

GENETIC CORRELATIONS BETWEEN CARCASS LENGTH, FAT AND MUSCLE DEPTHS AND PRIMAL CUT WEIGHTS IN THE FRENCH LARGE WHITE SIRE LINE

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SUMMARY

Records for the French national Large White sire line were collected between 1999 and 2008 for 65,082 pigs on farm and for 2,429 carcasses of siblings measured in three test stations. Ultrasonic measures of backfat and muscle depth were recorded *in vivo* on farm. In addition, fat and muscle depth as well as length were recorded on carcasses of littermates. Weights of primal cuts included back leg, loin with the skin and fat trimmed as well as shoulder and belly weights. Heritability estimates were moderate to high for the four primal cuts, ranging from 0.21 for shoulder to 0.46 for back leg weight. Estimates of genetic correlations (r_a) showed back leg weight was genetically independent from loin (r_a : 0.06) and shoulder (r_a : 0.01) weights. Belly weight was negatively correlated with the weight of the three other cuts (r_a : -0.57 to -0.33). The heritability of carcass length was high (0.64) but the genetic correlations between this trait and weights of primal cuts were low (r_a : 0.05 to 0.26) limiting its use as a potential selection criterion for these traits. Estimates of genetic correlations between fat and muscle depth with primal cut weights were generally higher for fat and muscle depth measured on the carcass in contrast to *in vivo* measures.

INTRODUCTION

In pig production, genetic selection has greatly improved body composition towards a higher lean meat content and a lower fat deposition. Breeding goals are subject to change and may be directed towards yield of primal cuts to better reflect the market value of the carcass. Weights of primal cuts vary for carcasses with a fixed weight and fat depth. This variation in weights of primal cuts resulted in a higher return per pig of \$7 (farm gate level) and \$21 (wholesale/retail level) for the top 10% of carcasses in comparison to the group average (Mérour and Hermesch 2008). Currently, pig producers would receive a similar price for these carcasses in France and Australia. However, new technologies are being developed in both countries to better quantify variation in weights and quality of primal cuts. Selection for weight of primal cuts requires genetic parameters for these traits as well as other traits that may be used as selection criteria. Few studies about genetic parameters for back fat and muscle depth measured *in vivo* and on the carcass, carcass length and primal cuts weights have been found in the literature. Estimates of genetic parameters for these traits are presented in this study.

MATERIALS AND METHODS

Data for this study were based on the French national Large White sire line (LWM) developed in France since 1998 based on the French national Large White dam line. The aim was to create a new breed complementary to the Pietrain breed to produce a terminal boar with not only good conformation but also high growth rate. Since 2000, there has been no gene transfer between the French national Large White sire and dam lines.

Performance recording of the national breeding program in France is based on on-farm testing combined with central testing. Siblings of on-farm tested animal candidates are sent to test stations

* AGBU is a joint venture of NSW Department of Primary Industries and University of New England

Pigs

for post-slaughter recording. Data for this study consisted of 65,082 records from ten herds and 2,429 records from three stations collected between 1999 and 2008. Males and females tested on farm were housed in pens of 10 to 15 pigs and fed *ad libitum*. All farms practiced batch management with a batch consisting of at least 18 animals from the same sex and minimal variation in age (maximum range of 15 days). Ultrasonic backfat thickness (**USBF**) and muscle depth (**USMD**) were measured four cm right and left from the chordal spine between the third and fourth last ribs at an average live weight of 97.2 kg (± 10.7 kg). For each of the latter two traits, the right and left measurements were averaged for analysis. Litter mates (only castrates) of pigs tested on farm were sent to the three test stations. Pigs from each herd were tested in at least two stations. Pigs arriving at the station over a period of two weeks formed a batch, which consisted of at least two herds. Pigs were a maximum age of five weeks at arrival. Animals from the same herd were housed in groups of 12 animals and fed *ad libitum* with individual electronic feeders. When pigs reached the target weight of 105 kg (108.7 ± 6.13), they were slaughtered in one of two commercial abattoirs. Fat and muscle depths (**CBF** and **CMD**) between the third and fourth last ribs were recorded on the carcasses using a fat and lean sensor (Sydel CGM – reflectance measurements). Carcass length (**LEN**) was measured 24 h *post mortem* from the atlas to the anterior edge of the pubic symphysis. The right half of each carcass was submitted to a normalised cutting procedure (Métayer and Daumas 1998), and weights of primal cuts including back leg (**LEG**), loin with the skin and fat trimmed (**LOIN**), shoulder (**SHLDR**) and belly (**BELLY**) were recorded.

