Genotype comparisons for meat and eating quality traits

Kim Bunter[1] and Colin Bennett[2]

[1]*Animal Genetics and Breeding Unit, University of New England, Armidale, NSW, 2351*
[2]*QAF Meat Industries, Redlands Road, Corowa, NSW, 2646*

Introduction

The National Genetic Evaluation Program (NGEP), a project coordinated by the National Pork Producers Council (NPPC) with geneticists and commercial producers in America, provided good evidence for significant differences between terminal sire lines in progeny performance for production, carcase, meat and eating quality traits. The project identified "differences among sire lines for many muscle quality traits that are directly related to eating quality and consumer acceptability of pork" (National Hog Farmer, 1995, pg 19). Moreover, considerable re-ranking of sire lines for commercial profit of producers was evident when differences in meat quality traits were considered. A subset of results from this study is shown in Table 1.

Table 1: A subset of sire line differences reported by the NGEP (converted to metric measures)

	Berkshire	**Duroc**	**NGT Large White**	**Yorkshire**
ADG (kg/day)	0.841	0.886	0.850	0.836
FCR (kg/kg)	3.07	2.91	2.94	2.93
+BF (10^{th} rib, mm)	31.8	28.7	29.7	26.7
+Muscle area (cm^2)	37.0	39.6	36.3	39.8
+Carcase lean (%)	47.0	49.0	47.7	49.9
***Colour score**	3.1	2.9	3.0	3.0
***Ultimate pH**	5.91	5.85	5.84	5.84
***Drip loss (%)**	2.43	2.75	2.92	2.85
***IMF (%)**	2.41	3.03	2.15	2.33
***Cooking loss (%)**	22.5	23.1	22.9	23.5
***Tenderness score**	3.50	3.38	3.16	3.26
Index 1 ($/pig)	-4.14	0.64	-0.97	0.74
Index 2 ($/pig)	-4.05	10.51	-8.87	-1.70

+ measured on carcase; * measured on the loin; Index 1: includes days to 250 pounds, FCR and BF10 (backfat-based market); Index 2 contains days to 250 pounds, FCR, BF10, IMF, pH, drip loss %, loin muscle area and tenderness (wholesale or retail pork market).

In some countries (eg Germany) results from random sample tests of the commercial product are routinely published. However, given the increasing privatisation and competitive nature of pig breeding elsewhere, comprehensive commercial product evaluation is not generally widely conducted and/or published. As a result, Australian producers are generally unable to access objective comparisons of either commercial end-product genotypes or alternatively progeny from available sire line genotypes for any economically important traits. In particular, comparisons for meat and eating

quality traits are problematical due to the necessity of standardising production and slaughter conditions, and obtaining feedback on individual animals of known parentage from the abattoir.

While breeding animals of Australian seed stock producers represent a smaller genetic base and less diversification of genotypes (eg. breeds) used for slaughter pig production than is the case overseas, it is likely that sire line differences in meat and eating quality traits do exist, given initial breed differences and some diversity of breeding goals within the Australian industry. These differences should be quantified for the terminal sire line genotypes used within Australia, to provide breeders and producers with objective information on meat quality differences. For this reason, Australian Pork Limited (APL) funded a project (APL1927) entitled "Quantifying meat and eating quality differences between major Australian pig genotypes". The purpose of this project was to:

1. evaluate the magnitude of differences between major terminal sire line genotypes for meat and eating quality traits, and;

2. investigate whether temperament measures on live animals have any phenotypic and genetic associations with meat and eating quality traits

Only brief results for objective 1 are reported in this document.

Material and methodology

1. Sire-breed comparisons

Semen from Large White (LW), Landrace (LR), Duroc (DU) and Duroc synthetic (DS) sires was obtained for inseminating commercial genotype females (Large White/Landrace base) at the QAF Meat Industries Balpool operation. Six breeders participating in the National Pig Improvement Program (NPIP) donated semen for this project: Anderlea (LW); Belmont (LW & LR); Caminda (LW, LR & DU); Gatton (LW & DU) and Yelmah (LW, LR and DU). In addition, Wandalup Farms (WA) donated semen from LW and LR sires, while Aztec Farms donated semen from LW synthetic sires, subsequently included in the LW *sire genotype group*. Concurrently, QAF provided semen from a stabilised synthetic Duroc line (DS) for evaluation.

