

EFFECT OF SIRE LINE AND SELECTION INDEX CATEGORY ON PIG GROWTH
PERFORMANCE FROM WEANING TO HARVEST AND CARCASS CHARACTERISTICS

BY

NATHANIEL MARK STAS

THESIS

Submitted in partial fulfillment of the requirements
for the degree of Master of Science in Animal Sciences
in the Graduate College of the
University of Illinois at Urbana-Champaign, 2017

Urbana, Illinois

Advisor:

Professor Mike Ellis

Abstract

The objective of this study was to compare 3 sire lines and the effect of selection index category within sire line on growth performance (from 6.1 ± 0.29 to 129.8 ± 2.16 kg BW) and carcass characteristics of pigs under commercial conditions. A randomized complete block design (blocking factor being day of start on test) was used with a 3×2 factorial arrangement of treatments: 1) Sire Line (Green line vs. Blue line vs. Yellow line) and 2) Selection Index Category (High vs. Low). The lines were representative of those widely used in the industry. The High Index Category sires were from the top 25% index values within each line; the Low Index Category sires were at the mean index value for each line. Ten sires from each Selection Index Category from each line were mated to approximately 15 crossbred dams each; dam lines were equally represented across sires. Progeny ($n = 2880$) were housed in mixed-sex groups (barrows and gilts) of 32 pigs (15 replicates) at a floor space of $0.66 \text{ m}^2/\text{pig}$. Pigs had *ad libitum* access to feed and water throughout the study period. Pen was used as the experimental unit and data were analyzed using PROC MIXED of SAS; the model accounted for the effects of Sire Line, Selection Index Category, 2-way interaction, block, and replicate. There were Sire Line by Selection Index Category interactions ($P < 0.05$) for most measurements. For ADG, there was no difference ($P > 0.05$) between High Index Category and Low Index Category for the Green line (0.76 vs. 0.77 kg, respectively) or the Yellow line (0.76 vs. 0.76 kg, respectively), however, ADG was greater ($P < 0.05$) for High Index Category than Low Index Category for the Blue line (0.83 vs. 0.80 kg, respectively). For G:F, there was no difference ($P > 0.05$) between High Index Category and Low Index Category for the Green line (0.402 vs. 0.410 kg:kg, respectively) or for the Blue line (0.425 vs. 0.429 kg:kg, respectively), however, G:F was greater ($P < 0.05$) for High Index Category than Low Index Category for the Yellow line (0.432 vs. 0.419 kg:kg,

respectively). For carcass lean, there was no difference ($P > 0.05$) for High Index Category and Low Index Category for the Green line (53.34 vs. 53.51 %, respectively) or for the Blue line (53.44 vs. 53.30 %, respectively), however, carcass lean was greater ($P < 0.05$) for High Index Category than Low Index Category for the Yellow line (54.71 vs. 54.18 %, respectively). In addition, there were main effect differences ($P < 0.05$) between sire lines for growth and carcass characteristics. The Blue sire line had higher carcass weight ADG than the Green and Yellow lines, which were similar (0.62, 0.59, and 0.59 kg, respectively). For carcass weight G:F, the Blue and Yellow lines were similar ($P > 0.05$) and had greater carcass G:F than the Green line (0.327, 0.327, and 0.313 kg:kg, respectively). The Blue line had lower ($P < 0.05$) carcass yield than the Green and Yellow lines (74.31, 75.17, and 75.00 %, respectively), and the Yellow line had lower ($P < 0.05$) ultrasonic backfat depth than the Green and Blue lines (12.95, 15.49, 14.22 mm, respectively). The difference between sire lines for *Longissimus* muscle depth was similar for measurements taken on the live animal (ultrasonic) or the carcass (Fat-O-Meater), with the Blue line having lower ($P < 0.05$) muscle depth than the Green and Yellow lines which were similar (55.88, 58.17, and 57.40 mm, and 58.42, 62.23, and 62.74 mm, respectively). These results show commercially important differences in growth performance and carcass characteristics between sire lines. They also suggest that the relative differences between progeny of sires with high and low selection index differs between sire lines which probably reflects differences in the weighting given to traits in each line-specific index, a finding that warrants further investigation.

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Chapter 1: Literature Review

Sire Line Performance Differences

Introduction: The choice of which sire line to use on a commercial swine operation is critical because it sets the genetic potential of the pigs for growth and carcass and meat quality characteristics, and ultimately determines the profitability of the business. When developing a breeding program, it is important to recognize that there are substantial differences in the genetic potential, and therefore, the performance levels of sire lines that are currently available to an industry. There is a range of commercial sire lines on the market, and in theory, it is necessary to evaluate the performance of each one in order for the producer to determine the best one to use for the operation. Historically, pure breeds formed the basis of the genetics available to the swine industry; however, currently, specialized sire and dam lines developed by breeding companies or organizations are widely used in most countries. Evaluation of pure breeds dates back over 100 years; however, since most breed evaluations were carried out several years ago, such comparisons are of historical interest only. Given that the genetic improvement of economically important traits is a continuous process, it is important that comparisons of breeds and genetic lines are carried out with the populations currently available to the industry. And therefore, it was chosen to exclude any breed comparisons from this review and to focus on sire line comparisons that have been published relatively recently. Unfortunately, there are relatively few comprehensive sire line comparisons that have been published in the scientific literature in recent years. With genetic improvement, sire lines change over time, and with markets and animal husbandry practices evolving, it is necessary to reference the most current literature. The following literature review summarizes recently published studies that have compared the performance of a range of sire lines.

Effect of Sire Line on Growth Performance, and Carcass and Meat Quality: In any review of published information on sire line performance, it is important to focus on studies that have evaluated lines that are representative of those currently utilized in the industry. Sire lines that have been evaluated have been formed with a wide range of breeds. However, this review will focus mainly on terminal sire lines that have Pietrain, Duroc, and Hampshire ancestry, as these breeds have been the foundation of many of the sire lines used in the industry today.

In a study by Gu et al. (1992), the growth performance and carcass characteristics of five genotypes of pigs were evaluated from 59 to 127 kg live BW. One hundred and twenty seven barrows representing five genotypes, 1) Hampshire × Hampshire-Duroc, 2) Synthetic terminal sire line, 3) Hampshire-Duroc × Landrace [Yorkshire-Duroc], 4) Landrace × Yorkshire-Duroc, and 5) Yorkshire × Landrace were placed on test. Samples of the genotypes were slaughtered at 59, 100, 114, or 127 kg live BW. No growth performance differences were reported. For all four weight periods, genotype 2 progeny had heavier carcasses. Genotype 2 and 3 had greater carcass lean percentage than the other genotypes. Genotype 4 had higher backfat thickness measurements at the final two weight periods than the other genotypes. However, bone and skin weights were similar across the genotypes. These results suggest a difference in compositional development among the genotypes tested. Although the pigs were slaughtered at similar live weights, the pig's carcass composition at each weight was vastly different. This is most likely due to the different selection programs used for these genotypes. Similarly, in a study by Ellis et al. (1996) three sire lines were evaluated for growth performance, carcass characteristics, and meat quality. Sire line A, B and C all had similar growth performance from start (35 kg) to harvest weight (120 kg). In terms of carcass characteristics and meat quality, Sire line A produced progeny with greater fat depths and smaller *Longissimus* muscles, higher visible

marbling, firmer backfat, and more acceptable meat with a lower shear force compared to lines B and C progeny that had similar growth performance and carcass and meat quality. These two studies illustrate that sire line has a significant effect on carcass composition and meat quality, two factors that could ultimately impact the profitability of a business.

