Development of a Duroc x Pietrain Swine Resource Population

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Introduction

The pork industry is diversifying into multiple pork chains. These chains have specific attributes relative to the consumer base they serve. Many chains have specifications regarding carcass lean and meat quality. There is concern that the quality merit of pork filling these chains may be eroding. This is fueled by preliminary results from the 2003 National Pork Quality Audit that revealed that the frequency of pale, soft and exudative (PSE) pork in the U.S. has increased from 10.2% in 1996 to 15.5% (Dr. D. Meisinger, National Pork Board, personal communication). This increased frequency in PSE pork may be due in part to unfavorable correlated change accumulated as lean yield improved in U.S pork. Selection for rapid lean growth rate in swine frequently results in production of animals that yield inferior quality meat. Significant genetic correlations of carcass leanness to ultimate pH (-0.13), reflectance (0.16) and drip loss (0.05) (Sellier, 1998) all indicate lowered meat quality with increased carcass leanness. Additionally, Wood (1985) reported increased occurrence of less juicy pork products with leaner pigs.

This unfavorable correlated change in meat quality can be overcome by inclusion of meat quality attributes and their related associations with lean growth in the selection objective of terminal as well as maternal lines and breeds. However, collection of meat quality data requires animal harvest and is expensive, thus limiting the utility of this option. In addition, geographic locations of nucleus herds to slaughter plants may prohibit regular collection of meat quality data. An alternative can be selection for markers or major genes that have a significant and favorable association with meat quality traits under selection consideration.

Crossing two populations that are genetically dissimilar creates linkage divergence (van Arendonk, et al., 1994). This linkage divergence creates unique genomic marker genotypes in resource populations developed from founder animals from two diverse breeds or lines. Typically, specific marker genotypes are then associated with performance measurements in the F_2 and later generations to determine the locations of markers or genes that are near chromosomal regions that have a significant association with performance traits. These regions are often called Quantitative Trait Loci (QTL).

A limited number of swine resource populations have been developed around the world using indigenous or rustic breeds crossed with commercial breeds or populations. These studies have reported QTLs for backfat thickness and carcass merit (for example; Andersson et al., 1994, Gelderman et al., 1996, Grindflek et al., 2001, Harlizius et al., 2000, Milan et al., 2002, Malek et al, 2001a, Nezer et al., 2002, Pazek et al., 2001, Rohrer et al., 1998a,b, Varona et al., 2002). In addition, putative QTLs for several meat quality traits have been reported (for example; Gelderman et al., 1996, Harlizius et al., 2000, Malek et al., 2001b). These studies have yielded clues to what portions of the porcine genome may have major control over developmental and meat quality characteristics. However, many of the markers for these putative QTL were determined to be of high frequency within the more commercially usable breeds. This limits the opportunity to utilize these markers for further improvement of domesticated breeds by marker-assisted selection (MAS). Studies that have used more commercially viable breeds for resource population development have also reported putative QTL for carcass merit and meat quality traits, albeit fewer in number (Grindflek et al., 2001, Malek et al, 2001a,b, Nezer et al., 2002) . These results indicate that favorable QTL are segregating for carcass merit and meat quality traits and may be exploited within commercial breeding schemes. Locating and utilizing specific favorable genes and/or markers in genetic improvement schemes for traits that cannot be measured on selection candidates will allow for direct selection among prospective parents and can be more cost effective than traditional methods.

Experimental Plan

A three-generation resource population is nearing completion at Michigan State University. Foundation grandparents of RYR1 normal Pietrain females were mated to Duroc males from a closed unselected control population (Kuhlers et al., 2003). The Pietrain and Duroc breeds were chosen because of their commercial significance worldwide and their widely different performance traits. Pietrain sired pigs have been reported to have poorer growth rate (Edwards et al., 2001) with less backfat thickness at market weight (Edwards, et al., 2003), when compared to Duroc sired pigs. At slaughter, Pietrain sired pigs had a higher percentage carcass lean (Edwards, et al., 2003) when compared to Duroc sired pigs. However, loin chops from Pietrain sired pigs had less marbling, lower ultimate pH , poorer color, and poorer water holding capacity (Edwards, et al., 2003) as compared to Duroc sired pigs.

