From genetic to phenotypic trends

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Optimal improvement of performance

The performance of pigs is influenced by genetic and environmental factors. Both the genetic merit of the pigs and the environment they are raised in have to be improved continuously to optimise progress in performance. In addition, the requirements of genotypes available today may have changed due to selection and the management of pigs has to be adopted accordingly to maximise phenotypic performance.

This document has two main components. Firstly, genetic and phenotypic trends are summarised for Australian pig populations and genetic trends are compared with those achieved in the Australian sheep and beef industries. Secondly, data were available from an on-farm trial to evaluate the effect of feeding a high energy diet on performance. This information may be a starting point to explore avenues to improve pig performance in Australia by matching management practices to the specific requirements of different genotypes available in the industry.

Genetic trends

1. Genetic trends of Australian pig populations

A total of 28 PIGBLUP data files from 10 herds with at least 8 years of data were used in the analyses. The majority of data sets included information from 1995 to 2005. Estimated Breeding Values (EBVs) for performance traits were derived from a multivariate analysis. Reproductive traits were analysed in a separate multivariate evaluation and some data sets had information on litter weight traits available. However, only genetic trends for litter size are summarised. Genetic trends were obtained through within-herd evaluations using PIGBLUP. Average genetic trends were obtained for each trait by regressing mean EBVs for each year available from PIGBLUP on year.

The economic benefits of genetic gains were evaluated using economic weights presented by Cameron and Crump (2001). The economic weight for muscle depth was derived using the approach outlined by Hermesch (2005) assuming a reduction of the base price of 2.30 by $ 0.10 for every 5 mm decrease in muscle depth and an increase of $ 0.10 for every 5 mm increase in muscle depth below and above the mean of 60 mm. The $Index expressed on a per pig basis ($/pig) was:

$$\$Index = 0.049 * EBV_{ADG} - 2.05 * EBV_{BF} - 21.1 * EBV_{FCR} + 1.0 * EBV_{LMD} + 3.56 * EBV_{NBA}$$

where ADG is lifetime average daily gain, BF is back fat, FCR is feed conversion ratio, LMD is muscle depth recorded with ultrasound on the live animal, NBA is number of piglets born alive.

The average annual economic gain resulting from genetic improvement was $1.06 per pig from 2000 to 2005 (Table 1). The top 25% group had an increase in the $Index of $1.92 per pig each year in comparison to an annual genetic gain of $0.35 per pig for the bottom 25% of populations.

The average annual genetic gain was 5.02 g/day for growth rate, -0.15 mm for back fat, -0.01 kg/kg for feed conversion ratio, 0.05 mm for muscle depth and 0.07 piglets for litter size from during last 5 years.

There is considerable variation between populations in annual genetic gain for all traits. Genetic gains in feed conversion ratio were largest in populations that recorded feed conversion ratio and juvenile IGF1. Muscle depth was not recorded in most populations and genetic gains were the result of correlated responses to selection on back fat and growth rate. Annual genetic gains were largest in herds that recorded live muscle depth. Overall, emphasis on litter size has increased during the last five years and considerable genetic gains have been achieved in some populations.

Table 1. Mean genetic trend of 28 pig populations in Australia along with genetic improvement in the top 25% and bottom 25% from 2000 until 2005.

Trait	Mean	Top 25% Mean[1]	Bottom 25% Mean[1]	Top 25% ranked within each trait separately
Growth rate (g/d)	5.02	7.52	2.68	9.59
Backfat (mm)	-0.15	-0.26	-0.07	-0.28
Feed conversion ratio (kg/kg)	-0.01	-0.027	-0.002	-0.028
Live Muscle depth (mm)	0.05	0.014	0.029	0.20
Number born alive (piglets)	0.07	0.12	0.001	0.18
$Index ($/pig)	1.06	1.92	0.35	

[1] Populations were ranked on overall $Index

Although there are multiple reasons why genetic trends differ between individual herds, there are some main factors that distinguish the top and bottom 25% of populations. Genetic gains were higher if an experienced person was in charge of the breeding program, who ensured that high selection intensities were achieved. Maintaining high selection differentials for sires and for dams were shown to be the first and second most important factors affecting rate of genetic gain in Australian beef populations (Johnston and Moore, 2005).

All herds with populations in the top 25% have participated in R&D projects and most of them have received technical advice through fee-based consultancies. Genetic gains in litter size have been enhanced through importation of superior genetics from other Australian sources in some populations.

