Proc. Assoc. Advmt. Anim. Breed. Genet. ***16****: 137-140*

GENETIC PARAMETERS FOR CHARACTERISTICS OF PORK BELLIES

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SUMMARY

Belly characteristics including predicted fat percentage of the belly (FATPC), joint area of the rib bone and muscle (RBMA), between muscle fat area (BMFA), subcutaneous fat area (SFA) were recorded on 2,403 pigs along with fat depth at the P2 site (P2). These traits were derived from image analysis of the anterior side of pork bellies. Data were available for juvenile insulin-like growth factor-I (18,398 records), lifetime growth rate (35,074 records), backfat (35,404 records) and muscle depth (34,869 records). Heritability estimates ranged from 0.23 to 0.34 and litter effect estimates were 0.07 or lower for belly traits. Genetic correlations between FATPC and individual fat measurements were high (range: 0.71 to 0.85). Genetic correlations between BMFA and subcutaneous fat measurements differed from unity (range: 0.47 to 0.63). Only muscle depth had a significant genetic correlation with RBMA of 0.39. Genetic correlations between belly and performance traits show that selection based on reduced juvenile-IGF1, backfat and muscle depth will reduce overall fat levels in the belly. However, genetic improvement of individual muscles requires specific measurements and practical pig breeding programs require measurements that can be routinely recorded on the slaughter line.

Keywords: Heritabilities, genetic correlations, belly composition, pigs

INTRODUCTION

Pork bellies are one of the five major cuts from a pork carcase. In the Australian domestic market, a good meaty streak in the belly is required for manufacturing of bacon rasher. The absence of this meaty streak often leads to rejection and return of the product by manufacturers. The composition of pork bellies is also of concern for a number of overseas markets where the belly may be used in stir-fry type meals, barbeques as well as in soup and general cooking. In summary, the belly is a valuable cut of pig carcases with different markets having different requirements. In order to supply each market with the desired belly product it is necessary to be able to predict the composition of the belly and have a good understanding of the factors that influence belly composition. Genetic selection is one avenue to change belly composition. This requires genetic parameters of characteristics describing belly composition along with their genetic relationships with other performance traits used in pig breeding programs. The aim of this paper is to present genetic parameters for fat percentage of the belly, a trait of economic importance, along with four individual belly characteristics and performance traits recorded on farm.

MATERIAL AND METHODS

Belly characteristics were recorded on 2,403 pigs at QAF Meat Industries between August 2001 and April 2003. Pigs were derived from three lines selected for efficient leant meat growth and were predominantly entire males (N=2,026). Belly traits were based on image analysis of the anterior side of the belly. Fat percentage of the belly (FATPC) was predicted from the joint area of the rib bone and muscles (RBMA), the intermuscular fat area (BMFA), the subcutaneous fat area (SFA) and backfat recorded at the P2 site on the carcase (P2) (Shaw and Rosetto, 2003). The mean predicted fat percentage of the belly was 24.8% with a standard deviation of 5.55%. The coefficients of variation of belly traits ranged from 17% for RBMA to 48% for BMFA. Lean bellies had a soft surface, which distorted area measurements and BMFA was most affected. Pictures were only taken from well-chilled carcases, which reduced this distortion somewhat.

Performance data recorded between January 2001 and July 2003 were available for juvenile insulin-like growth factor-I (IGF-I), lifetime growth rate (ADG) and backfat at the P2 site (BF) and muscle depth between the third and fourth last ribs (MD), both recorded with realtime ultrasound.

