GENETIC VARIATION BETWEEN CROSSBRED WEANER CALVES IN TRIACYLGLYCEROL FATTY ACID COMPOSITION

B.D. Siebert, A.E.O. Malau-Aduli, M.P.B. Deland' C.D.K. Bottema and W.S. Pitchford

University of Adelaide, Dept. Anim. Sci., Waite Campus, Glen Osmond, S.A. 5064, Australia
[1] Primary Industries SA, Struan Research Centre Naracoorte, S. A. 5271, Australia

SUMMARY

This study compared the fatty acid composition of subcutaneous biopsies of 324 weaner progeny by Angus, Belgian Blue, Hereford, South Devon, Wagyu, Jersey and Limousin sires mated to Hereford dams. The aim was to investigate sire genotype and sex differences in triacylglycerol fatty acids in a grass-fed management system. Results indicated that sire genotype and sex were significant sources of variation in individual fatty acids and summations of their proportions, while the effects of sire genotype by sex interaction and sire nested within sire genotype were not significant. Limousin crosses had the highest proportion of 18:0 and total saturated fatty acids, but the lowest proportion of 16: 1 and total monounsaturated fatty acids. Jersey crosses had the highest percentage of 16: 1 while Wagyu crosses had the highest proportions of 18: ln-9 and total monounsaturated fatty acids. Total polyunsaturated fatty acids did not differ between genotypes. Heifers contained higher 16: 1, 18: ln-9 and total monounsaturated fatty acids but lower proportions of 18:0 and total saturated fatty acids than steers.

Keywords: Genetic variation, fatty acids, triacylglycerols, adipose tissue, crossbred calves.

INTRODUCTION

Research has shown that while it is possible to change fatty acid composition in monogastrics by altering their diets, the attempt in ruminants has been disappointing due to rumen degradation (St. John *et* al. 1987). This has aroused an alternative interest in selectively breeding cattle to increase monounsaturated at the expense of saturated fatty acids since genetic improvement is permanent, cummulative and usually, highly cost-effective (Simm and Murphy, 1996). Genetic improvement demands that breed differences be established between the genotypes being selected and an estimation of the trait's heritability determined. Siebert *et* al. (1996) have reported breed differences in fatty acid composition between early and late maturing cattle genotypes. However, the cattle were all raised in the feedlot. There is a need to investigate genetic variation in triacylglycerol fatty acid composition between young grassfed cattle and this paper aims to meet this need.

MATERIALS AND METHODS

Animals and management. Adipose tissues were biopsied from 324 weaner progeny of 26 sires (Angus 3, Belgian Blue 4, Hereford 3, Jersey 4, Limousin 4, South Devon 4 and Wagyu 4) crossed to Hereford dams. The animals were part of the Southern Crossbreeding Project raised on grass on two properties. The herd's location and management practices have been

described in detail (Rutley *et* al., 1995). Subcutaneous adipose tissues from the weaners were biopsied by a technique described in detail (Malau-Aduli *et al.,* 1995).

Laboratory procedures. Chloroform-methanol fat extraction procedure described by Siebert *et al.*(1996) was used. The resulting extract was methylated by an acid-catalysed procedure (Malau-Aduli *et al.* 1996). The fatty acid methyl esters (FAME) were analysed by gas-liquid chromatography. A detailed description of the gas chromatograph's calibration has been published (Malau-Aduli *et al.* 1997). Fatty acid retention times were calculated as normalised percentages.

Statistical analyses. Total saturated (SFA), monounsaturated (MUFA) and polyunsaturated (PUFA) fatty acids were summed to look at overall trends (Table 1). An index of Δ^9-desaturase enzyme activity was calculated to estimate the proportion of stearate (18:0) that was converted to oleate (18: ln-9) when a double bond is inserted by the desaturase enzyme at the 9^{th} carbon atom on the fatty acid chain. Least squares analysis of variance was carried out using PROC GLM (SAS 1989) and the model included the fixed effects of sex, location, genotype, sire nested within genotype and the interactions between them. All the interactions were later dropped from the model because they were not significant sources of variation. The effect of genotype was tested against sire nested within genotype, while all other effects were tested against the residual (error term).

