Differences in carcass traits, meat quality and chemical composition between the pigs of different CAST genotype

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Abstract. The study was carried out on 89 Pig Improvement Co. (PIC) pig carcasses, with the aim to investigate the differences between three CAST loci in carcass and meat-quality traits, as well as chemical composition of longissimus dorsi (LD) muscle. The differences among genotypes at CAST/HinfI locus were significant in all carcass traits measured, where AB genotype exhibited preferable values in carcass lengths, ham length, muscle thickness, loin eye area, fat thickness and fat area. Among meat-quality traits analysed, genotypes at CAST/HinfI locus differed in pH\textsubscript{45} in SM muscle, both pH\textsubscript{24} in semimembranosus (SM) and LD muscles, as well as luminosity; genotypes at CAST/MspI differed in pH\textsubscript{24} and EC\textsubscript{24} measured at LD muscle and in red muscle intensity, level of yellowness and hue angle; while genotypes at CAST/Rsal differed in pH\textsubscript{45} and EC\textsubscript{45} in SM muscle, pH\textsubscript{24} in LD muscle, paleness and redness, as well as in shear force and calpain activity. EF genotype at this locus exhibited the highest pH values and the lowest CIE L*, with more pronounced red colour, but also highest shear force and lowest calpain activity values. Furthermore, significant differences in chemical composition of LD muscle were found only among genotypes at CAST/Rsal loci, where FF genotype had the lowest intramuscular fat and the highest relative share of protein.

Additional keywords: CAST genotype, calpain activity, carcass composition, meat quality, pig.

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Introduction

The perception of meat quality from consumer aspect refers to sensory attributes such as colour, flavour and meat tenderness. Among these traits the consumers are complaining mainly about large variability in meat tenderness (Maltin et al. 2003). Despite the efforts to control and optimise conditions before, during and after the slaughter, still large variability in this trait can be found on the market. This fact suggests that it is a very complex quality attribute and is influenced by many structural and metabolic factors, mainly connective tissue concentration, final pH, muscle contraction during rigor mortis, and probably the most important, activity of proteolytic enzymes (calpains and cathepsins). It seems that the role of calpains is most pronounced in early post mortem tenderisation of meat, after which their activity is decreasing due to pH decline, giving a lead to cathepsins released from lysosomes (Cong et al. 1989b; Cong and Goll 1993).

Calpastatin is an endogenous inhibitor of calpains, proteins considered to be the main determinants of meat tenderness (Cong et al. 1989a; Cong and Goll 1993). The molecule is consisted of one L domain, coded by Exons 2–8 and four repeating domains, coded by Exons 9–14 (Stearns et al. 2005). Meyers and Beever (2008) found that heterozygosity in the first 60 kb of calpastatin gene was concordant with the quantitative trait loci for tenderness in their Illinois Meat Quality Pedigree population. In this block, non-coding regions appeared to be more polymorphic than coding regions, presumably due to less selection pressure on non-coding sequences. This suggests that the causative mutation resides in regulatory region (Lindholm-Perry et al. 2009).

Unlike calpains, which are coded by at least 14 genes (Kemp et al. 2010), calpastatin is coded by only one gene – CAST, mapped on SSC2 in Region 2q2.1–q2.4 (Ernst et al. 1998). Ciobanu et al. (2004) sequenced complete CAST gene and identified two single nucleotide polymorphisms (SNPs) associated with meat tenderness, namely Arg249 Lys and Ser638Arg. The influence of these polymorphisms on the quality of raw meat and dry-cured products has been investigated by several authors (Ramos et al. 2005; Stalder et al. 2005; Škrlep et al. 2010, 2012; Gou et al. 2012); however, their findings were rather inconsistent.