It is common practice in genetic improvement programs for swine to select for a minimum number of traits in order to maximize genetic progress in the most economically important traits. This is illustrated in a study by Friesen et al. (1994) that evaluated 120 pigs from two genotypes that were selected for either high or medium lean tissue gain. The study was conducted between 44 and 127 kg live weight as a factorial with sex and dietary lysine as additional treatments; however, no treatment interactions were detected. Friesen et al. (1994) reported that the high-lean growth pigs had increased average daily gain and gain:feed ratio compared with the medium-lean growth pigs. The increase in growth performance of the high-lean growth pigs is thought to be due to the increase in lean accretion when compared with the medium-lean growth pigs. Likewise, the medium-lean growth pigs had increased lipid accretion compared to high-lean growth pigs. These results are in line with previous research (Cameron and Curran, 1994) which has shown that genetic increases in lean deposition and genetic decreases in fat deposition are accompanied by genetic improvement in feed efficiency through a reduction in the energy required per unit of gain. Therefore, evaluation and utilization of a leaner-type sire line will be beneficial in terms of improved feed efficiency, as well as increased carcass leanness, as the majority of pigs sold in the U.S. are on a lean percentage basis, ultimately maximizing profit potential.

As previously discussed, sire line is a major contributory factor to variation in growth performance and carcass characteristics and meat quality. Meat quality has become an important

concern of consumers and, consequently, is a topic of interest for the industry that needs to be considered when deciding on which genetic lines should be incorporated into breeding programs. Unfortunately, there are relatively few published studies that have evaluated differences between commercial sire lines for the major meat quality characteristics; however there is an abundance of published studies evaluating the effects of the halothane genotype on quality attributes. Although it is important to understand the impacts of single genes such as the halothane gene, the main focus of this review is on recent and relevant literature on differences between sire lines. The following references discuss the effects of the halothane genotype as well as line differences in growth performance and carcass and meat quality. Miller et al. (2000) evaluated the effect of three sire lines that differed in halothane genotype on growth performance and carcass characteristics and meat quality. Sire line A was a halothane positive line that produced carrier progeny, sire line C was a halothane negative genotype that produced negative progeny, and sire line B was a cross between A and C and was a halothane carrier line which produced both carrier progeny as well as negative progeny within the same litter. The halothane gene is known for its positive effect on carcass leanness; however, it is generally thought to have negative impacts on meat quality parameters. Sire line A progeny had slower growth than the other two lines due to decreased feed intake, however, gain:feed ratio was similar among all three lines. The halothane gene did not have a significant effect on growth performance which was unexpected. Dressing percentage was higher for the progeny of sire line A and B compared to line C, but differences in other carcass measurements were small and inconsistent. Line A produced pigs that had greater shear force, suggesting tougher meat, than those from the other two lines, and line A and B pigs had lower taste panel tenderness and juiciness scores compared with line C progeny. Miller et al. (2000) concluded that, although the halothane gene did not

have an effect on growth performance, it did appear to have a negative effect on some meat quality characteristics. These results indicate the importance of considering all sire lines, as well as any genes with major effects on growth performance and carcass and meat quality characteristics when selecting a sire line to incorporate into a breeding program.

When discussing genes with major impacts on meat quality it is also important to discuss the Rendement Napole (RN^-) gene, as some lines may have the unfavorable allele of this gene. Although this is not intended as a thorough review of the effects of this gene, because evaluation of sire lines is the main focus, it is important to be aware of the effects of Rendement Napole gene on growth performance and meat quality. A study by Le Roy et al. (2000) evaluated the effects of the three RN genotypes, homozygous dominant (RN^-/RN^-), heterozygous carrier (RN^-/rn^+), and homozygous recessive (rn^+/rn^+), on growth performance and meat quality traits. There was no difference between the RN^- genotypes for growth performance; however, pigs with the RN^- allele had significantly leaner carcasses. In addition, the RN^- gene had an effect on meat quality producing muscles with increased glycolytic potential levels, decreased ultimate pH, increased L^* score (paler meat), and decreased water-holding capacity. Le Roy et al. (2000) stated that eating quality was also affected by the Rendement Napole gene, with meat from pigs with the RN^- allele having a more acidic taste. As previously discussed, with meat quality becoming a more common topic of interest in the industry, single gene impacts need to be understood and considered when selecting a sire line.

One area of interest that has been evaluated in a limited number of studies is sire line differences in feeding patterns. In a study by Augspurger et al. (2002) two sire lines (Line A: Pietrain ancestry versus Line B: Synthetic line) were evaluated for the effect on growth performance and feeding patterns. Line B progeny had greater growth rate due to increased feed

intake, resulting in similar gain:feed ratio compared to line A progeny. Line B sired pigs had smaller *Longissimus* muscle depths but had greater overall lean growth rate in comparison with Line A progeny. In terms of feeding patterns, Line B progeny had a higher feed consumption rate but lower daily feeder occupation time compared to Line A sired pigs. This is in contrast with the results of the study of De Haer and Vries (1993) that showed that the fastest growing line spent less time at the feeder, but had more frequent feeder visits, and consumed smaller meals at each visit. Augspurger et al. (2002) concluded that genetic ancestry has a major influence on growth performance and feeding patterns in growing-finishing pigs. Likewise, feeding patterns changed at different rates with increasing live weight for each genetic line. Rate of change in feeding patterns can be associated with differences observed in overall growth performance and lean deposition in finishing pigs. These studies illustrate the potential importance of evaluating feeding patterns to assist with selection of sire lines for breeding programs.

In summary, this literature review described a number of studies that showed relatively large differences in economically important traits between commercially-available sire lines. The studies reviewed showed large variation between sire lines for growth performance, carcass characteristics, meat quality, and behavioral characteristics, such as feeding patterns. Although there were some inconsistencies in the differences between the sire lines evaluated, this review has highlighted the importance of evaluating each sire line in order for producers to determine the best line to use in the operation to maximize profit potential. As previously mentioned, the research presented showed the impact of sire line on various performance measures; however, as genetic progress is made and production systems evolve, it is important to continue these evaluations. In addition, inconsistencies in results related to differences between genetic lines

may be the result of differences in the selection approach and variation in selection indices throughout different testing environments, ultimately, resulting in a genotype by environment interaction. These topics of interest will be discussed in more detail.

Index Based Selection

As previously discussed, genetic improvement is the main objective for a genetic company or a production company with an internal genetic selection program. Determining the most appropriate selection objectives and selection criteria is an ongoing discussion and various approaches have been evaluated. The selection objective is the description of traits to be improved to increase profitability and the selection criteria being the traits that will actually be measured to meet the selection objective. Including the most economically important traits in the selection objective will help assure maximum profit potential to the business. In addition, various methods of selection have been utilized, including, random selection, phenotypic selection, which includes single-trait, independent culling levels, and multi-trait index selection, and selection based on Best Linear Unbiased Prediction (BLUP). The following sections of the literature review summarize historical published studies that discuss variation in both selection objectives and selection criteria, and, also, differing forms of selection methods.

