

Genetic Analyses of Carcass Characteristics in Crossbred Pigs: Cross between Landrace Sows and Korean Wild Boars

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ABSTRACT : Carcass characteristics of 241 crossbred pigs (Korean wild boars × Landrace sows) were analyzed to examine variations in fasted body weight (FASTWT), carcass weight (CARCWT), dressing percentage (DP), back fat thickness (BFT) and longissimus muscle weight (LMW), and to estimate genetic and phenotypic parameters using three different slaughter-end points. Covariates in the least squares full sib model were slaughter age, fasted body weight and back fat thickness of the carcass. Coefficient of variation was highest for BFT followed by LMW, CARCWT, FASTWT and DP in magnitude. Regressions of three covariates on traits were all linear. However, slaughter age was not significant as a linear covariate for five traits while FASTWT was significant for CARCWT and LMW and BFT was significant for all remaining traits. Genetic and phenotypic variation was considerably reduced by regressing FASTWT or BFT in the model. Heritability estimates of FASTWT, CARCWT, DP and BFT were 0.68, 0.61, 0.11 and 0.49, respectively, using slaughter age as covariate (model 1). Those of CARCWT, DP, BFT and LMW were 0.15, 0.15, 0.30 and 0.11, respectively, using FASTWT as covariate (model 2). Heritability estimates of the traits using LMW as covariate (model 3) were similar to the estimates from Model 1 except that the estimate of CARCWT was reduced to 0.39. Genetic or phenotypic correlations among FASTWT, CARCWT and BFT were all positive and moderate to high. Those between BFT and LMW were also positive and low to moderate. However, genetic and phenotypic correlations between DP and CARCWT were positive while those between DP and FASTWT were negative. It was suggested from this study that differences in carcass yield traits be determined using slaughter age or back fat thickness as slaughter-end point and carcass quality traits using fasted body weight as slaughter-end point. (*Asian-Aust. J. Anim. Sci.* 2002, Vol 15, No. 8 : 1080-1084)

Key Words : Carcass Weight, Longissimus Muscle, Back Fat Thickness, Crossbred, Genetic Correlation

INTRODUCTION

Carcass traits are observed only after the animals are slaughtered. Therefore, it is economically valuable to identify animals with favorable genotypes for human use earlier in their life. This can be done with considerable work on searching for genetic markers, molecular or any other visual tools. Recent molecular and bioinformatic works on finding quantitative trait loci involved in carcass characteristics have revealed several genes in porcine genome (Rothschild and Plastow, 1999). It is essential that the experimental population have an identifiable amount of variation due to heterozygosity in the trait loci. And the efficient and informative genetic markers linked to this trait locus should have polymorphic patterns. However, to clearly figure out the genetic differences between animals

regarding the traits of interest, it is indispensable to clear out all identifiable and significantly embedded environmental variation and leave mainly genetic variation in raw observations.

This study aims to verify the existence of genetic variation in a population generated by crossing two divergent swine species, a line of Korean domestic wild type and a line of Landrace bred for generations. In addition, we examined the effect of three different slaughter end points to adjust carcass measures for genetic evaluation: constant age, constant body weight or constant fat deposition. These adjustments were made by regressing trait characteristics on those as the first and second order covariates in covariance models.

MATERIALS AND METHODS

Animals

Carcass measures of 241 pigs were taken from an experiment as part of a swine genome mapping project of Ministry of Agriculture and Forestry in Korea. Pigs were the second-generation animals from crosses between five Korean native (domesticated wild) boars and ten Landrace sows. Out of progeny in F1 generation, one boar in each full-sib family were then *inter se* mated to the gilts in the family (2 to 6 gilts, average 3.4 gilts per boar) to produce 21.9 pigs per boar on average from a total of 37 litters. Average litter size per mate was 6.3 piglets ranging from 4

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to 8 piglets.

Body weight changes of pigs after weaning were tested in five groups depending on age. They were randomly assigned to one of twelve feeding chambers for each sex. Each chamber held ten to twelve pigs and tester diet (distributed by feed unit of National Livestock Cooperatives' Federation, Korea, and especially formulated for pig performance testing program) was provided *ad libitum*. Starting age averaged 84.8 days ranging from 69 to 111 days and the age at slaughter averaged 216.4 days ranging from 201 to 246 days. Pigs in each test group were slaughtered and weights of body parts, and characteristics were measured at the slaughterhouse of National Livestock Research Institute, Suwon, Korea from January to mid February in 2001 due to limitation in work capacity. Carcass weight was the weight measured after slaughtering, bleeding, scalding, removal of legs and head, and extraction of digestive organs. Animals were stunned applying electric current of 1.25-1.50 amperes (approximately 300 volts) for 1-5 seconds. Bleeding was performed at vertical position to minimize changes post-mortem. Scalding tank was maintained at around 60°C and the process was made no longer than 6 minutes. Back fat thickness was measured by taking average thickness between 11th and 12th dorsal vertebrae and between the last dorsal vertebra and the first lumbar vertebra on the left half carcass. Longissimus muscle between 6th thoracic vertebra and 6th lumbar vertebra was cut 3 cm wide parallel to the bacon with 3-5 mm fat thickness and weighed for longissimus muscle weight (LMW).

