RESEARCH REPORT
PORK QUALITY

Title: Continued selection for rapid growth: Implications for pork quality **- NPB #05-097**

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Industry Summary

It is hypothesized that a genetic selection for improved growth rate will result in a significant change in fresh pork quality. This study focused on two objectives. The first objective of this study is to determine the extent to which selection for improved growth rate influences pork quality. It is important to understand if this selection practice will have a negative impact on pork quality similarly to selecting for improved lean growth, or if this selection practice will possibly result in a positive impact on pork quality. The results of this objective will determine if this is a selection practice that can be successfully used by the industry without having a detrimental influence on pork quality. If there are variations in pork quality as a result of selecting for improved growth rate, it is important to understand the causes of the quality variations and determine how relationships between pork quality traits may have changed as a result of the selection method. The second objective of this study is to determine the extent to which selection for improved growth rate influences relationships between pork quality traits that can be used to explain variations in ultimate pork quality. Understanding how these relationships are influenced will lead to a further understanding of how these traits can be used to decrease the amount of variation in pork quality and ultimately be beneficial to the industry by increasing consumer acceptance of fresh pork products.

The findings of this study show that selection for improved growth rate can be implemented as a successful selection method without having a detrimental impact on pork quality. They also highlight the importance of genetic selection on pork quality variations. As a result, it is important to account for the genetic predisposition of the animal in addition to the selection practice used as both are of importance in determining ultimate pork quality. In addition, they highlight the importance of not using a single trait selection method as the trait may be changed as a result of the genetic background of the animal. Combining selection practices with the genetic background of the animal potentially changes how many factors interact with each other and can account for subsequent differences in pork quality traits such as water-holding capacity and sensory attributes. Overall, the findings demonstrate that this selection practice can be used to significantly reduce the days necessary for pigs from these sires to reach 125 kg without having a negative influence on pork quality. Future work addressing the causative agents controlling the variation in quality will be beneficial when selecting progeny for improved growth rate performance.

The results of the genetic marker testing document a clear link between growth, metabolism, meat quality and meat composition. Genetic markers (MC4R, PRKAG3) have major effects on pork quality and their use in marker-assisted selection within pig populations will be effective in improving product characteristics. Moreover, the genetic background of the animals should be considered for the genotypic analysis and prediction of response to selection.

Scientific Abstract

The objective of this study was to investigate if genetic selection of sires for improved growth rate is associated with changes in fresh pork quality. A sample derived from the cross between a commercial line of Duroc sires and white line dams was subdivided according to the sires' estimated breeding value (EBV) for age at 125 kg. Differences in age at 125 kg were achieved by assigning pigs sired by High EBV growth boars (n=48), Low EBV growth boars (n=48) or a control group (n =32). Loin pH and temperature decline were monitored on each carcass. Fresh pork quality characteristics and water holding capacity were monitored at 2 d postmortem. Sensory traits (juiciness, tenderness, chewiness, flavor, and off-flavor) and star probe texture were measured 10 d postmortem. Proteolysis was estimated by desmin degradation and µ-calpain autolysis at 2 d postmortem.
Fresh pork quality characteristics and water-holding capacity was monitored at 2 d postmortem. Sensory characteristics (juiciness, tenderness, chewiness, flavor, and off-flavor) and star probe texture were measured 10 d postmortem. Pigs in High (Fast Growth) EBV for growth were younger at 125 kg (153 d vs. 177 d), which established that our criteria was successful in separation of growth rate. Growth rate group did not affect pH decline in the longissimus dorsi, however, temperature at 6 h was significantly lower in the slow growth line. Loin color and drip loss were not affected by growth rate. Loins from carcasses in the fast growth group had higher subjective marbling scores and higher lipid content than loins from carcasses in the slow growth group. Growth rate did not affect star probe or sensory quality of fresh pork loin. Selection for rapid growth by improving days of age at 125 kg did not significantly affect the quality of fresh pork loin. Therefore this method of selection can be used without compromising fresh pork quality.
The genotypes for MC4R, and PRKAG3 (I199V) were determined. Associations between the genotypes and the phenotypic traits were tested using the general linear model procedure with a model including EBV group, genotype, sex, sire within EBV group, dam within sire and EBV group, interaction between EBV group and genotype, and slaughter day. PRKAG3 genotype 22 had lower ($P<0.05$) pH at 10 d postmortem (5.65) compared to genotype11 and 12 (pH =5.75 and 5.71). PRKAG3 genotype 22 also resulted in higher ($P<0.05$) off-flavor score (4.3) than genotypes 11 or 12 (3.0 and 3.6 respectively). A significant interaction between growth EBV and PRKAG3 was demonstrated as genotype 11 resulted in higher ($P<0.05$) subjective color score (3.5) than genotype 12 or 22 (2.5 and 2.6) in loins from pigs sired by fast growing boars. MC4R genotype 12 had higher pH at 48 hr (5.68 vs. 5.62), darker L values (45.95 vs. 47.01) and less drip loss (2.1 % vs. 2.7 %) than genotype 22 ($P<0.05$). There was an interaction between growth EBV and MC4R genotype for marbling scores (genotype 12, 2.2; genotype 22, 1.5) observed in loins from pigs sired by fast growing boars ($P<0.05$). These results confirm main effects of the selected genes but also that these genotypic effects depend on the background genetic merit for growth.