Selection Objectives and Selection Criteria. The following information is summarized from a comprehensive literature review of selection objections and criteria from Harris and Newman (1994). At the start of animal breeding, selection was based on the visual appearance of the animal. As data collection and objective forms of selection became more common, deciding on the selection objectives and the approach to meeting the objectives through selection criteria became a critical decision. It is important to base these objectives on economic values such as feed and labor (input) costs, and pig value at different stages of production (output). Similarly,

traits should be weighted according to the profit potential from an increase in one unit of improvement in the particular trait of interest. Historically, feed costs have been the most significant input cost in swine production, and this is true today. Therefore, selection for feed efficiency, directly or indirectly, ranks among the most important traits to include within a selection index. Selection on the basis of genetic correlations can assist and improve index accuracy when indirectly selecting for a trait. Harris and Newman (1994) stated that there are four components to creating an effective breeding program. First, statistical procedures to predict genetic differences in economic traits. Second, a testing and selection process to increase selection intensity and decrease generation interval, but also accurately measuring the desired traits. Third, a plan to disperse any genetic improvement down through each production phase and a payment plan to encourage any breeders involved. Lastly, an economic breeding objective to drive the profit potential of production. These authors concluded that feed efficiency, reproductive performance, and longevity were the most economically important traits to incorporate into selection objectives. The selection criteria relative to these objectives could require measurements of backfat, average daily gain, number of pigs weaned, and culling rates within the sow herd.

In the U.S. swine industry many factors contribute to the profitability of pork production. It is important to recognize the most economically important traits within the selection objective and weigh them accordingly. In a study by Baker (1974), five methods of constructing an index without the use of economic weights were evaluated. Economic weight was defined by Willis (1991) as being the relative economic value for each trait (i.e. how much is a unit of gain worth compared with a unit of feed efficiency). The selection objective was increased growth rate and feed efficiency. The first index was based on phenotypic values when no estimates of genetic or

phenotypic parameters are available and all traits are considered of equal importance. The second index was based on the breeder's desired gains of each trait, realizing that each trait is of different importance. The final three indices were based on multivariate statistics and were determined to be impractical for use in a breeding program. In each case the selection criteria was directly related to the selection objectives. The first two indices were found to be of practical use to a breeding program; however, increasing performance data collection as well as incorporating economic specific weights to the traits of interest will improve selection accuracy and efficiency. In addition, as markets change and production practices evolve, it is necessary to adjust the index to maximize selection efficiency. Selection efficiency was defined by Yonezawa (1999) as the ratio of achieving the desired genetic gain to the cost of that gain.

One approach is to select for traits either directly or indirectly, this can be used to make improvements in multiple traits using selection for a single measurement and exploiting favorable correlations between each trait in the selection objective. For example, feed costs consistently make up the highest input cost, but as feed ingredients decrease in price, feed efficiency becomes a less important factor. The majority of the market pigs sold in the U.S. are sold on a lean percentage basis, meaning, maximizing the percent carcass lean content of a pig will maximize profit potential. Average daily gain and backfat thickness measurements tend to be accurate indicators of these traits and represent indirect measures for feed efficiency and carcass lean content.

The use of genetic correlation between traits and indirect selection criteria can be utilized to maximize selection intensity while minimizing cost of data collection. In a study by Hazel (1943), three selection indices, 1) weight at 180 days + market score of the animal, 2) Index 1 + productivity of the dam, 3) Index 2 + average weight and score of the animals litter, were

evaluated for the effect on net genetic efficiency. The selection criteria became more complex as more traits were added to the index and began to incorporate the utilization of genetic correlation between traits to include indirect selection. In comparison with index 1, index 2 and index 3 were 8.8 and 11.3 percent more efficient, respectively. Likewise, 36 to 40 percent gain was achieved with these indices in comparison with the genetic gain utilizing the perfect index (i.e., if the exact composition of every animal is known). Hazel (1943) suggested that with proper control of the environment, accurate measuring of differences in phenotype, and by including relative's performance measures, the percentage of improvement in comparison to the perfect index can be improved. Although, with an increase in measuring accuracy, the generation interval may also increase and could offset the genetic gain by the improved accuracy and decrease the rate of genetic improvement. This study illustrates the need for overall balance between maximized genetic improvement and practicality in the resources needed to measure each trait.

Similarly, in a study by Swiger et al. (1979), five selection indices were evaluated for the effect on net genetic gain. Although the indices were not described in detail, some inferences were discussed. Pigs selected on the basis of individual feed intake (i.e., individually housed and fed) showed a 9% increase in genetic gain compared to pigs selected on the basis of a group feed intake (i.e., housed and fed in groups). In addition, including feed efficiency data on a littermate would increase genetic gain by 7%. Swiger et al. (1979) stated that feeding two littermates together offsets the loss of the combined feed data and results in an increase of 6% in genetic gain. Similarly, boosting selection intensity by utilizing ultrasound carcass measures to predict carcass lean content resulted in greater genetic gain compared to decreasing selection intensity by slaughtering littermates to collect carcass data. Ultimately, testing a greater number of

littermates, economically weighting each trait, and incorporating feed efficiency data will help assure maximum genetic gain.

Selection Methods. Various methods of selection have been used in the swine industry and throughout the history of genetic improvement. The following is a description of the common methods utilized for selection; definitions have been derived from Willis (1991).

Random Selection: Selection in the simplest form would be random, which would involve selecting replacement males or females based strictly on the number of animals needed to maintain the proper replacement rate. Random selection often involves visual selection, which will be referred to as selection based on appearance in the literature discussed. Selection based on the appearance of the animal can include a multitude of aspects, but is generally a subjective procedure based on the animal's conformation.

For both subjective and objective forms of selection, either single-trait selection (one trait of interest) or multiple-trait selection (2 or more traits of interest) can be carried out. The following forms of selection will incorporate objective measures into the selection procedure:

Tandem selection is the selection for a single-trait until a level of improvement is made, then a second trait is selected for, then a third, and so on. Tandem selection incorporates a multiple-trait selection objective while utilizing a single-trait selection criteria.

Independent culling levels are a form of selection in which minimum levels of performance are determined for each trait of interest and if an animal falls below this level for any trait it will be culled and not selected. This can be single-trait but is often a multiple-trait selection method.

Selection index is selection for multiple objectives by combining data into a single value. Index selection can be complex, however, it can incorporate many selection criteria into one net index.

The construction of an index will combine the heritability and phenotypic variance of each trait of interest, both genetic and phenotypic correlations between the traits of interest, and the relative economic value for each trait included in the index (economic weight).

The following index based values are defined by Abutarbush (2008):

Estimated breeding value (EBV) is the ability of an animal to produce superior offspring based on phenotypic measurements from the animal itself and relatives.

Expected progeny difference (EPD) is the difference in performance to be expected from future progeny. The EPD is normally one half of the value of the EBV.

Best linear unbiased prediction (BLUP) as defined by Mrode (2014) is a selection index in which the correlation between the true breeding value and the predicted breeding value is maximized and estimates realized values for a random variable using unbiased statistical methods. BLUP corrects for multiple environmental factors (location, diets, years, etc.) as long as a common sire, known as a reference sire, is tested in each environment. BLUP increases the selection accuracy when comparing differing sires.

