Phenotypic and Genetic Variability of Estimated Growth Curve Parameters in Pigs

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SUMMARY

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. *Heritabilities* of estimated *growth curve* parameters were: K (0.202±0.070), R (0.036 ± 0.030) and t^* (0.815±0.141). Estimated genetic correlations suggest that t^* may be useful in selecting for increased body weights at 20th or 24th week of age and decreasing mature weight. Estimated genetic correlations suggest that t^* may be useful in selecting pigs for increased body weights at 24th week of age which is very closure to slaughtering age and simultaneously for decreased mature body weight.

Keywords: Growth curve, Heritability, Genetic correlation, Phenotypic correlation, Pig, Logistic model, Inflection parameter.

1. INTRODUCTION

The relationship between body weight and age is particularly important in meat animals such as beef cattle, pig etc. Besides meat, growth is the foundation on which the other forms of production such as milk, meat and work rest. 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

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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 to accomplish the above in pig.

2 MATRIALS AND METHODS

2.1 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 experiment is still going on there under aegis AICRP. The growth data is available at 13 different point 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 week pigs are either slaughtered or used for mating. The body weights at 28th and 32nd week did not consider because the body weights was available for those points only for few animals. 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.

2.2 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

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

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 (Rutledge *et al.* 1972; Brown *et al.* 1976; McCarthy and Bakker 1979). This problem can be avoided by first estimating the unknown m and the replacing it by its estimated value in (1). 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 the 100 randomly selected animals. The estimate of m was obtained as 1.1005 ± 0.0374 by nonlinear least-squares. This estimate of m in (1) uggested 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

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

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

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

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 (1966).

2.3 Estimation of Growth Curve Parameters

Estimation was done by nonlinear least-squares (Draper and Smith 1966; 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; Timon and Eisen 1969; Rutledge *et al.* 1972; Brown *et al.* 1976; McCarthy and Bakker 1979, Goonewardene *et al.* 1981; Parratt and Barker 1982; Kachman *et al.* 1988).

2.4 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 full sib mixed linear model considering sex as fixed effect was used:

$$Y_{ijkl} = \mu + S_i + s_j + d_{jk} + e_{ijkl} \qquad (4)$$

where Y_{ijkl} = observed or estimated value of variate

S_i = fixed effect of sex *i*
s_j = random effect of sire *j*
d_{jk} = random effect of dam *k* and mated to sire j
e_{ijkl} = random residual

It was assumed that $s_j \sim (0, \sigma_s^2)$ $d_{jk} \sim (0, \sigma_d^2)$ and $e_{ijkl} \sim (0, \sigma_e^2)$, 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 8.2e.

Ignoring the non-additive effects, the following relationships hold (Willham 1963)

$$\sigma_s^2 = 0.25 \ \sigma_{Ao}^2$$

$$\sigma_d^2 = 0.25 \ \sigma_{Ao}^2 + \sigma_{AoAm} + \sigma_{Am}^2 + \sigma_{Em}^2$$

$$\sigma_e^2 = 0.50 \ \sigma_{Ao}^2 + \sigma_E^2$$

where σ_{Ao}^2 is additive "direct" genetic variance, σ_{Am}^2 is additive genetic variance of maternal effects, σ_{AoAm} is covariance between direct and maternal genetic effects, σ_E^2 is variance of individual environment effects and σ_{Em}^2 is variance of maternal environment effects. Although there are five unknown parameters, only three variances (of linear function thereof) can be estimated using (4). Similarly, covariance components between pair of traits can be written in terms of genetic and environmental components of covariance.

