

Genetics of pork quality

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Introduction

Fresh pork quality has become important and has received more attention as producers and processors try to meet consumer demand for high quality, nutritious products. Many different traits have been investigated as indicators of consumer acceptance of fresh pork. These include color, firmness, pH, intramuscular fat percentage (marbling), water-holding capacity, tenderness, juiciness, and flavor. Each of these has been shown to be low to moderately heritable (Sonesson et al., 1998; Knapp et al., 1997) and to impact consumer acceptance of fresh pork products. However, measuring these traits in the live animal is difficult.

Intramuscular fat percentage (IMF) is one of the meat quality traits which has the potential to be measured in the live animal and has favorable genetic correlations with many of the remaining meat quality traits. Therefore, the primary objective of my Ph.D. research has been the investigation of intramuscular fat percentage of the loin. This has included measuring IMF in the live animal using real-time ultrasound, estimation of genetic parameters for IMF predicted from real-time ultrasound and its relationship with other meat quality traits, the implementation of IMF estimation into a selection project to increase IMF in a population of Duroc swine, and a comparison of different models to estimate breeding values for IMF.

Prediction of IMF

Purebred Durocs (n=207) were used to develop a model to predict loin intramuscular fat percentage (PIMF) of the longissimus muscle in live pigs. A minimum of four longitudinal, real-time ultrasound images were collected 7 cm off-midline across the 10th - 13th ribs on the live animal using an Aloka 500V SSD ultrasound machine fitted with a 3.5 MHz, 12.5 cm linear-array transducer (Corometrics Medical Systems, Inc., Wallingford, CT). An example longitudinal image is shown in Figure 1. A trained technician used texture analysis software to interpret the images and produce 10 image parameters. Backfat and loin muscle area were measured from a cross-sectional image at the 10th rib. After harvest, a slice from the 10th-11th rib loin interface was used to determine carcass loin intramuscular fat percentage (CIMF) using the method of Bligh and Dyer (1959).

The model to predict loin intramuscular fat percentage was developed using linear regression analysis with CIMF as the dependent variable. Initial independent variables were off-test weight, live animal ultrasonic 10th rib backfat and loin muscle area, and the

10 image parameters. Independent variables were removed individually until all variables remaining were significant ($P < 0.05$). The final prediction model included live animal ultrasound backfat and five image parameters.

Multiple coefficient of determination (R^2) and root mean square error (RMSE) for the prediction model were 0.32 and 1.02%, respectively. An independent data set of Duroc ($n=331$) and Yorkshire ($n=288$) pigs from two replications of the National Pork Board's Genetics of Lean Efficiency Project were used for model validation. The product moment correlation and rank correlation coefficients between PIMF and CIMF were 0.60 and 0.56, respectively, in the Duroc population. Duroc pigs provided the best validation of the model. This demonstrates that real-time ultrasound image analysis can be used to predict intramuscular fat percentage in live swine.

Estimation of genetic parameters

Since we had developed the ability to estimate IMF on live pigs, we needed to determine the effects of selecting for improved IMF on other meat quality traits. Data from two national progeny testing programs were used to compare the relationships of intramuscular fat percentage of the loin predicted using real-time ultrasound (PIMF) and chemical intramuscular fat percentage (CIMF) with meat quality traits in pigs. A total of 821 purebred (Yorkshire, Duroc, Chester White, Poland China, and Berkshire) barrows and gilts were ultrasonically scanned 5 d prior to harvest with an Aloka 500 SSD ultrasound machine. A minimum of four longitudinal and one cross-sectional ultrasound image were collected. Intramuscular fat percentage was predicted using the model described above.

Chemical intramuscular fat percentage was determined as previously described (Bligh and Dyer, 1959). Meat quality traits measured were: Minolta reflectance and Hunter L (Minolta CR-310, Minolta Camera Co., Ltd., Japan), and pH at 24 and 48 h post-mortem (PH star probe, SFK Ltd, Hvidovre, Denmark); water holding capacity by the filter paper method of Kauffman et al (1986) (reported in mg of water absorbed by the filter, so higher water-holding capacity values are undesirable) and subjective visual scores for color, marbling, and firmness (48 h); tenderness (Oltrogge, 1987) using a star probe attached to an Instron Universal Testing Machine (Instron Corp., Canton, MA), cooking loss, and trained sensory panel evaluations (5 d).