In the already mentioned study of Ciobanu et al. (2004), apart from meat tenderness identified, SNPs were also associated with cooking loss and juiciness of the pig meat. The authors stressed the possibility of significant improvements in production of pig meat by the use of these polymorphisms in marker-assisted selection. In that way, naturally tender and juicy pork could be produced avoiding the additional processing steps. Investigation of Stalder et al. (2005) showed that polymorphism at Ser638Arg in pigs was a significant source of variation for moisture content in cured hams and a tendency of influencing the ham yield. Although Ramos et al. (2005) could not detect the influence of CAST polymorphisms on any trait of dry-cured hams, Škrlep et al.
(2010) reported the significant influence of CAST Lys249Arg and CAST Lys249Arg polymorphisms on ham weight and colour, respectively. In the study of genetic polymorphisms connected to quality traits of hams, Gou et al. (2012) identified Arg/Arg CAST genotype at both loci (249 and 638) as the most favourable for quality of Spanish dry-cured hams. Despite the fact that introns do not translate into protein, mutations in these parts of gene can influence phenotype, if they are located in the regulatory region. Their influence is manifested through the improvement of transcription effectiveness or by their effect on mRNA stability (Le Hir et al. 2003). Furthermore, there is a large possibility that intronic variants can be in linkage disequilibrium (LD) with causative mutations that might not be in introns, particularly for variants near the intron and exon boundaries (Koufariotis et al. 2014). As earlier stated, the causative mutation seems to be located in regulatory region, which indicates that it may affect the amount of CAST mRNA either by regulating expression, by affecting mRNA stability or half-life, or by alternate splicing rather than the amino sequence of the protein (Lindhолm-Perry et al. 2009). Numerous investigations in Introns 6 and 7 showed that many of the meat-quality and carcass traits were connected with the genotypes detected in intronic part of the CAST gene (Emnett et al. 2001; Koćwín-Podsiadła et al. 2004; Krzęcio et al. 2007a; Rybarczyk et al. 2010). For that reason, polymerase chain reaction–restriction fragment–length polymorphisms (PCR–RFLP) in intronic part of CAST gene are still considered interesting markers for improvement of pig-meat and carcass quality. The study of Ropka-Molik et al. (2014) showed that polymorphisms at CAST/HpaI and CAST/RsaI, located in Intron 6 of CAST gene, had the greatest effect on water holding capacity, meat pH, firmness and toughness for most breeds analysed. Furthermore, the investigation of Gandolfi et al. (2011) showed a significant influence of CAST EU137105: g.76872 G > A, SNP located in Intron 6 on the activity of autolysed calpain and drip loss; the effect of the specific CAST genotype on the shear force was not significant.

Therefore, the aim of the present paper is to evaluate the effect of nine genotypes identified in Intron 6 of CAST gene and meat-quality traits, as well as the chemical composition of hybrid pigs, with special emphasis on shear force and calpain activity.

Materials and methods

Animals

The study was conducted on 89 pig carcasses originating from P337xC23 PIC hybrid fatteners (45 gilts and 44 barrows). In accordance with European legislation (2008/120/EC 2008) on available floor space, the animals were kept in the collective pens with 12–15 animals/pen, resulting in an available floor space of 0.65–1.00 m² per pig. The animals were fed same diets and kept in the same environmental conditions with ad libitum access to food and water. The pigs were fed three different diets consisted of 13.58 MJ ME and 17.36 g/kg crude protein (CP) to 30 kg liveweight (LW); 13.26 MJ/ME and 16.05 g/kg CP from 30 kg to 70 kg LW; and 12.95 MJ/ME and 14.06 g/kg CP from 70 kg LW to slaughter weight. Pigs remained within the same pen the entire fattening period so as to prevent aggression resulting by mixing. LW of the animals included in the experiment was in the range of 110–150 kg. Animals were slaughtered in a commercial abattoir following electrical stunning (225–380 V, 0.5 A, 5–6 s). The carcasses were dressed according to the conventional procedure.

Carcass composition

After 24 h of cooling, the carcass length ‘a’ (from os pubis to atlas), length ‘b’ (from os pubis to 1st rib), ham length (from the anterior edge of the symphys pubis to the hock joint), together with the ham circumference at its widest point, were measured. Back-fat and loin eye area were measured by geometric procedure according to Comberg et al. (1978) and expressed as the fat : loin eye ratio.