RESULTS AND DISCUSSION

Sex differences. Weaner heifers significantly differed from steers in all fatty acids except 16:0 (palmitate) and PUFA (Table 1). Heifers had more 16: 1 (palmitoleate) and MUFA, but less 18:0 and SFA than steers. This observation agrees with those of Waldman *et al.* (1968) and Terre11 *et al.* (1969) on the influence of sex on bovine lipids. It is probable that this could be due to hormonal differences between heifers and steers. Prior *et al.* (1983) reported that the manipulation of hormone status of living cattle influenced lipid metabolism in the adipose tissue which in turn influences their enzymatic systems. Since heifers had more MUFA than steers, the Δ9-desaturase enzyme presumably has higher activity in female cattle as indicated by our calculated index (Table 1).

Table 1. Sex and genotype variation in triacylglycerol fatty acids (LSM± s.e.% total fatty acids)

	16:0	16:1	18:0	18:1n-9	SFA	MUFA	PUFA	Δ9-desat.
Sex								
Heifers (n=152)	30.0 ± 0.2	5.7 ± 0.1	12.5 ± 0.3	33.7 ± 0.3	49.7 ± 0.3	46.5 ± 0.3	3.8 ± 0.2	73.0 ± 0.4
Steers (n=172)	30.3 ± 0.2	5.4 fO.1	13.5 ± 0.2	32.5 ± 0.2	51.3 ± 0.3	44.9 ± 0.3	3.6 ± 0.1	70.8 ± 0.4
Significance	0.29ns	0.02*	0.01**	0.01**	0.01**	0.01**	0.28ns	0.01**
Genotype								
Angus (n=38)	30.6 ± 0.4	5.2 ± 0.2	13.3 ± 0.5	32.9 ± 0.5	51.5 ± 0.6	45.2 ± 0.6	3.3 ± 0.3	71.3 ± 0.8
Belgian Blue (n=56)	29.9 ± 0.4	5.9 ± 0.2	12.5 ± 0.4	33.4 ± 0.4	49.7 ± 0.5	46.4 ± 0.5	3.9 ± 0.3	72.9 ± 0.7
Hereford (n=39)	30.6 ± 0.4	5.4 ± 0.2	13.7 ± 0.5	32.5 ± 0.5	51.9 ± 0.6	44.3 ± 0.5	3.8 ± 0.3	70.4 ± 0.8
Jersey (n=50)	30.6 ± 0.4	6.5 ± 0.2	11.5 ± 0.4	33.2 ± 0.4	49.5 ± 0.5	46.6 ± 0.5	3.9 ± 0.3	74.3 ± 0.7
Limousin (n=48)	30.2 ± 0.4	4.9 ± 0.2	15.2 ± 0.4	32.4 ± 0.4	52.5 ± 0.5	43.7 ± 0.5	3.8 ± 0.3	68.6 ± 0.7
South Devon (n=38)	29.7 ± 0.5	5.4 ± 0.2	13.0 ± 0.5	32.2 ± 0.5	50.5 ± 0.6	45.6 ± 0.6	3.9 ± 0.3	71.4 ± 0.8
Wagyu (n=55)	29.2 ± 0.4	5.6 ± 0.2	11.9 ± 0.4	35.1 ± 0.4	48.3 ± 0.5	48.1 ± 0.5	3.6 ± 0.3	74.6 ± 0.7
Significance	0.07ns	0.01**	0.01**	0.01**	0.01**	0.01**	0.84ns	0.01**

*Only the major fatty acids shown, *P<0.05, **P<0.01, ns=not significant
SFA= 14:0+16:0+18:0, MUFA= 14:1+16:1+18:1n-9+18:1n-7
PUFA= 18:2n-6+18:3n-3+18:3n-6+18:4n-3
Δ9-desaturase(C 18) enzyme activity index=(18: 1 n-9)/(18:0+ 1-8: 1 n-9) x 100

