Are We Making Genetic Progress In Growth Performance And Carcass Characteristics In The South African Pig Industry?

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Introduction

The South African Pig Performance Testing Scheme is conducted to extend and improve the National Pig Herd by means of scientifically founded and proven methods and practices. Conventional pig breeding programs select mainly for performance traits because of the high economic value of these traits (Sonesson *et al*., 1998). In South Africa, selection has mainly been on average daily gain and reduced backfat. Most pig enterprises aim to produce fast growing pigs that consume minimum feed to attain market weight, reducing feed costs, which constitute a high proportion of the production costs (Hoque *et al*., 2007). South African producers are rewarded for the lean content of their products based on the PORCUS system. Meat quality and inputs in the raising of the pig are therefore important, while success of pork production is measured through profitability, which depends on product yield and quality. Thus, pig characteristics that are positive for profitability are high growth rate, low food conversion ratio and low carcass fatness (McPhee & MacBeth, 2000). Breeding strategies that maximize profit need to balance genetic potential for carcass yield with correlated changes in product quality.

In the history of the South African pig performance testing scheme focus has mainly been on recording the relevant traits and identifying superior animals for the industry. Less emphasis has been placed on evaluating the success of the improvement scheme itself. Despite a fairly sophisticated commercial pig industry, there is no information on the evaluation of genetic performance of the pig population. Therefore, the objectives of this study were to: (i) estimate the genetic parameters for growth and carcass traits, and (ii) compute genetic trends in order to evaluate the performance of the improvement scheme over the last 14 years.

Materials and Methods

Animals. The data comprised of 4900 performance tested animals from 1990 to 2008 and 2 843 carcass evaluated animals between 1993 and 2007 from 20 herds. These animals were tested at one of three testing centres, Irene, Elsenburg and Cedara under Phase B. Every year each member submitted 44 pigs (22 boars and 22 gilts) for testing at 18 to 24 kg. Before the test, animals were treated for internal and external parasites and quarantined, were individually penned on solid concrete floors and fed until they commenced testing at ±27 kg. During the test period, animals were individually housed and fed *ad lib* using individual feeders and water was available *ad lib*.

Measurements. The pigs were weighed weekly during the test period without any change in the feeding routine and feed consumption was calculated. Backfat measurements were taken using an ultrasonic backfat probe at about ±77 kg and at slaughter (±86 kg), 6.5 cm from the midline of the last rib (t23 position). At the completion of the test, age was recorded and the animals were humanely slaughtered in an ethically approved way and measurements were taken on the carcasses. After chilling for 24 hours, cold carcass weights were taken and carcass fat thickness measured using a ruler at the shoulder (thickest) and mid section (thinnest), before each carcass was split along the midline. Measurements for the t23 fat and diameter were taken at the t23 position. Eye muscle length and three measurements of eye muscle width at different points were taken using a ruler.

Traits. Carcass traits calculated from the measurements taken were; lean percentage (LEAN), drip-free lean percentage (DLEAN), dressing percentage (DRESS), eye muscle area (AREA) and carcass fat (CFAT). CFAT was the average of the thinnest and thickest carcass fats. AREA was calculated by multiplying eye muscle length by the average of the three eye muscle width measurements. DRESS was cold carcass weight expressed as a percentage of slaughter weight. Growth traits measured were ultrasonic backfat thickness (UFAT), test period weight gain (TPG), test period feed conversion ratio (FCR) and age at slaughter (AGES). FCR was calculated as kg of feed consumed to gain 1 kg of body weight and LEAN was used to calculate DLEAN as shown below (Bruwer, 1992).

$$\text{LEAN (\%)} = 72.5114 - (0.4618 \times \text{t23 fat}) + (0.0547 \times \text{t23 depth})$$

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$$\text{DLEAN (\%)} = 29.37 + (0.56 \times \text{LEAN \%}) - 3.1\sqrt{(\text{t23 fat})}$$

where, t23 fat and t23 depth are fat thickness and eye muscle diameter at t23 position, respectively.

