



## Genetic Parameter Estimation of Carcass Traits of Duroc Predicted Using Ultrasound Scanning Modes

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**ABSTRACT :** A total of 6,804 records for Duroc breed were collected from three farms registered at the Korean Animal Improvement Association (KAIA) from 1998 to 2004 of which both records from two ultrasound modes (A and B) were analyzed to estimate the variance components of carcass traits. Three carcass traits backfat thickness (bf), loin eye muscle area (lma) and lean meat percentage (lmp) were measured. These traits were analyzed separately as bf1, lma1 and lmp1 for ultrasound mode A and bf2, lma2 and lmp2 for ultrasound mode B with multiple trait animal model by using MTDFREML (Boldman et al., 1993). All the traits revealed medium heritability values. Estimated heritabilities for bf1, bf2, lma1, lma2, lmp1 and lmp2 were 0.45, 0.39, 0.32, 0.25, 0.28 and 0.39, respectively. Estimated genetic correlations for traits bf1 and bf2, lma1 and lma2, lmp1 and lmp2 were positive but low. Specifically, genetic correlations between bf1 and bf2 was 0.30 while the estimates for lean traits between lma1 and lma2 and between lmp1 and lmp2 were 0.15 and 0.18, respectively. Conversely, high negative genetic correlations existed between bf1 and the lean traits lma2, lmp2. Likewise, the estimated genetic correlations between lma1 and lma2 and lmp1 and lmp2 were low. (**Key Words :** Duroc, Genetic Parameters, Carcass Traits, Ultrasound Mode)

### INTRODUCTION

With the changes in the swine industry, the knowledge of genetic control of pork quality traits is required to implement selection programs which maximize the genetic gain in the swine population that emphasize product quality. Meat quality becomes increasingly important to meat processors and consumers as ready-made meat products, microwave consumption and the incidence of eating outside the home increase (Sloan et al., 1984). Real-time ultrasound measurements of backfat thickness and longissimus muscle area are being used increasingly in swine selection programs. The technology eliminates the need to slaughter animal and enables the breeder to monitor lean growth and to predict growth curves which are vital for animal evaluation and selection.

Ultrasound mode A gives point estimate of characteristics of the tissue of interest. According to Moeller (2002) it is accurate for backfat depth but inconsistent for loin depth. In contrast, the ultrasound mode B gives highly accurate results for both backfat and loin muscle area. Although the accuracy of mode A was often less than ideal, the relatively low investment cost and the perceived ease of operation made them widely used for seedstock selection, central testing programs, university, industry research and on-farm applications.

The Korean swine industry is dominated by three breeds Yorkshire, Landrace and Duroc. Registration and record keeping maintained by Korean Animal Improvement Association (KAIA) and Korean Swine Association (KSA) kept records for average daily gain, age to reach 90 kg and carcass characteristics through ultrasound scanning. In the year 2000, the government started training program for swine performance test technicians for the use of ultrasound mode B owing to its accuracy in order for the quality of pork to be globally competitive. However, swine growers have difficulty in adapting the use of ultrasound mode B because of the high cost of machine and the additional cost incurred from the services of the technicians. For reason of low investment cost still today, many swine growers are using ultrasound mode A technology for measuring backfat

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**Table 1.** Number of animals by farm, ultrasound mode, year of birth sex, season and parity

Farm	No. of pigs	Ultrasound mode*		Year of birth		Sex	Season**		Parity	
		A	B	Year	No. of pigs	No. of pigs	No. of pigs		No. of pigs	
A	374	175	199	1998	645	Gilts	1	1,785	1	1,704
B	2,426	369	2,057	1999	1,040	2552	2	1,840	2	1,499
C	4,004	418	3,586	2000	633	Boars	3	1,626	3	1,312
				2001	609	4252	4	1,553	4	833
				2002	838				5	589
				2003	1,882				>6	867
				2004	1,157					
Total	6804				6,804	6,804		6,804		6,804

\* No animals was scanned for both ultrasound mode A and B.

\*\* Season: 1, December to January; 2, March to May; 3, June to August; 4, September to November.

thickness and other carcass traits. In Duroc population only three (3) farms collected data using both the modes A and B. The purpose of this study was to estimate the genetic parameters of carcass traits using data collected by both ultrasound modes and investigate the genetic correlations between ultrasound modes.