Within *sire genotype group* (*SGG:* LW, LR, DU and DS), a minimum of 8-10 AI sires were used. For breeders participating in the NPIP, only those boars above the within breed average for the terminal sire index were included in this project, and boars were also chosen to reduce common parentage. For each *SGG*, ~36-65 matings (depending on the number of available sires) were made over a 6 week period. Matings for each *SGG* were made concurrently, with over-mating to maximise the probability of achieving the desired number of progeny for recording at slaughter. QAF sires were used to link data across weeks, since it was not possible to generate weekly matings for every sire.

2. Data collection for meat quality traits

All resulting project animals were identified to litter at birth (representing 52 sires and 157 dams) and earmarked accordingly. Weaned animals were reared in separate sex weaner eco-shelters until 10 weeks of age, followed by grow-out and finishing in contracted commercial eco-shelters at Temora until their slaughter at 22 weeks of age. Eco-shelters contained single-sex groups of 400 weaners, formed by mixing age-constant project and non-project weaners from the same source. Groups of project animals were subsequently slaughtered in weekly batches on six separate occasions (weeks 33 to 38), reflecting the flow of groups formed at mating and weaning. No sorting of project progeny occurred prior to their slaughter, although heavy non-project males and females were removed from eco-shelters approximately two weeks prior to slaughter.

Carcase weights and P2 were recorded on all project animals. However, a technical problem reduced the total number of P2 records recorded on-line. In addition, only a sub-sample of project animals were individually recorded for meat and eating quality traits. These progeny represented 40 sires (target: 16/sire), and were sampled from litters to balance sex within sire, where possible. The carcase and meat quality traits recorded were as follows:

1. Hot standard carcase weight (HSCW): head on.
2. Carcase fat depth (CP2): using the Hennessy-Chong probe at the P2 site
3. pH at ~24 hours post slaughter (pH24)
4. Colour (COL): L-value of the Minolta chromameter ~24 hours post-slaughter
5. Cooking loss (CL%): of two chops per pig ~ 48 hours post slaughter
6. Intra-muscular fat content using NIR analysis (IMF%): two replicates
7. Shear force (SF): Warner-Bratzler; three replicates per chop×two chops per pig
8. Fat % of the belly (BF%): from image analysis

The collection of belly data for analysis was not completed in time for inclusion in this document, while results for IMF are also preliminary since all data were not available. Only records for project animals slaughtered between 148-162 days of age were used for analyses.

3. Statistical analyses

For each trait, distributions were examined and data edited for outliers (of which there were few). Significant ($P<0.05$) systematic effects (main effects, their interactions, and covariates) were identified using SAS GLM Procedures (1988). For traits where *sire genotype group* was significant, least-square means (LSM) were computed. Predictions of average progeny performance for individual sires were obtained using ASREML (Gilmour et al., 1999) treating sire as a random effect, after removing *sire genotype group* from the analytical model.

Results and Discussion

Characteristics of the data after editing for outliers are presented in Table 2. Weekly averages for live weight ranged from 89 to 105*kg* (at 155 days), partially reflecting changes in disease challenge during this time. Live weight gain and slaughter weights were higher for females than males. Coefficients of variation were very low for pH and colour, but moderate for the remaining traits.

Table 2: Data characteristics after editing (N: number of records; SD: standard deviation; CV: coefficient of variation)

Trait*	N	Mean	SD	CV	Range
HSCW (*kg*)	1169	79.7	11.6	14.6	41-114
CP2 (*mm*)	909	11.8	2.86	24.2	4-22
pH (*pH units*)	686	5.58	0.14	2.51	5.22-6.18
COL (L* *units*)	687	46.6	3.09	6.63	37-60
IMF% (*%*)	559	2.55	0.78	30.6	0.65-5.75
CL% (*%*)	685	18.6	3.96	21.3	6.25-33.4
SF (kg)	687	4.10	1.00	24.4	1.43-7.32

***HSCW**: Hot carcase weight; **CP2**: carcase P2; **COL**: L-value of the Minolta chromameter; **IMF%**: intra-muscular fat percentage (average of two replicates); **CL%:** cooking loss percentage (average of two chops); **SF**: shear force (average of six cubes)