Statistical analysis. The fixed effects included in the analyses were determined using the generalized linear model in SAS (SAS, 2003). These fixed effects were contemporary group, feed intake and age at the start of test. Contemporary group was created by concatenating herd, year and season of testing. Feed intake was not included in the model for FCR, while age at the beginning of test was not included in the model for age at slaughter. Each contemporary group had at least five animals and two sires. Two seasons of testing considered were summer (October to March) and winter (April to September). Random effects were determined using the log likelihood ratio test and litter effects were not significant for all traits analyzed, and therefore not included. Univariate and bivariate analyses were conducted using an animal model to estimate the variance and covariance components. The analyses were done using REML procedures in ASREML-3 (Gilmour *et al*., 2009). The mixed model equation in matrix notation is as follows.

$$y = X\beta + Z_1 u_a + Z_2 u_m + e$$

where, y is the vector of observations, β is the vector of fixed effects, vectors of random effects consisted of random animal additive genetic (u_a), maternal genetic (u_m) and residual (e) effects. Incidence matrices X and Z_i (i = 1, 2) relate fixed, direct genetic and maternal genetic effects, respectively to y. The random effects were assumed to be sampled from a normal distribution with a mean of zero and variance-covariance structure of:

$$V\begin{bmatrix} u_a \\ u_m \\ e \end{bmatrix} = \begin{bmatrix} A\sigma_a^2 & A\sigma_{am} & 0 \\ A\sigma_{am} & A\sigma_m^2 & 0 \\ 0 & 0 & I\sigma_e^2 \end{bmatrix}$$

Vectors of the direct and maternal genetic effects were assumed to be distributed as:

$$\begin{bmatrix} u_a \\ u_m \end{bmatrix} \sim N(0, G_{am} \otimes A), \text{where } G_{am} = \begin{bmatrix} \sigma_a^2 & \sigma_{am} \\ \sigma_{am} & \sigma_m^2 \end{bmatrix}$$

Where A is the numerator relationship matrix, I is an identity matrix, G_{am} is the genetic covariance between direct and maternal effects, $\otimes$ denotes a direct product and σ_e^2 is the environmental variance.

Results and Discussions

Heritability estimates. The direct heritability estimates (Table1) for growth and carcass traits were moderate, while maternal heritabilities were generally low for growth traits. They ranged from 0.15±0.07 for DRESS to 0.63±0.10 for AREA. These estimates are generally within the range of literature estimates reported previously (Nguyen and McPhee, 2005; Chimonyo and Dzama, 2007; Gilbert *et al*., 2007). TPG had a heritability estimate of 0.28±0.06. This is higher than 0.13 reported previously by Chimonyo and Dzama (2007). The heritability estimate for FCR (0.21±0.03) is lower than 0.27±0.03 observed by Hoque *et al*. (2007). DLEAN had a heritability estimate of 0.34±0.08,which is lower than some previous literature estimates for lean percentage (Sonesson *et al*., 1998; Gilbert *et al*., 2007). These differences in estimates in heritability estimates may be attributable to different populations studied, trait definitions and selection pressures applied on the traits. Most of these traits are moderately heritable, suggesting that some genetic improvement may be expected if selective breeding is applied on them.

Maternal genetic effects (Table 1) were relatively low for growth traits. Carcass traits had comparatively higher estimates than previous reports (Chen *et al*., 2002; Chimonyo and Dzama). The maternal heritabilities were generally lower than the corresponding estimates for direct heritabilities indicating a greater genetic influence of the animal than its dam for the trait. No maternal genetic influence was observed in UFAT, FCR, CFAT and AREA. The maternal genetic effects ranged from 0.09±0.04 for TPG to 0.25±0.08 for DRESS. These were higher than those reported by Chimonyo and Dzama (2007) and Chen *et al*. (2002). The relatively large estimates of maternal effects could be due to confounding between common litter effects and maternal effects. The genetic correlations between direct and maternal effects were all negative, consistent with previous reports (Chen *et al*., 2002; Chimonyo and Dzama, 2007). The antagonism suggests that both direct and maternal components should be taken into account to achieve optimum genetic progress (Johnson *et al*., 2002).

