bareilly for the time period of 1994 to 2001 has been taken for study. The growth data is available at 13 different points of time namely, 0, 1, 2, 3, 4, 5, 6, 7, 8, 12, 16, 20 and 24 weeks of age. All the weights available are measured in Kg. After 32 weeks, pigs are either slaughtered or used for mating. The body weights at 28th and 32nd week were not considered because the body weights available for those points were very few. The animals were weaned at 8 weeks of age.

Two breeds of pig namely, Landrace and Desi were taken for crossing in the first year and in the subsequent generations progenies were mated in different combinations from which we can easily find out the half sib and full sib families.

3. Selection for a nonlinear growth model

A growth curve is usually sigmoid provided that a large range of ages is represented. Many functions can produce this general shape, and it is not practical to consider all of these to assess which one is "best". Attention was restricted to the Richards' family of growth functions (Richards 1959, 1969), because parameters could be related to various aspects of growth that were of biological interest. Also, the most commonly used growth curves are special cases of the Richards' function. Richards' function can be written as –

$$W(t) = \frac{K}{(1 \pm \beta e^{-rt})^{\frac{1}{m}}} \quad (1)$$

where, $W(t)$ = Body weight at age t , K = asymptotic body weight, β = time scale parameter of no biological significance, r = maturity rate and m = Inflection parameter. The value of m is always greater than or equal to -1. In (1), the positive sign applies when $m \geq 0$, and the negative when $m < 0$. The parameter K relates to mature body weight; β is connected to relative weight at time 0; r describes the rate at which the mature weight is achieved, and m gives the fraction of mature weight at which growth rate is maximum.

In estimating the parameters of (1) using iterative methods such as nonlinear least-squares, complications can arise with convergence of the solutions; this is particularly true for m (Brown *et al.* 1976; McCarthy and Bakker 1979). This problem can be avoided by assuming that m is unknown. In fact, $m = 1$ gives the Logistic function, $m = 0$ gives the Gompertz function, $m = -1/3$ gives the Von-Bertalanffy function and $m = -1$ gives the Monomolecular function.

In order to find an appropriate value for m , at first Richards' model was fitted to randomly selected 100 animals. Estimation of m in (1) by nonlinear least-squares using records from this group suggested the logistic function for application in the full data set. The function was then reparameterized to facilitate interpretation. With $m = 1$, putting $B = \exp(\log_e B)$ in (1) leads to

$$W(t) = K \left[1 + e^{r(\log_e B/r - t)} \right]^{-1} \quad (2)$$

Following Fitzhugh (1976), let

$$t^* = \frac{1}{r} \log_e \beta \quad \text{and} \quad R = rK/4$$

where t^* is the age at which growth rate is maximum (point of inflection of the curve) and R is maximum growth rate. Using these, (2) becomes

$$W(t) = \frac{K}{1 + \exp\{4R(t^* - t)/K\}} \quad (3)$$

In this form, the parameters have the following interpretation: K (asymptotic weight) is mature weight, R is maximum growth rate, and t^* (age at point of inflection) is related to age at puberty (Monterio and Falconer 1966). With this reparameterization, convergence would be directly to parameters of biological interest and not for some function of them, which is more reasonable from an estimation viewpoint.

Also, it facilitates the choice of initial guesses for iteration.

Body weights at 0, 1, 2, 3, 4, 5, 6, 7, 8, 12, 16, 20 and 24 weeks in the 698 pigs were used to estimate all the parameters in (3). Predicted body weights were compared with observed values to examine possible biases. The initial parameter estimates were obtained by using algorithm given by Draper and Smith (1998).

Estimation of growth curve parameters:

Estimation was done by nonlinear least-squares (Draper and Smith 1998; Daniel and Wood 1971) via Marquardt's algorithm. This procedure has been used previously for estimating growth curve parameters in mice and cattle (*e.g.*: Carmon 1965; Eisen *et al.* 1969, Brown *et al.* 1976; McCarthy and Bakker 1979; Parratt and Barker 1982; Kachman *et al.* 1988)

Estimation of genetic parameters:

Body weights at 0, 1, 2, 3, 4, 5, 6, 7, 8, 12, 16, 20 and 24 weeks of age and estimates of K , R and t^* in the 698 pigs were used to estimate genetic and phenotypic parameters. The following half sib mixed linear model considering sex as fixed effect was used:

$$Y_{ijk} = \mu + S_i + S_j + e_{ijk} \quad (4)$$

where, Y_{ijk} = observed or estimated value of variate.

$$S_i = \text{fixed effect of sex } i \quad i = 1, 2$$

$$S_j = \text{random effect of sire } j$$

$$e_{ijk} = \text{random residual}$$

It was assumed that $S_j \sim (0, \sigma_s^2)$ and $e_{ijk} \sim (0, \sigma_e^2)$, with all covariances between pair of random variables in the model being null. Estimates of variance and covariance components were obtained by REML method of estimation using the statistical package SAS 8e.

