GENETIC ASPECTS OF GROWTH CURVE SHAPE IN PIGS.

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SUMMARY

Growth curves of pigs from six genetic lines were estimated linearly (making use of on-test and off-test weights at ca 35 and 93 kg, respectively) and curvilinearly (making use of these and mid-test weights at ca 63 kg). The degree of curvilinearity (DEVN%) was quantified as the difference between actual mid-test weight and its linear prediction, expressed as a percentage of the latter. DEVN% showed line means from -5 to -2 %, with within-line standard deviations from 9 to 11 %. In the fastest-growing three lines, DEVN% showed h^2 values (estimated with a sire-dam model) close to zero while the h^2 of linear daily gain (LDG) ranged from 0.13 to 0.21; in the slower-growing three lines, h^2 values of LDG and DEVN% were of the same magnitude, ranging from 0.13 to 0.26 and from 0.16 to 0.35, respectively. Mean metabolic body weights MBW over the growth trajectory as estimated from on-test and off-test weight only and from these plus mid-test weight showed within-line correlation coefficients of ca 0.93. It is concluded that the degree of curvilinearity of the growth curve is a heritable trait in some of the lines. This has implications for the way MBW has to be accommodated in selection criteria that attempt to aim for net feed efficiency.

INTRODUCTION

The common breeding objective for growth and carcass traits in pigs nowadays comprises daily gain (DG), daily feed intake (DFI) and carcass lean content (LEAN). Many pig breeding companies have achieved substantial genetic progress in LEAN, which means that this will decreasingly be the trait of real interest. More probably, the rate of lean deposition and its efficiency, and ultimately net feed efficiency, will turn out as traits that some breeding companies will be able to improve more successfully than others. Hence the measurement of these traits, especially of the latter one, becomes of interest.

Net feed efficiency can be approached as DFI adjusted for production performance and metabolic body weight (MBW, an attempt to take care of the energy requirements for body maintenance, which cover about a third of total energy intake in growing pigs). This adjustment may take place in two ways. Either we explicitly calculate residual feed intake (RFI) figures as the residual from a multiple regression of DFI on DG, LEAN-related traits and MBW, and treat RFI as a trait to produce EBVs for in its own right, or we evaluate DFI together with DG, LEAN-related traits and MBW in a multivariate BLUP approach. Given properly estimated genetic parameters, the results should be very similar (Luiting et al., 1991).

In both cases, we need to establish data for MBW over the period during which DFI was measured; in fixed-length testing systems, this trait may show a considerable amount of variation. In this paper we report on the preliminary results of a study that considers the shape of the growth curve and its impact on MBW estimation.

MATERIALS AND METHODS

Data were available on 8840 male growing pigs, a subset of those tested in the Genetic Nucleus facilities of PIC-UK from May 1990 to June 1993. They belong to six genetic lines. Three of these (A, B, C) are Large White- or Landrace-based, the other three (D, E, F) are Pietrain/Large White/Belgian Landrace and Meishan/Landrace synthetics and a Duroc-based line. Numbers are in table 1.

Body weight of each of these pigs was measured three times: when placing them on-test (WT1, at 35.6 ± 5.4 kg), in mid-test after 35.5 ± 1.4 days (WT2, at 63.5 ± 9.4 kg), and when taking them off-test (WT3, at 93.2 ± 12.5 kg).

Table 1. Numbers of animals, sires and dams per line.

line	animals	sires	dams
A	1460	71	306
B	1787	95	384
C	2225	88	398
D	1302	65	292
E	1243	70	317
F	823	56	246

Each pig's WT1, WT3, and DAY1 and DAY3 (the on-test and off-test dates) were used to calculate linear daily gain, LDG = (WT3-WT1)/(DAY3-DAY1), and this regression was used to predict the weight on DAY2 (the date on which WT2 was measured). The deviation of the actual WT2 from this predicted mid-test weight E[WT2] was used to produce a measure of curvature, DEVN% = 100 * (WT2 - E[WT2]) / E[WT2].

We approach MBW here as body weight (in kg) raised to the power 0.75; mean MBW over the testing period was estimated in two ways: as a function of WT1 and WT3 (MBW_{13}), following De Haer et al. (1993), and as a function of WT1, WT2 and WT3 (MBW_{123}):

$$MBW_{13} = \frac{WT3^{1.75} - WT1^{1.75}}{1.75 * (WT3 - WT1)}$$

$$MBW_{123} = \frac{(WT2^{1.75} - WT1^{1.75}) * (DAY2 - DAY1)}{1.75 * (WT2 - WT1) * (DAY3 - DAY1)} + \frac{(WT3^{1.75} - WT2^{1.75}) * (DAY3 - DAY2)}{1.75 * (WT3 - WT2) * (DAY3 - DAY1)}$$

Preliminary variance components of LDG and DEVN% were estimated using the REML option of SAS-VARCOMP (SAS, 1989) fitting the model $y = \mu$ + month + year + sire + dam + residual, where the fixed effects month and year pertain to DAY2.