Key Words: Pork, Quality, Growth

Introduction

One of the main goals of the swine industry is to produce the highest quantity of meat at the least cost. However, it is becoming increasingly apparent that attention must also be paid to the production of uniform, high quality pork (Lonergan et al., 2001) as consumers are becoming more discriminating and will no longer accept pork of inferior quality (Cassens, 2000). As such, pig breeding companies are now paying more attention to meat quality and are including quality traits as integral parts of selection programs (Plastow et al., 2005) in addition to controlling the known negative effects on pork quality when incorporating the halothane gene or the

Rendement Napole (RN-) gene in selection programs in light of their known associations with production benefits (Brewer et al., 2002; Channon et al., 2000; Copenhafer et al., 2006). Thus, selection practices have become increasingly important in influencing pork quality.

Lonergan *et al.* (2001) demonstrated that selecting for improvements in lean growth efficiency has been shown to be successful in improving carcass composition by decreasing the amount of backfat on the carcass and increasing the yield of lean cuts. However, the selected line was also observed to have a lower pH early postmortem and a decrease in the presence of degraded troponin-T when compared with the control line which led to higher Warner-Bratzler shear force values and higher drip losses in the selected line, indicating product that was tougher and had poorer water-holding capacity (Lonergan et al., 2001). Thus, selecting for improvements in *lean* growth has been shown to have a negative effect on pork quality. However, questions still arise as to the effect of selecting for *growth rate* independent of lean growth potential in terms of influencing early postmortem changes in fresh pork and ultimately in pork quality. It is therefore hypothesized that selection for improved growth rate will influence early postmortem changes in pork quality and translate to differences in the quality of fresh pork between the progeny of sires selected for two different growth rates. The first objective of this study was to determine the extent to which selection for increased growth impacts fresh pork quality. Determining the extent of impact will lead to further knowledge of how selection practices can influence pork quality and consumer acceptance. In addition, if there are variations in pork quality as a result of selecting for growth rate, it is important to understand the causes of the quality variations and determine how relationships between pork quality traits may have changed as a result of the selection method. It is therefore also hypothesized that selecting for improved growth rate will change the relationship between pork quality traits and alter how they can be used to explain pork quality variations. The second objective of this study was to determine the extent to which selection for increased growth influences relationships between pork quality traits that can be used to explain variations in pork quality. Understanding how these relationships are influenced will lead to a further understanding of how these multifactorial traits can be used to decrease the amount of variation in pork quality and ultimately be beneficial to the consumer acceptance of fresh pork products.

Objectives

Research Objective 1: Determine the extent to which selection for rapid growth influences biochemical mechanisms underlying meat quality traits in the longissimus dorsi.