Statistical analyses

Traits involved in the study were fasted body weight before slaughter (FASTWT), carcass weight (CARCWT), dressing percentage (DP) calculated as percentage of carcass weight divided by fasted body weight, back fat thickness (BFT) and weight of longissimus muscle sample taken from the last rib.

Three statistical models of full-sib family structure with different covariates were fitted: age at slaughter, fasted body weight and back fat thickness.

$$\text{Model 1 : } Y_{ijklm} = \mu + \text{sex}_i + \text{testgrp}_j + \text{sire}_k + \text{dam/sire}_{lk} + \beta_1(\text{age}) + \beta_2(\text{age})^2 + e_{ijklm}$$

$$\text{Model 2 : } Y_{ijklm} = \mu + \text{sex}_i + \text{testgrp}_j + \text{sire}_k + \text{dam/sire}_{lk} + \beta_1(\text{fastwt}) + \beta_2(\text{fastwt})^2 + e_{ijklm}$$

$$\text{Model 3 : } Y_{ijklm} = \mu + \text{sex}_i + \text{testgrp}_j + \text{sire}_k + \text{dam/sire}_{lk} + \beta_1(\text{bft}) + \beta_2(\text{bft})^2 + e_{ijklm}$$

Where, Y_{ijklm} is a matrix composed of column vectors of observations on FASTWT, CARCWT, DP and BFT in model 1, CARCWT, DP and BFT in model 2, and FASTWT, CARCWT and DP in model 3. Sex, testgrp are the fixed effect of sex of pigs and test group of pigs while performance testing. Sire and dam/sire are the effects presumed to be random sire and dams within sire groups. β_1 and β_2 are the regression coefficients of traits on corresponding first order and second order covariates in each model and e's are the residuals also presumed to be random.

Least squares procedures for the analysis of variance were run with generalized linear model procedure (proc glm) of SAS (SAS Institute, 1990) with multivariate option (MANOVA). Average of sire and dam components of variation were used to calculate estimates of heritability and phenotypic or genetic correlation coefficients between traits by Henderson's method 3 (Henderson, 1953).

RESULTS AND DISCUSSIONS

Simple statistics of the traits we dealt with in this study are shown in table 1. There was little difference in the means of all traits between sexes. However, the variation among male pigs was slightly higher in all the traits than that among female pigs. Variation in back fat thickness was the highest among the traits studied with the coefficient of variation being 35.7% followed by longissimus muscle weight, the CV of which was 22.4%. Body fat reserve and fat content in longissimus muscle also showed higher variation (CV=120%) than the other carcass characteristics. It seems likely that great difference in fat deposition represents appreciable variation in growth pattern and degree of maturity at slaughter age of the pigs.

Results of the analyses of variances are summarized in table 2 with p-values for each effect in three models.

When age at slaughter was used as covariates (model 1), the effect of test group was not significant for all the variables. Sexual differences were found in carcass weight and back fat thickness. Significant genetic variation from differences among sires or among dams within sire groups was found in all the traits except in dressing percentage. Linear or quadratic regressions of traits on age at slaughter

Table 1. Summary statistics of the carcass traits of crossbred pigs (F2 generation)

Traits ¹	N	Mean	Range	CV	N	Mean	Range	CV
	Female				Male			
FASTWT	113	88.1	55-125	15.9	128	89.2	46-138	16.1
CARCWT	113	70.9	41.6-103.0	17.1	128	69.9	30.7-112.1	17.3
BFT	113	23.3	6-45	31.9	128	19.6	6-47	37.7
DP	113	80.6	50.4-115.7	7.7	128	78.6	51.6-109.1	9.0
LMW	113	3.4	2.1-5.5	21.2	128	3.5	1.4-5.3	23.2

¹ FASTWT=Fasted body weight before slaughter; CARCWT=Carcass weight; DP=Dressing percentage; BFT=Back fat thickness; LMW=Longissimus muscle weight.

