

Genetic Parameter Estimates of Production, Meat Quality, and Sensory Traits in Duroc Swine

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Summary and Implications

Heritability estimates detected for carcass composition, meat quality, and sensory measures indicate that improvement in these traits may be attained if adequate selection pressure is applied. Estimates obtained within the current population illustrate that substantial genetic relationships exist between many economically relevant traits. Genetic parameters estimated after 6 generations of selection for intramuscular fat indicate that the use of ultrasound technology may provide a non-invasive method for genetic improvement of IMF and other meat and eating quality components. However, genetic improvement programs aimed at meat quality improvement should be aware of possible adverse effects on carcass leanness, muscling, and loin color.

Introduction

Specific goals of breeding programs are subject to change due to alterations in economic values associated with different production parameters. However, such industry goals have been met with limitations specific to the processing of pork carcasses that do not allow accurate and easy-to-measure methods for evaluating meat quality indicators on a routine basis.

In light of such industry changes, accurate and non-invasive methods to evaluate components of meat quality on the live animal have received more attention in breeding programs. Recent developments in real-time ultrasound technology have allowed accurate prediction of intramuscular fat percentage (IMF) in the live animal to augment traditional sib and progeny testing methods of genetic improvement for IMF. Design of breeding programs requires knowledge of the variance components that exist for traits included in specific breeding goals, along with the genetic relationships that exist among traits of practical relevance.

The overall objective of this study was to evaluate the efficacy of selection for IMF with the use of real-time ultrasound technology. The second objective was to estimate genetic parameters associated with various economically relevant meat quality, eating quality, and production measures in a selected population of Duroc swine.

Materials and Methods

Using semen from Duroc boars available in regional U.S. boar studs, 2 generations of random mating were conducted to expand the population and produce the base generation of 56 litters. Littermate pairs of gilts from the base generation were randomly designated to either the control (CL) or select line (SL). Littermate pairs of females were then mated to the same boar (via natural mating or AI) to establish sufficient genetic ties between lines before selection was initiated. At weaning, up to 4 boars in each SL litter (when available) were randomly selected to remain intact to increase selection intensity.

Standard carcass collection procedures were followed to obtain carcass composition and meat quality measurements on all available barrows and randomly selected gilts within each generation after harvest at Hormel foods, Austin, MN. A section of bone-in loin containing the 10th to 12th ribs was removed from the carcass and transported to the Iowa State University Meat Laboratory for 48 hr measures of meat quality. A 3.2 mm slice from the 10th rib face was removed and utilized for percent lipid content analysis (CIMF). Water holding capacity was measured on the 11th rib face using the filter paper method described by Kauffman et al. (1986).

A trained sensory panel with 3 members evaluated cooked loin quality attributes on the 11th rib section. Three 1.3 cm³ cubes were removed from the center of the 11th rib sample and evaluated by the trained sensory panel for juiciness, tenderness, chewiness, flavor, and off-flavor using an end-anchored, 10-point scoring system (AMSA, 1995). Sample evaluations were averaged across panelists for analysis. The 12th rib section was evaluated for tenderness using an Instron Universal Testing Machine (model 1122; Instron Corp., Canton, MA).

Selection was based on estimated breeding value for CIMF. In the select line, the 10 boars and 75 gilts with the highest EBV were selected. Inbreeding coefficients of individuals and all possible matings among selection candidates were calculated with the use of the INBREED procedure of SAS. This information was utilized to design matings in both lines in an attempt to minimize inbreeding accumulation. Average inbreeding coefficients for progeny in generation 6 were 4.8% and 9.5% for the control and select lines, respectively.

Each trait was analyzed with a single trait model to obtain initial estimates for the components of variance due to animal additive genetic effects, common environment effects of birth litter, and residual. Heritability was calculated as the ratio of animal genetic variance to the sum of additive genetic, common environmental and residual variances (i.e. total variance). Variance components due to

common environment that described less than 1% of the phenotypic variance for a trait were removed from subsequent multi-trait models. Genetic analysis involved a 12-trait animal model that included measures of growth performance, carcass composition, meat quality, and eating quality. Estimates of variance components and corresponding heritabilities are presented in Table 3.