Selection Methods. Selection based on a selection index as described previously in this review is the most commonly used method in genetic improvement programs for swine. Historically, it has been discussed that selection based on a multiple-trait index will increase the rate of genetic gain in overall genetic merit compared to selection based on other simpler methods, such as tandem or single-trait selection. Hazel and Lush (1943) evaluated three methods of selection, 1) tandem selection, 2) total score method (index selection), and 3) independent culling levels. Selection based on total score (index) resulted in greater selection efficiency when compared to tandem selection, with independent culling level selection being

intermediate. However, independent culling level selection did allow for earlier selection, which can have a positive impact on other parts of the genetic program such as on the generation interval. Hazel and Lush (1943) stated that selection within industry is typically a combination of the total score method (index) and the independent culling levels method. With independent culling levels and total score (index) selection, the number of traits included and the intensity of culling will determine efficiency.

Historically, selection based on the appearance of the animal was common, but as technology advances, more complex selection (index based selection) was adopted. In a study by Belonsky and Kennedy (1987), selection based on phenotype performance (index selection) was compared to selection based on best linear unbiased predictor (BLUP) of breeding value selection for one trait of interest at varying levels of heritability. Genetic gain was greater for BLUP selection compared to index selection; however, as heritability increased, the difference between the two approaches decreased. Selection based on BLUP had a relative advantage over index selection by 55% for traits of low heritability and by 10% for traits of moderate heritability. The rate of inbreeding increased at a more rapid rate with selection based on BLUP but tended to decrease as heritability increased; however, the opposite was observed for index selection, as heritability increased, inbreeding also increased. Belonsky and Kennedy (1987) showed that genetic variance was reduced further with selection on BLUP compared to index selection. In addition to the improved genetic gains of selection, when a superior animal was available within the replacement stock, additional breeding animals were culled; the additional culling increased genetic progress by creating higher replacement rates and decreasing the generation interval in both methods of selection. With traits with lower heritability, which can be

of significant economic importance, selection based on BLUP will help improve selection accuracy as well as selection efficiency.

Within the industry, genetic selection programs are costly ventures. As previously discussed, variation in pig performance must be understood and will determine the genetic improvement potential of the business. In a study by Ellis et al. (1988), selection based on an index including average daily gain, gain:feed ratio, and backfat thickness was compared to random selection in a control line for the effect on growth performance and carcass lean in an experiment that was carried out over an 11 year period. The index selected line showed improvements in backfat thickness (in the first six years) and the gain:feed ratio (+0.22 kg gain/kg feed). It had been understood that decreasing backfat thickness generally results in increasing the gain:feed ratio; however, the gain:feed ratio continued to improve while backfat thickness stayed constant. Similarly, Jungst et al. (1981) compared pigs selected directly for feed efficiency (single-trait selection) and pigs randomly selected over a five year period. The single-trait selected pigs had improved feed efficiency (+0.10 kg gain/kg feed); however, due to the resources needed, selection directly for feed efficiency may not be practical. Therefore, with the selection objective remaining the same, indirect selection criterion may be more practical to use and may result in similar improvements in feed efficiency. In the swine industry, a multiple-trait index is the most common method for genetic selection. Utilization of BLUP, EPD, and EBV can increase selection accuracy of index selection. Determining the most economically important traits, along with economical weights, is critical to maximizing profit potential.

Genotype by Environment Interaction

As previously discussed, the genotype of a pig establishes its performance potential and ultimately the potential profitability of a business. When evaluating the effects of sire line on

growth performance and carcass characteristics of pigs, all environmental conditions must be considered. Within the industry many environmental conditions will be encountered, including but not limited to differences in housing (individual versus group), feeding strategies (ad libitum versus restricted), and ventilation (mechanical versus natural). Similar to sire line evaluations, research has been conducted to evaluate variation in performance of weaning to finishing pigs in a multitude of environments, and determining the best sire line for each environment will help maximize the profit potential of the business. An interaction between these two factors is classified as a genotype by environment ($G \times E$) interaction. A review of $G \times E$ interaction literature is important to understand which environmental factors to balance for when evaluating sire lines. The following literature review summarizes historic and more recent published studies that have evaluated the importance of $G \times E$ interactions in swine.

Definition. Merks (1986) defined a $G \times E$ interaction as a change in relative performance of two or more genotypes measured in two or more environments. James (2009) classified genotype by environment interactions as being either of rank-type or of scale-type. James (2009) defined rank-type interactions as those in which genotype 1 may be superior over genotype 2 in the first environment, however, the reverse may be true when tested in the second environment. Merks (1986) made a similar classification for rank-type interactions. In addition to the rank-type classification, James (2009) defined scale-type interactions as those in which the differences between genotypes change in magnitude, but not in sign, with changes in environment. The implications of these interactions have to be considered when developing a breeding program. Although the magnitude of the performance differences may change with a scale-type interaction, the ranking of the genotypes for performance will stay the same; however, with rank-type interactions, the ranking of the genotypes for performance will change with a change in

environment. Therefore, rank-type interactions are potentially of more practical importance to a business.

Effect of Genotype by Environment Interaction. In the literature, environmental factors are often described by a single factor such as ventilation system or feeding strategies, as well as complete environments, such as specially designed testing stations or commercial facilities which tend to incorporate multiple environmental factors. In sire line evaluations, it has been previously thought that the genetic correlation between the same traits measured in different environments was close to one. This is an important correlation to recognize as typically breeding animals are evaluated in testing stations rather than commercial facilities. Merks (1986) stated that a $G \times E$ interaction is based on the idea that the phenotype for identical traits in differing environments may be controlled by different genes, and, therefore, a high genetic correlation between these traits may not be true. A study by Merks (1986) evaluated pigs in a central test station and on a commercial farm for the presence of $G \times E$ interactions. This study found only one significant $G \times E$ interaction. A genotype by batch interaction was present for average daily gain and the interaction was claimed to be due to differences in animal husbandry between the batches. Merks (1986) also estimated genetic correlations between similar traits measured on pigs at a central testing station and on a commercial farm and determined that the expectation of the correlation should be lower than 1. Specifically for carcass characteristics, the correlations ranged from 0.25 to 0.94. In another study, Merks (1989) evaluated Dutch Landrace and Dutch Yorkshire pigs in three different environments (central test station, on-farm test, and commercial fattening operation). Significant $G \times E$ interactions were present for all growth performance measures. The testing environments differed in the level of control over feeding

regimen, housing, and disease. Merks (1989) concluded that the genetic correlation for growth performance in the different environments is moderate and that for carcass characteristics is low.