The GLM (SAS 1999) procedure was used to derive the fixed effect model for each trait. Variance and covariance components were estimated in univariate and bivariate analyses using ASReml (Gilmour *et al.*, 2006). On-farm contemporary group (1455 levels) combining herd, year, batch and sex was fitted for ultrasonic measurements (USBF and USMD) along with the linear covariable of live weight and the direct additive genetic and permanent environment of the litter effects. Contemporary groups (99 levels) in station tested animals were based on year, batch and station and was fitted for primal cut weights and linear carcass measurements (LEN, CBF and CMD) along with the linear covariable of cold carcass weight (83.2 ± 5.26 kg). Random effects were the direct additive genetic and common litter effects for on-farm traits, whereas the litter effect was not significant for traits recorded in station.

RESULTS AND DISCUSSION

Heritabilities. Moderate to high heritability estimates were obtained for carcass traits (Table 1). Primal cuts with higher lean to fat ratio (LOIN and LEG) were more heritable (0.43 and 0.46) than belly and shoulder (0.35 and 0.23). Definition of primal cuts differed between studies and it is difficult to directly compare these heritability estimates with literature values. Nevertheless, Johansson *et al.* (1987) reported heritabilities of 0.43, 0.40 and 0.35 for ham, loin and shoulder percentages for a Yorkshire breed, whereas van Wijk *et al.* (2005) estimated heritabilities of 0.40 and 0.29 for leg and loin weights. The heritability estimate of carcass length (0.64) was slightly higher than literature values, ranging from 0.44 to 0.62 (Engelland *et al.* 1997; Johansson *et al.* 1987). Other studies (Johnson and Nugent III 2003; Nakavisut *et al.* 2006) reported lower heritabilities of 0.12 to 0.41 for body length. Differences in the measurement position may have contributed to variation in estimates. The heritability of backfat depth measured *in vivo* was lower than the one measured on carcass (0.37 versus 0.59), whereas estimates were the same for both *in vivo* and *post mortem* muscle depth measures (0.30). The litter effect estimates were 0.04 ± 0.003 and 0.04 ± 0.004 for ultrasonic backfat and muscle depth recorded on farm.

Table 1. Number of records, means and coefficients of variation (CV), heritability estimates (h^2) with standard errors (s.e.) and phenotypic variance (σ_p^2) for carcass traits and *in vivo* depth

Trait (unit, abbreviation)	N	Mean	CV	h^2	s.e	σ_p^2
Leg weight (kg, LEG)	2,422	9.8	7.1 %	0.46	0.06	0.15
Loin with skin and fat trimmed (kg, LOIN)	2,426	10.9	8.8 %	0.43	0.06	0.28
Belly weight (kg, BELLY)	2,424	4.7	11.8 %	0.35	0.06	0.14
Shoulder (kg, SHLDR)	2,422	9.3	6.8 %	0.23	0.05	0.12
Carcass length (mm, LEN)	2,418	984	3.0 %	0.64	0.06	668
Fat depth abattoir (mm, CBF)	2,396	15.0	20.5 %	0.59	0.06	8.11
Muscle depth abattoir (mm, CMD)	2,400	54.4	10.1 %	0.30	0.05	20.3
Ultrasound <i>in vivo</i> backfat (mm, USBF)	65,082	9.1	19.2 %	0.37	0.01	1.45
Ultrasound <i>in vivo</i> muscle depth (mm, USMD)	55,036	52.7	10.1 %	0.30	0.01	12.5

