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THE EFFECT OF GENOTYPE AND CARCASS HANGING METHOD ON MEAT QUALITY

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Introduction

There are many reports that suggest differences in meat quality due to genotype (Chambaz *et al*., 2003, Monson *et al.*, 2004, and Sinclair *et al.*, 2001), whilst other reports suggest no or limited differences in meat quality due to genotype (Gariepy *et al.*, 1999, and Laborde *et al.*, 2001). Currently 53 and 47% of prime beef production in Northern Ireland originates from the beef and dairy herd, respectively. Based on various economic projections from the Department of Agriculture and Rural Development in Northern Ireland (DARDNI), these figures are likely to change in a subsidy free environment, which we have just entered, with beef from the dairy herd having a greater importance to prime beef production.

Lundesjo *et al*., 2002 reported that with the use of pelvic suspension (tender stretch) young bulls could approach the tenderness of heifers, both through sensory and instrumental evaluation. Hwang *et al.*, 2002 reported tender stretched hung carcasses produced meat with a longer sarcomere length, a lower shear force requirement and a higher tenderness ratings relative to Achilles tendon hung carcasses. The influence of production factors on meat quality are reported in the literature to account for 40% of the variation in meat eating quality (Polkinghorne, 1998). However, a change in post-slaughter treatment such as a change in carcass hanging method may alter the effects of production factors. Indeed, it should be noted that many researchers that have undertaken studies observing the effect of genotype on meat quality have not stated the method of hanging in their methodology.

Objectives

The aim of this study was to investigate the effect of genotype (dairy versus beef genotype) and hanging method (Achilles tendon versus Tender stretch) on meat quality.

Methodology

Animal Husbandry

The study involved 20 Charolais (CH) steers (greater than 75% CH genetics), initial weight range 409-639kg, and 20 purebred Holstein (HOL) steers, initial weight range 440-669kg. The animals were sourced from farms across Northern Ireland and taken to the Agricultural Research Institute of Northern Ireland for finishing. Animals were penned in groups of 3, according to genotype and live-weight and were finished indoors on a common diet, for the duration of the finishing period, which lasted 98 days. The finishing diet consisted of grass silage fed *ad libitum* supplemented with 4.5 kg beef concentrate.

Animal Performance

Animals were weighed on two consecutive days at the start and end of the study, to enable an initial and final live weight be calculated. Growth rate was calculated as the weight difference between the initial and final weight, divided by the duration of the study.

Slaughter procedure

At the end of the study all animals were taken to the abattoir on the night prior to slaughter and after clipping, were randomly penned according to genotype. On the morning of slaughter, after 11 hour in lairage, the animals were put through a cattle crush and allocated a kill number. Immediately afterwards the animals were sent for slaughter. The order of kill was a batch of CH, followed by a batch of HOL, followed by the remaining CH and then the remaining HOL animals. The animals were stunned with a captive bolt stun gun before being stuck, and were dressed according to the European standards. None of the carcasses were electrically stimulated.

Carcass Measurement

The internal kidney, channel and cod (KCC) fat were collected and weighed. The carcasses were graded by a Livestock and Meat Commission (LMC) grader for conformation score and fat classification according to the European scale. For the purpose of statistical analysis the conformation scores (EUROP) were converted to numerical values with E =5, U=4, R = 3, O+ = 2.5, O =2, O- =1.75 and P=1; while fat classification was converted to 1=1 (lean), 2=2, 3 =3, 4L =4, 4H =4.5 and 5 = 5 (fat).

28 hours post-mortem carcasses were split between the 10^{th} and 11^{th} rib (but not quartered) and marbling score assessed according to the USDA marbling scale, also subcutaneous fat measurements were taken at 3 points.

Hanging method

At 40 minutes post-mortem one side of each carcass was hung by the Achilles tendon (AT), while the other side was re-suspended from the pelvis using the tender stretch (TS)

procedure. The first batch of CH and HOL carcasses had their right side hung by the AT and their left by TS, whist the second batch had their right side hung TS and left side AT. Carcasses entered the chill 45 minutes post-mortem and were chilled under standard commercial conditions.