Traits were grouped for analysis and each group included chemical and predicted IMF. Genetic parameters were estimated within each trait group using the multiple-trait option of derivative-free maximum likelihood (DFREML) of Meyer (1991). The animal model fitted was: $\mathbf{y} = \mathbf{Xb} + \mathbf{Za} + \mathbf{Hd} + \mathbf{e}$, where \mathbf{y} = the vector of observations; \mathbf{b} = the vector of fixed effects (project, breed, and sex), \mathbf{a} = the vector of random additive genetic effect, which includes the numerator relationship matrix among animals; \mathbf{d} = the vector of harvest date effects, which is assumed to be uncorrelated with the random animal effects, \mathbf{e} = the vector of residuals. The incidence matrices relating observations to fixed, random animal, and harvest date effects are \mathbf{X} , \mathbf{Z} , and \mathbf{H} , respectively.

The heritability estimates for CIMF and PIMF were 0.45 and 0.52, respectively, and the genetic correlation between them was 0.76. Estimates were consistent across trait groups. Genetic correlation estimates for PIMF and CIMF with pH measured 48 hours post-mortem were 0.40 and 0.27, respectively. The genetic correlations between PIMF and tenderness, juiciness, and flavor evaluated by a sensory panel were 0.29, 0.67, and 0.66, respectively. The genetic correlations between CIMF and tenderness, juiciness, and flavor were 0.35, 0.53, and 0.54, respectively. Genetic correlation estimates for PIMF and CIMF with water-holding capacity were -0.40 and -0.25, respectively. The genetic correlations of PIMF and CIMF with remaining meat quality traits were similar. Selection for intramuscular fat percentage estimated from chemical analysis or by real-time ultrasound should yield similar genetic changes in meat quality traits in pigs.

Selection for Increased IMF

A selection project to increase intramuscular fat percentage was initiated at the Bilsland Memorial Swine Breeding Farm at Iowa State University in 1998. The project was started by purchasing 40 Duroc gilts from Midwest breeders. Two generations of random mating using Duroc boars available at regional boar studs was used to expand the population, and to ensure that the population represented genetics that were currently available in the Duroc breed. A base population of 56 litters was produced in 2000. At weaning, two boars in each litter were randomly selected to remain boars. All other boars in the litter were castrated. At an average weight of 110 kg, pigs were ultrasonically evaluated with an Aloka 500V SSD ultrasound machine for measurement of 10th rib off-midline backfat depth and loin muscle area. A minimum of four longitudinal images were collected 7 cm off-midline across the 10th-13th ribs. Predicted IMF was determined by the method described above

All barrows within each litter meeting the minimum weight requirement (> 97 kg) were harvested 5 d after scanning. If no barrows were available, a randomly chosen gilt was harvested. After harvest, a slice of the longissimus muscle from the 10th – 11th rib interface was analyzed for carcass IMF as previously described (Bligh and Dyer, 1959). In total, 379 pigs were scanned and 141 pigs harvested.

From the litters produced, littermate pairs of gilts were randomly chosen to produce the next generation. One gilt in each littermate pair was assigned to the select line and one littermate was assigned to the control line. Littermate gilts across both lines were mated to the same boar (via natural mating or artificial insemination) to maintain genetic ties between the lines for production of generation 1. A total of 24 sires from 14 sire families were used to produce 50 control and 45 select line litters. At weaning, two boars in each litter were randomly selected to remain boars and all other boars in the litter were castrated. When generation 1 animals reached an average of 110 kg, pigs were scanned and harvested according to the protocol previously described. In total, 324 and 283 pigs from the control and select lines, respectively, were scanned. A total of 148 pigs (85 control and 63 select) from generation 1 were harvested.