Genetic correlations. Leg weight was genetically uncorrelated with loin weight, suggesting that selection for high leg weight does not result in a high loin weight (Table 2). In comparison, van Wijk *et al.* (2005) found a genetic correlation of 0.31 between leg and loin weight. The weights of the two valuable cuts, leg and loin, had negative genetic correlations with belly (-0.49 and -0.57) and fat depth measurements (range from -0.58 to -0.35). Loin and belly weights had stronger genetic correlations with carcass muscle depth (0.55 and -0.30) than live muscle depth (0.23 and 0.03). Both muscle depth traits had no genetic association with leg weight. These genetic correlations were considerably lower than comparable estimates published by Hermesch *et al.* (2000) and van Wijk *et al.* (2005) for trait combinations involving weights of loin and leg along with fat and muscle depth traits. Due to the cost of recording these traits, the sizes of data sets were limited and there was a large range in standard errors of genetic correlations from 0.05 to a maximum of 0.38.

Shorter carcasses were genetically associated with heavier legs (-0.24) and lighter loins (0.26), both adjusted for carcass weight. Therefore, selection for shorter length would lead to muscular pigs with proportionally larger ham weights similar to the characteristics of the Pietrain breed. However, these aspects of conformation of pigs were not necessarily reflected in genetic correlations between carcass length and the four fat and muscle depth traits. These estimates were all negative, ranging from -0.30 to -0.20 for backfat and -0.42 to -0.39 for muscle depth. Nakavisut *et al.* (2006) also reported negative genetic relationships between body length and backfat or muscle depth while Engellandt *et al.* (1997) found negative genetic correlations between carcass length and lean meat percentage (-0.38) or *longissimus dorsi* area (-0.37).

CONCLUSIONS

Estimates of heritabilities of primal cut weights were moderate to high in the Large White sire line, implying that the weight of primal cuts and ultimately market value of the carcass can be improved via selection. Given the higher genetic correlations with primal cuts weight along with similar or larger heritabilities and variation, measurements of fat and muscle depth on the carcass may be better selection criteria for loin and back leg weights than *in vivo* measurements. However, *in vivo* measurements can be recorded prior to selection often on more animals. Index calculations are required to evaluate implications of these genetic parameters for pig breeding programs. Genetic correlations between primal cut weights and carcass length were of lower magnitude than estimates between fat or muscle depth and primal cut weights.

Table 2. Genetic correlations (above diagonal) along with environmental (r_e) and phenotypic correlations (r_p ; both below diagonal) between carcase traits¹

Traits ²		LEG	LOIN	BELLY	SHLDR	LEN	CBF	CMD	USBF	USMD
LEG			0.06	-0.49	0.01	-0.24	-0.40	0.04	-0.35	-0.05
LOIN	r_e	-0.10		-0.57	-0.22	0.26	-0.58	0.55	-0.47	0.23
	r_p	-0.03								
BELLY	r_e	-0.12	-0.23		-0.33	0.05	0.37	-0.28	0.39	0.03
	r_p	-0.27	-0.36							
SHLDR	r_e	-0.08	-0.15	-0.15		-0.08	-0.16	-0.30	-0.07	-0.25
	r_p	-0.05	-0.20	-0.20						
LEN	r_e	-0.08	0.27	-0.06	0.02		-0.30	-0.42	-0.20	-0.39
	r_p	-0.16	0.26	-0.01	-0.02					
CBF	r_e	-0.22	-0.45	0.14	0.001	-0.24		0.04	0.73	0.19
	r_p	-0.31	-0.51	0.24	-0.06	-0.28				
CMD	r_e	0.09	0.05	-0.05	-0.01	-0.07	-0.21		-0.17	0.70
	r_p	0.07	0.23	-0.12	-0.09	-0.22	-0.09			

¹ Standard errors of the genetic correlations presented in this table ranged from 0.05 to 0.13.

² For traits abbreviations see Table 1.

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