Body length and its genetic relationships with production and reproduction traits in pigs

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Introduction

Body length in pigs has been reported to be heritable with heritability estimates ranging from 0.12 to 0.62 (Kim et al., 1996; Cho et al., 1998; Johnson and Nugent, 2003; Hofer, 2004). Body length is directly associated with carcass length. Measuring body length is simple and not costly. Compared to reproduction traits body length can be measured on younger animals and from both sexes. Considering these characteristics, body length could be used as one of the selection criteria to improve production and reproduction traits in pigs. However, studies on genetic relationships between body length and other production and reproduction traits have not been found in the literature. The aim of this study was to estimate genetic correlations of body length with production and reproduction traits.

Material and methods

Data structure. Data consisted of 7665 performance-test records and 10984 litter records from 1431 Duroc (DU), 2712 Large White (LW) and 3522 Landrace (LR) animals and 1203 DU, 4742 LW and 5039 LR litter records. The data were collected from Government pig reeding farms in Thailand from 1992 to 2003. Pigs were performance-tested in individual pens and given ad libitum access to feed from approximately 30 kg to 90 kg of bodyweight. At the end of performance test, final date and weight were recorded together with body length (BL) from the mid point between the ears to the starting point of the tail. The average numbers of tested pigs per sire were 9.0, 11.4 and 11.2 and tested pigs per litter were 2.5, 2.8 and 2.7 for the DU, LW and LR breeds, respectively.

Production traits consisted of average daily gain over the test period (ADG), ultrasonic backfat thickness (BF) measured at 6.5 cm from the dorsal mid-line (P2) and muscle depth (MD) at the same position as BF. Reproduction traits included number of piglets born alive (NBA), number of piglets weaned (NW), litter weight at birth (LWB) and litter weight at weaning (LWW). The descriptive statistics for the studied traits by breed are presented in Table 1. Landrace pigs had the longest body of all breeds (108 cm), LW pigs were intermediate (106 cm) and the DU breed had the shortest body (103 cm). Body length had low coefficients of variation (3.1% to 4.3%).

Breed	Duroc			Large White					Landrace			
Trait	X	SD	Min	Max	X	SD	Min	Max	X	SD	Min	Max
BL (cm)	103	3.7	90.0	117	106	4.6	92	127	108	4.4	91	127
ADG (g)	794	111	500	1170	777	111	404	1375	836	122	476	1386
BF (mm)	13.5	2.5	6.5	24	12.9	2.8	3.0	49.5	12.1	2.7	4.0	23.0
MD (mm)	50.1	7.5	28.0	74	48.4	6.8	10.5	87.5	51	6.7	28.0	88.4
NBA (pigs)	7.8	2.5	1.0	14	9.0	2.7	1.0	18.0	8.7	2.6	1.0	17.0
NW (pigs)	6.9	2.4	1.0	13	8.2	2.7	1.0	17.0	8.1	2.6	1.0	15.0
LWB (kg)	11.9	4.0	1.0	25.6	13.0	4.1	0.5	29.9	13.1	4.2	1.0	29.8
LWW (kg)	32.9	12.4	2.1	74.9	39.6	14.2	1.0	122	42.4	14.2	2.0	128

Table 1. Means (X), standard deviations (SD), minima (Min) and maxima (Max) forbody length, production and reproduction traits.

BL: body length, ADG: average daily gain, BF: ultrasonic backfat, MD: muscle depth, NBA: number of piglets born alive, NW: number of piglets weaned, LWB: litter weight at birth and LWW: litter weight at weaning

Statistical analyses. Genetic analyses were performed separately within breeds using restricted maximum likelihood methodology with the program ASReml (Gilmour et al., 2002). Variance components for BL, ADG, BF and MD were estimated using a single trait animal model. The model included fixed effects of sex, contemporary group of test herd-year-season, genetic group of country of origin of the base populations introduced to Thailand, covariate of age at entering the test for ADG and covariate of final weight for BL, BF and MD. The additive genetic effects of animal and common litter effects were included as random effects. For reproduction traits, all univariate analyses were carried out using repeatability animal models, treating reproduction traits from different parities as a single trait with repeated records. Fixed factors in the mixed model included farrowing herd-year-season, genetic group of country of origin, age class of sow at farrowing, parity number and litter breed for the LW and LR breeds. Random effects for reproduction traits included the direct additive effects of animal and permanent environmental effects of repeated litter records of the sow. Genetic and phenotypic correlations between BL and production or reproduction traits were estimated using bivariate animal models with the same fixed and random effects as in the univariate analyses.

