A THIRD ALLELE (V199I) AT THE RN LOCUS WITH EFFECT ON CARCASS COMPOSITION AND MEAT QUALITY

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Background

The effect of a dominant allele (RN^-) causing lower processing yield of cured cooked ham was reported in Hampshire pigs and Hampshire crosses already in the mid-1980s (Naveau, 1986; Le Roy et al., 1990). This dominant allele has thereafter been found to influence several meat quality parameters. In comparison with the normal allele, rn^+, it gives higher lean meat content (Enfält et al., 1997a, Le Roy et al., 2000), higher muscle glycogen content (Fernandez et al., 1992), lower ultimate pH and processing yield, and higher internal reflectance values (Lundström et al., 1996; Enfält et al., 1997a). The RN^- allele has been found to influence the eating quality in a positive way, leading to higher tenderness, juiciness, meat taste and acidulous taste (Jonsäll et al., 2000).
Mariani et al. (1996) found that the RN locus was located at chromosome number 15. The causative mutation was then found as a missense substitution (R200Q) in the PRKAG3 gene, which encodes a muscle-specific isoform of the regulatory γ subunit of adenosine monophosphate-activated protein kinase (AMPK) (Milan et al., 2000). However, evidence for a third allele caused by another mutation (V199I) has recently been found in other breeds than Hampshire (Ciobanu et al., 2001), giving six possible genotypes. In comparison with the normal allele, the V199I allele gave higher ultimate pH (pH_u), lower muscle glycogen content, lactate and glycolytic potential. Also the colour, measured as Minolta L*, a* and b* values was influenced (Ciobanu et al., 2001).

Objectives

The purpose of this study was to compare the three alleles of the PRKAG3 gene (RN^-, rn^+, and V199I, from now on called rn*), concerning carcass composition and meat quality.

Methods

The animal material consisted of 337 pigs, entire males and females, from three different breed crosses, HxLH, LHxH, and LHxLH, raised at three breeding herds. All pigs were slaughtered at one commercial slaughterhouse with an average slaughter weight of 79.6 kg (range 65.1 – 99.6kg). The stunning procedure at the slaughterhouse changed during the experiment, from individual stunning with CO_2 (224 pigs) to group stunning with CO_2 (groups of 5, total 113 pigs). The carcasses were assessed 24 hours *post mortem* (p.m.) according to the procedure in the Swedish pig progeny testing scheme. pH was measured (Knick portable pH meter 911 equipped with a Xerolyte® electrode) in *M. longissimus dorsi* (LD) at the last rib 45 minutes, 3, 5, 24 and 48 hours p.m. and in *M. semimembranosus* (SM) and *M. biceps femoris* (BF) at 24 hours p.m. Internal reflectance was registered in all three muscles 24 hours p.m. using a fibre optic probe (FOP, 900 nm; TBL Fibre Optic Groups, Leeds, UK). The following registrations were made on the LD muscle: drip loss, shear force (INSTRON Universal testing Machine 4301), cooking loss and chemical composition. The alleles within the PRKAG3 gene were determined according to Milan et al. (2000). The presence of PSE in the ham was subjectively scored using a four graded scale from 0=normal meat to 4=fully PSE. Statistical evaluation was performed using the Procedure Mixed in SAS (Ver. 8e, SAS Institute Inc., Cary, NC, USA). The model contained the fixed effects of genotype, breed cross, sex and the random effects of herd and sire. The fixed effect of stunning system was included for the meat quality parameters and carcass weight was included as a covariate when significant for the carcass composition measurements.

Results and discussion

Six different genotypes were identified at the RN locus among the animals used in this study, and the frequency of these is shown in Table 1. The three genotypes carrying the dominant RN^- allele were the most common ones, adding up to 80% of all pigs, whereas the new mutation, rn*, was rare in the breed crosses presented here. The frequency of the dominant allele is known to be high in the Swedish Hampshire population (Enfält et al., 1997b). The low number of animals carrying the rn* allele in our study is in agreement with results by Ciobanu et al. (2001), who estimated the gene frequency in five different breeds, Landrace, Large White, Berkshire, Duroc and Duroc Synthetic and found the highest frequency in Berkshire (0.74) with low frequencies in the others, especially in Landrace (0.02).

Table 1. Number and frequency of animals with different genotypes in the PRKAG3 gene

	RN^- RN^-	RN^- rn^+	RN^- rn*	rn^+ rn^+	rn^+ rn*	rn* rn*	Sum
Number, (%)	79 (23.4)	80 (23.7)	112 (33.2)	28 (8.3)	29 (8.6)	9 (2.7)	337

