

## NEW DNA MARKER AFFECTING MUSCLE GLYCOGEN CONTENT: PRACTICAL IMPLICATIONS FOR PORK QUALITY

Fields B.<sup>1</sup>, Klont R.E.<sup>1</sup>, Jungst S.J.<sup>1</sup>, Wilson E.R.<sup>1</sup>, Plastow G.S.<sup>2</sup>, Sosnicki A.A.<sup>1</sup><sup>1</sup>PIC USA, P.O. Box 348, Franklin KY, 42135-0348 USA.<sup>2</sup>Sygen International, Fyfield Wick, Abingdon, Oxfordshire, OX13 5NA, U.K.**Background**

Ultimate pH (pHu) of pork is an important quality characteristic affecting meat quality. A higher ultimate pH is associated with a better water holding capacity, translating into lower drip or purge losses during storage, and a higher yield when processing (Eikelenboom et al., 1995). The RN gene is known as a major gene influencing muscle glycogen content and ultimate pH in Hampshire based pig genotypes (Monin and Sellier, 1985; Milan et al., 2000). Recently new economically important alleles have been identified in the protein kinase adenosine monophosphate-activated  $\gamma$ 3-subunit gene (PRKAG3) located on pig chromosome 15, which are associated with lower muscle glycogen levels (Ciobanu et al., 2001). Because of their prevalence in the more common commercial breeds, the potential implications for the pig industry and consumers may be greater than the original RN mutation.

**Objectives**

To study the practical implications of the new PRKAG3 marker on meat quality characteristics of pigs slaughtered under commercial circumstances.

**Methods**

Semen from Duroc and RN gene free Hampshire boars was used to inseminate Camborough 22 and Camborough 24 sows at the PIC research farm in Franklin, KY USA. All pigs were individually identified during processing by inserting duplicate numbered button ear tags into the pigs' left and right ears. Individual DNA samples were also collected at this time and typed for the PRKAG3 marker (I199V, see Ciobanu et al., 2001). A total of 375 pigs were used in the study. The favorable allele for PRKAG3 is 199I which is referred to as the "1" allele and therefore, the favorable genotype is 1.1 and carries both copies. Genotype 1.2 is a heterozygote and genotype 2.2 has no copies of the favorable allele.

Upon reaching the target market weight of 145 kg or 214 days of age pigs were shipped to a commercial packing facility where carcass quality and pH were recorded for each individual. Ultimate pH (pHu) in the loin was measured at approximately 24-hours post-mortem in the *longissimus* muscle between the tenth and eleventh rib while the carcasses hung on the rail in the holding cooler. Ham pH was also measured in the cooler in the *Semimembranosus* muscle. Data were analyzed using SAS PROC MIXED. Fixed effects for harvest date, sire line, dam line, PRKAG3 genotype, and gender were included in the model.

**Results and discussion**

Results from this commercial trial showed positive trends for pHu in both the loin and the ham for carcasses carrying one or more of the favorable PRKAG3 allele. Although the PRKAG3 marker is associated with the RN gene, Table 1 demonstrates the effectiveness of the marker in breeds other than Hampshires. The Duroc sired pigs had a higher ham pHu in the 1.1 genotype than the 2.2 genotype while the 1.2 genotype, or heterozygote, was intermediate but not statistically different. The Hampshire sired population showed higher ham pHu for the 1.2 genotype compared to the 2.2 genotype. In both populations, loin pHu tended to be higher for the favorable 1.1 genotype, but was not statistically significant, presumably due to the small sample sizes.

Table 1. Effects of PRKAG3 Genotype by Sire Line

Sire Line	Duroc			Hampshire		
	1.1	1.2	2.2	1.1	1.2	2.2
PRKAG3 Genotype						
Number of observations	39	90	113	23	68	42
Loin pHu	5.92	5.88	5.88	5.91	5.88	5.86
Ham pHu	6.07 <sup>a</sup>	5.99 <sup>ab</sup>	5.95 <sup>b</sup>	5.93 <sup>ab</sup>	6.01 <sup>a</sup>	5.87 <sup>b</sup>

<sup>a,b</sup> Means within a row lacking a common superscript differ ( $P < .05$ ) within sire line

Upon further analysis, data were pooled across sire lines, as there were no significant interactions between sire line and PRKAG3 genotype. This allowed for larger numbers in the analysis and a better assessment of the PRKAG3 marker effects across all pigs. Table 2 represents the pooled data and shows similar results to the individual sire line analysis. The 1.1 and 1.2 genotypes had a higher ham pHu than the 2.2 genotype. Furthermore, the loin pHu indicated higher values in the 1.1 genotype although the difference was not significant ( $P > .10$ ).

Table 2. Pooled Effects of PRKAG3 Genotype

PRKAG3 Genotype	1.1	1.2	2.2
Number of observations	62	158	155
Loin pHu	5.92	5.87	5.88
Ham pHu	6.01 <sup>a</sup>	5.99 <sup>a</sup>	5.93 <sup>b</sup>

<sup>a,b</sup> Means within a row lacking a common superscript differ ( $P < .05$ )

The results of this test are consistent with previous research findings (Ciobanu et al., 2001) and suggest a positive, additive effect of the allele on the population with a larger effect in hams than in loins. Moreover, the commercial validation of markers such as this allow for genetic

companies such as PIC to use them as an additional tool in the selection and improvement process of the herd. Selecting animals with the favorable genotype can more rapidly accomplish the improvement of traits such as meat quality as opposed to quantitative selection alone. This increased rate of selection for economically important traits like pHu will translate into increased value to all sectors of the pork chain and ultimately a better product for the consumer.

**Pertinent literature**

Eikelenboom, G., Van der Wal, P.G., De Vries, A.G. 1995. The significance of ultimate pH for pork quality. Proc. 41<sup>st</sup> ICoMST, August 20-25, 1995, USA. Vol II, pp. 654-655.

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