

PE1.64 Generation of pork samples divergent in intramuscular fat level for genomic studies 408.00

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Abstract—Intramuscular fat is an important meat quality trait that has a genetic and environmental component. The overall aim of this study is to obtain an improved understanding of the mechanisms underpinning intramuscular fat deposition in pork. In order to generate a meat resource in which intramuscular fat was variable for further genomic analysis, an experimental diet with restricted lysine was applied during the finisher period of growth (0.7% lysine) to 11 Duroc and 11 Pietrain animals. A control group (n=11 Duroc, n=11 Pietrain) received a non-restricted (1.3% lysine) diet. At 2 days post mortem two muscles were analysed for composition. The restricted lysine treatment had a significant effect on intramuscular fat (IMF) level in muscle tissue with IMF being increased relative to the control group. *Semimembranosus* (SM) muscle from animals offered a restricted diet displayed higher levels of intramuscular fat in both breeds. The *longissimus* muscle (LTL) displayed an overall lower level of fat compared to the SM. The experimental diet had a significant effect on LTL IMF level in Duroc animals but there was no difference between treatments in pork LTL of Pietrain background. These muscle samples will provide a resource for gene expression analysis.

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Index Terms— flavour, intramuscular fat, pork quality

I. INTRODUCTION

THERE is a growing dichotomy in consumer preferences in relation to pork and other meat products. From a health perspective, consumers seek to reduce the overall fat content of their diet, but they also display a preference for improved meat quality, flavour and juiciness (Ventanas, et al., 2007). In pork meat, these consumer drivers are linked to the level of intramuscular fat.

In order to develop an increased understanding of the biochemical pathways active in the control of intramuscular fat in porcine muscle, we aimed to

produce a panel of pork muscle samples which differed in intramuscular fat content. It is known that restriction of lysine in the diet of grower-finisher pigs promotes the deposition of intramuscular fat in porcine muscle (D'Souza, et al., 2008; Zhang, et al., 2008). Additionally, divergent breeding goals over time have led to the development of porcine breeds which differ in their capacities for muscle lean growth and fat deposition (Gispert, et al., 2007). The Pietrain breed is characterized by excellent conformation and muscle development and displays a very low intramuscular fat content, whereas the Duroc breed is also characterized by good conformation but has a moderate intramuscular fat content. Duroc and Pietrain breeds also differ in other meat quality traits such as water-holding capacity and loin colour (Latorre, et al., 2009).

We selected animals of Pietrain and Duroc genetic backgrounds and applied a dietary treatment of restricted and unrestricted lysine diets, with a view to producing muscle samples which diverge in fat content for genomics analysis. Future research will focus on exploiting this resource through gene expression profiling to identify the metabolic pathways relevant to the regulation of intramuscular fat deposition in porcine muscle.

II. MATERIALS AND METHODS

A. Animal sampling

Forty-four purebred Pietrain and Duroc animals, of mean weight 50 kg, comprising 12 females and 10 males of each breed were assigned to four treatment groups according to breed and diet and balanced for sex and weight until slaughter. Diets were formulated to have identical concentrations of energy (14 MJ/ kg), but differed in dietary lysine level. The control diet included 1.3 % lysine whereas the restricted diet included 0.7 % lysine. Animals were offered 1.87 kg feed per day until slaughter. After overnight lairage, animals were stunned and exsanguinated under controlled conditions at an EU-licensed pilot-scale abattoir and meat was aged for 7 days. At 2 days post mortem, samples of LTL and SM muscle were excised and stored at -20 °C until further analysis.

B. Biochemical analysis

Composition analysis of the muscle samples was carried out according to the protocol of Bostian et al. (1985).

C. Statistical analysis

Intramuscular fat level for both LTL and SM muscles were analysed using the General Linear Model procedure of SAS (Statistical Analysis Systems Institute, 1985). Models for both LTL and SM muscles included main effects of breed, diet, sex and day of slaughter and the interaction between breed and diet and between sex and diet. Mean intramuscular fat level was contrasted among individual groups (Pietrain muscle restricted diet, Pietrain muscle control diet, Duroc muscle restricted diet, Duroc muscle control diet) using the Tukey Kramer test in SAS for LTL and SM.

III. RESULTS AND DISCUSSION

A. Intramuscular fat in relation to breed

There was no significant effect of gender or slaughter date on fat content in either muscle, therefore average values across males and females and three slaughter dates are presented in Table 1. Overall fat content was relatively low in all animals and means ranged from 0.59 % to 2.89 % across treatment groups. The sampled animals originated in commercial lines, which have been subject to selection for lean growth which may have led to a reduction in intramuscular fat (Renand et al. 2003). However, although the level of fat in the muscle was low, the GLM revealed that, with the restricted diet, there was a significant effect of breed on intramuscular fat level in the LTL ($p = 0.003$). Tukey Kramer analysis indicated that intramuscular fat was higher in lysine-restricted Duroc muscle compared with lysine-restricted Pietrain muscle (Table 1), which is in line with previous research indicating these breeds differ in IMF and other meat quality traits (Latorre et al., 2009). However, an overall breed effect was not observed in the SM muscle ($p = \text{NS}$) and Tukey Kramer contrast analysis across breeds within treatment groups was not significant in this muscle.

Table 1 Least-squares mean IMF in LTL and SM of Duroc and Pietrain breeds and associated p-values from Tukey Kramer contrasts. Significant p-values are highlighted in bold

| | | 0.7 % lysine diet (restricted) Mean \pm S.E | 1.3 % lysine diet (control) Mean \pm S.E. | Diet p- value |
|---------------|----------|---|---|------------------|
| LTL | Duroc | 1.96 \pm 0.20 | 1.22 \pm 0.21 | 0.03 |
| | Pietrain | 0.76 \pm 0.20 | 0.59 \pm 0.20 | 0.90 |
| Breed p-value | | 0.003 | 0.23 | |
| SM | Duroc | 2.89 \pm 0.31 | 1.59 \pm 0.30 | 0.001 |
| | Pietrain | 2.19 \pm 0.32 | 1.07 \pm 0.31 | 0.03 |
| Breed p-value | | 0.48 | 0.74 | |

B. Intramuscular fat in relation to lysine restriction

According to the GLM, there was a significant effect of lysine restriction in both muscles overall (LTL; $p = 0.02$, SM; $p < 0.001$). Tukey Kramer analysis of treatment groups indicated that a significant difference in intramuscular fat content was associated with treatment in LTL samples of Duroc, but not of Pietrain origin, whereas intramuscular fat content was significantly higher in SM samples from animals on the restricted diet in both Duroc and Pietrain (Table 1).

C Interaction of breed and diet on intramuscular fat level in two muscles

No significant interaction effect was observed between breed and diet in the GLM analysis for either muscle ($p > 0.1$ in both cases). However, overall fat level was lower in LTL muscle. Muscle from the Duroc breed was more responsive to the diet than was that of Pietrain, with Tukey Kramer contrast being significant for both muscles in meat from Duroc animals whereas only the SM varied significantly in Pietrain. This indicates likely variation in the modulation of biological pathways relevant to protein and fat metabolism, suggesting that there is considerable scope for exploration of the biochemical basis of intramuscular fat deposition by gene expression analysis of these samples.

IV. CONCLUSION

This study has resulted in the development of a pork quality resource, divergent for intramuscular fat. The biochemical pathways underpinning intramuscular fat development will be further investigated by gene expression analysis.

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