Genotype differences. Least squares analysis of variance showed that there were significant differences between the genotypes in palmitoleate (16: 1), stearate (18:0), oleate (18: 1n-9), total saturated (SFA) and monounsaturated (MUFA) fatty acids (Table 1). Jersey x Hereford calves had the highest 16:1 content of 6.5% and Limousin x Hereford the least (4.9%). Since

the melting points of the MUFAs 16: 1(1°C) and 18: 1 n-9 (16°C) are low relative to SFAs (>62°C), the fat of Jersey x Hereford would be expected to be softer than the other breeds.

18:0 is the second most abundant saturated fatty acid after palmitate (16:0) in the adipose tissue accounting for 13-15% of the total fatty acids (Table 1). It is converted to 18: 1 n-9 through the introduction of a double bond by Δ9-desaturase enzyme. A calculated index of this enzyme showed that Wagyu and Limousin had the highest and lowest activities, respectively. Wagyu crosses had the most 18: ln-9 and South Devon crosses the least. Monounsaturated fatty acids are highly desirable in human diets because they lower cholesterol levels (Grundy *et* al. 1988). The MUFA levels in this study however, were not as high as those reported by Siebert *et* al. (1996) where the animals spent 300 days in the feedlot and thus were older and fatter. Limousin x Hereford had the most SFA (52.5%) and Wagyu x Hereford the least (48.3%), while MUFA was highest in the Wagyu x Hereford (48.1%) and least in the Limousin x Hereford (43.7%). Previous studies (Malau-Aduli *et al.* 1997) showed that the adipose tissue of Limousin raised on pasture was more saturated than that of Jersey.

In conclusion, this study has demonstrated that a wide variation exists in fatty acid composition between crossbred cattle genotypes, thus providing a useful tool for selective breeding. Wagyu crosses had higher monounsaturated fatty acids than all the other genotypes studied. The fact that nesting sire within genotypes did not produce significant variation might indicate that the heritability of these fatty acids at weaning is generally low.

REFERENCES

Grundy, S.M., Florentin, L., Nix, D. and Whelan, M.F. (1998). *American J.Clin.Nutr. 45:* 1185

Malau-Aduli, A.E.O., Siebert, B.D., Pitchford, W.S. and Bottema, C.D.K. (1995) *Proc. Australian Assoc. Anim. Breed. Genetics* **11: 554-557**

Malau-Aduli, A.E.O., Siebert, B.D., Bottema, C.D.K. and Pitchford, W.S. (1996) *Proc. Asian Australasian Assoc. Anim. Prod.* **2**:32-33

Malau-Aduli, A.E.O., Siebert, B.D., Bottema, C.D.K. and Pitchford, W.S. (1997) *Australian J. Agric. Res.* **48**:715-722

Prior, R.L., Smith, S.B., Schanbacher, R.D. and Mersmann, H.J. (1983). *Anim. Prod.* **37**:8 1

Rutley, D.L., Deland, M.P.B. and Pitchford, W.S. (1995) *Proc. Australian Assoc. Anim. Breed. Genetics* **11: 15** 1- 154

SAS (1989) SAS User's Guide: Statistics. Version 6, SAS Institute, Cary, NC

Siebert, B.D., Deland, M.P.B. and Pitchford, W.S. (1996) *Australian J. Agric. Res.* **47**:943-52

Simm, G. and Murphy, S.V. 1996. *Anim. Sci. 62: 255*

St. John, L.C., Young, C.R., Knabe, D.A., Thompson, L.D., Schelling, G.T., Grundy, S.M. and Smith, S.B. (1987) *J. Anim. Sci. 64: 1441*

Terrell, R.N., Suess, G.C. and Bray, R.W. (1969) *J. Anim. Sci.* **28**:449

Waldman, R.C., Suess, G.C. and Brungardt, V.H. (1968). *J. Anim. Sci.* **27**:632