Meat Quality

The sides were quartered 30 hours post–mortem and a small sample of *longissimus dorsi* (LD) muscle was taken for determination of the sarcomere length using the laser diffraction method as described by Okeudo and Moss (2004). Carcasses were boned out 48 hours post-mortem and the fore-rib joints (6^{th} - 10^{th} ribs) were taken back to the laboratory for meat quality assessment. The LD was removed from the fore-rib joint and sliced into 2.54 cm steaks. These were vacuum packed and stored in a cold room at $<4^{o}$C, until 7 days post-mortem, when further meat quality assessments were undertaken.

Ultimate pH was measured in the laboratory by inserting a spear point ISFET pH probe (Sentron, Model 1072 LanceFET^{TM}) attached to a portable pH meter (Sentron 3001).

Steaks were cooked in the vacuum bag in a hot water bath at 75^{o}C for 50 minutes. The meat was thereafter cooled in a bucket containing ice for 1 hour. The cooked meat was subsequently patted dry with paper towel and placed in a self sealing polythene bag and stored in a refrigerator overnight ($<4^{o}$C). Cooking loss was the weight loss during cooking divided by fresh sample weight and expressed as a percentage. Ten cores were drilled from each sample along the muscle bundle long axis using a 1.27cm diameter cork borer. The measurement of texture was carried out by shearing the core transversely on a 1kN load cell attached to a Warner-Bratzler shearing device mounted on an Instron Universal Testing Instrument (model 6021). The instrument was calibrated to measure over a range 0-20.38 kg and sheared each core of meat at a speed of 100 mm/minute. Texture was recorded as peak shear force (kg.cm-^{2}).

Steaks were removed from the vacuum packs, a 4 mm slice was removed from each steak, discarded and the remaining 2.5 cm slice allowed to bloom with the freshly cut surface uppermost prior to taking the colour measurement. Reflectance spectra of the freshly cut meat surface were measured using a $0^{o}/45^{o}$C illumination viewing geometry-head, attached to a Monolight 6800 Spectrophotometer (Macam Photometrics, Liveingston, Scotland,UK). The instrument was standardized by using black, grey and white reference tiles. The reflectance spectra were recorded continuously from 380nm to 800nm. The spectral data were analysed by computer to provide data in the CIE (Commission Internationale de l'Elairage) tristimulus colour values X,Y and Z and then transformed to CIE L*, a* and b* values.

Statistical Analysis

Data were analysed using analysis of variance for the main effects of genotype (CH vs HOL) and hanging method (AT vs TS) and their interactions. The meat quality data was adjusted by covariance for age at slaughter and carcass weight. In addition relationships of meat quality parameters to carcass parameters were tested for linear relationships.

Results & Discussion

Animal Performance

The main effects of genotype on animal performance are presented in Table 1. Genotype had no effect ($P>0.05$) on live weight gain. CH steers had a higher kill out percentage ($P<0.001$) and produced heavier ($P<0.001$), better conformed ($P<0.001$) carcasses, with a lower KCC fat ($P<0.001$) content and marbling score ($P<0.001$) relative to HOL steers. Although genotype had no significant ($P>0.05$) effect on fat classification, when genotypes were compared at constant carcass weights (Lively et al., 2005) CH carcasses were leaner ($P<0.01$) than HOL carcasses.

Meat quality

The main effects of genotype and hanging method on meat quality are presented in table 2. Neither genotype nor hanging method had any significant effect on meat colour as assessed by L*, a* or b* or ultimate pH. CH meat had a significantly ($P<0.001$) higher cooking loss and Warner Bratzler shear force (WBSF) relative to the HOL meat, but had no significant ($P>0.05$) effect on sarcomere length. Tender stretching significantly ($P<0.001$) decreased WBSF and increased sarcomere length, but did not alter ($P>0.05$) cooking loss. There was a significant ($P<0.001$) genotype by hanging method interaction for WBSF. The TS hanging had a greater improvement on WBSF for the CH genotype (4.3 and 3.0 kg cm^{-2} for AT and TS, respectively) than the HOL genotype (2.8 and 2.3 kg cm^{-2} for AT and TS, respectively).