The F_2 generation of the MSU resource population is approaching 1,000 F_2 progeny. Sixteen F_0 Pietrain dams and four F_0 Duroc sires propagated the F_1 generation. From F_1 progeny, 51 females and 6 males (sons of three F_0 sires) were retained to produce the F_2 generation. Females were retained across multiple parities to produce the projected F_2 progeny number. A minimum of 25 pre-harvest and 30 post-harvest and meat quality traits have been measured (Table 1). Additionally, from serial weight and ultrasound estimates of backfat thickness and loin muscle area, lean growth accretion and and lipid deposition rates will be calculated. Phenotypic data collection of F_2 progeny will be completed in February, 2004.

Genotyping of microsatellite loci in F_0 individuals in order to identify a set of informative markers for use in a genome scan has been initiated. A range of three to eight alleles was observed for 11 loci (Table 2) with five of the loci exhibiting six or more alleles. Thus, it will be possible to easily identify a set of informative markers for genotyping.

Table 1. Phenotypic characteristics measured in F_2 progeny.

Pre-Harvest Traits	**Post-Harvest Traits**	**Meat Quality Traits**
Birth weight, three week and six week weight	Androstenone and skatole concentration	Loin muscle (LM) pH at 45 minutes and 24 hour post harvest
Weight at 10,13,16,19 and 22 weeks of age and at harvest	Hot carcass weight, Carcass Length	LM temperature at 45 minutes and 24 hours post harvest
Plasma IGF-1 at 10 weeks of age	Midline 1st rib, last rib, last lumbar backfat thickness	Subjective LM scores at 24 hours post harvest for: Color (1-6 scale), Marbling (1-10 scale) and Firmness (1-5 scale)
Last and 10th rib backfat at 10, 13, 16, 19 and 22 weeks of age, measured by B-mode ultrasound	Off midline 10th rib backfat thickness and loin muscle area	Other LM measures: CIE Color (L*, a* and b*), drip loss (24-48 hours post harvest), cooking loss and shear force
Loin muscle area at 10, 13, 16, 19 and 22 weeks of age, measured by B-mode ultrasound	Wholesale cuts weights of: Picnic, Boston Butt, Belly, Spareribs, Loin and Ham	Loin chop tenderness, juiciness and off-flavor sensory panel analysis

Table 2. Determination of alleles segregating at microsatellite loci in foundation animals from a
Duroc by Pietrain swine resource population.

Marker[a]	Pig Chromosome	# of Alleles	Marker[a]	Pig Chromosome	# of Alleles
S0113	1	4	S0178	8	6
S0002	3	4	S0539	9	5
S0097	4	7	SW249	10	6
S0005	5	8	SW1008	13	8
S0220	6	3	S0210	14	4
S0101	7	4			

[a]Microsatellite primers distributed by the US Pig Genome Coordinator

Initial Study

The objective of our initial study is to determine QTL for lean growth and selected meat quality traits and how they may interrelate. This study will utilize a subset of the traits evaluated and incorporate a selective DNA pooling strategy (Darvasi and Soller, 1992, 1994; Dekkers, 2000). Two DNA pools, each comprised of DNA from F_2 pigs that exhibited extreme favorable and unfavorable phenotypic performance for selected traits will be created. Each pool will be evaluated for 120 microsatellite markers evenly spaced across the entire porcine genome. The position of a QTL can be estimated from differences in allele frequencies for two flanking markers between individuals with high and low phenotypes (Dekkers, 2000). Three QTL for each trait determined to be significant from this initial screen will be further characterized in individual animals by evaluation of five markers within the genomic region where the QTL resides. Initial traits of interest for this study will include lean growth from 10 to 22 weeks of age, intramuscular fat, cook loss, shear force, and sensory panel estimates for tenderness and juiciness.

Initial analysis for QTL will include both single trait (Haley et al., 1994) and multitrait least squares methodologies (Knott and Haley, 2000). For the analyses of longitudinal data, such as our lean growth data, we will associate DNA markers with parameters from our growth functions as suggested by Rodriguez-Zas et al. (2002).

Future Objectives

Our future efforts will include a more comprehensive genome scan, utilizing a larger number of markers across the genome and determining marker associations with all traits measured. In addition, functional genomic studies will be conducted for longissimus muscle and subcutaneous adipose tissue utilizing RNA extracted from these tissues harvested from selected F_2 animals and evaluated by cDNA microarray analysis.

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