Table 1: Estimates of the phenotypic variance (σ^2_p), direct genetic (h^2), maternal genetic (m^2), correlation between direct and maternal genetic (r_{am}) and environmental (e^2) effects in Large White pigs

	h^2	m^2	r_{am}	e^2	(σ^2_p)
UFAT	0.50±0.04			0.50±0.04	5.35±0.16
TPG	0.28±0.06	0.09±0.04	-0.39±0.19	0.70±0.04	6528.00±208.60
FCR	0.21±0.03			0.79±0.03	0.04±0.00
AGES	0.24±0.05	0.11±0.04	-0.41±0.19	0.69±0.04	32.31±0.80
DLEAN	0.34±0.08	0.21±0.08	-0.98±0.11	0.71±0.06	2.86±0.08
CFAT	0.25±0.09			0.75±0.09	13.88±0.73
DRESS	0.15±0.07	0.25±0.08	-0.95±0.23	0.78±0.05	4.89±0.13
AREA	0.63±0.10			0.37±0.10	23.89±1.38

UFAT – ultrasonic backfat thickness, TPG – test period weight gain, FCR – test period feed conversion efficiency, AGES – age at slaughter, DLEAN – drip-free lean percentage, CFAT – carcass fat, DRESS – dressing percentage, AREA – eye muscle area

Genetic correlations. Table 2 contains genetic correlations among the traits studied. Genetic correlations among growth traits ranged from -0.15±0.07 between UFAT and AGES to high (-0.94±0.01) between TPG and AGES. These estimates are generally comparable to most literature estimates (Nguyen and McPhee, 2005; Hoque *et al*., 2007). The highest genetic correlation among carcass traits was 0.65±0.32 between DRESS and AREA, while the lowest was 0.02±0.19 between AREA and CFAT. A high genetic correlation (0.64±0.20) was observed between DLEAN and AREA. Comparable estimates have been reported in literature (Knap *et al*., 1997; Nguyen and McPhee, 2005). Genetic correlations between growth and carcass traits ranged from no correlation between AGES and CFAT to -0.91±0.03 between DLEAN and UFAT. There was also a high positive genetic correlation (0.66±0.22) between UFAT and CFAT. These estimates are similar to some literature estimates (e.g. Nguyen and McPhee. 2005; van Wijk *et al*., 2005). Selecting for improved growth rate will reduce slaughter age and improve feed utilization. Improving drip-free lean percentage and dressing percentage will reduce carcass fat, improve yield and water holding capacity.

Table 2: Genetic correlations among growth and carcass traits

	TPG	FCR	AGES	DLEAN	CFAT	DRESS	AREA
UFAT	0.26±0.06	0.37±0.08	-0.15±0.07	-0.91±0.03	0.66±0.22	-0.10±0.23	-0.31±0.25
TPG		-0.56±0.08	-0.94±0.01	0.05±0.19	-0.13±0.26	-0.02±0.26	-0.34±0.27
FCR			0.93±0.02	-0.40±0.13	-0.09±0.24	0.38±0.12	0.29±0.11
AGES				-0.28±0.20	0.02±0.22	0.18±0.26	0.51±0.27
DLEAN					-0.49±0.22	0.06±0.23	0.64±0.20
CFAT						0.42±0.46	0.02±0.19
DRESS							0.65±0.32

UFAT – backfat thickness, TPG – test period gain, FCR – feed conversion efficiency, AGES – age at slaughter, DLEAN – drip-free lean percentage, CFAT – carcass fat, DRESS – dressing percentage, AREA – eye muscle area

Genetic trends. Genetic trends for growth traits are shown in Figure 1 and they show a slight improvement up to 1997, followed by a decrease until 2006. These genetic trends confirm the genetic correlations between them. Carcass traits (Figure 2) did not show clear and consistent trends. Chen *et al*. (2002) reported decreasing trends for backfat thickness and days to 113.5 kg in four different breeds. Kennedy *et al*. (1996) suggested that 1.7 to 2.9 % improvement per year for backfat thickness and 1.5% per year for days to slaughter would be realistic for industry breeding programs. These trends might have been a response to selection on these or other correlated traits and show that the traits are responsive to selection, hence selection can be successfully applied on them. The deterioration observed after 1999 in growth traits and the inconsistency of carcass traits underscore the need to revise the selection objectives in order to improve the performance of the pig industry.

