Technological meat quality in carriers and non-carriers of the RN allele in Hampshire crosses with a low or high lean meat content

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Background

Technological and sensory quality traits are of major importance for pork meat. In Sweden, as in other countries, the Hampshire breed is used in slaughter pig production as terminal sire in three-way crosses, where the dams are Landrace-Yorkshire crossbreeds. The specific characteristics of the Hampshire breed, including low pH and technological yield and high glycogen content (e.g. Monin & Sellier, 1985), have been attributed to the presence of the dominant RN gene (Naveau, 1986; Estrade et al., 1993; Le Roy et al., 1995; Lundström et al., 1996, 1998; Enfält et al., 1997). Carriers of the dominant allele in Hampshire crosses (RN carriers) have also been found to have lower protein content (Estrade et al., 1993; Enfält et al., 1997), higher drip and cooking losses, and higher internal reflectance values (Lundström et al., 1996, 1998). The yield of cured cooked products is thus dependent on muscle, RN phenotype and processing method, and to our knowledge nothing has been published on how the yield of cured-smoked loins varies according to RN phenotype and lean meat content.

Objectives

The purpose of this investigation was to study the effects of the RN allele on technological meat quality traits in Hampshire crossbred pigs in carcasses containing a low or a high lean meat content.

Methods

The material used in this study comprised 90 pigs from commercial herds slaughtered at one abattoir. The pigs were selected from herds producing crossbred pigs for slaughter using purebred Hampshire or Hampshire x Yorkshire boars and Swedish Landrace \times Swedish Yorkshire sows. The experimental material was chosen from low lean and high lean carcasses (< 61 or \ge 61 percent meat at grading; head not included in the definition of meat percent) from the same herd between 71 and 88 kg weight (head not included). To avoid confounding between meatiness and sex, only female pigs were selected. The carcasses were assessed at least 48 hours post mortem, according to the procedure in the Swedish pig progeny testing scheme. The right half of the carcass was cut into primary cuts and further to de-fatted ham and back. An estimation of the lean meat content was made using the following prediction equation: Lean meat, % = -20.832 + 0.294* (% ham in carcass) + 0.668* (% meat and bone in carcass) + 0.065* (% back in carcass) + 0.234* (% meat and bone in back). This estimate of the lean meat percent was used when finally dividing the material into a low lean meat class (< 61%) and a high lean meat class (\ge 61%; head not included in the definition of meat percent).

Technological meat quality was measured at cutting on *M. longissimus dorsi* (LD), at the last rib. Reflectance values (surface reflectance 'EEL-Y' and internal reflectance 'FOP'), ultimate pH (pH_u), and drip loss were determined as described by Lundström et al. (1996), and filter paper wetness according to Kauffmann et al. (1986). Samples for drip loss were weighed 5 consecutive days. Marbling was subjectively determined on a cross section of LD using a 5-point scale ranging from 1 (low) to 5 (high) marbling.

LD muscles used for processing of cured-smoked loins ('kassler') were vacuum packed at cutting, frozen on the fourth day after slaughter, and kept frozen for maximum 3 months. The processing was done in a commercial plant. The muscles were thawed overnight, cured by injecting with brine containing 13% NaCl (0.45% nitrite in the NaCl), after which they were tumbled, smoked and steam-boiled to an internal temperature of 67°C. Muscle weights were registered at cutting and after each step in the process.

Glycogen was determined as the sum of glycogen, glucose and glucose-6-phosphate and is expressed in µmol glucose equivalents per gram muscle, wet weight (Talmant et al., 1989).

Statistical analyses. The Hampshire crosses were divided into RN phenotypes, using the threshold from Lundström et al. (1996), i.e. animals with a glycogen concentration $\geq 40~\mu$ mole/g in the LD muscle were regarded as carriers of the RN allele. Assuming that the RN allele was transferred only from the Hampshire sires, all pigs were either heterozygous carriers or non-carriers and thus of known RN genotype. All calculations were performed using the Statistical Analysis System (SAS Institute, Release 6.12). Proc GLM was used when analysing meat content and technological quality. The statistical model used included the fixed effects of lean meat class, RN genotype and day of slaughter. The interaction between lean meat class and RN genotype was non-significant and therefore ignored (p > 0.05). For traits concerning meat content, carcass weight was included as covariate.