The SAS procedure GLM (SAS, 1990) was used to derive the fixed effect model for each trait. The effects fitted for belly characteristics included date of slaughter, line (RBMA, BMFA and P2 only), sex of the animal, and the linear covariates of age of the animal at slaughter (FATPC, SFA and P2 only) and live weight. Live weight was also fitted as a quadratic covariable for RBMA. Fixed effects for juvenile IGF-I included the contemporary group consisting of the assay batch within date of bleeding, sex of the animal, line and parity of the sow and age at bleeding as a linear covariable. The contemporary group for further performance traits was based on the week of recording, the testing system (conventional pens with *ad libitum* feeding versus electronic feeders with restricted feeding) and the sex of the animal. The weight of the animal at end of test was fitted as a linear covariable for BF and as a linear and quadratic covariable for MD. Genetic parameters were estimated in univariate and bivariate analyses using ASREML (Gilmour *et al.* 1999) fitting an animal model, with litter as a second random effect.

RESULTS AND DISCUSSION

The fixed effect model explained 42 to 52% of the variation observed in belly traits (Table 1). Slaughter date, which accounted for differences in slaughter procedures and operators, and weight of the animal were the most important effects. Predicted fat percentage of the belly had a heritability of 0.34. Heritabilities ranged from 0.23 to 0.32 for other belly characteristics similar to estimates of 0.27 and 0.31 for lean meat content of the belly, which was based on AutoFOM measurements (Tholen *et al.* 2001). Litter effects were 0.07 or lower for all carcase traits supporting earlier findings (i.e. Hermesch *et al.* 2000; Tholen *et al.* 2001). The heritabily of 0.21 for juvenile IGF-I with a litter effect of 0.11 is well in agreement with previous estimates summarised by Bunter *et al.* (2005). Heritability estimates were similar for ADG and MD and lower for BF in comparison to Hermesch *et al.* (2000).

The three fat measurements recorded on the carcase were part of the prediction equation, which contributed to their high genetic correlations with FATPC (range: 0.71 to 0.85; Table 2). In comparison, the genetic correlation between RBMA and FATPC had a lower magnitude (-0.48). Genetic correlations between RBMA and further fat measurements were not significantly different from zero and show that selection for reduced fatness levels will not improve RBMA. The moderate genetic correlations between BMFA and other subcutaneous fat measurements (range: 0.56 to 0.63) support results by Kouba *et al.* (1999) who reported that, relative to other fat depots, intermuscular fat was more developed in genetically lean than in genetically fat pigs. This could be the result of selection of pigs against subcutaneous fat only and selection for leanness has been less successful in reducing intermuscular fat.

Table 1. Number of records (N), coefficients of determination (R^2), heritabilities (h^2) and estimates of litter effects (c^2) with standard errors (se) along with phenotypic variance (σ^2_p) for belly characteristics, juvenile IGF-1, lifetime growth rate, backfat and muscle depth.

Trait*	N	R^2	h^2	(se)	c^2	(se)	σ^2_p
FATPC (%)	2,331	0.43	0.34	0.06	0.05	0.03	18.8
RBMA (cm^2)	2,339	0.42	0.25	0.05	0.04	0.03	40.7
BMFA (cm^2)	2,400	0.48	0.23	0.05	0.05	0.03	8.48
SFA (cm^2)	2,396	0.52	0.32	0.06	0.07	0.03	24.3
P2 (mm)	2,316	0.40	0.26	0.06	0.03	0.03	4.50
IGF1 (ng/mL)	18,398	0.32	0.21	0.02	0.11	0.01	814
ADG (g/d)	35,074	0.16	0.30	0.02	0.08	<0.01	4,757
BF (mm)	35,404	0.38	0.33	0.02	0.04	<0.01	3.65
MD (mm)	34,869	0.37	0.23	0.01	0.02	<0.01	22.0

* Abbreviations: **FATPC**: Predicted fat percentage of the belly IGF-1; **RBMA**: Rib bone and muscle area; **BMFA**: Between muscle fat area; **SFA**: Subcutaneous fat area; **P2**: Fat depth at P2 site, carcase; **IGF1**: Juvenile insulin-like growth factor 1; **ADG**: Lifetime average daily gain; **BF**: Backfat recorded at finishing at the P2 site, **MD**: Muscle depth between third and fourth last ribs.

Table 2. Genetic (below diagonal) and phenotypic (above diagonal) correlations between belly characteristics (standard errors).