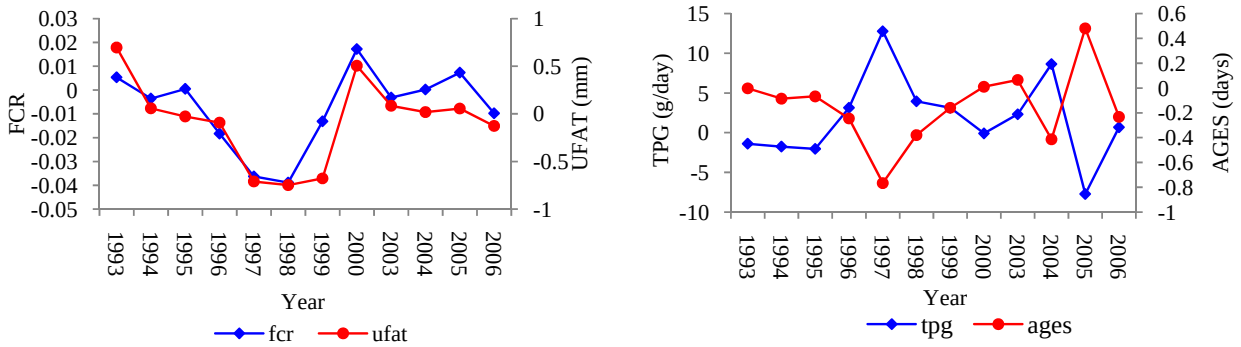

Figure 1: Estimated genetic trends for growth traits in South African Large White pigs

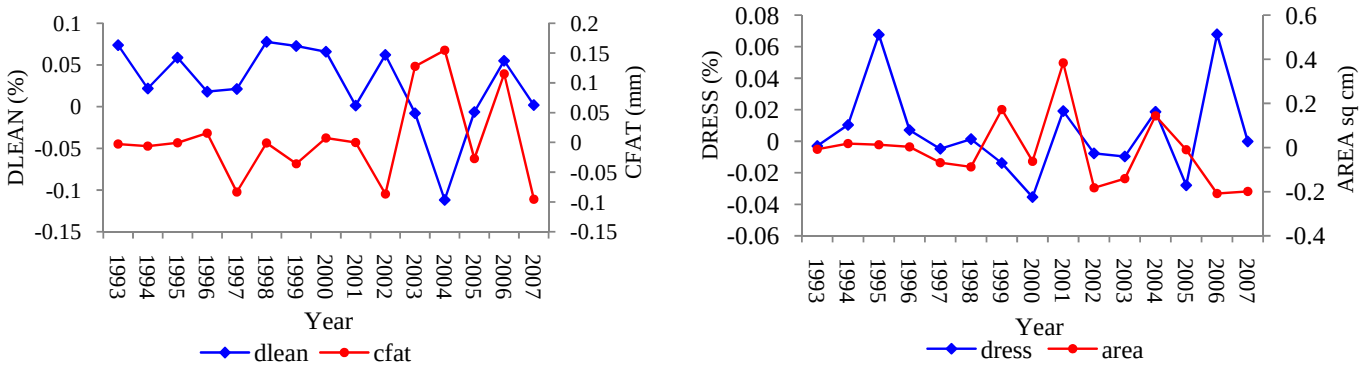

Figure 2: Estimated genetic trends for carcass traits in South African Large White pigs

Conclusions

Substantial genetic progress in growth and carcass traits studied can be expected if selection is applied on them. Selection for drip-free lean percentage can improve carcass leanness, water-holding capacity and yield, while ultrasonic backfat thickness may be used as an indicator for carcass leanness. Improving growth rate may result in improved feed utilization efficiency, hence reduced slaughter age. Improved feed efficiency would also improve carcass leanness. Both direct and maternal genetic effects should be considered in selection programmes. There has been some deterioration of growth traits after 1999 and no consistent performance in carcass traits in the South African pig industry. It is imperative therefore, that the South African pig industry redefine its breeding objectives for growth and carcass traits of pigs in order to meet market demands.

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