Genetic gains in individual traits were reduced due to lack of data, either direct or indirect for traits like feed conversion ratio, muscle depth, carcase and meat quality traits as well as litter weight records of the sow. In addition, avoidance of additional

increase in inbreeding levels and pre-selection of pigs for structural soundness and other conformation traits may have contributed to reduced genetic gains.

2. Comparison of genetic trends in the Australian pig, beef and sheep industries

The rate of genetic gains achieved in Australian pig populations can be compared with other industries by expressing them on the basis of genetic standard deviation for each trait. The average rates of genetic gain were 0.15 and -0.11 (downward selection) genetic standard deviations for growth rate and back fat, respectively (Figure 1). These values were lower in magnitude for feed conversion ratio (-0.07) and litter size (0.08). As most breeding programs do not consider live muscle depth the genetic gain was lower (0.03 genetic standard deviations). In comparison, the top 25% group achieved genetic gains of 0.13 to 0.22 (absolute values) genetic standard deviations for growth rate, back fat, feed conversion ratio and litter size.

Rates of genetic gains were lower in Border Leicester sheep and higher in Terminal Sire Sheep (Figure 2, information from Daniel Brown, 2006). The sheep industry considers a similar number of traits to the pig industry. However, higher selection intensities are possible in pigs in comparison to sheep and the generation is slightly lower in pigs. Therefore, annual genetic gains should be higher in pigs in comparison to sheep or beef. Australian Angus breeders include a substantially higher number of traits in their breeding programs (Figure 3) but were still able to achieve genetic gains in individual traits of 0.02 to 0.19 genetic standard deviations. Barwick and Henzell (2005) demonstrated how the rate of genetic gain in profitability in Angus increased from 1985 until 2005. The breeding objective used in Angus includes carcase, meat quality and cow reproductive traits like retail beef yield, intra muscular fat content, days to calving and calving ease and genetic gain has been achieved in these traits. This shows that it is possible to achieve genetic gains in reproduction, carcase and meat quality traits alongside production and Australian pig breeders should consider a wider range of traits in their selection decisions.

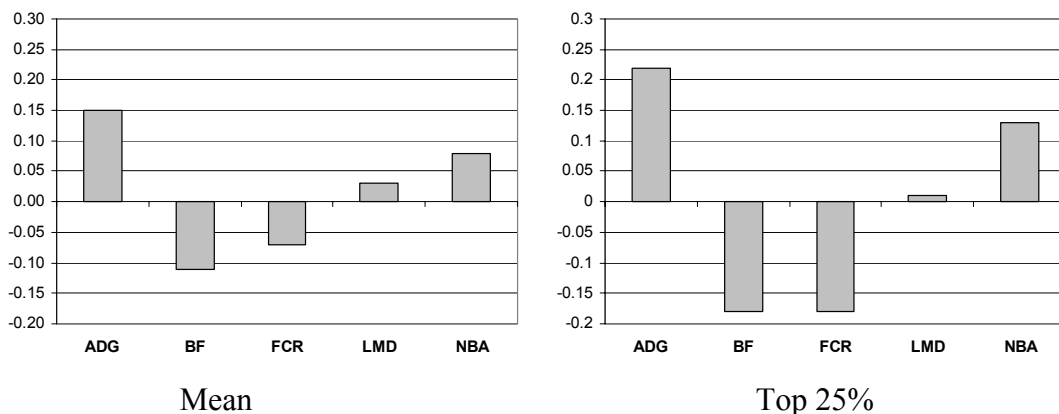Mean   Top 25%

Figure 1. Rates of annual genetic gain from 2000 to 2005 in individual trait EBVs for 28 Australian pig populations (Mean) and top 25% of those populations (Top 25%) expressed in genetic standard deviation of each trait. ADG: lifetime growth rate; BF: back fat, FCR: feed conversion ratio; LMD: live muscle depth; NBA: number born alive.