Results and discussion

It should be mentioned that it was quite difficult to find carcasses from female pigs with either low or high lean meat content from the same herd, and the high lean carcasses were slightly over-represented. The distribution between non-carriers and carriers of the RN allele was 34 vs. 56, i.e. 62% of carriers, which is in accordance with earlier studies on Swedish pigs of the same breed-cross. Three carcasses from the low lean non-carrier group had to be excluded when analysing meat quality and yield traits due to DFD-condition (pH 5.79, 5.90 and 6.31).

As can be seen from Table 1, the carcasses from the low lean group were somewhat heavier compared with the high lean class (79.8 vs. 78.0 kg; p = 0.018), but the opposite pattern was seen for the LD muscle (3.16 vs. 3.46 kg; p = 0.001; values not shown). No weight differences were found between the RN genotypes. When the LD muscles were thawed before processing, the thawing loss was lower in the low lean meat class (10.8 vs. 11.9%; p = 0.018), but did not differ between the RN genotypes (values not shown). There was only a small difference in processing yield after curing and smoking between loins from the low and high lean meat class (98.8 vs. 97.4 %; p = 0.08), while the difference between the two RN genotypes was as large as 2.2 percentage units (p = 0.01). The



low yield in general was dependent on the freezing and thawing before processing the loins, as fresh muscles will have approximately 5 percentage units higher yield than frozen (Lundström et al., unpublished). The difference between RN genotypes is in accordance with other reports on hams processed with tumbling (Le Roy et al., 1995), but lower than the 4 percentage units difference when processing of the ham muscle *semimembranosus* was done without tumbling (Lundström et al., 1998).

Results for the technological traits of the LD muscle are presented in Table 1. In general, the quality was higher in LD muscle from carcasses belonging to the low lean group or to non-carriers of the RN allele (higher pH, lower FOP-value, higher water holding capacity). In addition, these groups also had higher marbling score, while there was no difference among groups for surface reflectance measurements (EEL-Y; values not shown). No difference was found in fibre area between the low and high lean loins. This is in contrast to the results by Tornberg et al. (1994) who found a tendency to larger fibre areas in loins from leaner carcasses. However, a difference in fibre types was found between RN genotypes as can be seen in Fig. 1, with a higher relative area of type IIA (p=0.004) and a lower area of type IIB (p=0.06) in carriers of the RN allele.

Conclusions

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Both RN genotype and lean meat content had significant effects on the technological quality of *M. longissimus dorsi*. The effect of genotype was, however, generally larger.

Acknowledgements

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Table 1. Differences in carcass weight, meat percent, processing yield and technological quality among *M. longissimus dorsi* from low and high lean carcasses with or without the RN allele (least-squares means ± standard errors)