Results and Discussion

Descriptive statistics and trait abbreviations are detailed in Table 1. Estimates of variance components and genetic correlations are presented in Tables 2 and 3, respectively.

Heritability estimates

Estimates of h^2 were highest for ultrasonic and in-plant measures of carcass composition. These h^2 estimates present opportunities for efficient genetic progress in these traits. However, AGE at a constant off-test weight had the lowest h^2 estimate in the current study. As indicated by the large litter effect estimated for AGE, preweaning environment may have a substantial influence on growth measured from birth to market. Intramuscular fat, measured ultrasonically or through chemical lipid extraction, was moderately heritable ($h^2 = 0.31$ and 0.38 for UIMF and CIMF, respectively). Additive genetic variation described a smaller proportion of phenotypic variance in subjective color scores ($h^2 = 0.30$) when compared to objective Hunter L values ($h^2 = 0.50$). In general, meat quality and sensory attributes of loins resulted in the lowest estimates of h^2 (range 0.09 to 0.38). Due to the possibility of various environmental influences that exist for such traits, this result is not surprising. The relatively low h^2 values for sensory attributes observed in this study (Table 2) may limit the genetic progress that can be made for these traits. These results also substantiate the potential value of genetic

indicators that are easier to phenotypically evaluate and contain a larger genetic component.

Genetic Correlations

Genetic correlations estimated in the current investigation support the general impression that selection for decreased backfat should lead to a correlated increase in loin muscle area ($r_g = -0.77$ between CBF and CLMA). Here, we also find that growth performance does not have a strong genetic relationship with carcass composition measures. With the exception of objective loin color, genetic relationships among meat and eating quality characteristics were desirable (Table 3). Moderate to strong genetic correlations were estimated between 48 h pH and all other meat quality and sensory traits, except IMF measures. Based on estimates obtained in this study, genetic improvement in pH should have a desirable effect on loin color, tenderness, and palatability characteristics. Moderate to high genetic associations were detected among the three sensory measures evaluated in the current study (range of 0.51 to 0.77). Additionally, a moderate genetic correlation (antagonistic in nature) was detected between INST and carcass measures of CBF and CLMA.

Intramuscular fat measures obtained on the carcass (CIMF) and predicted with the use of ultrasound technology (UIMF) were highly correlated ($r_g = 0.86$). Estimated genetic relationships of either IMF measure and other traits evaluated were generally consistent. Notable correlations were detected between IMF measures and carcass and ultrasonic measures of backfat and loin muscle area. Based on estimates in this study, genetic improvement in IMF will lead to products with more desirable tenderness and flavor. However, estimates of genetic correlations also imply that more backfat and paler objective measures of loin color may result when selection is directed toward increased IMF.

Table 1. Descriptive statistics of production traits evaluated in a study involving selection for intramuscular fat in a population of purebred Duroc swine.

Trait	Abbr.	No. of records	Mean	SD	Min	Max
Carcass intramuscular fat, %	CIMF	862	3.83	1.46	1.07	10.67
Ultrasound intramuscular fat, %	UIMF	3,925	3.91	1.01	0.51	8.22
Age at off-test, d	AGE	4,094	180.58	10.40	146.00	214.00
Carcass 10 th rib backfat, mm	CBF	836	19.99	5.85	6.76	43.95
Ultrasound 10 th rib backfat, mm	UBF	3,998	17.04	4.75	6.08	40.80
Carcass 10 th rib loin muscle area, cm ²	CLMA	837	40.77	5.41	25.15	59.34
Ultrasound 10 th rib loin muscle area, cm ²	ULMA	3,998	41.05	5.29	26.12	60.31
Subjective color ^a	C	821	3.27	0.62	1.00	6.00
48 h Hunter L score ^b	HUN	400	47.63	2.65	39.73	54.77
48 h pH	pH	466	5.69	0.14	5.36	6.27
Instron tenderness, kg	INST	612	5.64	0.97	2.88	9.39
Juiciness score ^c	JS	608	6.10	1.25	1.67	9.33
Tenderness score ^c	TS	608	6.27	1.41	1.67	10.00
Flavor score ^c	FS	608	2.82	1.12	1.00	9.00