## MATERIALS AND METHODS

The data set used 6,804 performance records of pure breed Duroc from three farms which collected data both for ultrasound mode A and B that were registered at KAIA from 1998 up to 2004 (Table 1). The traits were backfat thickness (bf), loin eye muscle area (lma) and lean meat percentage (lmp). These were analyzed separately as bf1, lma1 and lmp1 for ultrasound mode A and bf2, lma2 and lmp2 for ultrasound mode B.

Each animal was scanned either by ultrasound mode A or B but no animal was scanned for both modes. For backfat thickness mode A, Piglog105<sup>TM</sup> ultrasound machine (bf1) was used for the three scanned points at P1 (shoulder), P2 (mid-back) and P3 (loin) adapted from Iowa State University. The average of the three measurements were calculated and adjusted to 90 kg using formula (equation 1) as prescribed by the KAIA Swine Performance Testing Program. On the other hand backfat thickness ultrasound mode B (bf2) was measured using Sonoace 600 V<sup>TM</sup> ultrasound machine scanned 5 cm from the midline at the 10<sup>th</sup> rib and adjusted to 90 kg using the same formula as bf1 (equation 1).

$$bf1 \& bf2 = \frac{\text{backfat at end test} + (90\text{kg} - \text{end weight}) \times \text{backfat at end test}}{(\text{end weight} - 11.34)}$$

For loin eye muscle area (mode A, lma1) the depth of loin muscle area at scanned point 5 cm from the last rib was first measured. The depth of lma multiplied by 6.4516 was calculated prior to adjusting to 90 kg using equation 2. Moreover, loin eye muscle area (mode B, lma2), 5 cm from the 10<sup>th</sup> rib was measured, the image was drawn and area was calculated then adjusted to 90 kg using the following

formula (equation 2):

$$lma1 \& lma2 = \frac{\text{loin meat area end test} + (90\text{kg} - \text{end weight}) \times \text{loin meat area at end test}}{(\text{end weight} + 70.31)}$$

To compute for lmp1 the backfat at the 10<sup>th</sup> rib and 10cm before the last lumbar vertebrae were measured first then measured the depth of lma1 at the 10<sup>th</sup> rib point and Piglog 105<sup>TM</sup> automatically calculated the lmp1. For lmp2, Sonoace 600 V<sup>TM</sup> using both lma2 and bf2 automatically calculated the lmp2.

All traits were initially analyzed using GLM procedure of Statistical Analysis System (SAS 8.2) to determine the significant fixed effects using the following model:

$$Y_{ijklm} = \mu + S_i + F_j + B_k + M_l + P_m + e_{ijklm}$$

where

$Y_{ijklm}$  = observation of traits (bf1, bf2, lma1, lma2, lmp1 and lmp2)

$\mu$  = general mean

$S_i$  = fixed effect of the  $i^{\text{th}}$  sex ( $i = 2$ ; gilts and boars)

$F_j$  = fixed effect of the  $j^{\text{th}}$  farm ( $j = 1, 2$  and  $3$ )

$B_k$  = fixed effect of  $k^{\text{th}}$  year of birth ( $k = 1 \dots, 7$ )

$M_l$  = fixed effect of  $l^{\text{th}}$  season ( $l = 1 \dots, 4$ )

$P_m$  = fixed effect of  $m^{\text{th}}$  parity ( $m = 1 \dots, 6$ )

$e_{ijklm}$  = random residual error

The following animal model was used to estimate the genetic parameters:

$$y = Xb + Z\mu + e$$

where,  $y$  is vector of observations for traits (bf1, bf2, lma1, lma2, lmp1 and lmp2),  $X$  is known incidence matrix relating to observations of fixed effects (sex, farm, year of birth, season and parity),  $b$  is vector of fixed effects (sex, farm, year of birth, season, parity),  $Z$  is known incidence matrix relating observations of random effect (animal),  $\mu$  is vector of random additive genetic effects and  $e$  is vector of random residual error. Only the significant ( $p < 0.01$ ) fixed effects were included in the final animal model therefore