Significant systematic effects for each trait, including interaction terms, are presented in Table 3. Slaughter date, which encompassed rearing group, transport, slaughter and abattoir conditions common to animals slaughtered on that date, was very highly ($P<0.0001$) significant for all traits. Sow parity group was highly significant for final slaughter weight, with offspring from first parity litters often lighter at slaughter. However, sow parity had no influence on carcase composition (eg CP2) or meat quality traits. Sex significantly affected carcase weights and P2 measurements, along with pH, intra-muscular fat and cooking loss percentages. Generally, females had heavier carcase weights, higher CP2 and IMF%, along with lower pH and cooking loss than males. Significant differences also existed between *sire genotype groups* for all traits, excluding pH and COL (reported later).

Table 3: P-values for significant systematic effects (Sire genotype group in bold) along with the model R^2 (- without SGG; + with SGG in the model)

	Factors							Model R^2 (%)	
Trait*	**SPG**	**SD**	**SPG×SD**	**Sex**	**SPG×Sex**	**SD×Sex**	**SGG**	**-SGG**	**+SGG**
HSCW	.0009	.0001	.024	.0001	.003	ns	**.008**	18.3	19.1
CP2	ns	.0001	ns	.0001	ns	.0001	**.0001**	38.7	41.8
pH	ns	.0001	ns	.0005	ns	ns	**ns**	21.7	22.0
COL	ns	.0001	ns	ns	ns	ns	**ns**	11.8	12.2
IMF%	ns	.0001	ns	.0002	ns	ns	**.0022**	35.1	36.8
CL%	ns	.0001	ns	.0003	ns	.027	**.047**	18.9	19.9
SF	ns	.0001	ns	ns	ns	ns	**.0001**	4.8	8.2

* for trait abbreviations, see Table 2; **SPG**: sow parity group (3 levels: 1: parity 1; 2: parities 2-4; 3: parities 5-9); **SD**: slaughter date (6 levels); Sex (2 levels: M or F); **SGG**: sire genotype group (4 levels: DU, LW, LR, DS).

Linear covariates (not tabulated) included age at slaughter for HSCW; HSCW for carcase fat (CP2) and intra-muscular fat percentage (IMF%); CP2 for pH (P<.003), COL (P<.015) and SF (P<.015); and chop weight (P<.0001) for CL%, which contributed to the reported model R^2 values (Table 2). Increasing age at slaughter increased HSCW by approximately 1 kg/day. Higher carcase weights were associated with increased carcase P2 and intra-muscular fat levels, while higher CP2 was associated with darker meat, higher pH and higher shear force values. Larger chops had a lower percentage cooking loss.

Overall, identifiable systematic effects accounted for much of the observed variation in CP2 (R^2: 41.8%) and IMF% (R^2: 36.8%), and to a lesser extent variation in HSCW, pH and CL% (R^2: ~20%) (Table 1). However, relatively little of the observed variation (~10%) in COL or SF was associated with known factors. Further, the difference between *sire genotype groups* accounted for only 0.3% (pH) to 3.4% (SF) of observed variation, whereas differences between sires generally contributed significantly more towards improvements in the model R^2 (not shown). This indicates generally that variation within a *sire genotype group* is relatively large compared to the observed differences between groups. The exceptions were CL% and IMF%, where differences between sires within *sire genotype group* were only approaching significance.

Least square means for *sire genotype groups* (SGG) for carcase, meat and eating quality traits are shown in Table 4. Progeny of Duroc synthetic (DS) and purebred Duroc (DU) sires were significantly heavier than progeny from LW or LR sires at slaughter. Carcase P2, adjusted for hot carcase weight, differed significantly between each level of SGG, in diminishing order: DU>LR>LW>DS. In contrast, pH and colour did not differ significantly between *sire genotype groups*. However, progeny of purebred DU sires had significantly higher intra-muscular fat and meat that was more tender than progeny sired by the other terminal *sire genotype groups*. Meat from progeny sired by LR or LW sires was less tender than that from progeny of DS sires. Cooking loss was lowest for LR, highest for LW, and intermediate for DU and DS sired offspring.

Table 4: LSM for Duroc (DU), Landrace (LR), Large White (LW) and Duroc synthetic (DS) sire genotype groups, for traits where this effect was significant (P<0.05).