^aSubjective color score (1 = pale pinkish gray to white; 6 = dark purplish red).

^bHunter L values are objective measures of exposed lean color (0 = black; 100 = white).

^cTrained sensory panel evaluations of juiciness (1 = dry; 10 = juicy), tenderness (1 = tough; 10 = tender), flavor (1 = little pork flavor, bland; 10 = extremely flavorful, abundant pork flavor).

Table 2. Phenotypic variance (σ_p^2), animal genetic variance (σ_a^2), common environmental variance of litter (σ_l^2), and heritability (h^2) estimates from a multi-trait animal model evaluation of purebred Duroc swine.

Trait	σ_p^2	σ_a^2	σ_l^2	h^2
CIMF	1.65	0.62	0.10	0.38
UIMF	0.59	0.18	0.03	0.31
AGE	55.70	2.19	47.60	0.04
CBF	21.06	8.36	3.30	0.40
CLMA	18.84	11.49	0.54	0.61
C	0.36	0.11	-	0.30
HUN	6.67	3.37	-	0.50
pH	0.02	0.01	-	0.38
INST	0.78	0.23	-	0.29
JS	1.42	0.13	-	0.09
TS	1.86	0.36	-	0.19
FS	1.17	0.14	-	0.12

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Table 3. Genetic correlation estimates (\pm SE) obtained from a twelve-trait analysis in a population of purebred Duroc swine.

Trait	UIMF	AGE	CBF	CLMA	C	pH	HUN	INST	JS	TS	FS
CIMF	0.86 (0.09)	0.16 (0.24)	0.42 (0.17)	-0.38 (0.15)	-0.16 (0.19)	0.01 (0.20)	0.52 (0.15)	-0.31 (0.19)	0.17 (0.31)	0.22 (0.22)	0.65 (0.25)
UIMF		0.18 (0.19)	0.59 (0.12)	-0.40 (0.12)	0.06 (0.15)	0.16 (0.15)	0.31 (0.14)	-0.25 (0.15)	0.12 (0.23)	0.05 (0.18)	0.60 (0.22)
AGE			0.13 (0.27)	-0.19 (0.23)	0.28 (0.31)	-0.16 (0.31)	0.00 (0.27)	0.63 (0.38)	0.17 (0.53)	-0.29 (0.39)	0.12 (0.43)
CBF				-0.77 (0.11)	0.06 (0.21)	-0.18 (0.22)	0.35 (0.20)	-0.38 (0.20)	-0.11 (0.35)	0.04 (0.25)	0.06 (0.29)
CLMA					-0.02 (0.18)	0.11 (0.19)	-0.42 (0.16)	0.25 (0.18)	0.10 (0.30)	0.04 (0.22)	-0.18 (0.25)
C						0.62 (0.17)	-0.85 (0.11)	0.33 (0.25)	0.44 (0.40)	-0.16 (0.29)	0.34 (0.31)
pH							-0.60 (0.15)	-0.24 (0.24)	0.78 (0.35)	0.43 (0.25)	0.73 (0.23)
HUN								-0.39 (0.23)	-0.31 (0.36)	0.20 (0.27)	-0.06 (0.32)
INST									-0.30 (0.37)	-0.79 (0.15)	-0.32 (0.31)
JS										0.73 (0.28)	0.77 (0.50)
TS											0.51 (0.30)