Linear Relationships

The linear relationships between the meat quality parameters (cooking loss, WBSF) and production / carcass parameters (age at slaughter, carcass weight, conformation score, fat classification, marbling score) are presented in table 3. Cooking loss and WBSF decreased significantly ($P<0.001$) as age at slaughter, carcass weight, fat classification and marbling score increased, regardless of hanging method. Cooking loss was inversely related to conformation score for the AT hanging method, but directly related for the TS hanging method. WBSF increased as conformation score got better (increasing from P to U). For the relationships between WBSF and age at slaughter, carcass weight, conformation score and fat classification the variation for the TS sides was approximately half the variation for the AT sides. This may be due to the reduction in variation of WBSF in the TS sides.

Conclusions

Charolais produced a larger, leaner, better conformed carcass relative to Holstein. LD from Holstein was more tender and had a lower cooking loss than beef from Charolais. Warner Bratzler shear force values were significantly lower in TS sides. Tender stretch hanging reduced the genotype difference for WBSF values. Thus when comparing production effects, we should use post slaughter conditions to optimise meat quality. Highly significant linear relationships were found between cooking loss, WBSF and production / carcass characteristics.

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Tables and Figures

Table 1. The effects of genotype on animal performance and carcass characteristics

	Genotype			
	CH	Hol	sed	Sig
Live weight gain (kg/d)	0.89	0.87	0.059	ns
Carcass weight (kg)	360	281	7.8	***
Kill out percentage (%)	55.5	48.7	0.36	***
Conformation[†]	3.37	1.29	0.106	***
Fat classification[‡]	2.96	3.14	0.114	ns
KCC fat (kg)	10.6	15.6	0.99	***
Marbling score[1]	1.57	2.89	0.156	***

[†] EUROP scale: 5, 4, 3, 2, 1 respectively; [‡] EU fat classification, where 5 = fat, 1 = lean;
[1]8 point scale : 1=low marbling, 8 = high marbling;
ns = not statistically significant ($p>0.05$); *** = $p<0.001$; ** =$p<0.01$; *=$p<0.05$

Table 2 The effect of genotype and hanging method on meat quality

	Genotype (G)		Hanging Method (H)		Significance			
	CH	HOL	AT	TS	sem	(G)	(H)	G*H
L* (lightness)	36.3	34.9	36.6	34.4	1.90	ns	ns	ns
a* (redness)	15.6	18.3	17.3	17.1	0.75	ns	ns	ns
b* (yellowness)	12.3	14.7	13.9	13.5	0.71	ns	ns	ns
Ultimate pH	5.61	5.59	5.61	5.59	0.019	ns	ns	ns
Cooking loss (%)	32.8	27.9	30.1	29.7	0.45	***	ns	ns
WBSF ($kg.cm^{-2}$)	3.7	2.6	3.4	2.6	0.16	***	***	***
Sarcomere length (μm)	2.4	2.5	2.4	2.6	0.12	ns	***	ns

Table 3. Linear relationship between meat quality and production / carcass parameters

	Cooking loss		WBSF	
	AT	TS	AT	TS
Age at slaughter				
Significance	***	***	***	**
Fit[1]	parallel	parallel	parallel	parallel
Slope[2]	-ve	-ve	-ve	-ve
% variance	52.4	48.5	36.4	17.5
Carcass weight				
Significance	***	***	***	*
Fit[1]	parallel	parallel	parallel	parallel
Slope[2]	-ve	-ve	-ve	-ve
% variance	46.8	41.3	35.6	16.9
Conformation score				
Significance	***	***	***	**
Fit[1]	parallel	common	common	common
Slope[2]	-ve	+ve	+ve	+ve
% variance	43.2	36.7	31.2	17.1
Fat classification				
Significance	***	***	***	*
Fit[1]	parallel	parallel	parallel	parallel
Slope[2]	-ve	-ve	-ve	-ve
% variance	59.6	45.0	34.2	16.3
Marbling score				
Significance	***	***	***	***
Fit[1]	parallel	parallel	parallel	common
Slope[2]	-ve	-ve	-ve	-ve
% variance	52.8	52.7	39.4	33.2

[1]parallel indicates slope not significantly different between genotype; common indicates both genotypes can be fitted by a single line

[2] –ve = negative; +ve = positive