In a classic study by Fowler and Ensminger (1960), pigs were tested for $G \times E$ interactions using two different genotypes and two different feeding strategies (*ad libitum* and restricted). The genotypes originally came from a single population within which selection for increased average daily gain was carried out based on the two feeding strategies. Selection occurred for six generations and improvements in average daily gain were realized. A scale-type $G \times E$ interaction occurred when each line was tested in opposing environments. Pigs selected under the restricted feeding level had greater growth rates compared to the *ad libitum* selected pigs in both environments; however, there was a greater magnitude of difference between the lines in the restricted feeding environment than in the *ad libitum* environment. Fowler and Ensminger (1960) determined that the selection program produced two very different genotypes; pigs selected under *ad libitum* feeding had increased feed intake to drive the increase in rate of gain, and pigs selected under restricted feeding had increased lean tissue deposition. Under the restricted conditions pigs could not express any variation in feed intake capacity, so for growth rate to increase, lean tissue deposition had to increase. This study supports the claim by Merks (1986) that selection for identical traits in different environments may be selecting for different genes and results in $G \times E$ interactions. Similarly, Minkema (1970) evaluated genotype (9 to 11 sires) by feeding level (*ad libitum* and restricted) interactions and found contradicting results to those of Fowler and Ensminger (1960). In fact, in this study there were no significant interactions for genotype by feeding level. Due to low interaction occurrence, Minkema (1970) estimated genetic correlations around 1 for most traits except for backfat thickness, ham percentage, and ham shape, for which the correlations were 0.90, 0.82, and 0.90, respectively. In

contrast, Merks (1986) estimated genetic correlations for backfat thickness and ham percentage measured in 2 environments and found these to be relatively low (0.25 and 0.60, respectively).

A study by Bereskin et al. (1990) evaluated genotype by dietary protein level interactions over six generations of selection. Selection was based on an index including average daily gain and backfat thickness. Pigs were tested using either high (24% crude protein) or low (12% crude protein) dietary protein levels. Two lines were developed that were either selected for a high index (select line) or for the mean index (control line). During the fifth and sixth generations, pigs were assigned to two environments, either high (24% crude protein) or low (12% crude protein) dietary protein levels and days to 91kg live weight, average daily gain, backfat thickness, and *Longissimus* muscle area was measured. When the pigs were fed low protein diets, pigs from the high index line selected on low protein diets required less days to reach 91 kg live weight and had greater average daily gain compared to pigs from the high index line selected on high protein diets; however, the opposite was true when pigs from these 2 lines were fed high protein diets, indicating a rank-type $G \times E$ interaction. Conversely, for carcass characteristics there were little to no interactions. Bereskin et al. (1990) concluded that traits with low to moderate heritability (e.g., growth performance traits) are more likely to exhibit a $G \times E$ interaction compared to traits with high heritability (e.g., carcass characteristic traits). This supports the findings of Merks (1989) that a $G \times E$ interaction is more likely to occur in growth performance traits compared with carcass characteristic traits. Bereskin et al. (1990) suggested that selection for age at a fixed weight and average daily gain should be practiced under similar dietary conditions to those that future progeny would experience; however, this would not be necessary for carcass measurements.

Schinckel et al. (1999) carried out 3 studies to investigate the potential for interactions between genetic potential for lean growth, sex, antibiotic treatment, and health status conditions. In trial I, 288 pigs were evaluated from two genetic populations (European Terminal cross and Yorkshire-Landrace cross) with either a high potential for lean growth or an average potential for lean growth, respectively. Pigs were assigned to two environments, either a segregated early weaning, three-stage production system, or a conventional continuous flow, two-stage production system. There were significant scale-type $G \times E$ interactions for average daily gain, daily feed intake, days to market, backfat thickness, percent lean, and death loss. The European Terminal cross gilts were leaner compared to the Yorkshire-Landrace gilts in both environments; however, the magnitude of the difference was greater in the early weaning environment. In addition, the European Terminal cross pigs had greater death loss in the continuous flow environment; however, there was no difference between lines in the early weaning environment. In trial II, three sire lines with different potentials for lean growth (low, medium, and high) were evaluated and these were tested in the same two environments as trial I. Schinckel et al. (1999) found significant $G \times E$ interactions for average daily gain, days to 250lb, feed efficiency, and morbidity. Pigs with the lowest potential for lean growth had the highest feed intake and growth rate, and required less days to reach 250lb live BW in the continuous flow system; however, there was no differences between the genotypes for these traits in the segregated early weaning environment. In another study, Schinckel et al. (1999) used 288 pigs from two genetic populations (Duroc and Duroc-Hampshire F_1 crosses). Pigs were tested under the same environmental conditions as the previous 2 studies. Once again, Schinckel et al. (1999) found $G \times E$ interactions. In the segregated early weaning environment both lines performed similarly for average daily gain and average daily feed intake. However, in the continuous flow environment

the Duroc-Hampshire F₁ pigs had lower feed intake and average daily gain compared to the Duroc line. In all three studies, Schinckel et al. (1999) showed significant G × E interactions for growth performance and concluded that evaluation of sire lines in one environment cannot be used to predict the performance of pigs reared in a different environment. Both greater economic and genetic improvement can occur if superior sires can be identified in the production environment in which the progeny will be reared. Schinckel et al. (1999) also suggested comparing performance improvement trends over time of differing genetic lines in the same environment. Different performance improvement trends over time between the genotypes would suggest increased potential for important G × E interactions.

In a study by Hamilton et al. (2003) 736 pigs were used to test for G × E interactions. Two sire lines (A and B) were evaluated at two floor spaces (unrestricted and restricted) and growth performance and protein and lipid accretion were measured. Hamilton et al. (2003) reported no G × E interactions for any of the measures. The genetic lines used were from the same genetic source and had been selected under similar conditions. Hamilton et al. (2003) suggested evaluating more diverse genotypes under a wider range of environments to determine if G × E interactions were important. This is supported by the findings of Bereskin et al. (1990), by evaluating a wider range of environments or adding more environmental factors, a G × E interaction is more likely to be present. Hamilton et al. (2003) concluded that for the two lines tested, similar performance could be expected across a range of floor spaces.

This literature review outlines a number of studies that show the potential for G × E interactions. A range of environmental conditions have been evaluated, whether it is a single factor or complete environments to determine the potential importance of G × E interactions. Although there were differences between the number of environmental factors tested along with the type of

environmental factors tested in each study, $G \times E$ interactions do occur and need to be taken into consideration when developing a selection program, evaluating sire lines, and, also, when selecting the appropriate sire line to use in a commercial operation. It is inaccurate to assume the correlation between similar traits measured in different environments is close to one. Ideally, to maximize genetic gain and selection accuracy, evaluation of sire lines should be executed in the environment that their progeny will be reared.

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Chapter 2: Effect of Sire Line and Selection Index Category on Pig Growth Performance from Weaning to Harvest and Carcass Characteristics.

Introduction

The sire line utilized on a commercial swine operation sets the genetic potential for growth and carcass and meat quality characteristics, and, ultimately, determines the profitability of the business. There are substantial differences in genetic potential of sire lines that are currently available to any industry, and it is necessary to evaluate the performance of each one in order to determine the best one to use. Genetic improvement of economically important traits is a continuous process, therefore, it is important to carry out evaluations with the populations currently available to the industry.

Differences in performance between lines are the results of differences in selection objectives, selection criteria, and testing methods. The most widely used selection criterion is an index that combines information on economically important traits. Producers not only have a choice of which line to use but also which sires to use within each line. This choice is mainly based on the index value of the sire. Consequently, it is important to understand the relationship between changes in index value and changes in performance traits. This information will allow producers the economic benefit of using sires with higher index values and can also be used to determine the value of using reproductive technologies to reduce the number of sires needed.