**Table 2.** Least square means and level of significance of fixed effects of carcass traits of Duroc

Trait	LSmean±SE	Sex	Fixed farm	Effects <sup>1</sup> year of birth	Season	Parity
bf1 (mm)	13.37±0.34	**	**	**	**	**
bf2 (mm)	14.70±0.09	**	**	**	**	**
lma1 (cm <sup>2</sup> )	45.84±0.86	**	**	**	**	**
lma2 (cm <sup>2</sup> )	37.21±0.16	**	**	**	**	**
lmp1 (%)	58.13±0.31	**	**	**	**	ns
lmp2 (%)	45.27±0.05	**	**	**	**	ns

<sup>1</sup> Fixed effects fitted for each trait in General Linear Model (SAS, v9.1).

\*\* Significant,  $p < 0.01$ , ns: not significant,  $p > 0.05$ .

bf1: backfat thickness mode A; bf2: backfat thickness mode B; lma1: loin eye muscle area mode A.

lma2: loin eye muscle area mode B; lmp1: lean meat percentage mode A; lmp2: lean meat percentage mode B.

**Table 3.** Heritability estimate (diagonal), genetic correlation (above diagonal), phenotypic correlation (below diagonal) of carcass traits of Duroc

TRAITS	bf1	bf2	lma1	lma2	lmp1	lmp2
bf1	0.45	0.30	-0.07	-0.31	-0.83	-0.80
bf2	0.65	0.39	-0.11	-0.08	-0.20	-0.20
lma1	-0.06	-0.01	0.32	0.15	0.15	0.13
lma2	-0.14	-0.01	0.42	0.25	0.16	0.15
lmp1	-0.08	-0.12	0.20	0.20	0.28	0.18
lmp2	-0.13	-0.19	0.21	0.21	0.22	0.39

bf1: backfat thickness mode A; bf2: backfat thickness mode B; lma1-loin eye muscle area mode A.

lma2: loin eye muscle area mode B; lmp1: lean meat percentage mode A; lmp2: lean meat percentage mode B.

the traits bf1, bf2, lma1 and lma2 incorporated all the fixed (sex, farm, year of birth, season, parity). However, for traits lmp1 and lmp2 only sex, farm, year of birth and season were included in the animal model.

Variance and covariance components were estimated using Multi Trait Derivative Free Restricted Maximum Likelihood (MTDFREML) by Boldman et al. (1993). Since no animal had records for both ultrasound modes A and B, the error covariance was set to zero among all the trait combinations bf1 and bf2, lma1 and lma2, lmp1 and lmp2, bf1 and lma1, bf1 and lma2, bf1 and lmp1, bf1 and lmp2, bf2 and lma1, bf2 and lma2, bf2 and lmp1, bf2 and lmp2, lma1 and lmp1, lma1 and lmp2, lma2 and lmp1 and between lma2 and lmp2.

## RESULTS AND DISCUSSION

The data set included 6,804 records of bf1, bf2, lma1, lma2, lmp1 and lmp2. The mean bf1 was 13.37mm and bf2 was 14.70mm while lma1 was 43.51 cm<sup>2</sup> and lma2 was 40.45 cm<sup>2</sup>. The mean lmp1 and lmp2 was 58.13 and 45.27%, respectively (Table 2). Significantly lower bf1 compared to bf2 because mode A ultrasound frequently underestimated corresponding measurements on carcasses. Sather et al. (1986) hypothesized that the underestimation have been a function of the inability to consistently define the third layer of fat that covers the loin muscle of pig. Significant fixed effects ( $p < 0.01$ ) on sex, farm, year of birth, season and parity for traits bf1, bf2, lma1 and lma2 were observed therefore these were fitted in the final model for

MTDFREML. However, for traits lmp1 and lmp2 only the four fixed effects (sex, farm, year of birth and season) were significant ( $p < 0.01$ ) hence fitted in the final animal model.