Heritabilities and common litter environmental variance components were estimated as

$$h^2 = \frac{4 * \sigma^2_{sire}}{\sigma^2_{sire} + \sigma^2_{dam} + \sigma^2_{residual}} \quad \text{and} \quad c^2 = \frac{\sigma^2_{dam} - \sigma^2_{sire}}{\sigma^2_{sire} + \sigma^2_{dam} + \sigma^2_{residual}}.$$

RESULTS

In terms of LDG, the lines fall apart into two groups: lines A, B, and C as relatively fast-growing lines with LDG levels of 866 ± 123 to 914 ± 130 g/d, and lines D, E and F as slower-growing ones with 682 ± 126 to 797 ± 114 g/d. No such line differences are apparent for DEVN%, which shows levels of -3.6 ± 9.8 to -2.3 ± 9.0 % in lines A, B and C, and of -4.7 ± 10.4 to -1.5 ± 10.1 % in lines D, E and F. Its frequency distributions over lines are in figure 1.

DEVN% appears to be a trait with a considerable variation among animals. The h^2 and c^2 estimates indicate that this variation is not entirely due to measurement errors or unidentified environmental influences: the DEVN% h^2 estimates in lines D, E and F are of the same order of magnitude (0.21, 0.35 and 0.16, respectively) as the LDG ones (0.26, 0.25, 0.13). In contrast, the DEVN% h^2 values in lines A, B and C are close to zero (0.03, 0.03, 0.02) although those of LDG are of similar size as in the other lines (0.21, 0.25, 0.13). The c^2 estimates do not provide very

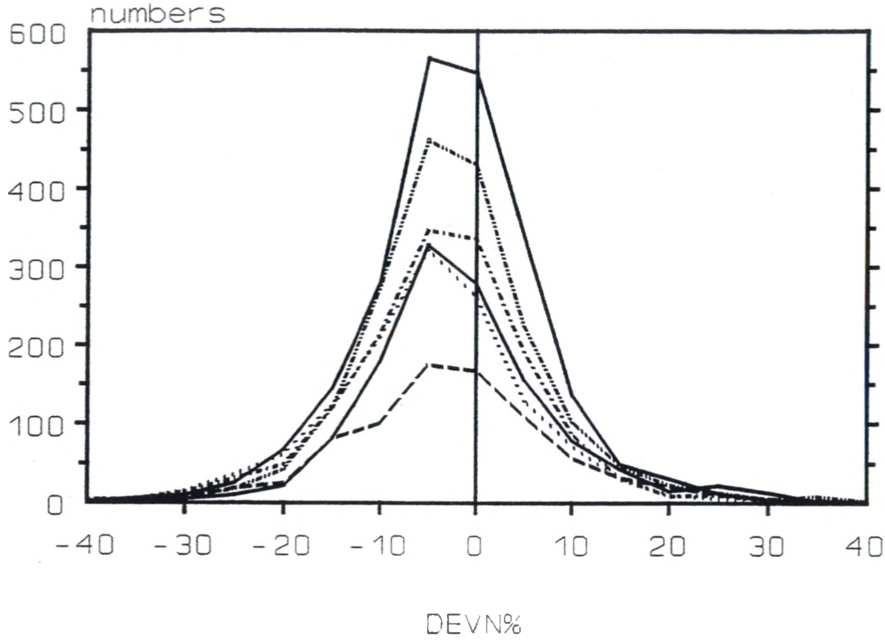

Figure 1. DEVN% frequency distributions.

useful information: they range from 0.00 to 0.08 for LDG and from 0.04 to 0.09 for DEVN%, without any clear pattern as regards the lines.

Correlations between MBW_{13} and MBW_{123} range among the lines from 0.92 to 0.94.

DISCUSSION

It appears from these preliminary results that the degree of curvilinearity of the growth curve of pigs between 35 and 95 kg shows a considerable amount of variation among animals within genetic lines. Furthermore, in our slower-growing lines, this variation seems to be of genetic origin to the same extent as is the case for linear growth rate; in the faster-growing lines, the variation in curvature appears to be largely non-genetic.

Metabolic body weights estimated without taking this curvature in consideration (i.e., making use of on-test and off-test weights only) show a high linear correlation with MBW values estimated from on-test, mid-test and off-test weights, but about 14 % (i.e., $1 - 0.93^2$) of the latter trait's variance remains still unaccounted for.

The heritability estimates of DEVN% in the slower-growing lines suggest that there is as much reason to consider variation in curvilinearity as a genetic issue as there is for linear growth.

These data need to be re-examined using an animal model to estimate the genetic parameters. Furthermore, considering the net feed efficiency issue, the body weight curves will have to be linked to the feed intake curves of the same pigs.

As a result of developmental changes in body composition (with consequences for the energy requirements for body protein turnover and thermal regulation) and physical activity over the test trajectory, the determinants of net feed efficiency are not entirely the same in young animals (up to 60 kg or so) as in older ones. In order to be able to quantify this development to the extent that we may use the information for genetic selection purposes, we need information on the development of body weight, DFI, and body composition during the growth trajectory. Treating all these processes (or traits) as linear cannot be adequate.

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