Table 2. Results of the analyses of variances with 3 statistical models

Source ¹	df	p-values				
		FASTWT ²	CARCWT	DP	BFT	LMW
Model 1						
SEX	1	0.2033	0.0353	0.0570	0.0007	0.3318
TESTGRP	4	0.1799	0.6312	0.2541	0.8221	0.2305
SIRE	11	0.0001	0.0003	0.1232	0.0002	0.6388
DAM/SIRE	25	0.0001	0.0001	0.3576	0.0215	0.0259
AGE_SL	1	0.1278	0.1642	0.9426	0.1836	0.6520
AGESL2	1	0.1357	0.1689	0.9614	0.1805	0.6796
Model R ²		0.45	0.42	0.25	0.44	0.41
Model 2						
SEX	1		0.0548	0.0777	0.0001	0.5034
TESTGRP	4		0.3924	0.2627	0.3773	0.0549
SIRE	11		0.0974	0.0867	0.0038	0.4805
DAM/SIRE	25		0.2031	0.2274	0.1610	0.0820
FASTWT	1		0.0009	0.7355	0.1052	0.0001
FSWT2	1		0.7803	0.5955	0.8862	0.0004
Model R ²			0.84	0.25	0.64	0.62
Model 3						
SEX	1	0.0002	0.0011	0.4151		0.0053
TESTGRP	4	0.0072	0.2796	0.1404		0.0447
SIRE	11	0.0001	0.0112	0.0892		0.0847
DAM/SIRE	25	0.0001	0.0039	0.2041		0.0214
BFT	1	0.0061	0.0001	0.0043		0.0001
BFT2	1	0.8977	0.2891	0.0563		0.0001
Model R ²		0.65	0.71	0.31		0.56

¹ Effects in each model. TESTGRP=Group number at performance testing; SIRE=Sire of the pig; DAM/SIRE=Dams within sire; AGE_SL=Age at slaughter (days); AGESL2=Squared AGE_SL; FASTWT=Fasted body weight (kg); FSWT2=Squared FASTWT; BFT=Back fat thickness (cm); BFT2=Squared BFT.

² FASTWT=Fasted body weight before slaughter; CARCWT=Carcass weight (kg); DP=Dressing percentage (kg); BFT=Back fat thickness; LMW=Longissimus muscle weight sample (kg).

were not significant at all for five traits. Regression coefficients of the covariates from three models (table 3) show that quadratic effects of all three covariates were small enough to consider them as zeros. Positive estimates of linear regression of fasted weight, carcass weight or back fat thickness and negative estimate of dressing percentage on the age at slaughter means that older pigs have heavier body weights and inner muscling and thicker back fat at slaughter without improvement in the percentage of edible portion of the body. This implies retarded growth around maturity that changes physiological differences in the growth of muscle and fat portions of the body.

In model 2 four carcass variables were regressed on linear and quadratic covariates of fasted weight. The effect of sex was significant only for back fat thickness, and that of test group was not significant for any traits in this model. The genetic effect was only significant for back fat thickness from source of variation among sires. However, both the linear and quadratic covariates were all highly significant for longissimus muscle weight, and linear covariate only was significant for carcass weight. However, any fixed, random effects in the model did not affect dressing percentage significantly. Linear regression

coefficients of four trait variables in this model on fasted body weight were all positive and significantly different from zero for carcass weight and longissimus muscle weight. Quadratic effects of fasted weight were negligible (table 3). Positive regression coefficients for all traits mean that on the constant weight basis, carcass weight, back fat, longissimus muscle weight and slaughter weight all increase as pigs weigh heavier at slaughter.

Linear covariates of back fat thickness were all positive and significant for fasted body weight, carcass weight and dressing percentage or for longissimus muscle weight in model 3 (table 2, 3) while quadratic effect was also significant for longissimus muscle weight. Effect of sex was significant in this model for fasted body weight, carcass weight and longissimus muscle weight. Effect of performance test group was a significant source of variation for fasted body weight and longissimus muscle weight. Genetic effect (sire or dams within sire) was significant for all the traits except dressing percentage.

Model R² was greatly improved in model 2 and model 3 compared to model 1 (table 2). However, dressing percentage was not explained well by any of the three covariates in the models.

Table 3. Partial regression coefficients of carcass traits on three covariates

Covariates	Traits ¹	FASTWT	CARCWT	DP	BFT	LMW
Age ²	Linear	22.07	17.71	-0.58	10.50	0.37
	Quadratic	-0.047	-0.038	0.001	-0.023	-0.001
FASTWT	Linear		0.81**	0.10	0.36	0.12**
	Quadratic		-0.000	-0.001	-0.000	-0.000**
BFT	Linear	1.08**	1.46**	0.75**		0.15**
	Quadratic	0.001	-0.007	-0.011		-0.003**

¹ FASTWT=Fasted body weight before slaughter (kg); CARCWT=Carcass weight (kg); DP=Dressing percentage (%); BFT=Back fat thickness (cm); LMW=Longissimus muscle weight (kg).