Research Objective 2. Determine the extent to which known candidate genes for meat quality contribute to variation in pork quality

Materials and Methods

Animals

A pig population was derived from a cross between a commercial line of Duroc sires and synthetic white line dams. Progeny were subdivided into two groups according to the sires' estimated breeding value (EBV) for growth rate based on the genetic merit of the sire to improve progeny growth rate, in this instance age at 125 kg. High EBV sires were the fast growth EBV and Low EBV sires were the slow growth EBV. Progeny (n=128) consisted of 50% barrows and 50% gilts to account for any sex differences and were slaughtered on two different slaughter dates. The first slaughter group included the most rapid growing pigs sired by High EBV growth boars (n=48; 150 d at 125 kg), and a reference group that included pigs sired by Low EBV growth boars (n=8; 160 d at 125 kg) and High EBV growth boars (n=8; 160 d at 125 kg). The second slaughter group consisted of the slowest growing pigs sired by Low EBV growth boars (n=48; 180 d at 125 kg), and a reference group that included pigs sired by Low EBV growth boars (n=8; 174 d at 125 kg) and High EBV growth boars (n=8; 169 d at 125 kg). Each group was harvested at a commercial slaughter facility using conventional chilling practices. Carcass weight, composition, and meat quality data were collected. Loins were removed from the carcass, vacuum packaged and shipped to the ISU Meat Laboratory.

Growth and carcass composition

Age of progeny at 125 kg, calculated based on performance data, and carcass composition data were collected at the time of harvest. The growth and carcass composition traits evaluated were: off-test weight, days to 125 kg, days to produce a 90 kg hot carcass, average daily gain on test, hot carcass weight, and backfat thickness of the carcass.

pH and Temperature measurements

Longissimus dorsi pH was measured 2, 6, 24, 48, and 240 h postmortem. Temperature of the longissimus dorsi was measured at 2, 6, and 24 h postmortem. Temperature and pH measurements were taken by a penetration probe on right side loins using a Hanna 9025 pH/ORP meter (Hanna Instruments, Woonsocket, RI). The pH probe was calibrated with temperature at each time period using two buffers (pH 4.2 and 7.10). Calibration was monitored after each 5 carcasses.

Meat quality traits

Loin quality scores were evaluated 48 h postmortem according to National Pork Board standards (2000). Loins were assigned a score for color, firmness, wetness, and marbling while a trained panel (n = 2) was used to determine a color score (1 = pale, 6 = dark) for each loin eye (National Pork Board, 2000). Firmness and wetness were evaluated on a three point scale (1 = soft and wet, 3 = firm and dry). Marbling values were based on NPB standards. Loin meat was also evaluated for lipid composition (AOAC, Hexane extraction) and moisture composition (AOAC). Hunter L*, a* and b* values were determined at 1 day postmortem on 2.54 cm thick chops. Samples were allowed to bloom for 1 hour at room temperature and were analyzed on a calibrated Hunter Labscan colorimeter (Hunter Association Laboratories, Inc.; Reston, VA.) A CIE D/65 10° standard observer and a 1.27 cm viewing port were used to obtain three color measurements on each of three chops. All nine color measurements were used to determine an average color score for each loin. Calpastatin activity was determined as described by Lonergan *et al.* (2001).

Drip loss

Loin chops were evaluated for drip loss at 48 h postmortem. Drip loss was determined using 2.54 cm-thick boneless chops (two per loin) by similar method to Lonergan *et al.* (2001). Drip loss was evaluated as weight lost from the entire chop, done in duplicate. Drip loss percentage was calculated by the following equation: [(initial weight – final weight)/initial weight] x 100.

Star probe

Star probe measurements were taken as an instrumental indication of texture of the loin, through analysis of cooked loin chops, by similar method to Lonergan *et al.* (2007). Star probe is a measurement of the peak load necessary to puncture and compress the product to 20% of its height. The star probe consists of a circular, five-pointed star probe measuring 9 mm in diameter with 6 mm between each point, and it punctures the product at a crosshead speed of 3.3 mm/second. Samples consisted of two chops from each loin 2.54 cm thick and aged for 7 days. Chops were then cooked to an internal temperature of 71°C in a convection oven prior to texture analysis. Each chop was compressed three times and all six measurements used to determine an average for each loin.

Sensory Panels

A trained sensory panel (n = 5) evaluated loin chops for sensory traits using a similar method as described by Lonergan *et al.* (2007). Loin chops were evaluated for sensory tenderness, chewiness, juiciness, flavor, and off-flavor. A scale of 1-10 was used (1 = not tender, chewy, juicy, flavorful, no off-flavor; 10 = very tender, chewy, juicy, flavorful, high off-flavor) to evaluate all chops. Samples consisted of loin chops 2.54 cm thick aged for 10 days. Prior to analysis, samples were cooked to an internal temperature of 71°C using an electric oven broiler.