Meat quality

Post mortem measurements of muscle pH were taken at m. semimembranosus (SM) and m. longissimus dorsi (LD) 45 min and 24 h post mortem with Mettler MP 120-B portable pH meter (Mettler-Toledo, Schwerzenbach, Switzerland). Drip loss was measured by a bag method according to Kauffman et al. (1992) after 48 h of cooling the samples at 4°C. Light reflectance scores for CIE L*ab* (CIE 2007) and hue angle were obtained by Minolta CR-300 colourimeter (Konica Minolta Sensing Ltd, Singapore) calibrated against a white plate (L* = 93.30; a* = 0.32 and 1.8; b* = 0.33) with a D65 light source and 10-degree standard observer. For the purpose of instrumental tenderness evaluation, 2.54-cm-thick chops of LD muscle were frozen for 2 weeks, defrosted for 24 h at 4°C, sealed in vacuum bags, cooked in water bath to 73°C internal temperature and cooled at 4°C overnight. Cooking loss was calculated from weights taken before and after cooking of LD chops and expressed as a percentage. Shear force was measured on at least six 1.27-mm thick cores using a TA. XTplus Texture Analyser (Stable Micro Systems, London, UK) fitted with a 1-mm-thick Warner–Bratzler shear attachment. The mean value of maximal strength necessary for cutting the samples was calculated using a Texture Exponent 4.0 Software (Stable Micro Systems) and presented as Warner–Bratzler Shear Force (WBSF, N).

Calpain-activity assay

Calpain activity was quantified using a Calpain Activity Assay Kit (Abcam, UK), according to the manufacturer’s instructions. Frozen muscles (30 mg) were pulverised and homogenised on ice in the extraction buffer provided by the manufacturer. Homogenates were centrifuged at 10000 g, 4°C for 5 min and the supernatant was collected. Protein content was determined using Bradford method (Bradford 1976) with bovine serum albumin as a standard. After quantification of protein in the supernatant, 100 µg of protein was used for the calpain-activity assay with Acetyl–Leu–Leu–Tyr–7-amino-4-trifluoromethylcoumarin (Ac–LLY–AFC), a fluorescent calpain substrate. Active calpain I and calpain inhibitor (Z-Leu–Leu–Tyr–fluoromethylketone) were used for positive and negative controls, respectively. The reaction was carried out at 37°C in the dark for 1 h and fluorescence of released free AFC was monitored using a Fluoroscan Ascent microplate reader (Labsystems, Vantaa, Finland) equipped with a 400-nm excitation filter and a 505-nm emission filter. The enzyme activity
was expressed as relative fluorescence units per milligram of protein (RFU/mg proteins) of each sample.

**Chemical composition**

Relative contents of water, intramuscular fat (IMF), protein and collagen in LD muscle were determined by NIR spectroscopy (AOAC 2007) using the FoodScan™ Meat analyser (Foss, Hillerød, Denmark).

**DNA analysis**

Total DNA was isolated from 50 mg of pig tissue using a commercially available High Pure PCR Template Kit (Roche Diagnostics GmbH, Mannheim, Germany), according to the protocol provided by manufacturer. The genotypes at different CAST loci were identified with HinfI, MspI and Rsal restriction enzymes according to the method described by Ernst et al. (1998). PCR was performed in a reaction mixture of 20 μL containing 50 ng genomic DNA, standard PCR buffer, 1.5 mM MgCl2, 200 μM of each dNTP, 5 pmol of each primer and 1 U Taq DNA polymerase (Fermentas, Vilnius, Lithuania). Cycling conditions consisted of initial denaturation at 95°C for 5 min, followed by 35 cycles of denaturation at 95°C (45 s), annealing at 58°C (45 s) and extension at 72°C (1 min), with a final extension at 72°C for 6 min. PCR products were purified using High Pure PCR Clean Up Micro Kit (Roche Diagnostics GmbH) and digested with three restriction enzymes (HinfI, MspI, Rsal) in a total volume of 15.0 μL containing 12.0 μL of PCR product, 10 × reaction buffer and 1 U of each restriction endonuclease (Fermentas). The resulting digests were incubated at 37°C for 2 h and resolved on 3% agarose gel stained with ethidium bromide.