### Heritability

Generally the heritability estimate of all carcass traits measured were low to moderate ranging from 0.25 to 0.45. The heritability estimate of bf1, bf2, lma1, lma2, lmp1 and lmp2 was 0.45, 0.39, 0.32, 0.25, 0.28 and 0.39, respectively. The value for bf1, 0.45 was close with the findings of Hicks et al. (1999) which was 0.43. Furthermore, the value was within the range of previous estimates (Arganosa et al., 1969; Lundstorm, 1975; Kennedy et al., 1985; Bereskin, 1987; van Diepen and Kennedy, 1989; Kaplon et al., 1991). However, Kim et al. (2004) reported a lower value of 0.25 for average backfat. For bf2 it was lower than the values reported by Lo et al., 1992 which was 0.54. Likewise, Li and Kennedy (1994) reported estimates of 0.55. Other estimates of heritability of bf2 in the literature ranged from 0.23 to 0.79 (Kennedy et al., 1985; Bereskin 1987; Bryner et al., 1992; Kuhlert and Jungst, 1992; Ferraz and Johnson, 1993; Mrode and Kennedy, 1993). The values for bf1 and bf2 were higher than those reported by Choi et al. (2004) which ranged from 0.28 to 0.31.

Higher heritability of bf1 compared to bf2 could be attributed to the three measurements taken before taking the average in which case the variability of the three scanned points might be considered as one of the factors. Conversely, for bf2 there was only 1 scanned point.

For lma1, it was slightly similar to those reported by

Bereskin (1987) which was 0.31. Other researchers have reported higher estimates Lo et al. (1992) using data from 2×2 diallel mating system involving Landrace and Duroc pigs, estimated heritability of lma measured ultrasonically at the last rib at 103.6 kg of body weight to be 0.46. Stewart and Schinckel (1990), using a weighted average results published in research papers from the United States and Europe, reported a heritability of 0.47 for lma. Higher heritability was likewise reported by Swiger et al. (1979), using carcass data from swine tested at the Ohio Swine Evaluation Station, estimated heritability of 0.56.

Estimates for lmp1 and lmp2 were lower than the results of Choi et al. (2004) ranged from 0.50 to 0.60. Similarly, higher values were reported by Li and Kennedy (1994), 0.55. In a literature review conducted by Hutchens et al. (1981), heritability for probed backfat was 0.38. The National Swine Improvement Federation (NSIF) assumed a heritability of 0.40 in constructing selection indexes (NSIF, 1987).

#### Genetic and phenotypic correlations

Positive but low genetic correlations for traits bf1 and 2, lma1 and lma2, lmp1 and lmp2 were revealed. Specifically, genetic correlation between bf1 and bf2 was 0.30 while for lean traits lma1 and lma2 and lmp1 and lmp2 was 0.15 and 0.18, respectively. The positive and low genetic correlation between bf1 and bf2 could be attributed to the fact that bf1 used three scanned points wherein variation from each point is wide while bf2 used only one scanned point. The anatomy of swine backfat is arch shaped wherein the middle point has the least variation in terms of distance from the midline as opposed to the 4<sup>th</sup> rib or P4. This is evidenced by the results of the study of Kim et al. (2004) on three different scanned points using ultrasound mode A that backfat measurements at shoulder, mid-back and loin, the genetic correlation between backfat measurements at shoulder and mid-back was the lowest in Duroc, Landrace and Large White. Moreover, the third layer of backfat could be detected close to 90 kg only using ultrasound mode B however bf1 can not detect exactly the third layer (Sather et al., 1986). This indicated that both traits were loosely related. Likewise, lma1 and lma2 and lmp1 and lmp2 revealed low genetic correlations suggesting also the same loose genetic relationship. Conversely, high negative genetic correlation existed between bf1 and lean traits lma2, lmp1 and lmp2. This finding corroborated with the existing body of knowledge that backfat thickness is negatively correlated with lean traits (Lo et al., 1992; Wilson, 1992; Moeller and Christian, 1998).

The phenotypic correlations between bf1 and 2, lma1 and lma2 were high 0.65, respectively although for lmp1 and lmp2 was unusually low, 0.22. The high phenotypic

correlations between bf1 and bf2 and lma1 and lma2 could be due to differences in the accuracy of the ultrasound device as a function of transducer accuracy. Also the inconsistency of anatomical location and the lack of experience of the operator might have some contribution to the differences.

#### IMPLICATIONS

The attempt to correlate the use of ultrasound mode A and B in order to substitute ultrasound mode B with mode A was not convincing due to the low genetic correlations. Therefore, in the conduct of across farm genetic evaluations the use of multiple trait animal model is highly recommended treating each of the carcass traits separately.

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