Trait*	**DU**	**LR**	**LW**	**DS**
HSCW (kg)	79.2^{ab}	78.4^{a}	78.5^{a}	81.0^{b}
CP2 (mm)	12.6^{a}	12.1^{b}	11.5^{c}	11.1^{d}
IMF% (%)	2.82^{a}	2.59^{b}	2.60^{b}	2.51^{b}
CL% (%)	18.8^{a}	18.1^{ab}	19.1^{ac}	18.8^{ac}
SF (kg)	3.72^{a}	4.13^{bc}	4.28^{bc}	4.03^{b}

*abbreviations were described with Table 2.

Differences between predicted progeny values of sires for each trait are illustrated using box-plots by breed in Figure 1. Each 'box' contains the middle 50% (2 quartiles) of sires with a horizontal line representing the median value, while each whisker extends to include sires ≤1.5 times the inter-quartile distance from the box. Outliers for that breed group are then illustrated with a dot point outside the whiskers. For reference, the number of sires represented in each box-plot by breed and trait is shown in Table 5.

Table 5: The number of sires with progeny recorded by sire genotype group.

Trait(s)	*DU*	LR	LW	DS
HSCW	9	16	17	10
CP2	8	15	16	10
PH, COL, IMF%, CL%, & SF	8	11	13	9

Generally, the box-plots show that there was considerable overlap between sires from different *sire genotype groups*. In most cases, the best sire from the worst *sire genotype group* for any particular trait was competitive against at least some sires from the best group. However, differences in variability of sires within groups were apparent. For example, while there were similar numbers of sires represented in the LW and LR *sire genotype groups*, variability amongst LR sires for HSCW and CP2 was greater. This may reflect more diversity of breeding goals amongst breeders supplying LR sires to the project, and/or the sample of sires used in this study. In contrast, relative to all other *sire genotype groups*, the LR sires tended to display less variation in colour, pH and cooking loss, but similar variation to other groups in shear force value. DU sires showed considerable variation in cooking loss, contributing to their lack of a significant difference from results for other *sire genotype groups* for this trait (Table 4).

Results from other studies

The 1995 NGEP study (see Table 1 for sample data) compared progeny from 3261 slaughter pigs representing nine sire lines: Berkshire; Duroc; Spotted; Yorkshire; Hampshire; and four company lines: Danbred HD; NGT Large White; Nebraska SPF Duroc and Newsham Hybrid. Similar to results presented here, progeny from Duroc based sire lines had the best growth performance but less acceptable carcase fat compared to company lines (eg Danbred HD and Newsham Hybrid), although the latter could also have contained Duroc ancestry. Only Hampshire sired progeny differed significantly from other sire lines in meat colour (Minolta L), consistent with the lack of a significant difference evident from this study. Similarly, Duroc and Nebraska SPF Duroc, NGT Large White, and Yorkshire did not significantly differ in ultimate pH, as was the case here for pH measured at 24 hours. Significant differences were more evident between sire lines for intramuscular fat, cooking loss and tenderness. Duroc based sire lines had higher intra-muscular fat, combined with reduced cooking loss and significantly better tenderness than LW or Yorkshire pigs in the NGEP. Thus, results from the NGEP study are very similar to that observed here, despite the fact that NGEP pigs were substantially heavier (~115*kg*) and fatter (>25*mm*) at slaughter. Landrace sire lines were not included in the NGEP study (National Hog Farmer, 1995).

The Stotfold trial report (MLC, 1989) compared production and meat quality characteristics of Meat Type and White sires using progeny from 347 litters representing four breeding companies: Cotswold; Masterbreeders; NPDC and PIC. Meat type (MT) sires were described as containing infusions of "muscular European and North American breeds" while White (W) sires included both Large White or Landrace sires. Each company provided boars representing both sire types along with their own hybrid gilts, making this trial more closely represent a product comparison trial. In the Stotfold trial, the relative performance of the two sire groups differed according to company. Further, differences between companies were larger than

differences between the two sire types for most of the traits measured. This probably reflects the contribution from each company's females to the commercial end products, along with company differences in breeding goals and the sample of sires used, which is a useful point to keep in mind when interpreting results from this study. That is, in our study DU, LW and LR *sire genotype groups* represent several breeding companies with potentially diverse breeding goals.