**Statistical analyses**

Kolmogorov–Smirnov normality tests followed by Levene’s test for equality of variances were performed for all 27 traits as a whole and within each of the genotypes separately. For the traits where Levene’s test showed significance, the Kruskal–Wallis analysis of variance (ANOVA) was used to evaluate heterogeneity of the means across genotypes. Kruskal–Wallis ANOVA was followed by Mann–Whitney U test as a post hoc test for two-genotype comparisons. For the traits where Levene’s test showed no significance, the differences between different genotypes at CAST loci were analysed using mixed ANCOVA (analysis of covariance), a procedure of the general linear model with genotype and sex as the main factors and batch number as a covariate. Since genotype × sex interaction was not observed, gender was excluded from further analysis. Hot carcass weight was used as a covariate when proved to be significant for a trait. The differences between genotypes were determined by Fisher’s l.s.d. test, where P < 0.05 was classified as significant difference and P < 0.1 as a tendency. All data were analysed using Statistica 10 (StatSoft Inc., Tulsa, OK, USA).

**Results**

The differences among investigated genotypes in carcass traits are presented in Table 1. AB genotype had the highest carcass length (‘a’ and ‘b’), ham length, muscle thickness and loin eye area. This genotype also had the lowest fat thickness and fat area. However, this genotype did not differ from AA genotype in

<table>
<thead>
<tr>
<th>Genotype</th>
<th>CAST/HinfI</th>
<th>CAST/MspI</th>
<th>CAST/Rsal</th>
<th>HinfI</th>
<th>MspI</th>
<th>Rsal</th>
<th>L</th>
<th>CC</th>
<th>CD</th>
<th>DD</th>
<th>MSE</th>
<th>P</th>
</tr>
</thead>
<tbody>
<tr>
<td>AA</td>
<td>9.200b</td>
<td>9.483a</td>
<td>0.933a</td>
<td>0.86</td>
<td>0.21</td>
<td>0.69</td>
<td>0.15</td>
<td>0.121</td>
<td>0.78</td>
<td>0.121</td>
<td>0.78</td>
<td>0.121</td>
</tr>
<tr>
<td>AB</td>
<td>9.360a</td>
<td>9.532b</td>
<td>0.923b</td>
<td>0.87</td>
<td>0.05</td>
<td>0.65</td>
<td>0.13</td>
<td>0.205</td>
<td>0.77</td>
<td>0.142</td>
<td>0.77</td>
<td>0.142</td>
</tr>
<tr>
<td>BB</td>
<td>10.466b</td>
<td>11.53b</td>
<td>0.75</td>
<td>0.31</td>
<td>0.04</td>
<td>0.65</td>
<td>0.13</td>
<td>0.88</td>
<td>0.77</td>
<td>0.138</td>
<td>0.77</td>
<td>0.138</td>
</tr>
</tbody>
</table>

| Length a (cm) | 92.00b     | 94.83a    | 0.86  | 0.121 | 0.78 | 0.121 |
| Length b (cm) | 93.76a     | 94.78b    | 0.78  | 0.034 | 0.78 | 0.034 |
| Ham length (cm) | 112.12a   | 112.36a   | 0.78 | 0.142 | 0.78 | 0.142 |
| Ham circumference (cm) | 34.04AB | 34.72AB   | 0.77 | 0.138 | 0.77 | 0.138 |
| Loin eye area (cm²) | 54.36b    | 53.36b    | 1.39  | 0.067 | 1.39 | 0.067 |
| Fat area (cm²) | 20.82a    | 22.92a    | 1.26  | 0.026 | 1.26 | 0.026 |
| Fat to meat ratio at LD cut | 0.36b     | 0.38b     | 0.43  | 0.079 | 0.43  | 0.079 |
meat: fat ratio at the LD muscle cut. Three obtained genotypes at CAST/MspI locus differed in ham length, fat area and loin eye area, where the lowest fat thickness was found in CD genotype, while the lowest fat area and fat: meat ratio at LD cut was found in CC genotype. As for the CAST/Rsal locus, significant differences among genotypes were found in ham circumference, fat area and fat: meat ratio at LD cut. EE genotype had the highest ham circumference, with the highest fat: meat ratio.