Genetic and phenotypic correlations were of main interest. Formulae for these parameters are

$$r_A = \frac{\hat{\sigma}_{sxsy}}{\sqrt{\hat{\sigma}_{sx}^2 \hat{\sigma}_{sy}^2}} \quad \text{and} \quad r_p = \frac{\hat{\sigma}_{sxsy} + \hat{\sigma}_{exey}}{\sqrt{(\hat{\sigma}_{sx}^2 + \hat{\sigma}_{ex}^2)(\hat{\sigma}_{sy}^2 + \hat{\sigma}_{ey}^2)}}$$

respectively.

Here, σ_{sx}^2 , σ_{dx}^2 and σ_{ex}^2 are sire, dam and residual variance component for the character X

σ_{sy}^2 , σ_{dy}^2 and σ_{ey}^2 are sire, dam and residual variance component for the character Y

σ_{sxsy} , $\sigma_{dx dy}$ and σ_{exey}^2 are sire, dam and residual covariance component between the character X and Y.

Standard error of genetic correlation was approximated using the following formula

$$S.E. (\hat{r}_A) = \frac{1 - \hat{r}_A^2}{\sqrt{2}} \sqrt{\frac{S.E.(\hat{h}_x^2) S.E.(\hat{h}_y^2)}{\hat{h}_x^2 \hat{h}_y^2}}$$

4. RESULTS AND DISCUSSION

Model selection

Richard's model was fitted to each of the 698 animals to describe body weight-age relationship. Estimates of m parameter were 0.909 with standard error as 0.0374. Clearly, this result suggests that the logistic growth model should be adequate for describing the growth of pig because $m = 0.909$ which is much nearer to 1. It should be noted that the coefficient of variability of m is quiet low.

Fitting of Logistic growth model

The logistic growth model was fitted to each of the 698 animals. Means and standard deviations of estimated growth curve parameters of logistic model are in the table 1. The mean estimated asymptotic body weight (K) in case of logistics growth model was 79.670 kg. with standard error as 2.205 kg. The mean estimated maximum growth rate (R) and mean estimated age at point of inflection were 2.672 ± 0.050 kg per week and 23.242 ± 0.343 weeks.

The estimates (with standard error) of growth curve parameters of logistic model by sex are in table 2. Females had faster maximum rates of gain than males on average. The females also had higher estimated asymptotic weights and later ages at point of inflection than males. It was found that the parameter estimates of male and female pigs are significantly differing. The estimates of K (Asymptotic Body Weight) and R (Maximum Growth Rate) have been significantly different in male and female by 5% level of significance whereas estimate of t^* (Age at Point of Inflection) was significantly different in male and female pigs by 1% level of significance. So it indicates that we should use mixed model considering sex as fixed effect for estimation of genetic parameters.

Table 1: Estimated values of growth parameters (logistic) with standard error

Growth Curve Parameters	Estimates	S.E.
K (kg)	79.670	2.205
R (kg per week)	2.672	0.050
t^* (week)	23.242	0.343

Table 2: Estimated values of growth curve parameters of logistic model with standard error by sex

Growth Curve Parameters	female		male	
	Estimates	S.E.	Estimates	S.E.
K	84.645	3.239	74.945	2.985
R	2.776	0.070	2.574	0.072
t^*	24.329	0.473	22.210	0.489

Estimates of genetic parameters:

The mixed half-sib model (Eq. 4) considering sex as fixed effect was fitted to estimate the genetic correlations of the body weights and also estimated growth curve parameters. REML method of estimation was used for estimation of variance and covariance components.

Genotypic correlation among body-weights at different ages:

The estimated genetic correlations of body weights at different ages obtained using half-sib mixed model are given in table 3. The genetic correlations between body-weights decrease as the time between weights increase. For example the genetic correlation between body-weights at 1st and 2nd week of age is 0.818 while

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that between 1st and 5th week of age is 0.317. The estimated genetic correlation between 1st and 24th week of body weight further reduces to 0.081.

The estimates of genetic correlations within pre-weaning weights were in general positive except for the body weight at birth and most of them were more than 0.650. Again the genetic correlations within post-weaning weights were also positive and ranged from 0.776±0.055 to 0.979±0.005. Except for the body-

weights at birth, the estimates of genetic correlation between pre- and post-weaning weights were ranged between -0.314±0.135 and 0.803±0.051.

The genetic correlation of the body weights at 7th or 8th weeks of age with the body weights at 16th, 20th and 24th week of age were ranging from 0.393 to 0.732. It indicates that improvement in body weight at 7th or 8th weeks of age will increase the body weights at 16th, 20th and 24th weeks of age.