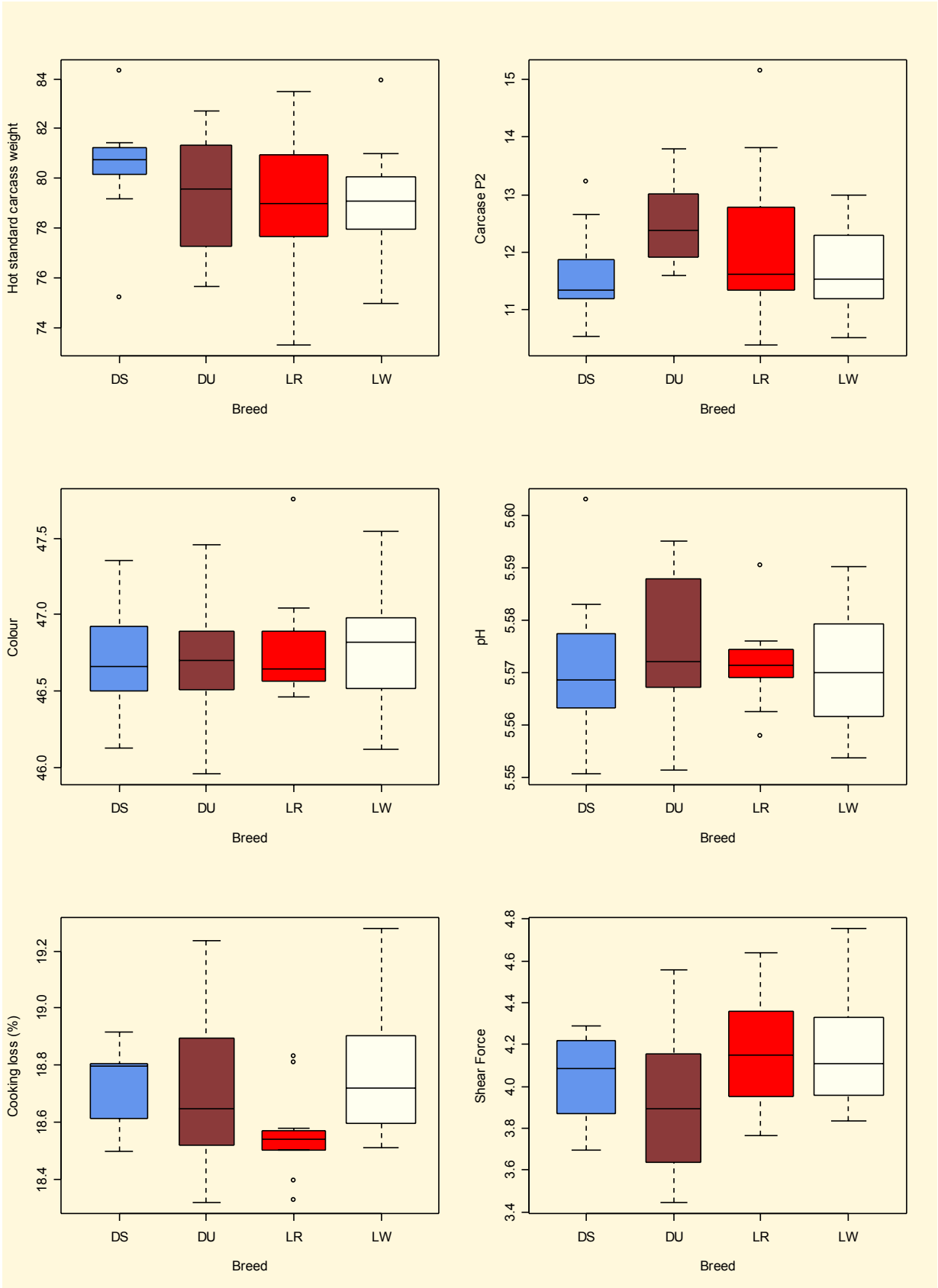

Figure 1. Boxplot illustrating variation between sires by sire genotype groups: horizontal lines indicate the median value; each box contains 50% of sires; whiskers extend to a maximum of 1.5×interquartile region; outliers indicated by a point.