Finally, sire lines may be tested for and selected in a variety of environments. Due to this, there may be interactions between the genotype and the environment. These such interactions are classified as genotype by environment ($G \times E$) interactions, defined by Merks (1986) as a change in relative performance of two or more genotypes measured in two or more environments. The

testing environment conditions may be a contributor to $G \times E$ interactions. Due to the possibility of $G \times E$ interactions, it is important that sire lines are evaluated on the basis of the performance of their progeny in the specific commercial environment in question.

Therefore, the objectives of this research were to: 1) compare three commercial sire lines based on progeny growth performance and carcass characteristics and 2) evaluate how sire value changes as the line-specific index changes.

Materials and Methods

This study was carried out at the Georgia Technology Center of The Maschhoffs, LLC located near Carlyle, IL. This is a standard commercial wean-to-finish facility that is equipped to collect data on growth performance and feed intake under typical commercial conditions. The protocol for this experiment was approved by the University of Illinois Institutional Animal Care and Use Committee prior to the start of the study.

Experimental Design and Treatments. This study was conducted as a randomized complete block design (blocking factor was day of start on test) with a 3×2 factorial arrangement of the following treatments:

1. Sire Line
 - a. Green
 - b. Blue
 - c. Yellow
2. Selection Index Category
 - a. High
 - b. Low

Selection of Sires and Matings. The three Sire Lines were from three different breeding companies and were selected based on preliminary data collected by The Maschhoffs suggesting all three lines had economic merit.

Selection of sires within each line to use for matings for the study was carried out as follows:

- Each company used a line-specific selection index that combined the EBVs for the traits that they included in the index together with the economic weights that were used by that company. In other words, the selection index used for each line differed in terms of the specific traits that were included in the index, and the weightings that were placed on the traits in the index. The companies were not at liberty to release the traits included in the line-specific selection index.
- For each sire line, all of the sires that were potentially available to use for matings in this study had a **revised selection index** computed using the sire's EBVs for the specific traits that were in the company selection index weighted by the economic value of the trait to The Maschhoff production system.
- Twenty sires were selected per Sire Line, 10 for each Selection Index Category, from the population of sires available from that line based on the **revised selection index**.
- The High Index Category treatment sires were the 10 sires from the population available from each line that had the highest **revised selection index**.
- The Low Index Category treatment sires were 10 sires that had **revised selection index** values that were closest to the mean index of the population of sires available from that line.

- Details of the *revised selection index* values of the selected boars from each Sire Line and Selection Index Category used for the matings are presented in Table 1.

Each sire was mated to approximately 15 dams that were from 4 crossbred dam lines. Dams were in the parity range 1 to 6, with parity and dam line being balanced across all treatments using the following parity classification: P1 (females bred after 1st litter), P2 (females bred after second litter), and P3+ (females bred after 3rd litter and greater).

Sows were mated using 2 single sire inseminations, the first was at first indication of standing estrous and the second was 24 hours later. Sows were housed and managed according to standard unit protocol during gestation and farrowing. The females were mated and farrowed at Deer Run Sow Farm of The Maschhoffs, LLC located near Huntsville, IL and the progeny from these females were transported to the Georgia Technology Center at weaning. Piglets were individually tagged at birth with the tag representing the Sire Line and Selection Index Category subclass that they represented.

Animals and Allotment to Growth Study. A total of 2,880 animals were used in the study. Pigs from this study came from sows that were previously on a two treatment study and previous sow treatment was used as an allotment criteria. On the day of weaning, pigs were individually weighed and sorted into outcome groups of the same Sire Line × Selection Index Category and gender. Pigs were randomly allotted to pens from within the outcome group and the process was repeated until there were 6 pens with 32 pigs per pen (16 barrows and 16 gilts). Selected pigs were a representative sample of each population of Sire Line and Selection Index Category combinations that arrived at the barn that day, based on live weight, variation in live weight, and individual sire representation. The mean age of the pigs was calculated for each pen and pigs were exchanged between pens as needed so that all 6 pens within a replicate had a mean age

within ± 0.5 days. All 6 pens within a replicate had similar numbers of pigs (± 2) from each dam line used, previous sow treatment category, and parity classification. Pigs were retagged with a unique identification number, moved to the allotted pen, and immediately started on test. The growth study was carried out between start and end BW of 6.1 ± 0.29 kg and 129.8 ± 2.16 kg.

Housing. Pigs were housed in two rooms of a tunnel ventilated wean-to-finish building that had fully-slatted concrete flooring. Pen divisions consisted of gates with horizontal steel rods, and adjustment gates were located in the back of each pens to allow for the size of the pen to be changed in the event of a pig death or removal to maintain the same floor space per pig. Floor space allowance for the study period was 0.66 m^2 per pig. Each pen was equipped with one 5-hole wet/dry box feeder and two cup water drinkers.

Diets. Diets were formulated to meet or exceed the recommendations of NRC (2012) for the nutrient requirements of swine; pigs had *ad libitum* access to feed and water throughout the study period.

Growth Measurements. Pigs were individually weighed at the start and end of the study period. Group pen weights were collected at the start and end of the study and every 2 weeks throughout the study period. All feed additions to the feeders were recorded and the feed remaining in the feeder was measured at the time of pig weighing and these data were used to calculate feed intake and gain:feed ratio. At the end of test, pigs were individually weighed and a transverse ultrasound scan was taken at the 10th rib using an Aloka model 500V B-mode scanner with an Aloka 5011 probe (Corometrics Medical Systems, Wallingford, CT). Backfat depth (over the middle of the *Longissimus* muscle), *Longissimus* muscle depth, and *Longissimus* muscle area were measured on the image.

Harvest and Carcass Measurements. At the end of the growth study, entire pens of pigs were taken off test and transported to a commercial plant for harvest and collection of carcass measurements which were taken on the slaughter line. Hot carcass weight and Fat-O-Meater measurements, including backfat depth and *Longissimus* muscle depth at the 10th rib, and a predicted carcass percent lean were obtained for each carcass.

Statistical Analysis. The pen was used as the experimental unit for all growth and carcass measurements. All data were tested for normality using the PROC UNIVARIATE procedure of SAS (SAS Institute Inc., Cary, NC). Morbidity and Mortality data were not normally distributed and were transformed using the PROC FREQ procedure of SAS prior to analysis. Data meeting the criteria for normality were analyzed using the PROC MIXED procedure of SAS. Data were analyzed as a randomized complete block design with the model accounting for the fixed effects of Sire Line, Selection Index Category and the two-way interaction, and the random effect of block and replicate. Least-squares means were compared using the PDIF option of SAS.

Results and Discussion

Growth Performance:

Least-squares means for the effect of Sire Line by Selection Index Category interaction on wean-to-finish growth performance are presented in Table 2. There was no effect ($P > 0.05$) of either Sire Line or Index Category on morbidity and mortality (Table 2). There were Sire Line by Selection Index Category interactions ($P < 0.05$) for weaning weight (start of test weight), week 20 weight, days on test, overall live weight average daily gain, and overall live weight gain:feed ratio (Table 2).