Trait*	FATPC	RBMA	BMFA	SFA	P2
FATPC		-0.38 (0.02)	0.67 (0.01)	0.73 (0.01)	0.68 (0.01)
RBMA	-0.48 (0.12)		0.14 (0.02)	0.07 (0.02)	-0.07 (0.02)
BMFA	0.71 (0.08)	0.03 (0.17)		0.50 (0.02)	0.29 (0.02)
SFA	0.84 (0.05)	-0.09 (0.15)	0.56 (0.11)		0.42 (0.02)
P2	0.85 (0.05)	-0.24 (0.14)	0.63 (0.10)	0.73 (0.07)	

* See Table 1 for trait abbreviations.

Belly characteristics describing fat levels had low positive genetic correlations with juvenile IGF-I (range: 0.18 to 0.25; Table 3) and downward selection for juvenile IGF-I as described by Bunter *et al.* (2005) will also lead to a slight reduction in belly fat content. Genetic correlations between fat levels in the belly and BF differed from unity for FATPC (0.80±0.05), BMFA (0.47±0.09) and SFA (0.76±0.05). In addition, among performance traits only MD had a significant genetic correlation of 0.27(±0.09) with RBMA. Overall, these genetic relationships show that genetic improvement of certain fat and muscle characteristics requires specific measurements of these traits. In this respect, further studies of the belly should include additional measurements of the lean meat area of the belly.

Table 3. Genetic (rg) and phenotypic (rp) correlations between belly characteristics and juvenile IGF-I, growth rate, backfat and muscle depth (standard errors).

Trait*		FATPC	RBMA	BMFA	SFA	P2
IGF-I	rg	0.20 (0.10)	0.08 (0.11)	0.18 (0.12)	0.25 (0.10)	0.21 (0.11)
	rp	0.11 (0.02)	-0.05 (0.02)	0.08 (0.02)	0.10 (0.02)	0.06 (0.03)
ADG	rg	0.33 (0.09)	-0.11 (0.11)	0.35 (0.10)	0.29 (0.09)	0.16 (0.10)
	rp	0.25 (0.03)	-0.11 (0.03)	0.16 (0.03)	0.17 (0.03)	0.05 (0.03)
BF	rg	0.80 (0.05)	-0.09 (0.10)	0.47 (0.09)	0.76 (0.05)	0.95 (0.03)
	rp	0.60 (0.01)	-0.08 (0.02)	0.36 (0.02)	0.52 (0.02)	0.58 (0.01)
MD	rg	-0.16 (0.08)	0.27 (0.09)	0.04 (0.09)	-0.14 (0.08)	-0.05 (0.09)
	rp	-0.07 (0.02)	0.11 (0.02)	0.03 (0.02)	-0.05 (0.02)	-0.03 (0.02)

* See Table 1 for trait abbreviations.

CONCLUSIONS

Predicted fat percentage of the belly and individual belly characteristics used in the prediction equation were moderately heritable and had coefficients of variation similar to other carcase traits. Therefore, these traits can be improved through selection. Intermuscular fat area was genetically a different trait than subcutaneous fat measurements. In addition, the joint area of bone and rib muscles (RBMA) had no genetic relationship with fat measurements, juvenile IGF-I and lifetime growth rate. Only muscle depth recorded on the live animal had a low positive genetic correlation with RBMA. Selection based on backfat, growth rate and muscle depth will increase lean meat content of the whole carcase. However, genetic improvement of individual fat and muscle characteristics requires specific measurements. Belly characteristics were derived from image analysis of the anterior side of the belly and are not routinely available on the slaughter line. Practical breeding programs require traits that can be routinely recorded on the slaughter line similar to the AutoFOM system that provides detailed carcase information including belly composition analysed by Tholen *et al*. (2001).

ACKNOWLEDGEMENT

This study was funded by Australian Pork Limited under project 1637. Diligent data collection by Helen Grigg and Tania Shaw at QAF Meat Industries is gratefully acknowledged.

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