Whole-muscle sample preparation for gel electrophoresis

Samples were prepared from muscle (.2 g) taken at 2 d postmortem from the longissimus dorsi for SDS-PAGE analysis and Western blotting of desmin degradation and µ-calpain autolysis. Whole-muscle protein

extraction (extraction buffer consisted of 10 m*M* sodium phosphate and 2% [vol/vol] SDS; pH 7.0) and gel electrophoresis sample preparation was conducted according to Lonergan *et al.* (2001). Protein concentration was determined using the method described by Lonergan *et al.* (2001) using premixed reagents (Bio-Rad Laboratories, Hercules, CA). Gel samples, containing 4 mg/mL of protein, were frozen and stored at -80°C until subsequent analysis.

Gel electrophoresis and Western blotting

Ten percent polyacrylamide separating gels (acrylamide:bisacrylamide = 100:1 [wt/wt], 0.1% [wt/vol] SDS, 0.05% [vol/vol] TEMED, 0.05% [wt/vol] APS, and 0.5 *M* Tris·HCl, pH 8.8) were used for determination of desmin degradation at 2 d of storage. Nine percent polyacrylamide separating gels were used for determination of µ-calpain autolysis at 2 d of storage. Both gels were used with 5% polyacrylamide stacking gels (acryalmide:bisacrylamide = 100:1 [wt/wt], 0.1% [wt/vol] SDS, 0.125% [vol/vol] TEMED, 0.075% [wt/vol] APS, and 0.125 *M* Tris·HCl, pH 6.8) to fractionate muscle proteins.

Gels (10 cm wide x 8 cm tall x 1.5 mm thick) for analysis of desmin degradation were run on Hoefer Mighty Small II SE 250/SE 260 electrophoresis units (Hoefer Scientific Instruments, San Francisco, CA). Gels (10 cm wide x 12 cm tall x 1.5 mm thick) for analysis of µ-calpain autolysis were run on Hoefer Tall Mighty Small SE 280 electrophoresis units. The running buffer used for electrophoresis contained 25 m*M* Tris, 192 m*M* glycine, 2 m*M* EDTA, and 0.1% [wt/vol] SDS. Gels were loaded with 40 µg per lane of total protein for desmin or 80 µg per lane of total protein for µ-calpain. Gels were run at a constant voltage of 120V for approximately 2.5-2.75 h.

Gels for both desmin and µ-calpain were transferred to polyvinylidene (PVDF) membranes (Millipore Corporation, Bedford, MA) using a Hoefer TE22 Mighty Small transfer tank electrophoresis unit (Hoefer Scientific Instruments) at a constant voltage of 90V for 1.5 h. The transfer buffer used consisted of 25 m*M* Tris, 192 m*M* glycine, 2 m*M* EDTA, and 15% [vol/vol] methanol. The temperature of the transfer buffer was maintained between 4°C and 8°C using a refrigerated circulating water bath (Ecoline RE106; Lauda Brinkmann, Wesbury, NY).

Western blots. Western blotting and chemiluminescent detection were done as described by Lonergan *et al.* (2001) and Melody *et al.* (2004). Desmin degradation was indicated by a decrease in intensity of an approximately 55-kDa intact band and the presence of an increasing intensity desmin degradation product band of approximately 38-kDa (Melody et al., 2004). Intact desmin degradation ratio was calculated as the intensity of each immunoreactive desmin band over the intensity of the immunoreactive desmin band in a determined reference sample for consistency of intact desmin that was loaded on each gel. µ-calpain autolysis was indicated by the presence of a non-autolysed 80-kDa band in addition to the presence of an intermediate 78-kDa autolysis product and the presence of a 76-kDa autolysis product. Autolysis of µ-calpain was calculated as the percentage of non-autolysed 80-kDa subunit as well as the percentage of the 78-kDa and 76-kDa subunit autolysis products.