² Age at slaughter (days).

*, ** Those regression coefficients are significantly different from 0 at $\alpha=0.05$ (*) and at $\alpha=0.01$ (**).

Heritability estimates and phenotypic and genetic correlation coefficients are summarized in table 4. These values were calculated from the average of sire and dam variance components, the variances or covariances of which contain (co)variances from twice the maternal effects and a half the dominance effect in addition to additive genetic effect (Becker, 1984). Heritability of fasted body weight was estimated to be moderate to high from models 1 and 3. The heritability estimate of carcass weight was the highest (0.61) by age adjustment and the lowest (0.15) by body weight adjustment with medium estimate of 0.39 by fat adjustment. This is because of a high genetic correlation somewhat higher than phenotypic correlation between two weights and between carcass weight (model 1 and 3) and back fat thickness (model 2). Therefore, regressing on body weight or back fat thickness reduced genetic variances of carcass weights relative to environmental variances. Total variation of body weight was reduced by taking back fat thickness as covariates instead of age at slaughter. Heritability estimates of dressing percentage were low from all three models in the range of 0.11 (model 1) to 0.16 (model 3). Stewart and Schinckel (1989) and Ducos et al. (1993) estimated higher values (0.41 and 0.45, respectively) than those from our population. Heritability estimates of longissimus muscle weight were low, but the genetic and phenotypic correlations with body weight measures were moderate to high enough to say that heavier pigs at slaughter yields heavier (or larger) longissimus muscle and that there is genetic relationship between whole body size and the size of body parts. Robison et al. (1999) also found that lines with heavier body weights tended to have larger longissimus muscle area. Heritability estimates of back fat thickness were medium with a somewhat higher estimate from age adjustment (table 4). Heritability estimates in the literature are variable from 0.12 to 0.74 (Clutter and Brascamp, 1998) depending on the population studied or the method and models of estimation. Negative phenotypic correlations between dressing percentage and fasted body weight (-0.08 in model 1 and -0.44 in model 3, -0.07 genetic in model 1) coincide with the negative genetic correlation (-0.32) between killing out percentage and carcass length (Stewart and Schinckel, 1989). In relation to positive genetic or phenotypic relationships between dressing percentage and carcass weight or back fat thickness, we suggest that heavier and fatter animals at

Table 4. Genetic and phenotypic correlations between carcass traits of the experimental population (heritability estimates on the diagonal, genetic correlations over the diagonal and phenotypic correlations below the diagonal)

Trait ¹	FASTWT	CARCWT	DP	BFT	LMW
Model 1					
FASTWT	0.68	0.98	-0.07	0.79	0.87
CARCWT	0.89	0.61	0.15	0.93	0.47
DP	-0.08	0.32	0.11	0.81	-1.92
BFT	0.66	0.77	0.24	0.49	0.34
LMW	-. ²	-	-	-	-
Model 2					
CARCWT		0.15	-	-	-
DP		0.98	0.15	-	-
BFT		0.53	0.50	0.30	-
LMW		0.42	0.41	0.09	0.11
Model 3					
FASTWT	0.64	1.00	-		0.79
CARCWT	0.80	0.39	-		0.39
DP	-0.44	0.17	0.16		-
LMW	0.51	0.63	0.09		0.02

¹ FASTWT=Fasted body weight before slaughter (kg); CARCWT=Carcass weight (kg); DP=Dressing percentage (%); BFT=Back fat thickness (cm); LMW=Longissimus muscle weight (kg).

² Not a number. Negative variances on the denominator or the estimates out of parameter space.

slaughter yield smaller proportions of carcass relative to live body weight of the animal.

As to the selection of the model using three different slaughter-end points as covariates, faster growth of the animals can be favored by slaughtering at the same age or at the same fat thickness considering the heritability estimates from this study. However, for breeding towards greater longissimus muscle weight, slaughtering at the same body weight would be recommended. Shanks et al. (2001), however, could not see any significant differences in the proportion of genetic variation in carcass traits by applying different covariates of slaughter-end points in Simmental-sired cattle populations.

Cundiff et al. (1969) suggested use of carcass weight as a covariate because differential growth between body

components could be accounted for Slaughter age in their study when put in the model along with carcass weight as a covariate was not a significant source of variation while carcass weight was still significant. High correlations among body weight, carcass weight and longissimus muscle weight suggest that constant age or back fat thickness be used as slaughter-end points for estimation of genetic variation in weight or yield traits.

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