Border Leicester   Terminal Sire
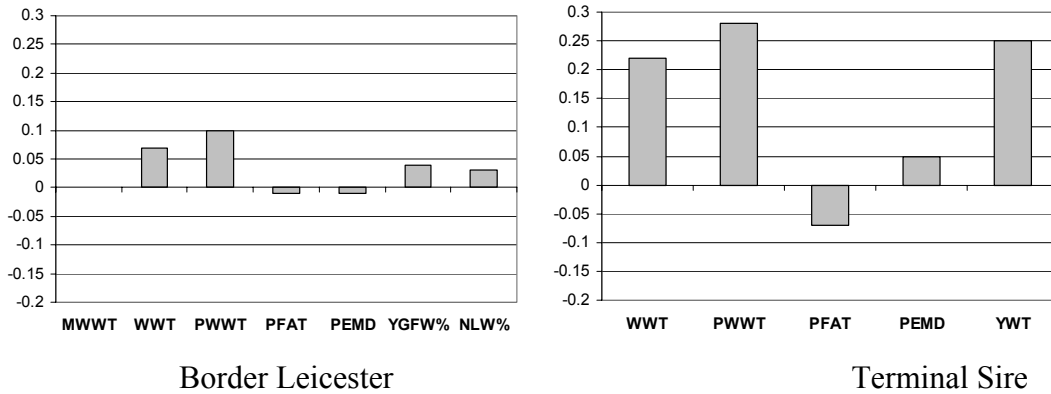
Figure 2. Rates of annual genetic gain from 2000 to 2005 in individual trait EBVs for Australian Border Leicester and Australian Terminal Sire sheep expressed in genetic standard deviation of each trait (D. Brown, pers. comm. 2006). MWWT: Maternal weaning weight; WWT: Weaning weight; PWWT: Post Weaning weight; PFAT: Post weaning fat depth; PEMD: Post weaning muscle depth; YGFW%: Yearling Greece Fleece Weight; NLW%: Number of lambs weaned;
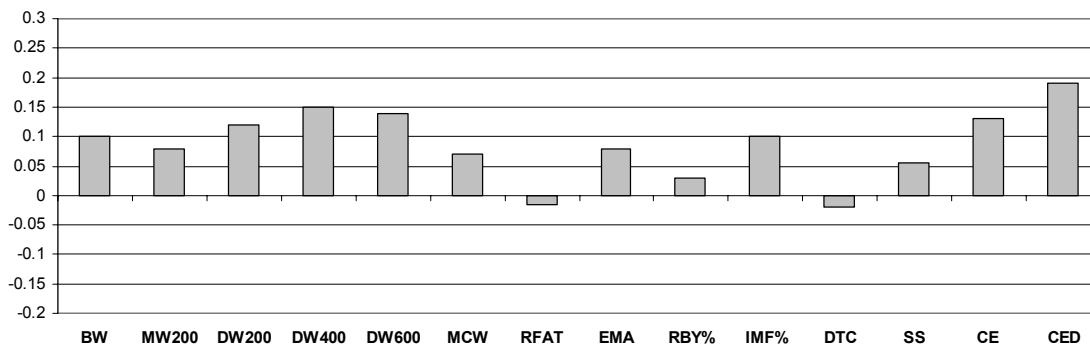

Figure 3. Rates of annual genetic gain from 1998 to 2003 in individual trait EBVs for Australian Angus expressed in genetic standard deviation of each trait (from Barwick and Henzell, 2005). BW: Birth Weight; MW200: Maternal weaning weight 200-day; DW200: 200-day weight, direct; DW400: 400-day weight, direct; DW600: 600-day weight, direct; MCW: Mature cow weight; RFAT: Rump fat; EMA: Eye muscle area; RBY%: Retail Beef Yield; IMF%: Intramuscular Fat Content; DTC: Days to calving; SS: scrotal size; CE: Calving ease (direct); CED: Calving ease daughters.

Phenotypic trends

Mean performance in litter size (NBA), lifetime growth rate (ADG), back fat (BF) and live weight were summarised from eight herds based on their Large White population. Only Large White are shown because it is the largest population within each herd and phenotypic trends did not differ greatly between breeds within a herd.

Phenotypic trends were favourable for all traits (Table 2). Performance in growth rate was lowest in 2003, which may reflect the poorer quality of feed available during the drought years. Mean back fat levels were reduced from 11.1 mm in 2000 to 10.5 mm in 2003 and have remained at similar levels since then. This may indicate that a further reduction in back fat was not desired. The weight at recording has not changed significantly during the last 5 years.

Average annual phenotypic improvements in these eight Large White populations were 0.09 piglets for litter size, 3.8 g/d for growth rate and -0.10 mm for back fat. However, there was substantial variation in phenotypic trends between herds and this summary should only be regarded as an indication that phenotypic trends were of similar magnitudes to genetic trends. In addition, phenotypic performance differed substantially between years within herds which shows that changes in environmental conditions may fully over-ride genetic gains.