For the Green and Yellow sire lines, there was no difference ($P > 0.05$) between the High and Low Index Category for weaning weight (6.0, 6.1, 6.1, 6.0 kg, respectively); however, for the Blue line, the High Index Category had heavier ($P < 0.05$) weaning weights than the Low Index Category (6.3 and 6.1 kg, respectively) (Table 2). This difference in weaning weight could be due to either a greater birth weight or a greater growth rate between birth and weaning for the High compared to the Low Index Category, or a combination of the two. Birth weights were not collected in this study. However, for the Blue line, the High Index Category had greater wean-to-finish growth rates than the Low Index Category, which is discussed below, and this suggests that birth to weaning growth rates could have contributed to the differences in weaning weights between Index Categories for the Blue Line.

The treatment interactions for wk 20 live weight, days on test, live weight ADG, and ADFI were similar to the interaction for weaning weight. There was no difference ($P > 0.05$) in live weight ADG, wk 20 live weight, days on test, and ADFI between the Index Categories for the Green and Yellow sire lines; however, for the Blue line the High Index Category ($P < 0.05$) grew faster (0.03 kg, 3.6%), was heavier at wk 20 (4.4 kg, 3.5%), had fewer days on test (4 days, 2.6%), and had greater ADFI (0.07 kg, 3.6%) than the Low Index Category (Table 2). For live weight G:F, there was no difference ($P > 0.05$) between the Index Categories for the Green and Blue lines; however, for the Yellow line the High Index Category had greater ($P < 0.05$) live weight G: F (0.013 kg:kg, 3.0%) than the Low Index Category (Table 2).

These results suggest that the greater growth rates for the High compared to the Low Index Category for the Blue line were largely the result of greater feed intake. In addition, these results also suggest that the greater feed efficiency for the High compared to the Low Index

Category for the Yellow line was not due to differences in growth rate and more likely was because of differences in lean deposition rates which are discussed below.

There were effects ($P < 0.05$) of Sire Line, but not Selection Index Category, on carcass weight ADG and carcass weight G:F (Table 2). The Blue sire line had higher carcass weight ADG than the Green and Yellow lines, which were similar (0.62, 0.59, and 0.59 kg, respectively) (Table 2). In addition, carcass weight G:F was similar ($P > 0.05$) for the Blue and Yellow lines and greater ($P < 0.05$) for these lines than for the Green line (0.327, 0.327, and 0.313 kg:kg, respectively) (Table 2).

Thus, irrespective of Index Category, the Blue line grew faster than the other two lines when measured on both a live weight and carcass weight basis and the Green line had poorer feed efficiency than the other two lines on both a live weight and carcass weight basis.

Carcass Characteristics:

Least-squares means for the effect of Sire Line and Selection Index Category on carcass characteristics are presented in Table 3. There were Sire Line by Selection Index Category interactions ($P < 0.05$) for Fat-O-Meater (FOM) fat depth at the 10th rib and predicted carcass lean content (Table 3). For the Green and Blue sire lines, there was no difference ($P > 0.05$) between the High and Low Index Category for FOM backfat depth (18.54, 18.03, 16.51, and 16.00 mm, respectively) or for carcass lean content (53.34, 53.51, 53.44, and 53.40 %, respectively). However, for the Yellow line, the High Index Category had lower ($P < 0.05$) FOM backfat depth (1.02 mm, 6.5%) and greater carcass lean content (0.53 percentage units, 1.0%) (Table 3).

With the exception of the interactions reported above, there was no difference between the Selection Index Categories for any other carcass measurements. There were Sire Line effects ($P < 0.05$) for carcass yield, ultrasound carcass measurements (backfat thickness and *Longissimus* muscle depth and area) and for *Longissimus* muscle depth measured on the carcass (Table 3). The Blue line had lower ($P < 0.05$) carcass yield than the Green and Yellow lines (74.31, 75.17, and 75.00 %, respectively) and the Yellow line had lower ($P < 0.05$) ultrasonic backfat depth than the Green and Blue lines (12.95, 15.49, and 14.22 mm, respectively) (Table 3). The differences between the lines for *Longissimus* muscle depth was similar for the measurements taken on either the live animal using ultrasound or on the carcass with the Fat-O-Meater, with the Blue line having lower muscle depth than the other two lines which were similar for this measurement (Table 3).

Differences in carcass lean content can result from differences in feed intake or in lean growth rates. Pigs with low feed intakes and high lean growth rates are generally likely to be leaner than those with high feed intakes and low lean growth rates. In this study, the Yellow line produced the leanest carcasses and had lower feed intake than the other two lines (Table 2), suggesting that the reduced feed intake was, in part, responsible for the improved feed efficiency for the Yellow line. In addition, the Yellow line was the only line to show a difference between the High and Low Index Categories for carcass measures which indicated that the pigs from High Index Category were leaner than those from the Low Index Category. As previously discussed, there were no differences between the High and Low Index Categories of the Yellow line for growth rate and feed intake. However, the High Index Category had a greater live weight feed efficiency than the Low Index Category for the Yellow line. Collectively, these results suggest that the greater live weight feed efficiency for the High compared to the Low

Index Category of the Yellow line resulted from a greater lean growth rate. These results are in line with the results of the studies of Cameron and Curran (1994) and Friesen et al. (1994), which showed that genetic increases in lean deposition and genetic decreases in fat deposition are accompanied by genetic improvement in feed efficiency.

Relative to the Yellow line, the Green line had similar growth rates but higher feed intake, and poorer feed efficiency and produced fatter carcasses. This suggests that the greater feed intake of the Green line largely resulted in greater fatter deposition rates than the Yellow line. It has been suggested that lines of pigs with higher carcass fat levels may have improved pork quality relative to leaner lines (Le Roy et al., 2000); however, pork quality was not measured in the current study.

Summary Discussion:

The results of this study show practically important differences between the sire lines evaluated, and within line between Selection Index Categories, for growth and carcass characteristics that result largely from differences in feed intake and tissue deposition rates. The Blue line had greater performance for many of the growth traits while the Yellow line had improved feed efficiency and carcass lean traits, and the Green line had lower performance for growth rate and feed efficiency but had improved carcass yield and *Longissimus* muscle measurements. These results are generally in line with those of Gu et al (1992), Ellis, et al. (1996), and Augspurger et al. (2002) that not one sire line is superior for all growth performance and carcass characteristic traits.

The presence of Sire Line by Selection Index Category interactions suggests that the line-specific indexes that the three genotypes were originally selected for, place different emphasis on

growth and carcass traits. Relative to the other lines, the selection index used for the Blue line would appear to have a greater emphasis on growth rate and feed intake than the other lines and less emphasis on carcass characteristics. In contrast, the selection index for the Yellow line would appear to have a greater weighting on feed efficiency and carcass leanness. For the Green line, there were no significant differences between the High and Low Index Categories for any of the growth and carcass measurements, making it difficult to interpret which traits were emphasized in the selection index used for this line. As presented in the Materials and Methods, the High Index Category sires for all lines had index values that were, on average, approximately 1.4 standard deviations above the mean index for the population of sires available for use in this study. On this basis, it is surprising that there were no differences in any of the growth or carcass traits between High and Low Index Categories for the Green line. Further research would be needed to identify the reasons for this surprising result.

Conclusions

Conclusions:

The results of this study showed that there were important differences between the sire lines for growth and carcass traits that would impact the economic performance. However, no one line was superior in all respects. In general, the Blue line was faster growing and the Yellow line had greater carcass lean, with both lines having similar feed efficiency. The Blue line had lower *Longissimus* muscle measurements than the other two lines, which were similar.