Breeding values were estimated for predicted and carcass IMF by fitting a two-trait animal model and the full relationship matrix in MATVEC (Wang et al., 2003). Genetic and environmental variances used were estimated using predicted and carcass IMF values from the 289 pigs harvested using the following model: $\mathbf{y} = \mathbf{Xb} + \mathbf{Za} + \mathbf{Hd} + \mathbf{b} + \mathbf{e}$, where \mathbf{y} = the vector of observations; \mathbf{b} = the vector of fixed effects (scan contemporary group, harvest contemporary group, and sex), \mathbf{a} = the vector of random additive genetic effect, which includes the numerator relationship matrix among animals; \mathbf{d} = the vector of common litter effects, which is assumed to be uncorrelated with the random animal effects, \mathbf{b} = covariate of off-test weight, and \mathbf{e} = the vector of residuals. The incidence matrices relating observations to fixed, random animal, and common litter effects are \mathbf{X} , \mathbf{Z} , and \mathbf{H} , respectively.

Selection was based on EBV for carcass IMF. In the select line, the 10 boars and 75 gilts with the highest EBV were selected. To minimize inbreeding, no more than 2 boars per sire family were selected, selection of full-sib boars was not permitted, and no more than 4 gilts per litter were selected. In the control line, one boar from each of the 14 sire families and 50 gilts representing all 14 sire families were randomly selected. Animals within each line were randomly mated to produce generation 2, but matings were designed to control inbreeding and ensure several litters from each selected boar.

In generation 2, 56 select and 36 control line litters were produced. At weaning, three boars in each select litter and two boars in each control litter were randomly selected to remain boars and all other boars in the litter were castrated. When generation 2 animals reached an average of 110 kg, pigs were scanned and harvested according to the protocol previously described. A total of 637 pigs were scanned. A total of 103 pigs from generation 2 were harvested. The genetic evaluation described above was performed to make selections. Generation 3 pigs were born in July and August, 2003 and will be evaluated in January, 2004.

Comparison of Models to Estimate Breeding Values for IMF

Data from generations 0, 1, and 2 of this selection project were used to compare how animals rank based on breeding values estimated from either a one- or two-trait animal model. Breeding values were estimated using MATVEC and fitting a one- or two-trait animal model. The single-trait model estimated breeding values for PIMF (P1) from only PIMF for all pigs (n=1630) with gender and scan group as fixed effects, animal (genetic) and litter as random effects, and scan weight as a covariate. The two-trait model estimated breeding values for PIMF (P2) and CIMF (C2) from PIMF for all pigs and CIMF from those pigs (n=392) harvested. In addition to effects in the one-trait model, harvest group and harvest weight were added as a fixed effect and covariate, respectively, in the two-trait model. Spearman rank correlation coefficients were calculated between P2 and C2, P2 and P1, and C2 and P1. Correlations were calculated for all pigs with scan data, within year for all pigs scanned (n=379, 637, and 614 for Gen 0, 1, and 2, respectively), and by gender within year. The rank correlations between P2 and C2, P2

and P1, and C2 and P1 for all pigs with scan data were 0.95, 0.95, and 0.84, respectively. Rank correlations by year for all three EBV combinations increased over the three generations of the project. As expected, these results demonstrate that with more information, the two models rank animals more similarly. Results showed that similar animals would be selected when ranking was based on C2 or P1. When selecting the top 10 boars, 7 of the 10 boars selected were the same for both models.

Conclusion

Results from these projects presented in this paper show IMF can be estimated using real-time ultrasound technology. Additionally, selection for IMF predicted from real-time ultrasound should yield similar genetic changes in other meat quality traits. These results have been implemented into a selection project and after 1 generation of selection, the average percent IMF EBV for the select line is 0.50 greater than the control. This technology will offer seedstock producers the opportunity to select for improved IMF in live animals and hence speed genetic progress for this trait.

References

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Figure 1. Example ultrasound image used for prediction of intramuscular fat percentage.



^a Fat layers.

^b Trapezius muscle.

^c Region of Interest- 100 X 100 pixel area, 10 image parameters generated from this region.

^d 10th rib.