Among 16 investigated meat-quality traits, CAST/Hinfl locus influenced both pH45 and pH24 in SM muscle and ultimate pH values in LD muscle. Significant differences among genotypes at this locus were also found for hue angle ($\hat{h}$) and level of palenessness (Table 2). The most favourable pH values measured 24 h post mortem in LD muscle were observed in BB genotype and for SM muscle in AB genotype. As for the level of palenessness, the most favourable values were noticed in BB genotype. Furthermore, the same genotype exhibited the lowest $h^*$ values, indicating that meat from this genotype was redder with less MMb (AMSA 2012).

Genotypes obtained by the use of MspI restriction enzyme differed in pH34 and EC24 values measured in LD muscle and in almost all Minolta colour scores ($a^*$, $b^*$ and $h^*$), where CD genotype had meat with most pronounced red colour.

Genotypes at CAST/Rsal locus differed in pH and EC values measured 45 min post mortem in SM muscle, pH34 values of SM muscle, level of paleness and redness, as well as shear force and calpain activity. EF genotype had highest pH values in SM muscle and lowest CIE L*, with more pronounced red colour, but also highest shear force and lowest calpain-activity values.

The comparison between investigated genotypes for chemical composition of LD muscle is shown in Table 3. The only locus that influenced investigated traits was CAST/Rsal; FF genotype had the lowest IMF content and highest protein content.

### Discussion

It is known that calpain–calpastatin system plays a significant role in the muscle growth and development. This system is associated with apoptosis and myogenesis (Pandurangan and Hwang 2012), where calpain activity is required for myoblast fusion, cell proliferation and growth (Goll et al. 1998; Cruzen 2013). Increased skeletal muscle development may be a result of a reduced rate of protein degradation in muscle, which is connected with reduced activity of calpastatin mainly due to increased calpastatin activity (Goll et al. 1998).

The genotypes at CAST/Hinfl locus significantly differed in all investigated carcass traits. Genotype AB exhibited the most favourable values for all traits, which indicates its potential use as a marker for improved carcass traits in marker-assisted selection. Contrary to results of the present study, Kuryl et al. (2003) and Rybarczyk et al. (2010) did not determine significant influence of CAST/Hinfl locus on any of the carcass traits measured. However, the investigations of Koćwin-Podsiadła et al. (2004) showed a significant influence of this locus on back-fat thickness and weights of the back-fat with bones, ham, loin, shoulder and ham muscle tissue in fatteners free of RYR1 allele. The authors concluded that BB genotype at Hinfl and MspI loci can be used in selection on ham weight and AA genotype at the same loci can be used for selection on loin weight.