Heritabilities of direct genetic effects and genetic and phenotypic correlations were of main interest. Formulae for these parameters are

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

$$r_A = \frac{\hat{\sigma}_{sxsy}}{\sqrt{\hat{\sigma}_{sx}^2 \hat{\sigma}_{sy}^2}}$$

and

$$r_p = \frac{\hat{\sigma}_{sxsy} + \hat{\sigma}_{dxdy} + \hat{\sigma}_{exey}}{\sqrt{(\hat{\sigma}_{sx}^2 + \hat{\sigma}_{dx}^2 + \hat{\sigma}_{ex}^2)(\hat{\sigma}_{sy}^2 + \hat{\sigma}_{dy}^2 + \hat{\sigma}_{ey}^2)}}$$

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}, σ_{dxdy} and σ_{exey}^2 are sire, dam and residual covariance component between the character *X* and *Y*.

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

$$\hat{\sigma}_{h^2}^2 = 16 \ h^2 / T$$

and standard error of genetic correlation was approximated using the following formula (Robertson 1959)

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

3. RESULTS AND DISCUSSION

3.1 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.

3.2 Fitting of Logistic Growth Model

The logistic growth model has been fitted to each of the 698 animals. Means and standard deviations of estimated growth curve parameters of logistic model are given in 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) was 2.672±0.050 kg per week. The mean estimated age at point of inflection (*t**) was 23.242±0.343 weeks.

The mean of observed and predicted body weight (obtained using logistic growth model) at different ages along with percentage Prediction Error are listed in Table 2. From this table some undesirable features of logistic growth model are observed. For example, the estimated body weights at 0th, 1st and 2nd week were over-predicted by 227 %, 85% and 33% respectively. This tendency of the logistic model to over predict the early weights has also been noted by Kachman *et al.* (1987) in mice. However the body-weights were more or less rightly predicted from 4th week onwards.

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. Means of observed and predicted body weight at several ages using the logistic growth function

Age (weeks)	Observed body wt. (*O*) (Kg)	Predicted body wt.(*P*) (Kg)	$\frac{P-O}{O} \times 100$
0	0.851	2.788	227.550
1	1.731	3.201	84.932
2	2.768	3.678	32.870
3	3.748	4.223	12.676
4	4.782	4.844	1.291
5	5.701	5.545	−2.736
6	6.756	6.332	−6.263
7	7.778	7.211	−7.288
8	9.062	8.184	−9.686
12	13.447	13.099	−2.592
16	20.132	19.626	−2.516
20	25.839	27.301	5.660
24	33.796	35.310	4.479

Table 3. 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

The estimates (with standard error) of growth curve parameters of logistic models by sex are in Table 3. 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 *K* (Asymptotic Body Weight) and *R* (Maximum Growth Rate) have been significantly different in male and female by 5% level of significance whereas *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.

3.3 Estimates of Genetic Parameters

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

3.3.1 *Heritability Estimates of Body-Weights*

Heritability estimates along with their standard errors for different body weights as computed are shown in Table 5. The sire component heritability estimates of body weights upto 3rd week is not significant. But thereafter, from 4th week onwards, body-weights are moderately heritable. It indicates that selection for the body-weights may be effective from 4 weeks of age.

3.3.2 *Heritability Estimates of Growth Curve Parameters of Logistic model*

The Estimates of heritability of different growth parameters (logistic) obtained using full-sib mixed

Table 5. Estimates of heritability and approximate standard error for body weight at several ages

Trait	Heritability estimates	S.E.
W0	0.271	0.074
W1	0.376	0.087
W2	0.286	0.076
W3	0.319	0.080
W4	0.522	0.102
W5	0.626	0.112
W6	0.598	0.109
W7	0.601	0.119
W8	0.649	0.114
W12	1.083	0.147
W16	0.670	0.116
W20	0.574	0.107
W24	0.576	0.107

Table 6. Estimates of heritability of growth curve parameters of Logistic model (REML method of estimation and Full sib mixed model)

Trait	Sire comp.	S.E.
K	0.202	0.070
R	0.036	0.030
t^*	0.833	0.142

model are shown in Table 6. Heritability estimate of estimated asymptotic weight was 0.202±0.070. Heritability of estimated maximum growth rate was 0.036±0.030. Estimates for age at point of inflection was 0.833±0.142 which is quiet higher.

