

## BREED AND SIRE EFFECTS ON FATTY ACID COMPOSITION OF BEEF FAT

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### SUMMARY

The fat content of muscle and the fatty acid profile and melting point of subcutaneous fat was examined in the progeny of three years of crossbreeding Angus, Belgian Blue, Hereford, Jersey, Limousin, South Devon and Wagyu sires with Hereford cows. Significant cohort and sire breed effects were recorded for most traits. Heritability was moderate in most cases. As expected, significant breed differences were noted in the fat content of muscle, but also apparent was the difference in the degree of unsaturation in Jersey and Wagyu progeny. Angus, Hereford, Belgian Blue, South Devon and Limousin animals varied in some fatty acid measures. Jersey and Wagyu had fat with lower melting point (a function of fatty acid composition) and South Devon and Limousin had higher melting point than the remaining breeds.

**Keywords:** Fat, fatty acids, unsaturation, melting point

### INTRODUCTION

The amount of fat deposited in beef muscle and the fatty acid composition of that fat are known to affect the organoleptic qualities and value of meat. The early maturing breeds deposit fat earlier in life and at maturity contain more fat throughout the body (including the edible muscles) than the late maturing breeds. Intramuscular fat values (recorded as marbling) from the germ plasm evaluation program at Clay Center, Nebraska (Cundiff *et al.* 1994) are clearly higher in British breeds than in western European and *Bos indicus* breeds. To some extent fatty acid composition of deposited fat is related to breed partly because of stage of maturity (Leat 1977; Siebert *et al.* 1996; Malau-Aduli *et al.* 1997). Melting point of fat is a function of the fatty acid composition. Lowering melting point could 1) enable boning rooms to be maintained at lower temperatures, which is desirable for meat safety, and 2) affect the eating quality through its effect on flavour.

### MATERIALS AND METHODS

The animals used comprised the first 749 animals slaughtered as part of the "Southern Crossbreeding Project". Progeny from the crossing of Angus, Belgian Blue, Hereford, Jersey, Limousin, South Devon and Wagyu sires with Hereford dams born in 1994, 1995 and 1996 (heifers only) were weaned at 250-300 days. Heifers were raised on pasture for 400-500 days then in the feedlot for 70-90 days. Steers were at pasture for 500-600 days then in the feedlot for 180 days. At the end of this time, they were all slaughtered in a commercial abattoir when carcass measurements and tissue sampling were carried out. Animals were slaughtered generally within a few days and day of slaughter was shown not to be significant. Muscle samples were taken from the 12-13th rib interface and subcutaneous fat from an adjacent area. The muscle was used to obtain intramuscular fat (IMF)

content and the subcutaneous fat sample for both the melting point and fatty acid composition. Chemical analysis procedures were similar to those outlined by Malau-Aduli *et al* (1997). The data were analysed using the MIXED Procedure (SAS, 1996). Animals were arranged into four birth groups, depending on when they were born (early, mid 1, mid 2 and late) within the 7 week calving season. Day of birth was also fitted as a linear covariate within these four groups. Cohort groups were formed based on birth year (1994-1996), sex (heifer or steer), birth location (Struan or Wandilo) and post weaning group (generally 3). In this subset of 749 animals there were 24 combinations of cohort. Sire was fitted as a random effect nested within breed and breed differences were tested against the sire mean square. Significance is defined as  $P < 0.05$ . A total of 75 sires were considered. On average there were 6 heifer and 6 steer progeny per sire. The 749 animals comprised 3 heifer drops (94-96) and 2 steer drops (94-95). No IMF data were obtained for for the 1994 drop steers (162 animals).

## RESULTS AND DISCUSSION

Tests of significance used to analyse fat and fatty acid data for cohort groups and sire breeds together with heritability and phenotypic variance are shown in Table 1. Cohort differences were significant for all traits and accounted for a similar amount of variation as breed. Differences between birth groups and day of birth covariate were not significant for any of the traits analysed and are not presented. Heritability estimates from the between sires variance were considered moderate for the fatty acids (C16:0, C16:1(9c), C18:0, C18:1(9c), cis MUFA (total mono- unsaturated fatty acids)) and melting point, but low for IMF. The low value for IMF was probably the result of less data being available for this measurement.

**Table 1. Tests of significance for factors fitted for least squares analysis and heritability and phenotypic variance of various fat and fatty acid traits**

Trait	Cohort	Sire breed	Sire (within breed)	Phenotypic variance	Heritability
Intramuscular fat	**	**	ns	1.9	7
C16:0	**	ns	**	4.9	29
C16:1(9c)	**	**	*	1.0	19
C18:0	**	**	**	4.6	27
C18:1(9c)	ns	ns	*	10.2	21
cis MUFA	**	**	**	11.7	27
Melting point of fat	**	**	**	8.2	27

ns, not significant; \*  $P < 0.05$ ; \*\*  $P < 0.01$

The mean values of measurements made on tissues removed at slaughter from animals of the various sire breeds (straight bred Herefords and six Hereford crossbreeds) are shown in Table 2. Intramuscular fat for the early maturing Jersey, Wagyu and Angus were significantly ( $P < 0.05$ ) greater (4.7-4.8 %) than those of the later maturing crosses (3.2-4.2 %). Fatty acid composition

showed some differences in the degree of unsaturation. In the case of C16:1, Jersey animals showed significantly highest values whereas with C18:1, it was the Wagyu animals that had the highest although breed was generally not significant. When these values were summed (cis MUFA) with other minor components, it was these two breeds (Jersey and Wagyu) that had significantly greater values than other breeds.