### Table 2

<table>
<thead>
<tr>
<th>Genotype</th>
<th>AA</th>
<th>AB</th>
<th>BB</th>
<th>SME</th>
<th>P</th>
<th>CC</th>
<th>CD</th>
<th>DD</th>
<th>SME</th>
<th>P</th>
<th>Cast</th>
<th>Rsal</th>
<th>P</th>
</tr>
</thead>
<tbody>
<tr>
<td>pH45 LD</td>
<td>6.23</td>
<td>6.22</td>
<td>6.27</td>
<td>0.06</td>
<td>0.502</td>
<td>6.28</td>
<td>6.27</td>
<td>6.36</td>
<td>0.06</td>
<td>0.736</td>
<td>6.28</td>
<td>6.27</td>
<td>6.36</td>
</tr>
<tr>
<td>pH34 LD</td>
<td>5.84</td>
<td>5.81</td>
<td>5.80a</td>
<td>0.32</td>
<td>0.254</td>
<td>5.83</td>
<td>5.81</td>
<td>5.80a</td>
<td>0.32</td>
<td>0.254</td>
<td>5.83</td>
<td>5.81</td>
<td>5.80a</td>
</tr>
<tr>
<td>EC45 SM</td>
<td>5.42</td>
<td>5.43</td>
<td>5.40</td>
<td>0.03</td>
<td>0.734</td>
<td>5.43</td>
<td>5.42</td>
<td>5.40</td>
<td>0.03</td>
<td>0.734</td>
<td>5.43</td>
<td>5.42</td>
<td>5.40</td>
</tr>
<tr>
<td>pH24 LD</td>
<td>5.62</td>
<td>5.61</td>
<td>5.60</td>
<td>0.03</td>
<td>0.797</td>
<td>5.61</td>
<td>5.60</td>
<td>5.62</td>
<td>0.03</td>
<td>0.797</td>
<td>5.61</td>
<td>5.60</td>
<td>5.62</td>
</tr>
<tr>
<td>Calpain activity (RFU/mg)</td>
<td>9.54a</td>
<td>8.33b</td>
<td>9.30ab</td>
<td>0.31</td>
<td>0.011</td>
<td>9.54a</td>
<td>8.33b</td>
<td>9.30ab</td>
<td>0.31</td>
<td>0.011</td>
<td>9.54a</td>
<td>8.33b</td>
<td>9.30ab</td>
</tr>
<tr>
<td>CIE L*</td>
<td>51.72</td>
<td>51.62</td>
<td>51.51</td>
<td>0.12</td>
<td>0.484</td>
<td>51.72</td>
<td>51.62</td>
<td>51.51</td>
<td>0.12</td>
<td>0.484</td>
<td>51.72</td>
<td>51.62</td>
<td>51.51</td>
</tr>
<tr>
<td>Drip loss (%)</td>
<td>5.97</td>
<td>5.97</td>
<td>5.97</td>
<td>0.04</td>
<td>0.675</td>
<td>5.97</td>
<td>5.97</td>
<td>5.97</td>
<td>0.04</td>
<td>0.675</td>
<td>5.97</td>
<td>5.97</td>
<td>5.97</td>
</tr>
<tr>
<td>Shear force (N)</td>
<td>48.97</td>
<td>48.97</td>
<td>48.97</td>
<td>0.10</td>
<td>0.627</td>
<td>48.97</td>
<td>48.97</td>
<td>48.97</td>
<td>0.10</td>
<td>0.627</td>
<td>48.97</td>
<td>48.97</td>
<td>48.97</td>
</tr>
</tbody>
</table>
Ham length and circumference represent important traits due to the possibility of selecting the best carcasses for further processing into valuable dry-cured products, such as ham or prosciutto. In the present study, CC genotype at MspI locus exhibited the highest ham length and EE genotype at Rsal locus the highest ham circumference. The lowest fat thickness was found in CD genotype. Krzcio et al. (2007a) reported a significant effect of CAST/MspI locus on the ham thickness at the last rib, as well as the weights of LD muscle, ham and shoulder. In their investigation, DD genotype had higher belly weight, back weight and fat thickness than did other investigated genotypes. In addition, Kuryśl et al. (2003) determined the lowest fat thickness and the highest muscle area in DD genotype. In contrast to results of the present study, Kuryśl et al. (2003) also reported the lowest back-fat thickness in EE genotype.

Meat quality is characterised by traits that are the consequence of different metabolic processes in muscle caused by conditions related to the ante mortem handling of the animal, slaughter and carcass manipulation. Muscle acidity, i.e. pH value and its drop rate, represent the most important meat-quality trait due to its influence on the many related properties such as, for example, protein denaturation during meat aging, drip loss, colour and losses during thermal processing. The influence of calpastatin on pH values can be explained through its ability of calcium channel regulation (Lee et al. 1992) and the fact that phosphorylase responsible for glycogenolysis is also a calpain substrate (Lametsch et al. 2002). In this way, glycogen in post mortem muscle degrades at different rates, depending on the activity of calpain system regulated by the activity of calpastatin (Boehm et al. 1998). It is interesting to notice that all three investigated CAST loci influenced pH values measured in SM and LD muscle (Table 2), which is supported by other authors who have reported results similar to ours (Kočwin-Podsiała et al. 2003; Kapelański et al. 2004; Krzcio et al. 2004, 2007a, 2007b; Ngu et al. 2012). The electrical conductivity measured 24 h post mortem is often used as the predictor of drip loss in pork muscle; an increase in EC24 values is related to a decrease in water-holding capacity (Lee et al. 2000; Łyczynski et al. 2009; Czyzak-Runowska et al. 2010). From the results shown in Table 2, it can be noticed that CD genotype at CAST/MspI locus exhibited the highest (P < 0.1) EC24 values measured in LD muscles and the highest drip loss. Opposite to the results of the present study, Krzcio et al. (2004, 2008) reported a significant influence of Rsal mutation on EC values, water-holding capacity and drip loss, where EE genotype showed favourable values for these traits.