Table 2. Mean phenotypic performance of eight Large White purebred populations from 2000 until 2005

	2000	2001	2002	2003	2004	2005	Total change 2005 – 2000
Growth rate	634	629	628	620	630	653	19
Back fat	11.14	10.77	11.00	10.52	10.55	10.65	-0.49
Litter size	10.41	10.52	10.74	10.85	10.81	10.85	0.44
Weight	96.4	97.5	96.9	96.0	96.1	97.0	0.58

Feeding a high energy diet – a first trial

A feeding trial was conducted at Belmont by Brenden McClelland, following a seminar by Roger Campbell who had outlined the use of high energy diets to improve performance of genotypes available today. One batch of pigs was fed a high energy diet during the growth period with 15 MJ DE/kg during the grower and finisher phase. The available lysine per DE was 0.64 g/MJ in the grower and 0.60 g/MJ in the finisher diet. The standard diet had 14.2 MJ DE per kg feed with the same available lysine over DE ratio as the test diet. The trial diet costs approximately $30 more per tonne than the normal diet and contained about 3% oil.

The test batch included 182 pigs which were weighed at 61 (range 58 to 70 days), 82, 103, 122 and 151 (range 144 to 159) days of age with average live weights of 22, 40, 60, 76 and 108 kg, respectively. Back fat was recorded at the end of test. There was no control group which was fed the standard diet at the same time and a comparison was only possible based on the performance of pigs in the adjoining batches, which were fed the standard diet. There were 158 and 169 pigs in the batches recorded before and after the trial batch. The total data set included 265 Large White, 173 Landrace and 71 Duroc pigs with most Duroc pigs (N: 57) fed the higher energy diet. The batches either side of the test batch had only lifetime growth rate and back fat available and a comparison of both diets was only possible for these traits. Phenoytpic means of the unadjusted data showed a higher growth rate for the test batch accompanied by a higher weight and a higher back fat (Table 3). Overall coefficients of variation were similar across batches for most traits, only back fat had a higher coefficient of variation in the trial batch.

Table 3. Unadjusted means, standard deviations (sd) and coefficients of variation (CV) for performance traits recorded on the standard diet (pre and post-test batches) and a higher energy diet (test batch).

Trait	Pre-test batch		Test batch		Post-test batch	
	Mean (sd)	CV	Mean (sd)	CV	Mean (sd)	CV
Age (days)	152 (3.0)	1.9%	151 (3.8)	2.5%	148 (3.7)	2.5%
Weight (kg)	101 (9.5)	9.4%	108 (9.7)	9.0%	98 (8.5)	8.7%
Growth rate (g/d)	660 (61)	9.2%	718 (66)	9.2%	664 (59)	8.9%
Back fat (mm)	10.9 (1.56)	14.3%	12.0 (2.51)	20.9%	10.5 (1.34)	12.7%

The effect of batch on performance was evaluated using Proc Mixed (SAS OnlineDoc, V8, 1999) fitting batch, breed and sex as fixed effects. In addition, back fat was adjusted for weight at end of test. The sire and dam nested within sire were fitted as random effects for both traits.

Least squares means (LSM) for batch are shown in Table 4 for both traits. There was a significant effect of batch for growth rate. The LSM were 651, 719 and 652 for the three batches, clearly showing the effect of the higher diet on growth. The difference in LSM between the trial batch and the batches fed the standard diet were slightly higher then the observed means due to the larger number of Duroc animals in the test batch. The performance of Duroc animals was substantially lower than the other two breeds and the model accounted for these breed differences. There was no significant effect of batch for back fat and LSM were similar across the three batches. The higher backfat observed in the test group was due to the higher weight

In conclusion, this trial showed that the higher energy content in the diet led to a substantial increase in growth rate and had no effect on back fat. The economic benefits of this higher performance have to be compared with the higher feed costs of the high energy diet.

Table 4. Least squares means (LSM) for batch for growth rate and back fat (se: standard error)

Batch	Growth rate		Back fat	
	LSM	se of LSM	LSM	se of LSM
Pre-test batch	651	8.4	11.7	0.26
Test batch	719	7.2	11.4	0.26
Post-test batch	652	8.3	11.5	0.26

Acknowledgements

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