A sample of the *longissimus dorsi* muscle was collected after slaughter for all the animals and stored in a -80^{o}C freezer until DNA extraction. The PCR-RFLP tests for MC4R, and PRKAG3 I199V SNPs were done as described by Kim *et al.* (2000) and Ciobanu *et al*. (2001), respectively. Associations between the genotypes and the phenotypic traits were tested using the general linear model procedure (SAS procedure GLM, SAS institute, Cary, NC) with a model that included EBV group, genotype, sex, sire within EBV group, dam within sire and EBV group, interaction between EBV group and genotype. For the meat quality and sensory traits, slaughter day was also included. Least squares means for the genotypes and for the interaction between EBV groups and genotypes were obtained.

Statistical analyses

For the first objective, Data were analyzed using the GLM procedure of SAS and Least Squares Means by growth rate, through EBV group, for all traits of interest were computed. A series of models were used to analyze the data by sire EBV group. A model consisting of EBV group and gender was used to analyze off-test weight, age at 125 kg, days to produce a 90 kg hot carcass, calpastatin activity, lipid and moisture content, and

marbling. A model including EBV group, gender, and on-test weight was used to analyze average daily gain. A model including EBV group, gender, and age at harvest was used to analyze Hot Carcass Weight. A model including EBV group, gender, and Hot Carcass Weight was used to analyze yield and backfat thickness. Finally, a model including EBV group, gender, harvest day, and EBV group x harvest day interaction was used to analyze pH, temperature, Hunter color, subjective color, drip loss, sensory traits, and star probe. For the second objective to investigate changes in relationshops, data were analyzed in a one-way analysis of variance by sire EBV group for growth rate using JMP 6.0 (SAS Institute, South Cary, NC). Progeny were divided into groups based on sire EBV group for growth rate into a High EBV group and a Low EBV group. Least Squares Means were calculated for all traits of interests and then compared for both groups using a Tukey-Kramer HSD test. Pearson correlations were also calculated and evaluated for both groups. Correlations were defined as significant if pairwise correlations $P<.05$.

Results

Objective 1:

Table 1. Growth traits means of progeny from two different sire growth rate Estimated Breeding Values (EBV).

Item	Fast Growth EBV	Slow Growth EBV	Std. Error
Off-test weight, kg	131.8[a]	123.6[b]	1.0
Age 125 kg, days	153.3[a]	177.4[b]	1.0
Average daily gain, g/day	1101[a]	963[b]	22.0
Days 90 kg hot carcass wt., days	159.2[a]	179.9[b]	1.8

[a,b]Within a row, means without a common superscript letter differ (P<.01).

Table 2. Carcass traits means of progeny from two different sire growth rate Estimated Breeding Values (EBV).

Item	Fast Growth EBV	Slow Growth EBV	Std. Error
Hot carcass wt., kg (adj. for age)	89.9	89.6	1.1
Yield, %	76.6	76.7	0.01
Backfat thickness, mm	10.5	10.5	0.2

[a,b]Within a row, means without a common superscript letter differ (P<.01).

Table 3. Temperature and pH measurements means of progeny from two different sire growth rate Estimated Breeding Values (EBV).

Item	Fast Growth EBV	Slow Growth EBV	Std. Error
*Temperature, °C**			
2 h	25.6	25.1	0.4
6 h	14.4[x]	13.6[y]	0.2
24 h	2.5	2.3	0.1
*pH**			
2 h	6.18	6.2	0.04
6 h	5.9	5.92	0.03
24 h	5.65	5.61	0.02
48 h	5.67	5.67	0.02
10 d	5.66	5.67	0.02

[x,y]Within a row, means without a common superscript letter differ (P<.05).

*Measured by a penetration probe on right side loins using a Hanna 9025 pH/ORP meter (Hanna Instruments, Woonsocket, RI). pH probe was calibrated with temperature at each time period using two buffers (pH 4.2 and 7.10).

Table 4. Loin meat quality traits means of progeny from two different sire growth rate Estimated Breeding Values (EBV).

Item	Fast Growth EBV	Slow Growth EBV	Std. Error
Loin color score (1 to 6)*	2.5	2.4	0.1
Loin marbling score (1 to 10)*	2.0[a]	1.4[b]	0.1
Loin firmness score (1 to 3)*	1.9	1.8	0.1
Loin wetness score (1 to 3)*	1.8	1.8	0.1
Hunter L color**	46.7	47.54	0.41
Hunter a color**	6.24	6.23	0.1
Hunter b color**	9.27	9.37	0.15
Drip loss, %	2.5	2.28	0.25
Lipid, %	1.99[x]	1.22[y]	0.18
Moisture, %	73.67	73.75	0.14
Cook loss, %	19.55	19.39	0.38
Star Probe, kg***	5.43	5.54	0.11
Calpastatin, units of activity/g of tissue****	1.03	0.98	0.03

[a,b]Within a row, means without a common superscript letter differ (P<.01).

