

Heritability of growth curve parameters of pigs

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ABSTRACT

Most of the strategies of breeding plan in animal depend on heritability which is one of the most important genetic parameter. Data from 698 pigs were used to examine the potential usefulness 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 to model growth through 24 weeks of age. Estimates of asymptotic body weight (K), maximum growth rate (R) and age at point of inflection (t^*) have been obtained by non-linear 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 were used for computing genetic parameters. Heritabilities of estimated growth curve parameters were: K (0.301 ± 0.121), R (0.102 ± 0.070) and t^* (0.874 ± 0.228).

Key words: Asymptotic, Growth curve, Heritability, Inflection parameter, Logistic model, Pig

The relationship between body weight and age is particularly important in meat animals such as beef cattle, pig etc. Growth is the foundation on which the other forms of production such as milk, meat and work rest. As this relationship is of interest throughout lifetime of animal, so it is desirable 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 is 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.* 1992), body weight-age curves in poultry (Barbato 1991), body weight-age curves in mice (McCarthy and Bakker 1979, Kachman *et al.* 1988, 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 have been completely ignored in case of pigs.

The body weight-age relationship can be described with

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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 was to examine the possible usefulness of growth curve parameters as selection criteria.

Data description

The growth data of 698 pigs from piggery farm of IVRI, Izatnagar, for the time period of 1994 to 2001 has been taken for study. The growth data are 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 as weight in kg. 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 half sib and full sib families.

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

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

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. 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; which is particularly true for m (Rutledge *et al.* 1972; 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

$$t^* = \frac{1}{r} \log_e \beta$$

and

$$R = rK / 4$$

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 (Carmon 1965, Eisen *et al.* 1969, Timon and Eisen 1969, Rutledge *et al.* 1972, Brown *et al.* 1976, McCarthy and Bakker 1979, Parratt and Barker 1982, Kachman *et al.* 1987)

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 = fixed effect of sex i $i = 1, 2$

s_j = random effect of sire j

e_{ijk} = 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.

Heritabilities of direct genetic effects are of main interest. Formulae for this parameters are

$$h^2 = \frac{4 \hat{\sigma}_s^2}{\hat{\sigma}_s^2 + \hat{\sigma}_e^2}$$

Standard error of heritability were approximated using the following formula (Falconer 1996)

$$\hat{\sigma}_{h^2}^2 = 32 \frac{\hat{h}^2}{T}$$

where, $T = nN$, n and N being the average half-sib family size and N being the no. of Half-sib families.

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.

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

Growth curve parameters	Estimates	SE
K (kg)	79.670	2.205
R (kg per week)	2.672	0.050
t^* (week)	23.242	0.343

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

Growth curve parameters	Female		Male	
	Estimates	SE	Estimates	SE
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 heritabilities and also estimated growth curve parameters. REML method of estimation was used for estimation of variance components.

Heritability estimates of body-weights

Heritability estimates along with their standard errors for different body weights are shown in Table 3. The heritability estimates of body weights are quiet closure to 1 which seems quiet unreasonable. This may be due to the fact that the each sire was not mated with enough number of dams. It is very much tough to get any information weather the selection can be effective or not. This prompts us to look into the heritabilities of growth parameters instead of age specific body weights.

Table 3. Estimates of heritability and approximate standard error for body weight at several ages (REML method of estimation and Half sib mixed model)

Trait	Sire component	SE
W0	0.981	0.198
W1	0.895	0.217
W2	0.789	0.206
W3	0.954	0.213
W4	0.865	0.223
W5	0.778	0.126
W6	0.768	0.027
W7	0.875	0.212
W8	0.993	0.232
W12	0.856	0.176
W16	0.878	0.187
W20	0.992	0.212
W24	0.974	0.189

Heritability estimates of growth curve parameters of logistic model

The estimates of heritability of different growth parameters (logistic) obtained using full-sib mixed model are shown in Table 4. Heritability estimate of estimated age at point of inflection was 0.874 ± 0.228 . Heritability of estimated maximum growth rate and mature body weight were 0.301 ± 0.121 and 0.102 ± 0.070 respectively.

In general, it appears that estimated asymptotic body weight is lowly heritable whereas age at point of inflection

Table 4. Estimates of heritability of growth curve parameters of logistic model

Trait	Sire comp.	SE
K	0.301	0.121
R	0.102	0.070
t^*	0.874	0.228

was moderately heritable. Since the heritability of the age at point of selection is high, so we can use this parameter for selection purpose. The remaining two parameters cannot be used for selection purpose due to their low heritability.

In conclusion, it seems that it is possible to have pigs with higher body weight at ages of 20 th or 24 th 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 (more than 0.80).

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