Results and discussion

Estimates of heritabilities for body length were high and similar in all breeds ranging from 0.34±0.05 in the LW breed to 0.36±0.07 in the DU breed and 0.41±0.05 in the LR breed (Table 2). The heritability estimates for production traits were low to moderate. The heritability estimates for reproduction traits were low in the LW and LR breeds and moderate in the DU breed (Table 2). The litter effects for production traits and repeatability estimates for reproduction traits are also shown in Table 2. The results from this study show a similar trend to that from a study by Johnson and Nugent (2003). The heritability estimate for BL had a tendency to be higher in the LR breed than the DU and LW breeds. The heritability estimates for BL reported by Johnson and Nugent (2003) were 0.16, 0.23, and 0.32 and litter effect estimates were 0.22, 0.18, and 0.15, for the DU, Yorkshire and LR breeds, respectively. The sum of heritabilities and common litter effects were similar between these two studies. Sampling and different data structures between populations may result in different partitioning of additive genetic and common litter effect variances. The differences in the measurement positions may result in different estimates of heritabilities between studies. Hofer (2004) reported a high heritability estimate of 0.62 in female LW and LR pigs for BL (means of 97 cm and 99 cm for LW and LR, respectively). Most studies reported heritability estimates for BL to be high in the LW and LR breeds (0.47 by Cho et al. (1998) and 0.42 ± 0.03 by Kim et al.(1996)). Similar to BL, heritability estimates for carcass length were reported to be high. For example, Engellandt et al. (1997) estimated heritability for carcass length to be 0.44 in Pietrain and Belgian LR pigs.

		Heritability		Litter effects / Repeatability*				
Traits	DU	LW	LR	DU	LW	LR		
BL	0.36±0.07	0.34±0.05	0.41±0.05	0.12±0.03	0.12±0.02	0.10±0.02		
ADG	0.33±0.07	0.16±0.05	0.26±0.05	0.21±0.04	0.25±0.03	0.24±0.02		
BF	0.25±0.10	0.30±0.06	0.41±0.05	0.17±0.05	0.05±0.03	0.11±0.02		
MD	0.25±0.11	0.22±0.07	0.20±0.06	0.17±0.05	0.05±0.03	0.05±0.03		
NBA	0.22±0.08	0.12±0.03	0.07±0.02	0.24±0.04	0.15±0.02	0.14±0.02		
NW	0.29±0.04	0.07 ± 0.02	0.07 ± 0.02	0.29±0.04	0.14±0.02	0.14±0.02		
LWB	0.25±0.07	0.10±0.03	0.10±0.02	0.28±0.04	0.15±0.02	0.15±0.02		
LWW	0.27±0.08	0.11±0.03	0.07±0.02	0.32±0.04	0.18±0.02	0.17±0.02		

Table 2. Estimates of heritabilities, litter effects, repeatabilities, genetic and phenotypic correlations for and between body length and production or reproduction traits

*repeatability estimates for reproduction traits in italics and litter effect estimates for production traits in regular font style, DU: Duroc, LW: Large White, LR: Landrace.

The genetic correlation estimates between BL and the production traits studied were consistently lowly negative (Table 3). The highest magnitude of the genetic relationship with ADG was found in the DU breed (-0.43 ± 0.15). This suggests that genetically fast growing DU pigs have more compact bodies. In the LW breed, BL had moderately negative genetic relationships with backfat thickness (-0.34 ± 0.13). In the LR breed, BL had a moderately negative correlation with muscle depth (-0.39 ± 0.16). The results agree with Choi et al. (1996) who reported negative genetic relationships between carcass length and backfat thickness and Engellandt et al. (1997) who reported negative dorsi area of -0.38 and -0.37, respectively.

The genetic correlations between BL and litter traits were moderately positive $(0.30\pm0.16 \text{ to } 0.47\pm0.14)$ in the LW breed. In the DU and LR breeds, the r_g estimates between BL and litter traits were not significantly different from zero. In the LW breed, the moderate r_g estimates indicate that BL information may be used to improve reproduction traits in the long term. There are two reasons to support using BL in a breeding program to improve reproduction traits in the LW breed. Firstly, BL is much more heritable than reproduction traits. Secondly, BL can be measured earlier than litter traits and on both male and female pigs.

	Gen	etic correla	tion	Phenotypic correlation*				
Traits	DU	LW	LR	DU	LW	LR		
ADG	-0.43±0.15	-0.10±0.17	-0.14±0.11	-0.28±0.03	-0.17±0.02	-0.14±0.02		
BF	-0.08±0.24	-0.34±0.13	-0.20±0.11	-0.11±0.04	-0.09±0.03	-0.09±0.03		
MD	-0.03±0.26	-0.23±0.17	-0.39±0.16	-0.03±0.05	0.02±0.03	-0.10±0.03		
NBA	-0.06±0.21	0.47±0.14	0.11±0.16	0.01±0.05	0.00±0.03	0.01±0.03		
NW	0.03±0.19	0.46±0.16	0.07±0.16	0.00 ± 0.05	0.01±0.03	0.02 ± 0.03		
LWB	-0.19±0.20	0.37±0.16	-0.02 ± 0.14	-0.05 ± 0.05	-0.01±0.03	$0.00{\pm}0.03$		
LWW	-0.05±0.20	0.30±0.16	0.04±0.16	-0.06±0.05	-0.01±0.03	0.01±0.03		

Table 3. Estimates of genetic and phenotypic correlations between body length (BL) and production and reproduction traits

For abbreviations see note below tables 1 and 2

Conclusion

Genetic correlations between body length (adjusted for weight) and production or reproduction traits are inconsistent across the three breeds, possibly due to sampling. While genetic correlations would indicate that BL might be a suitable indicator trait to achieve higher accuracy of selection for reproduction traits particular at young ages and in males in the Large White breed, the r_g estimates in the other breeds do not support

this. As the standard errors of the estimated correlations are large, additional data from those populations or from other studies are required to develop recommendations with respect to body length for commercial performance recording programs. The recording of BL is continuing in the Thai Government breeding herds and updated results will become available.

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