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

3.3.3 *Genotypic Correlation Among Body-Weights at Different Ages*

The estimated genetic correlations of body weights at different ages obtained using full-sib mixed model are given in Table 7. The genetic correlations between body-weights decrease and then become negative as the time between weights increases. For example the genetic correlation between body-weights at 1st and 2nd week of age is 0.679 while that between 1st and 5th week of age is 0.433. The estimated genetic correlation between 1st and 24th week of body weight is -0.297.

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 0.236±0.219 to 0.987±0.003. Except for the body-weights at birth, the estimates of genetic correlation between pre- and post-weaning weights have ranged between -0.297±0.117 and 0.763±0.056.

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 0.404 to 0.763.

Table 7. Full-sib estimates of Genotypic correlation between body-weights using REML methods of estimation

	W1	W2	W3	W4	W5	W6	W7	W8	W12	W16	W20	W24
W0	0.679	0.073	0.234	0.228	0.063	−.245	−.311	−.252	−.375	−.458	−.247	−.216
W1		0.679	0.767	0.432	0.433	0.195	0.191	0.172	−.153	−.104	−.153	−.297
W2			0.705	0.724	0.703	0.643	0.673	0.812	0.089	0.444	0.236	−.007
W3				0.950	0.937	0.794	0.807	0.847	0.498	0.438	0.297	0.281
W4					0.997	1.001	0.966	1.030	0.604	0.560	0.369	0.304
W5						0.997	0.925	0.922	0.516	0.463	0.413	0.349
W6							0.960	0.933	0.469	0.498	0.580	0.371
W7								1.037	0.236	0.641	0.645	0.644
W8									0.469	0.763	0.721	0.652
W12										0.827	0.876	0.747
W16											0.933	0.853
W20												0.987

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.

3.3.4 Genotypic Correlation Between Growth Parameters (Logistic)

The Estimates of genetic correlations between growth curve parameters of logistic model are given in Table 8. The estimated genetic correlation between asymptotic body weights and age at point of inflection was 0.949±0.017. This indicates that animals that have a later age of point inflection would be expected to produce smaller mature weight.

Table 8. Estimates of genetic correlation of growth curve parameters of logistic model (REML method of estimation and Full sib mixed model)

	K	R	t*
K	1.00	0.091 (.373)	0.949** (.017)
R		1.00	−0.264** (.246)
t*			1.00

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

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

It is found that the estimated genetic correlation between estimates of mature weight and maximum growth rate was very low, only 0.091±0.373. Besides this estimates of genetic correlation between maximum growth rate and age at point of inflection was -0.264 ± 0.016. This indicates that change in age at point of inflection or in asymptotic weight does not result any change in maximum growth rate.

3.3.5 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 obtained using full-sib mixed model are in Table 9. 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 are 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

Table 9. Estimates of genetic correlation between estimated growth curve parameters and body weights (REML method of estimation and full sib mixed model)

Traits	K		R		t*	
	Estimate	S.E.	Estimate	S.E.	Estimate	S.E.
W0	0.131**	0.211	0.859**	0.087	−0.215**	0.144
W1	0.043	0.203	0.563**	0.213	−0.187**	0.138
W2	−0.340**	0.189	1.545**	−0.454	−0.633**	0.090
W3	−0.852**	0.069	−0.176**	0.378	−0.665**	0.099
W4	−0.697**	0.112	−0.049	0.333	−0.536**	0.109
W5	−0.686**	0.108	−0.396**	0.265	−0.506**	0.107
W6	−0.294**	−0.178	0.259**	0.280	−0.387**	0.116
W7	−0.446**	0.143	0.800**	0.099	−0.572**	0.084
W8	−0.495**	0.138	1.643**	−0.478	−0.697**	0.066
W12	−0.306**	0.143	1.240**	-0.131	−0.710**	0.055
W16	−0.618**	0.112	0.853**	0.076	−0.914**	0.021
W20	−0.962**	0.014	1.575**	−0.423	−1.060**	−0.016
W24	−0.935**	0.023	1.780**	−0.614	−1.005**	−0.001

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

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

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 3rd, 4th, 5th, 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.