The statistical analyses were performed both with the animals grouped into the six identified genotypes, and with animals devided into three groups, where all RN^-carriers were grouped together, rn+rn+ animals were in one group and all rn* carriers in a third. The results and conclusions concerning the technological meat quality traits were the same using both groupings, and for clarification, the results from using three groups are shown in Table 2. The RN^- / genotypes had a more rapid pH decrease, as shown by a lower pH_{45} value and a more rapid pH fall (larger δpH_3) between 45 min p.m. and three hours p.m. as compared to the other genotypes. This might be a part of the explanation of the higher drip loss in this group, as a low initial pH causes higher amount of protein denaturation. A higher degree of PSE was also found in the RN^- / genotypes. There was an interaction between genotype and stunning system for pH_u in LD and BF (see Figure 1); individual stunning resulted in higher pH_u for carriers of the recessive alleles (rn+ and rn*), whereas RN^- / carriers were not influenced by the stunning method. The higher pH_u as a result of individual stunning indicates that this is more stressful for the animals, and more glycogen is consumed before slaughter, causing the higher pH_u. The earlier results showing that the RN^- allele gives lower pH_u and protein content, and higher drip loss, cooking loss, water content and internal reflectance values (Lundström et al., 1996; Enfält et al., 1997b) were confirmed in the present study. However, the two recessive alleles did not differ to any large extent, except for a tendency to somewhat higher pH_u for rn* carriers and lower Hunterlab a* and b* values (see Lindahl et al., 2002). Intramuscular fat content (IMF) did not differ between the genotypes.
Estimated lean meat content in four of the genotypes is shown in Figure 2. The dominant allele gives the leanest and the rn* the fattest carcasses. There was no difference between the RN^- RN^- and RN^- rn^+ genotypes, so these genotypes were pooled, while it seems that the RN^-

allele is not fully dominant over the rn*, as indicated by the lower meat content in RN^- rn* compared to RN^- RN^- or RN^- rn^+. The higher meat content found in RN^- carriers is in agreement with previous results (Enfält et al., 1997a, Le Roy et al., 2000).

Table 2. Technological meat quality in different PRKAG3 genotypes and p-value for the difference between genotypes

	Genotype[1]			
Quality parameter	RN^- / *n=271*	rn^+ rn^+ *n=28*	rn*/ *n=38*	p-value
pH_{45min}	6.51^a	6.54^{ab}	6.58^b	**0.070**
δpH_3[2]	0.19^a	0.15^b	0.14^b	**0.001**
$Ph_{u\ SMA}$	5.39^a	5.48^b	5.51^c	**0.001**
FOP_{LD}	26.3	25.4	24.7	**0.251**
FOP_{SMA}	37.6^a	34.4^b	33.8^b	**0.001**
FOP_{BF}	41.5^a	37.9^b	36.1^b	**0.001**
$PSE\text{-}score_{ham}$	0.37^a	0.05^b	0.01^b	**0.001**
Drip loss, %	6.92^a	5.32^b	5.00^b	**0.001**
Cooking loss, %	30.9^a	26.9^b	26.7^b	**0.001**
Shear force, N	67.8	68.9	71.6	**0.513**
Water content, %	76.5^a	75.7^b	75.6^b	**0.001**
Protein content, %	21.1^a	22.7^b	22.7^b	**0.001**
IMF content, %	0.86	0.97	0.93	**0.197**

[1] RN^- / = (RN^- RN^- + RN^- rn^+ + RN^- rn*); rn^* / = (rn^+ rn* + rn* rn*); [2] δpH_3= rate of pH decline between 45 minutes and 3 hours p.m.

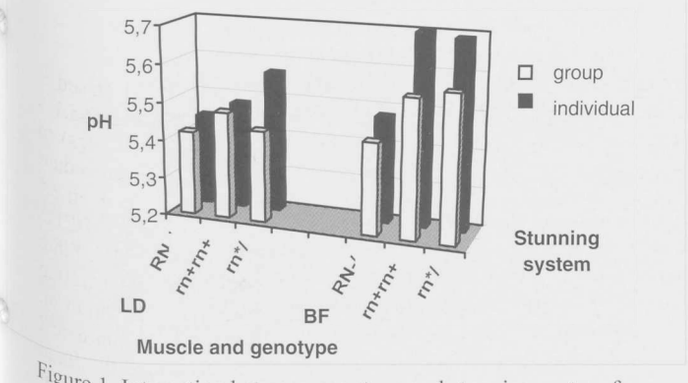

Figure 1. Interaction between genotype and stunning system for pH_u in the LD and BF muscles.

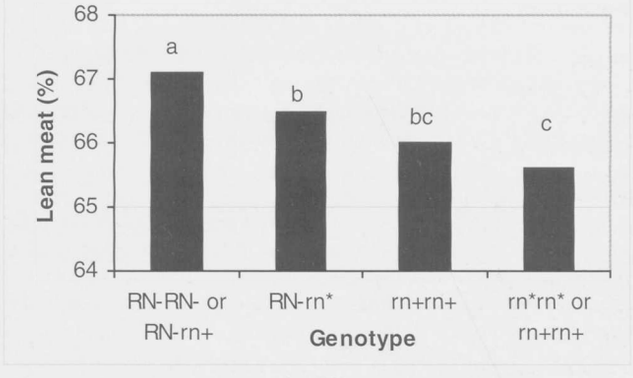

Figure 2. Lean meat content in different PRKAG3 genotypes.

Conclusions

It can be concluded that the new allele of the PRKAG3 gene, rn*, caused less lean carcasses compared to the two other alleles (RN^-, rn+). Concerning technological meat quality, the RN^- allele differed from rn^+ and rn* in the same way for drip loss, cooking loss, internal reflectance and chemical composition, while the pH_u is somewhat higher in rn*carriers compared to RN^- and rn^+.

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Pertinent literature

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