Table 3: Half-sib estimates of genetic correlation between body-weights using REML methods of estimation

	W1	W2	W3	W4	W5	W6	W7	W8	W12	W16	W20	W24
W0	0.564	0.339	0.185	0.015	-0.015	-0.278	-0.104	-0.094	0.045	-0.123	-0.010	0.022
W1		0.818	0.652	0.415	0.317	0.178	0.168	0.150	0.132	0.057	0.090	0.081
W2			0.811	0.684	0.577	0.488	0.461	0.474	0.314	0.226	0.358	0.330
W3				0.934	0.848	0.713	0.626	0.593	0.428	0.427	0.398	0.359
W4					0.953	0.866	0.774	0.728	0.588	0.551	0.539	0.438
W5						0.956	0.846	0.789	0.609	0.573	0.488	0.412
W6							0.920	2.140	0.636	0.640	0.495	0.393
W7								0.979	0.668	0.732	0.584	0.511
W8									0.705	0.803	0.697	0.635
W12										0.928	0.846	0.776
W16											0.960	0.887
W20												.979

Genotypic correlation between growth parameters (logistic):

The Estimates of genetic correlations between growth curve parameters of logistic model are given in table 4. The estimated genetic correlation between

asymptotic body weights and age at point of inflection was 0.947±0.021. This indicates that animals that have a later age of point inflection would be expected to produce smaller mature weight.

Table 4: Estimates of genetic correlation of growth curve parameters of logistic model (REML method of estimation and Half sib mixed model)

	<i>K</i>	<i>R</i>	<i>t</i> *
<i>K</i>	1.00	.392** (.306)	.947** (.021)
<i>R</i>		1.00	.143** (.258)
<i>t</i> *			1.00

Note: * denotes the significance in the 5% level of significance
 ** denotes the significance in the 1% level of significance

Genotypic correlation between estimated growth curve parameters (logistic) and body weights:

Estimates of genetic correlations between estimated growth curve parameters and body weights at various ages are in table 5. The genetic correlation between asymptotic body weight and body weight at a given age is always negative except the body weight at birth and 1st week and increased in value as the animal aged. The genetic correlation between asymptotic body weight and body weights both at 20th and 24th week of age were nearly perfect. Coupled with the heritability estimates, this implies that selection for body weight at 20th or 24th weeks of age would result in approximately the same genetic change for estimated asymptotic body weight as direct selection for the latter. Obtaining an estimate of asymptotic body weight involves recording body weight of animals in later ages. Hence, if mortality is high, selection intensity may be lower in direct selection

for estimated asymptotic body weight than in indirect selection for body weight at 20th and 24th weeks of age.

Genetic correlations between maximum growth rate and body weights at 1st, 20th and 24th weeks of age are negative whereas this is with the body weights at other ages are being positive. The genetic correlation between maximum growth rate and different body weight did not show any consistent pattern so it is very much tough to draw any conclusion from it.

The genetic correlation between estimated age at point of inflection and body weight is always negative and in general, the absolute correlation increases as the animal gets older. These correlations suggest that selection for decreased age at point of inflection would increase the body weights (at least upto 24th weeks of age). This type of selection might be conducted on pigs where animals are marketed at earlier ages.

Table 5: Estimates of genetic correlation between estimated growth curve parameters and body weights (REML method of estimation and Half sib mixed model)

Traits	K		R		t*	
		S.E.		S.E.		S.E.
W0	0.024	0.198	0.246**	0.244	-0.130**	0.142
W1	-0.079*	0.196	-0.004	0.258	-0.158**	0.140
W2	-0.127**	0.199	0.701**	0.134	-0.302**	0.133
W3	-0.075*	0.205	0.618**	0.167	-0.173**	0.145
W4	-0.106**	0.199	0.719**	0.128	-0.189**	0.141
W5	-0.135**	0.193	0.732**	0.119	-0.225**	0.136
W6	-0.076*	0.197	0.685**	0.138	-0.252**	0.135
W7	-0.251**	0.177	0.664**	0.139	-0.434**	0.112
W8	-0.338**	0.164	0.885**	0.053	-0.543**	0.095
W12	-0.336**	0.162	0.711**	0.118	-0.664**	0.074
W16	-0.395**	0.180	0.668**	0.155	-0.808**	0.054
W20	-0.663**	0.112	-0.456**	0.207	-0.988**	0.004
W24	-0.681**	0.103	-0.370**	0.218	-0.929**	0.019

Note: * denotes the significance in the 5% level of significance

** denotes the significance in the 1% level of significance

Mean estimated age at point of inflection was 23.242 weeks and, as noted earlier, its genetic correlation with weaning weight (weight at 8 weeks of age) is -0.543 ± 0.095 . Again the genetic correlations between the age at point of inflection and the body weights at 20th and 24th week are almost perfect and negative. Hence, selection for early age at point of inflection would be expected to increase the juvenile body weight as well as the body weight at 24 weeks of age. Again the sire-component heritability estimate of age at point of inflection is more than 0.80 and the body weights at 20th and 24th weeks of age were moderately heritable in all the four methods of estimation. Coupled with these heritability estimates, the higher genetic correlations of age at point of inflection with the body weights at different ages implies that increase in body weight is possible through selecting animals on the basis of decreased age at point of inflection.