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 -0.697±0.066. 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.

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 decrease in the parental stocks.

3.3.6 *Phenotypic Correlation Between Body-Weights at Different Ages*

The estimates of phenotypic correlation between body weights at different ages are given in Table 10. Strong positive correlations between body weights were found, but tend to decline as the interval between weights increase. For example, phenotypic correlations ranging from 0.844 between body weights at 2nd and 3rd weeks and 0.423 between body weights at 2nd and 12th weeks of age.

3.3.7 *Phenotypic Correlation Between Growth Parameters*

The estimates of phenotypic correlation between growth parameters (logistic) are given in Table 11. 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 0.923). Estimates of phenotypic correlation between age at point of inflection and maximum growth rate were 0.608.

Table 11: Full sib estimates of phenotypic correlation for growth curve parameter (logistic) using REML methods of estimation

Model: Full sib Method: REML			
	K	R	t*
K	1.00	0.913	0.827
R		1.00	0.608
t*			1.00

We have already seen that the genetic correlation between mature body weight and age at point of inflection was 0.949. So the phenotypic correlation

Table 10. Full-sib estimates of Phenotypic correlation between body-weights using REML methods of estimation

	W1	W2	W3	W4	W5	W6	W7	W8	W12	W16	W20	W24
W0	0.645	0.510	0.423	0.423	0.341	0.292	0.267	0.230	0.206	0.050	0.142	0.155
W1		0.781	0.688	0.594	0.535	0.466	0.414	0.395	0.321	0.160	0.292	0.274
W2			0.844	0.767	0.699	0.617	0.569	0.547	0.436	0.225	0.434	0.423
W3				0.910	0.836	0.731	0.670	0.622	0.522	0.265	0.483	0.449
W4					0.926	0.827	0.754	0.696	0.571	0.331	0.546	0.482
W5						0.931	0.855	0.811	0.647	0.338	0.574	0.521
W6							0.920	0.883	0.703	0.350	0.596	0.529
W7								0.937	0.759	0.394	0.657	0.597
W8									0.792	0.431	0.712	0.659
W12										0.448	0.764	0.711
W16											0.505	0.473
W20												0.927

between mature body weight and age at point of inflection is as per 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.

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.

3.3.8 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 12. It was seen that mature body weight were almost phenotypically uncorrelated with body weights at different age regardless the methods of estimation. The phenotypic

Table 12. Full sib estimates of phenotypic correlation between estimated growth curve parameters and body weights at several ages using REML methods of estimation

Model: Full sib	Method: REML		
Traits	K	R	t*
W0	0.006	0.023	−0.073
W1	−0.024	0.006	−0.136
W2	−0.010	0.066	−0.155
W3	0.053	0.116	−0.101
W4	0.029	0.100	−0.131
W5	0.009	0.088	−0.166
W6	0.001	0.063	−0.203
W7	−0.046	0.085	−0.258
W8	−0.042	0.081	−0.312
W12	−0.102	0.086	−0.385
W16	−0.097	0.083	−0.301
W20	0.236	0.021	−0.485
W24	0.214	0.047	−0.456

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 moderately correlated at the higher ages. For example, the phenotypic correlation of age at point of inflection with body weight at 2nd week is only −0.155 and that was −0.485 in the 20th week of age. The absolute phenotypic correlation increased with the advancement of age. This result conforms with 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, 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.

4. CONCLUSIONS

In conclusion, 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 age at point of inflection is highly heritable (more than 0.80) 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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