Meat percent	leat percent		Genotype		monds of
< 61 (n=36)	≥61 (n=51)	Level of sign.	rn ⁺ rn ⁺ (n=31)	RN ⁻ rn ⁺ (n=56)	Level
79.8 ± 0.6	78.0 ± 0.5	*	79.0 ± 0.7	78.7 ± 0.5	n.s.
57.52 ± 0.4	64.5 ± 0.3	***	60.9 ± 0.4	61.1 ± 0.3	n.s.
98.8 ± 0.7	97.4 ± 0.6	#	99.2 ± 0.7	97.0 ± 0.6	**
5.44 ± 0.02	5.40 ± 0.01	*	5.48 ± 0.02	5.36 ± 0.02	***
36.4 ± 1.1	37.5 ± 0.9	n.s.	34.6 ± 1.2	39.3 ± 0.9	***
7.0 ± 0.3	8.2 ± 0.3	**	6.9 ± 0.4	8.2 ± 0.2	**
1.6 ± 0.2	2.1 ± 0.1	#	1.7 ± 0.2	1.9 ± 0.1	n.s.
1.7 ± 0.1	1.4 ± 0.1	#	1.7 ± 0.1	1.3 ± 0.3	*
	<pre><61 (n=36) 79.8 ± 0.6 57.52 ± 0.4 98.8 ± 0.7 5.44 ± 0.02 36.4 ± 1.1 7.0 ± 0.3 1.6 ± 0.2</pre>	$\begin{array}{c} \text{(n=36)} & \text{(n=51)} \\ \\ 79.8 \pm 0.6 & 78.0 \pm 0.5 \\ \\ 57.52 \pm 0.4 & 64.5 \pm 0.3 \\ \\ 98.8 \pm 0.7 & 97.4 \pm 0.6 \\ \\ 5.44 \pm 0.02 & 5.40 \pm 0.01 \\ \\ 36.4 \pm 1.1 & 37.5 \pm 0.9 \\ \\ 7.0 \pm 0.3 & 8.2 \pm 0.3 \\ \\ 1.6 \pm 0.2 & 2.1 \pm 0.1 \\ \end{array}$	< 61 (n=36) ≥ 61 (n=51) Level of sign. 79.8 ± 0.6 78.0 ± 0.5 * 57.52 ± 0.4 64.5 ± 0.3 *** 98.8 ± 0.7 97.4 ± 0.6 # 5.44 ± 0.02 5.40 ± 0.01 * 36.4 ± 1.1 37.5 ± 0.9 n.s. 7.0 ± 0.3 8.2 ± 0.3 ** 1.6 ± 0.2 2.1 ± 0.1 #	< 61 (n=36) ≥ 61 (n=51) Level of sign. m^+m^+ (n=31) 79.8 ± 0.6 78.0 ± 0.5 * 79.0 ± 0.7 57.52 ± 0.4 64.5 ± 0.3 **** 60.9 ± 0.4 98.8 ± 0.7 97.4 ± 0.6 # 99.2 ± 0.7 5.44 ± 0.02 5.40 ± 0.01 * 5.48 ± 0.02 36.4 ± 1.1 37.5 ± 0.9 n.s. 34.6 ± 1.2 7.0 ± 0.3 8.2 ± 0.3 ** 6.9 ± 0.4 1.6 ± 0.2 2.1 ± 0.1 # 1.7 ± 0.2	< 61 (n=36) ≥ 61 (n=51) Level of sign. m^+m^+ (n=31) RN^-m^+ (n=56) 79.8 ± 0.6 78.0 ± 0.5 * 79.0 ± 0.7 78.7 ± 0.5 57.52 ± 0.4 64.5 ± 0.3 *** 60.9 ± 0.4 61.1 ± 0.3 98.8 ± 0.7 97.4 ± 0.6 # 99.2 ± 0.7 97.0 ± 0.6 5.44 ± 0.02 5.40 ± 0.01 * 5.48 ± 0.02 5.36 ± 0.02 36.4 ± 1.1 37.5 ± 0.9 n.s. 34.6 ± 1.2 39.3 ± 0.9 7.0 ± 0.3 8.2 ± 0.3 ** 6.9 ± 0.4 8.2 ± 0.2 1.6 ± 0.2 2.1 ± 0.1 # 1.7 ± 0.2 1.9 ± 0.1

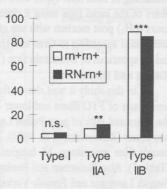


Figure 1. Fibre type composition (%) in non-carriers and carriers of the RN allele.

Levels of significance: n.s. = p > 0.10; # = $p \le 0.10$; * = $p \le 0.05$; ** = $p \le 0.01$: *** = $p \le 0.001$.

Without head, kidney and flare fat. ²Yield of loins based on muscle weight at cutting.