Again the mature body weight and age at point of inflection were positively and almost perfectly correlated genetically which implies that if we select animals for early age at point of inflection then mature weight would be expected to decrease. Hence, selection for early age at point of inflection would be expected to increase the body weight during slaughtering age with sizable concomitant decrease in mature body weight. Thus it seems that it is possible to alter the shape of

growth curve in ideal direction so that animals will have increased body weights during slaughtering age and decreased mature body weights simultaneously. This result seems to be as per of our interest because we want to increase the body weight during slaughtering age and at the same time to decrease the asymptotic body weight so that maintenance cost of animal decreases in the parental stocks.

Phenotypic correlation between growth parameters:

The estimates of phenotypic correlation between growth parameters (logistic) are given in table 6. It was found that phenotypic correlation of mature body weight with the age at point of inflection and maximum growth rate was strong and positive (0.827 and .912). Estimate of phenotypic correlation between age at point of inflection and maximum growth rate was 0.608.

We have already seen that the genetic correlation between mature body weight and age at point of inflection was 0.947. So the phenotypic correlation between mature body weight and age at point of inflection is almost same as genetic correlation between them. So from here we may draw conclusion that change in age at point of inflection will result change in the mature body weight, more specifically, the decrease in age at point of inflection will also result in decrease in mature body weight.

Table 6: Half sib estimates of phenotypic correlation for growth curve parameter (logistic) using REML method of estimation

	K	R	t*
K	1.00	0.912	0.827
R		1.00	0.608
t*			1.00

Unfortunately, the phenotypic correlations of maximum growth rate with mature body weight and age at point of inflection were not as per same as genetic correlation.

Phenotypic correlation between growth parameters and body weights at different age:

The estimates of phenotypic correlation between growth parameters (logistic) and body weights at different age are given in table 7. It was seen that mature body weight were almost phenotypically uncorrelated with body weights at different ages. The phenotypic correlation between the maximum growth rate with different body weights were also poor.

The phenotypic correlations of age at point of inflection were negative with the body weights through out the all-different ages. The phenotypic correlations were very low in the early ages and become moderate at the higher ages. For example, the phenotypic correlation of age at point of inflection with body weight at 2nd week is only -0.150 and that was -0.483 in the 20th week of age. The absolute phenotypic correlation increased with the advancement of age. This result conforms to genetic correlations but the absolute phenotypic correlations were much smaller than the absolute genetic correlations between age at point of inflection and body weights at different age. Therefore we may draw conclusion, on the basis of these results,

Table 7: Half sib estimates of phenotypic correlation between estimated growth curve parameters and body weights at several ages using REML methods of estimation

Traits	Model: Half sib		Method: REML	
	K	R	R	t*
W0	0.006	0.020	0.020	-0.070
W1	-0.025	0.007	0.007	-0.130
W2	-0.011	0.066	0.066	-0.150
W3	0.053	0.108	0.108	-0.091
W4	0.029	0.095	0.095	-0.124
W5	0.010	0.092	0.092	-0.160
W6	0.003	0.067	0.067	-0.200
W7	-0.048	0.078	0.078	-0.263
W8	-0.045	0.088	0.088	-0.317
W12	-0.101	0.090	0.090	-0.387
W16	-0.098	0.085	0.085	-0.304
W20	0.242	0.009	0.009	-0.483
W24	0.216	0.039	0.039	-0.456

that decrease in the age at point of inflection will increase the body weights. In reverse we can say animals that have higher body weight will reach point of inflection earlier.

Compounded with the negative phenotypic correlation of the age at point of inflection and mature body weight with the body weight at different ages and positive phenotypic correlation between age at point of inflection and mature body weight suggests that it is possible to have animal with higher early body weight and decreased mature body weight through selecting animal on the basis of decreased age at point of inflection. Remember that we have already reached this conclusion while discussing genetic correlation. Here it is important to remember that an ideal growth curve will be that which is characterized by higher body weight at early ages and decreased mature body weight.

5. Conclusions:

In conclusion, it seems that it is possible to have pigs with higher body weight at ages of 20th or 24th week which is very closure to slaughtering time and decreased mature body weight through selecting animals on the basis of early ages at point of inflection. This comes from the fact that the age at point of inflection is highly heritable and at the same time this is also negatively correlated (both genetically and phenotypically) with body weights at 20th and 24th weeks of ages and

positively correlated (both genetically and phenotypically) with the mature body weight.

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