[x,y]Within a row, means without a common superscript letter differ (P<.05).

*Evaluated 48 hr postmortem according to National Pork Board Standards (2000).

**Analyzed on a calibrated Hunter Labscan colorimeter (Hunter Association Laboratories, Inc.; Reston, VA.) A CIE D/65 10° standard observer and a 1.27 cm viewing port were used to obtain three color measurements on each of three chops. All nine used to determine average color score.

***Instrumental indication of loin texture by similar method to Lonergan *et al.* (2007).

****Determined 24 h postmortem as described by Lonergan *et al.* (2001).

Table 5. Sensory traits means of progeny from two different sire growth rate Estimated Breeding Values (EBV).

Item	Fast Growth EBV	Slow Growth EBV	Std. Error
Juiciness score (1 to 10)*	5.3	5.3	0.2
Tenderness score (1 to 10)*	5.9	6.4	0.2
Chewiness score (1 to 10)*	2.8	2.5	0.1
Flavor score (1 to 10)*	1.9	2.1	0.1
Off-flavor score (1 to 10)*	4.0	3.7	0.2

[a,b]Within a row, means without a common superscript letter differ (P<.01).

*Evaluated by a trained sensory panel using similar method as described by Lonergan *et al.* (2007). A value of 1 represents a low degree of juiciness, tenderness, chewiness, flavor, and off-flavor. A value of 10 represents a high degree of juiciness, tenderness, chewiness, flavor, and off-flavor.

Table 6. Proteolysis measurements of progeny from two different sire growth rate Estimated Breeding Values (EBV).

Item	Fast Growth EBV	Slow Growth EBV	SE
Desmin Day 2 Intact, ratio[1]	1.55[a]	1.10[b]	0.10
Desmin Day 2 Degraded, ratio[1]	1.91[x]	1.46[y]	0.13
µ-Calpain 78 kDa subunit, %[2]	5.37[x]	9.81[y]	1.29
µ-Calpain 76 kDa subunit, %[2]	94.63[x]	88.73[y]	1.60
Calpastatin, units of activity/g of tissue[3]	1.03	0.97	0.03

[a,b]Within a row, means without a common superscript letter differ (P<.01).

[x,y]Within a row, means without a common superscript letter differ (P<.05).

[1]Evaluated by similar method to Melody *et al.* (2004). Ratio expressed as intensity of intact and degradation product bands over intensity of bands in a reference sample.

[2]Evaluated by similar method to Gardner *et al.* (2005). Expressed as percentage of autolysis products present at 78- and 76-kDa subunits.

[3]Determined 24 h postmortem as described by Lonergan *et al.* (2001).

Table 7 Least squares means and standard errors for the associations between PRKAG3 genotypes and meat quality traits, interaction between EBV group and PRKAG3 I199V genotypes in commercial crossbred pigs. Number of animals per class is in parenthesis.

Main effects		Traits		
Gene	Genotype	Marb	Moist	OFF
PRKAG3 I199V	11 (26)	1.70±0.23a	73.66±0.20a	3.18±0.37a
	12 (53)	1.50±0.13a	73.93±0.11a	3.77±0.20a
	22 (40)	1.99±0.14b	73.48±0.12b	4.21±0.22b
		P<0.07	P<0.04	P<0.10
Interaction		EBV x Genotype interaction		
EBV	Genotype	HCW	LiveW	
Fast	11 (13)	85.73±3.61a	121.61±4.87a	
Fast	12 (29)	92.57±1.73b	130.96±2.34b	
Fast	22 (19)	91.00±2.32a	128.70±3.13a	
Slow	11 (13)	88.75±3.64a	125.71±4.91a	
Slow	12 (24)	85.93±2.20a	121.94±2.97a	
Slow	22 (21)	93.46±1.96b	132.01±2.64b	
		P< 0.06	P<0.06	

Traits: Marb: marbling score, correspond to lipid percentage; Moist: percentage of moisture; OFF: off flavor score, assigned as a 1 to 10 scale, being 1 the low and 10 the high degree; HCW: Hot carcass weight; LiveW: weight at slaughter (Kg). Same letter in the same column means no statistical difference between genotypes. Genotypes 11, 22 and 12: Homozygous for the non-mutated, homozygous for the mutated and heterozygous animals respectively.