Significant differences in CIE L* values were observed for CAST/Hinfl and CAST/Rsal loci, while genotypes at MspI locus differed in CIE a*, CIE b* values and hue angle. In concordance with our results Kapelański et al. (2004) and Ropka-Molik et al. (2014) reported that meat from animals of the AA genotype at CAST/Hinfl locus was characterised with shorter colour-dominant waves than that from animals of AB and BB genotypes, which indicates paler meat. On the other hand, Rybarczyk et al. (2010) found a significant influence of CAST/Hinfl locus on CIE b* and CIE a*, where BB genotype exhibited higher values of both CIE a* and CIE b* than did AB genotype, while Ngu et al. (2012) reported a significant influence of MspI mutation on the meat redness, where the reddest meat was observed in DD genotype. However, Krzcio et al. (2008) did
not determine the effect of CAST/RsaI on colour-reflectance scores.

Muscle is an ATP- and Ca^{2+}-sensitive organ. With slaughter process and consequent decrease of ATP, an increase of Ca^{2+} in muscle cell can be observed. The calpain system activates at the time when pH begins to drop and Ca^{2+} ions begin to leak out of the endoplasmic reticulum. Binding of Ca^{2+} ions to calpain cause molecule alterations that enable it to become active, but also allows interaction of calpastatin with enzyme (Moldoveanu et al. 2008). The amount of calcium required to allow half-maximal binding of calpastatin to calpain is lower than that required for half-maximal activity of the unautolysed and autolysed forms of calpain (Huff Lonergan et al. 2010). By further decrease of pH values, calpastatin is degraded due to the increase of calpain activity. The rate of its degradation depends on the rate of meat proteolysis and tenderisation (Lonergan et al. 2001), but the exact factors that regulate calpastatin degradation by calpains are still unknown (Huff Lonergan et al. 2010). In the present study, a relationship between calpain activity and shear force at CAST/RsaI locus was noticed, indicating its potential role in calpain activity regulation and meat tenderisation. Using the different methodology of tenderness evaluation, Kapelański et al. (2004) also found the most tender meat in EE genotype. These results suggest the possibility of using EE genotype at CAST/RsaI locus as a marker for increased tenderness in marker-assisted selection. The differences in all investigated chemical parameters of LD muscle were found only among genotypes obtained by RsaI restriction enzyme. Contrary to our results, Krzęcio et al. (2008) reported highest protein share and lowest IMF in EE genotype, while Cheng (2004) found a significant influence of MspI mutation on IMF in different breeds and suggested selection of the DD genotype at CAST/MspI for the improvement of its mean values.

Conclusions

Our study indicated an effect of CAST/Hinfl locus on economically important carcass traits in PIC hybrid pigs, suggesting its potential use as genetic marker for improvement of these traits. Furthermore, we found significant ($P < 0.05$) and suggestive ($P < 0.10$) differences among investigated CAST loci in most meat-quality traits. Most importantly, a relationship between shear force and calpain activity was noticed, where EE genotype at CAST/RsaI locus exhibited the highest calpain-activity and the lowest shear-force values. This result suggests a potential role of this intronic mutation in calpain-activity regulation and meat tenderisation of PIC fatteners.

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References


Polymorphisms at CAST locus exert meat quality of pigs


