Major Genes and Meat Quality

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▪ Introduction

In recent years, international trade regulations have undergone a number of changes. A new openness on world markets has translated into opportunities to stimulate growth and development throughout the entire pork network. This has also meant, however, more aggressive international competition and the introduction of new standards that are gradually replacing tariff barriers. Recent scientific and technological advances as well as the production of quality pork and processed products will serve as the basis for satisfying the growing demands of consumers and help to maintain a competitive edge on foreign and domestic markets. Currently, the Halothane (Hal) and Napole yield (RN) genes are the only two Amajor genes≅ that have been recognized for their significant effects on certain components of the technological quality of pork.

▪ The Halothane Gene

Malignant hyperthermia in pigs, also known as porcine stress syndrome (PSS), is a genetic disorder caused by the Halothane gene discovered in the early 1960s. Malignant hyperthermia leads to a rapid pH fall (pH 45 minutes post mortem <6.1) which results in a pale, soft and exudative meat (PSE meat). In pigs the Hal gene is located on chromosome 6 and is comprised of 2 alleles: a normal allele (Hal^N) and a recessive mutant allele (Hal^n). In 1991, Canadian researchers demonstrated that malignant hyperthermia in pigs was caused by a mutation at position 1843 of the gene encoding for the ryanodine receptor (locus ryr-1) (Fujii et al., 1991). It was also demonstrated that the Hal^n allele was present among Canadian populations of Duroc, Landrace, Yorkshire and Hampshire (Houde et al., 1993). The 3 possible genotypes (NN, Nn and nn) can now be specifically identified using a molecular test. Heterozygote pigs with the Hal gene generally produce a lower quality meat than pigs free of this gene (Table 1). Meat properties are also strongly influenced by slaughtering conditions. Generally, the advantages brought about by the Hal^n allele in terms of body composition do not offset its adverse effects on meat quality. This may explain why the Hal^n allele has been gradually removed over recent years from most pig populations.

Table 1. Effect of Hal gene on quality of loin.

Parameter	Heterozygotes (Nn)	Homozygotes (NN)	Significance (P <)
pH 45 minutes (LD)[1]	5.91	6.28	0.001
Reflectance L* (LD)[1]	46.8	44.5	0.05
pH 48 hours (LD)[1]	5.41	5.42	NS
Drip Loss (%)	5.02	3.62	0.001

[1]LD, *Longissimus dorsi* Source: Pommier *et al.*, 1998.

▪ The RN Gene

The RN gene (Rendement Napole) is a dominant gene discovered in France in 1985 by Naveau, Pommeret and Lechaux (Naveau et al., 1985), which can be identified by a Napole yield evaluation, an indicator of the technological yield of ham production, or by an evaluation of the glycolytic potential of muscle. This gene exists in the form of 2 alleles: the rn+ allele (normal allele) and the RN- allele (the allele with a negative effect on Napole yield). To date, the presence of this gene has been found in the Hampshire breed and Hampshire-based composite lines. The unfavourable allele (RN-) affects the technological quality of meat by radically increasing glycogen levels (approximately 70%) in the sarcoplasm of white fibres and reducing the protein content of muscle (22% for rn+ vs 21% for RN-). Unlike the Hal gene, the RN gene has an effect on the extent, but not the rate, of pH fall (pH 24 hours <5.5) which leads to the production of an acidic type of meat, better known as the Hampshire effect. The RN- allele causes a large drip loss in fresh meat (difference of 4%) and also increases cooking losses (difference of 8%) (Table 2), resulting in major financial losses per carrier pig. Recent advances in molecular genetics have led to locating the RN gene on chromosome 15 and a mutation in PRKAG3 gene associated with excess glycogen content could be identified with a new molecular test for better control of this gene (Milan et al., 2000).

Table 2. Effect of RN gene on quality of loin and ham.

	RN- (n = 51)	rn+ (n = 35)	Significance (P<)
Loins			
GP[1] biopsies (µmol lactate/g)	272.0 ± 9.7	154.9 ± 4.6	0.001
pH 24 hours	5.45 ± 0.05	5.77 ± 0.06	0.001
Reflectance L*	51.79 ± 0.97	47.70 ± 1.01	0.001
Drip Loss (%)	8.65 ± 0.76	4.52 ± 0.70	0.001
Hams			
pH 24 hours (GS)[2]	5.43 ± 0.03	5.67 ± 0.05	0.001
ETY[3] (%)	101.76 ± 2.21	114.53 ± 1.99	0.001
Protein content (%)	21.29 ± 0.19	22.07 ± 0.21	0.001
Slicing Yield (%)	73.04 ± 5.80	57.31 ± 7.53	0.008
Techn. Yield (%)	113.47 ± 1.99	121.00 ±0.88	0.001

[1]GP Glycolytic Potential; [2]GS *Gluteus superficialis*; [3]Experimental Technological Yield

Source: Gariépy *et al.*, 1999.

▪ Conclusion

The isolated or combined effects of environmental and genetic factors have major influences on pork quality. Some genes have a direct impact on the technological quality of meat and processed products, resulting in important economic losses. Characterization of the Halothane gene and its negative effects has been well documented and has led to systematic screening to eliminate it from pig herds. The RN gene, which also has a major negative impact, is the next genetic challenge to the technological quality of pork. Intense research into molecular genetics may provide geneticists with new selection tools to genetically improve the quality of pork, which may also have major impacts on competitiveness in the pork sector on foreign and domestic markets.

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