Table 8 Least squares means and standard errors for the associations between MC4R genotypes and meat quality traits, and the Least squares means and standard deviations for interactions between EBV group and MC4R genotypes in commercial crossbred pigs. Number of animals per class is in parenthesis.

Main effects		Traits				
Gene	Genotype	pH120	FLAV		OFF	
MC4R	12 (78)	5.70±0.01	2.08±0.07		3.80±0.13	
	22 (44)	5.66±0.02	1.77±0.11		4.25±0.22	
		P<0.08	P<0.02		P<0.08	
Interaction		EBV x Genotype interaction				
EBV	Genotype	pH48	Moist	pH120	Perc	Tender
Fast	12 (39)	5.71±0.03a	73.84±0.13a	5.71±0.02a	19.46±0.54a	5.84±0.24a
Fast	22 (25)	5.60±0.04b	73.42±0.21b	5.66±0.03b	20.79±0.85a	4.87±0.38b
Slow	12 (39)	5.66±0.02a	73.66±0.13a	5.69±0.02a	19.11±0.52a	6.34±0.23a
Slow	22 (19)	5.70±0.04a	73.73±0.17a	5.69±0.03a	18.46±0.72b	7.32±0.32c
		P<0.02	P<0.09	P<0.08	P<0.10	P<0.0004

Traits: pH 48: Meat pH 48 hours after slaughter; pH 120: Meat pH 120 hours after slaughter; Moist: Percentage of moisture; Perc: percentage of cooking loss; FLAV: Flavor score; OFF: off flavor score. Tender: tenderness score. FLAV, OFF and Tender were assigned as a 1 to 10 scale, being 1 the low and 10 the high degree of each trait. Same letter in the same column means no statistical difference between genotypes. Genotypes 12 and 22: heterozygous and homozygous for the non-mutated animals, respectively.

Discussion

Objective 1:

Selection for improved growth rate resulted in a significant difference in the offspring of the Fast Growth and Slow Growth EBV groups for all growth traits evaluated (Table 1). Fast Growth EBV pigs were heavier at time of slaughter and had a higher average daily gain than Slow Growth EBV pigs. In addition, Fast Growth EBV pigs took less days to produce a 90 kg hot carcass and reached 125 kg approximately 24 days faster than Slow Growth EBV pigs. Thus, the selection method used in this study was successful in improving growth rate.

Differences in growth traits did not translate to differences in carcass composition as the two groups did not differ for any of the carcass composition traits evaluated (Table 2). They did not differ in terms of their hot carcass weight, yield percentage, or backfat thickness. Thus, carcass composition was not negatively influenced by selecting for improved growth rate.

Temperature and pH decline of the loin were not significantly affected by selection for improved growth rate (Table 3). Temperature decline was only different at 6 h postmortem with the Fast Growth EBV group having a higher temperature. pH decline was not influenced by the selection method as the two sire EBV groups did not differ at any of the time points in which pH

was measured. Therefore, selection for improved growth rate did not result in a change in temperature or pH decline.

The only National Pork Board score that was influenced by selecting for improved growth rate was the loin marbling score, in which the Fast Growth EBV pigs had a higher marbling score than the Slow Growth EBV pigs (Table 4). Loins from both groups were not different for firmness or wetness scores, nor were they different for subjective or instrumental color score (Table 4). Moisture composition did not differ between the two groups, but the Fast Growth EBV group had a higher lipid composition in the loin than the Slow Growth EBV group (Table 4). Given the higher marbling score and higher lipid composition in the Fast Growth pigs, it may be that pigs were being selected based on their appetite as pigs with an increased appetite would develop more lipid in the muscle faster than pigs with less of an appetite.

Traits important for water-holding capacity were not influenced as a result of selection for improved growth rate as the two groups did not differ in their drip loss or cook loss percentages (Table 4). Star probe measurements of the loin were not different between the two groups (Table 4), as well, and therefore instrumental texture or tenderness was not influenced by the selection method. In addition, none of the sensory traits that were evaluated differed between the two groups (Table 5) and thus selection for improved growth rate did not have an influence on the sensory quality of the loin in this study.