Indices of desaturation can be calculated from these data and are similar to those that can be derived for other Australian cattle but considerably lower than those of Japanese cattle (Yang *et al.* 1999). Nevertheless, within the Australian environment it is clear that genetic differences exist and that the Jersey and Wagyu breeds possess the ability to desaturate the saturated fatty acids to a greater degree than the other breeds studied. It is not clear what the environmental effects are that limit desaturation in Australian cattle.

**Table 2. Least squares means of the effect of breed on the intramuscular fat content (% w/w) and the fatty acid concentration (% of total) and melting point (°C) of subcutaneous fat**

Sire breed	Measurement					
	IMF	C16:1(9c)	C18:0	C18:1(9c)	cis MUFA <sup>^</sup>	Melt. pt
Jersey	4.8±0.4 <sup>a</sup>	5.8±0.2 <sup>b</sup>	12.2±0.4 <sup>a</sup>	41.1±0.6 <sup>a</sup>	50.8±0.6 <sup>a</sup>	36.3±0.5 <sup>b</sup>
Angus	4.7±0.4 <sup>a</sup>	4.5±0.2 <sup>a</sup>	13.3±0.4 <sup>b</sup>	41.2±0.6 <sup>ab</sup>	49.5±0.7 <sup>b</sup>	38.8±0.6 <sup>a</sup>
Wagyu	4.7±0.4 <sup>a</sup>	4.9±0.2 <sup>a</sup>	12.6±0.4 <sup>ab</sup>	42.2±0.6 <sup>b</sup>	50.9±0.6 <sup>a</sup>	36.6±0.5 <sup>b</sup>
Hereford	4.2±0.4 <sup>b</sup>	4.5±0.2 <sup>a</sup>	14.2±0.4 <sup>c</sup>	40.5±0.6 <sup>a</sup>	49.6±0.7 <sup>b</sup>	39.1±0.6 <sup>a</sup>
South Devon	3.9±0.4 <sup>b</sup>	4.6±0.2 <sup>a</sup>	4.0±0.4 <sup>c</sup>	40.6±0.6 <sup>a</sup>	48.8±0.7 <sup>b</sup>	39.7±0.6 <sup>a</sup>
Limousin	3.2±0.4 <sup>c</sup>	4.8±0.2 <sup>a</sup>	13.6±0.4 <sup>c</sup>	40.8±0.6 <sup>a</sup>	49.1±0.6 <sup>b</sup>	40.0±0.5 <sup>a</sup>
Belgian Blue	3.2±0.4 <sup>c</sup>	4.9±0.2 <sup>a</sup>	13.3±0.4 <sup>b</sup>	40.8±0.6 <sup>a</sup>	49.3±0.6 <sup>b</sup>	38.5±0.5 <sup>a</sup>

a/b/c -Values with different superscripts are significantly different at  $P \leq 0.05$

<sup>^</sup> Sum of cis-mono unsaturated fatty acids

Desaturation takes place under the action of the enzyme  $\Delta 9$ -desaturase present in cattle in adipose tissue. The level of the saturated C16 fatty acid (palmitic) was consistent across the breeds (means 28.4-28.9 %). After desaturation to the C16:1 form, there can be elongation to C18:1(c11), but values for this fatty acid (not shown) were not significantly different between breeds. The enzyme is more active at the C18 level and although values of the product (C18:1(9c)) were not significantly different, those of the substrate (C18:0) were. This indicated that as desaturation took place, levels of this saturated fatty acid in Jersey and Wagyu fell to below those of the other breeds.

The mono-unsaturated fatty acids shown here are the cis form which have melting points much lower than the saturated fatty acids (1-16°C versus 60-70°C). Trans forms of C16:1 and C18:1 are present to a small degree in deposited fat. Because of their structure they have physical characteristics similar to the saturated fatty acids and the melting point of the C18:1 trans fatty acids is near 45°C. These acids are from the animal's rumen bacteria. They do influence the physical and chemical nature of the animal's fat. Despite this small extraneous influence, the melting point of fat is a function of the various fatty acids that compose the fat and to a large extent is a useful index of genetic differences between animals.

From the data presented here, it is clear that three groups of breeds could be identified from this parameter. The Jersey and Wagyu crossbred animals had the lowest melting points, significantly lower than an intermediate group (Angus, Belgian Blue and Hereford breeds) which were lower than South Devon and Limousin.

The above data collected from the progeny of three years of breeding demonstrates that the trait of desaturation of saturated fat is heritable. It is greatest in Jersey and Wagyu cross animals. The level of unsaturation in Australian cattle is not as high as in Asian cattle or in some instances in cattle from Britain and the United states. It may well be that differences between breeds in this trait would be expressed to a greater or lesser extent if they were raised in an environment that permits higher levels of unsaturation. In addition to differences between breeds, this study also indicates that there is opportunity for genetic change within breeds.

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