Overall, the Stotfold trial (MLC, 1989) demonstrated that the cost of producing a *kg* of lean was higher for White vs Meat type sires, more so in the worst compared to the best company. Progeny sired by Meat type sires tended to have slightly higher drip loss than the White type sired progeny, but this was not consistent across companies. Intra-muscular fat levels did not differ between sire types. A trained taste panel indicated meat from progeny of Meat type sires was more tender, but there were no significant differences in juiciness, flavour or odour. Further, consumer panels did not detect a significant difference between progeny of White and Meat type sires for any eating quality traits.

In a later trial at Stotfold, 721 slaughter pigs were used to evaluate the influence of growth rate, sex, and the proportion of Duroc genes on pork eating quality (Blanchard et al., 1999a,b,c). In their study, rapid growth prior to slaughter was favourably associated with many sensory characteristics of pork, but relationships were generally weak (Blanchard et al., 1999a). Correspondingly, faster growing boars produced more tender loin chops according to sensory panel testing. However, there was no significant sex difference in overall acceptability (Blanchard et al., 1999b), suggesting other factors were also important. In our study, meat from the faster growing females was no more tender than meat from their male contemporaries, although they did have higher IMF% and reduced cooking loss percentages. The study of Blanchard et al. (1999c) also demonstrated that progeny of purebred Duroc sires had higher intra-muscular fat levels and improved eating quality, but carcases were fatter, similar to the results found here. Slaughter, progeny with a proportion of only 0.25 Duroc genes had IMF levels, marbling scores and subcutaneous fat levels more similar to progeny of LW (0% Duroc) than DU (50% Duroc) boars, implying that a 50% Duroc inclusion is required to obtain demonstrable differences between Duroc infused genotypes in meat and eating quality traits. However, it is also possible that this result simply reflected differences amongst the female breeding stock purchased for the study.

D'Souza and Mullen (2003) reported on eating quality characteristics of 60 male pigs (entire, surgically or immuno-castrated) representing two genotypes (A: lean vs B: fat), whereby genotype A had a higher percentage of Duroc ancestry. Progeny of genotype A sires were leaner at slaughter but had higher IMF%. Genotype A animals also had significantly lower ultimate pH values and higher drip loss than Genotype B animals, along with some changes in meat colour (a* and b* values) but not meat lightness (L* value). However, since slaughter weight was fixed and average daily gain was lower in genotype A pigs, these pigs were also older at slaughter (D'Souza, pers. comm., 2004). Their study also showed that leaner carcases of entire males were accompanied by drier and tougher pork, with lower acceptability to a consumer taste panel. This observation is supported in our study by the lower IMF% and higher cooking losses for males. Overall acceptability of meat to consumers in the study of D'Souza and Mullen (2003) was influenced by a combination of genotype and castration method. For entire males and surgical castrates, overall acceptability of meat from genotype A was higher.

Litten et al. (2004) reported differences in growth performance (N=200 test pigs) and eating quality (N=80) as assessed by a trained taste panel for pigs from different maternal and/or paternal lines (Cotswold Pig Development Company). Significant subjective eating quality differences were not supported by significant differences in objective IMF% or pH. However, tenderness was not recorded and the number of slaughter pigs evaluated for meat quality traits was low.

None of the above studies illustrated variability between sires in the performance of their progeny for meat and eating quality traits.

Conclusions

This project has shown significant differences between *sire genotype groups* for production and some meat and eating quality traits. Progeny of purebred Duroc sires had higher IMF% and more tender meat, but more variable levels of cooking loss and less favourable carcase composition (CP2), than progeny representing sires from the alternative *sire genotype groups*. Favourable meat quality characteristics were not as evident in the progeny of Duroc synthetic line sires, although production characteristics differed. While meat pH and colour did not significantly differ between *sire genotype groups*, variation between average progeny performance for individual sires was evident. Such results are generally consistent with those reported for comparable genotypes studied elsewhere.

Comparisons between sires demonstrated that there was considerable overlap between sires for production and meat or eating quality traits from different *sire genotype groups*. Thus, while differences between *sire genotype groups* do exist, it is also possible to identify sires with desirable meat quality characteristics within groups which exhibit less favourable meat quality characteristics overall. In practice this would require routine performance testing for meat and eating quality traits to identify superior individuals within breed for these traits. Further, selection for meat quality characteristics (for which no direct payments are currently received) ultimately must be balanced with selection for production traits, which currently dominate returns to pig producers. Differences in production performance both within and between breeds were also evident from this study.

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