Objective 2:

The association analyses revealed many significant differences associated with genotypes and several meat quality traits. The interaction between EBV group and genotype was also significant for some traits. *PRKAG3* was first recognized as a major gene by Milan *et al.* (2000), and was identified as the causative mutation for the NAPOLE phenotype, (RN^-). Other mutations in the PRKAG3 gene, especially the I199V (Ciobanu *et al.*, 2001) have since been identified. Our data support the findings of previous work that *PRKAG3* I199V has significant effects in commercial populations as a marker not only for pork quality but also for growth traits (Table 2). Ciobanu *et al.* (2001) had already identified the association of this marker with pH and other traits, but in their paper, no association was found with off-flavor score, marbling and moisture as we describe here. More interesting is the interaction between EBV group and genotype for hot carcass weight and live weight, where both traits presented the same pattern, with the 12 and the 22 animals, respectively, being the heaviest ones in the Fast and Slow EBV groups ($P<0.10$).

The results reported for MC4R confirm this gene as one of the most important markers in pig production (Table 3). Due to the cross, no 11 genotype animals were observed. Genotype 12 was associated with higher pH 120 hours after slaughter, higher flavor and better off flavor score when compared to 22 animals. We detected an interaction between growth EBV and MC4R genotype for pH 48 and pH 120 hours after slaughter, percentage of cooking loss, moisture and tenderness, with the 22 genotype presenting the lower and the higher tenderness scores respectively in the Fast and Slow EBV groups. While MC4R effects on meat quality have been reported no interaction effects with growth background have been presented until now.

Results in table 5 summarize data that demonstrate an association of Myostatin genotypes and phenotypic traits. Notable are significant effects of genotype on star probe where the AA genotype is 1 kg less than AG or GG. The AA genotype also reached 125 kg approximately 9 d

earlier. **This suggests that improvement in growth rate can, under some circumstances also result in improved quality (in this case tenderness).**

Results in Table 6 show expression of SDHD (Succinate Dehydrogenase Complex II subunit D) is correlated with some growth, composition and meat quality traits. Succinate-ubiquinone oxidoreductase (cytochrome b) is an important enzyme complex in both the tricarboxylic acid cycle and the electron transport system required for aerobic respiration in both eukaryotic cells and prokaryotic organisms. The normalized expression of *SDHD* was correlated to growth, meat quality and sensory traits ($P<0.10$). These data demonstrate a linkage of metabolism, growth, meat composition and meat quality.

It is possible to detect genes with major effects on pork quality and their use in marker assisted selection within pig populations will be effective in improving product characteristics. Moreover, the genetic background of the animals should be considered for the genotypic analysis and prediction of response to selection.

Implications

Pork quality is multifactorial, meaning it is influenced by a number of interacting factors. Changing one or more factors has the potential to alter the relationship of pork quality traits. Proteolysis has been identified as one factor that can be used to account for variation in pork quality. In the present study, measurements of proteolysis were not important factors for sensory traits such as tenderness and chewiness in the Slow Growth EBV sired pigs but were very important in the Fast Growth EBV sired pigs. Therefore, we may conclude that selection for some economically important trait, such as improved growth rate, changes the relationships of traits known to be useful in controlling pork quality variations. Combining selection practices with the genetic background of the animal potentially changes how many factors interact with each other and can account for subsequent differences in pork quality traits such as water-holding capacity and sensory attributes. The results of this trial demonstrate clearly that improvement in growth rate and quality can be achieved with carefully developed genetic improvement programs. Future work addressing the causative agents controlling the variation in quality will be beneficial when selecting progeny for improved growth rate performance.

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Wagner, C.E., E. Huff-Lonergan, M.F. Rothschild, A.A.Sosnicki, S.B. Jungst, and S.M. Lonergan. Influence of selection for improved growth rate on pork quality. Meat Science (Submitted)

Wagner, C.E., E. Huff-Lonergan, A.A.Sosnicki, S.B. Jungst, and S.M. Lonergan. Selection for improved growth rate influences relationships between fresh pork quality traits. Meat Science (Submitted)

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