There were important Sire Line by Selection Index Category interactions for most of the important growth and carcass characteristics which suggested that the line-specific indexes, that were used to select the three lines, placed different emphasis on growth and carcass traits. The Blue line selection index appeared to emphasize growth rate, and the Yellow line selection index

appeared to emphasize feed efficiency and carcass leanness. However, the Green line showed no differences between Selection Index Categories for any of the growth and carcass traits making it difficult to interpret which traits were emphasized in the selection index used for that line.

Implications:

With the differences in performance for the traits of interest between the sire lines, a producer has the ability to determine the traits of most importance and select the appropriate sire line to use in their operation. In addition, for the lines that showed a reduction in performance for the Low compared to the High Index Categories (e.g., the Blue line for growth rate and the Yellow line for feed efficiency and carcass characteristics), it would be beneficial to use reproductive technologies to reduce the number of sires needed, making it possible to utilize only High Index Category sires. However, due to the Green line showing no differences between Selection Index Categories in growth and carcass traits, using reproductive technologies to reduce the number of sires used would provide no benefit to the genetic potential of the offspring, and ultimately, to the profit potential of the business.

Tables

Table 1. Summary of Selected Boars

Sire line	Index category	Mean index	Average standard deviation from the mean index
Green	High	\$4.90	1.399
Green	Low	\$2.61	-0.002
Blue	High	112.61 IU	1.369
Blue	Low	97.30 IU	0.143
Yellow	High	139.00 IU	1.389
Yellow	Low	121.53 IU	0.04

IU = Index units

Table 2. Least-squares means for the effect of terminal sire line and selection index category on growth performance of wean-to-finish pigs.

Item	Sire Line, (SL)			SEM	Index Category, (IC)			SEM	P-values		
	Green	Blue	Yellow		High	Low	SL		IC	SL × IC	
Number of pens	30	30	30	-	45	45	-	-	-	-	
Number of pigs	960	960	960	-	1440	1440	-	-	-	-	
Growth performance											
Live weight, kg											
Start of test (at weaning)											
Index Category, (IC)											
High	6.0 ^b	6.3 ^a	6.1 ^b	0.07	-	-	-	0.05	0.22	0.05	
Low	6.1 ^{ab}	6.1 ^b	6.0 ^b	-	-	-	-	-	-	-	
Week 20											
Index Category, (IC)											
High	113.2 ^{cd}	122.2 ^a	111.0 ^{de}	1.39	-	-	-	<0.001	0.06	0.02	
Low	114.2 ^c	117.8 ^b	109.9 ^e	-	-	-	-	-	-	-	
End of test	129.3	130.2	129.8	0.42	129.9	129.6	0.36	0.23	0.52	0.78	
Days on test											
Index Category, (IC)											
High	158 ^{ab}	148 ^d	160 ^a	1.1	-	-	-	<0.001	0.22	0.04	
Low	157 ^b	152 ^c	160 ^a	-	-	-	-	-	-	-	
Overall average daily gain, kg											
Live Weight											
Index Category, (IC)											
High	0.76 ^c	0.83 ^a	0.76 ^c	0.007	-	-	-	<0.001	0.45	0.05	
Low	0.77 ^c	0.80 ^b	0.76 ^c	-	-	-	-	-	-	-	
Carcass Weight ¹	0.59 ^b	0.62 ^a	0.59 ^b	0.004	0.60	0.60	0.004	<0.001	0.46	0.18	
Overall average daily feed intake, kg											
Index Category, (IC)											
High	1.90 ^{ab}	1.94 ^a	1.78 ^c	0.022	-	-	-	<0.001	0.23	0.01	
Low	1.89 ^b	1.87 ^b	1.81 ^c	-	-	-	-	-	-	-	
Overall gain:feed, kg:kg											
Live Weight											
Index Category, (IC)											
High	0.402 ^d	0.425 ^{ab}	0.432 ^a	0.0050	-	-	-	<0.001	0.87	0.02	
Low	0.410 ^{cd}	0.429 ^{ab}	0.419 ^{bc}	-	-	-	-	-	-	-	
Carcass Weight ²	0.313 ^b	0.327 ^a	0.327 ^a	0.0024	0.322	0.323	0.0021	<0.001	0.76	0.33	
Mortality and morbidity, %	8.02	6.77	8.54	1.018	8.34	7.22	0.850	0.42	0.33	0.87	

^{a,b,c,d,e}Means within a row with different superscripts are different ($P \leq 0.05$).

¹Carcass average daily gain = overall ADG × carcass yield.

²Carcass gain:feed = Carcass average daily gain / overall average daily feed intake.

Table 3. Least-squares means for the effect of terminal sire line and selection index category on carcass characteristics of wean-to-finish pigs.

Item	Sire Line, (SL)			SEM	Index Category, (IC)			P-values		
	Green	Blue	Yellow		High	Low	SEM	SL	IC	SL × IC
Number of pens	30	30	30	-	45	45	-	-	-	-
Number of pigs	960	960	960	-	1440	1440	-	-	-	-
Ultrasound measurements										
10 th rib backfat depth, mm	15.49 ^a	14.22 ^b	12.95 ^c	0.221	14.15	14.37	0.188	<0.001	0.33	0.40
10 th rib <i>Longissimus</i> muscle depth, mm	58.17 ^a	55.88 ^c	57.40 ^b	0.364	57.45	56.79	0.319	<0.001	0.06	0.92
10 th rib <i>Longissimus</i> muscle area, sq. cm	48.00 ^a	45.03 ^b	48.06 ^a	0.390	47.48 ^a	46.65 ^b	0.356	<0.001	0.01	0.60
Carcass characteristics										
Harvest live weight, kg ¹	129.4	130.2	129.8	0.42	129.9	129.7	0.36	0.31	0.62	0.77
Hot carcass weight, kg	97.3	96.7	97.3	0.36	97.3	96.9	0.30	0.47	0.33	0.90
Carcass yield, %	75.17 ^a	74.31 ^b	75.00 ^a	0.154	74.92	74.73	0.125	<0.001	0.29	0.40
10 th rib backfat depth, mm ²								<0.001	0.99	0.04
Index Category, (IC)										
High	18.54 ^a	16.51 ^b	14.73 ^c	0.335	-	-	-	-	-	-
Low	18.03 ^a	16.00 ^b	15.75 ^b	-	-	-	-	-	-	-
10 th rib <i>Longissimus</i> muscle depth, mm ²	62.23 ^a	58.42 ^b	62.74 ^a	0.618	61.68	60.59	0.507	<0.001	0.13	0.63
Predicted carcass lean content, %								<0.001	0.14	0.05
Index Category, (IC)										
High	53.34 ^c	53.44 ^c	54.71 ^a	0.138	-	-	-	-	-	-
Low	53.51 ^c	53.30 ^c	54.18 ^b	-	-	-	-	-	-	-

^{a,b,c}Means within a row with different superscripts are different ($P \leq 0.05$).

¹Harvest live weight = final farm live weight; average of all pigs sent for harvest.

²Measurements taken on the slaughter line using the Fat-O-Meater.

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