SEX AND BREED DIFFERENCES IN THE FATTY ACID COMPOSITION OF MUSCLE PHOSPHOLIPIDS IN CROSSBRED CATTLE

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SUMMARY

Phospholipid data from the *Longissimus dors* (eye muscle) of 117 weaners across 7 cattle genotypes were analysed. The aim was to investigate sex and breed differences in fatty acid composition of muscle phospholipids in an entirely grass-fed management situation. Results showed that sex was a significant source of variation in the levels of 18: ln-9, total monounsaturated fatty acids (MUFA) and calculated Δ^9-desaturase enzyme activity index. Heifers had higher percentages in all cases than steers. All the other individual fatty acids and the summations of their proportions did not differ between the sexes. Significant breed differences were apparent in 18: ln-9, 18:3n-3, MUFA and Δ^9-desaturase enzyme index. Wagyu and Belgian Blue crosses had the highest proportion of 18: ln-9 and Hereford the lowest. Jersey crosses and Hereford breeds had the highest 18:3n-3 levels and Belgian Blue the lowest. Δ^9-desaturase enzyme index was highest in the Wagyu crosses. There were no other breed differences detected in all the other individual fatty acids and their summations. This study suggests that in weaners, the fatty acid composition of muscle lipids differs between breeds and sexes. The magnitude of the differences is, nevertheless, more reflected in the adipose tissue than in the muscle phospholipids. Also, Wagyu and Belgian Blue genotypes produced muscles with the most monounsaturated fatty acids.

Keywords Fatty acids, muscle, phospholipids, crossbred cattle, breed, sex.

INTRODUCTION

Crossbreeding as a tool for introducing new genetic material has long been recognised in beef cattle breeding. The Southern Crossbreeding Project at the Struan Research Centre was designed to cross Hereford dams with a variety of sire breeds to investigate the genetics of lipid metabolism and meat quality traits. Phospholipids are structural lipids found in cell membranes. They have been shown to play significant roles in reproductive and skeletal muscle tissues (Simopoulos, 1994). In trimmed lean meat, phospholipids are the fats that are consumed by humans (Siebert et *al.* 1996), and should not be confused with intramuscular fat. This paper reports sex and breed differences in the fatty acid composition of phospholipids in the *Longissimus dorsi* muscles of seven cattle genotypes.

MATERIALS AND METHODS

Animals and management. The animals comprised of 117 weaner progeny of 26 sires (Angus, Belgian Blue, Hereford, Jersey, Limousin, South Devon and Wagyu) crossed to

Hereford dams. They were all raised on grass on two properties at the Struan Research Centre. The herd's location and management practices have been described in detail (Rutley ***et*** *al.* 1995). *Longissimus dorsi* muscle tissues from the weaners were biopsied by a technique described in detail (Malau-Aduli et ***al.,*** 1995).

Laboratory procedures. Chloroform-methanol lipid extraction procedure described by Siebert et *al.* (1996) was used. Phospholipids were separated from triacylglycerols by thin layer chromatography. 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.*** 1997a). 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: 1 n-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 differed from steers in the percentages of 18: ln-9, total MUFA and Δ9-desaturase enzyme activity index (Table 1). Heifers had higher percentages than steers in all cases. This finding agrees with that of Siebert et *al.* (1998) who reported a similar observation in the adipose tissue of these same weaners. It has been reported that hormonal differences between the sexes influence lipid metabolism and enzymatic systems in living cattle (Prior et al. 1983). It is worth mentioning that sex differences in the fatty acids were more apparent in the adipose than in muscle tissues.

Sire breed differences. Phospholipids are structural lipids found in muscle cell membranes. They consist mainly of long-chained polyunsaturated fatty acids which can be up to 28% in grassfed, purebred Jersey and Limousin cattle (Malau-Aduli et *al.* 1997b). In crossbred weaner cattle, Table 1 shows that there were significant breed differences in phospholipid fatty acids 18: 1 n-9 (oleate), 18:3n-3 (alpha-linolenate) and total monounsaturated fatty acids (MUFA). Oleate is the most abundant of all the fatty acids in beef muscle tissue accounting for up to 25% of the total fatty acids. It is a product of the desaturation of stearate (18:0) when Δ9-desaturase enzyme introduces a double bond between the ninth and tenth carbon atoms in the fatty acid chain.

Table 1. Sex and sirebreed differences in phospholipid fatty acids (LSM± s.e.% total fatty acids) [A]

	18:1n-9	18:3n-3	SFA	MUFA	P U F A	Δ9-desat.
Sex						
Heifers (57)	24.2 ± 1.1	2.9 ± 0.4	41.4 ± 1.5	37.4 ± 1.1	21.2f1.5	61.2f1.5
Steers (60)	21.6 ± 1.1	2.8 ± 0.4	42.1 ± 1.4	34.6 ± 1.0	23.2f1.4	57.6f1.4
Significance	0.02*	0.77ns	0.92ns	0.05*	0.23ns	0.03*
Sirebreed						
Angus (16)	19.7 ± 1.9	3.2 ± 0.6	43.9 ± 2.4	32.2 ± 1.7	23.9± 2.5	55.3± 2.4
Belg.Blue (16)	25.5 ± 1.8	1.7 ± 0.6	41.9 ± 2.3	38.5 ± 1.7	19.6± 2.4	60.5± 2.3
Hereford (16)	19.2 ± 1.8	3.9 ± 0.6	42.4 ± 2.3	31.1 ± 1.6	26.5± 2.4	55.2± 2.3
Jersey (16)	23.9 ± 2.1	3.9 ± 0.7	38.0 ± 2.7	40.2 ± 1.9	21.8± 2.8	60.7± 2.7
Limousin (16)	21.8 ± 1.9	2.1 ± 0.7	46.8 ± 2.5	35.1 ± 1.8	18.1± 2.6	56.2± 2.5
Sth Devon(15)	24.9 ± 1.9	2.9 ± 0.7	39.7 ± 2.5	36.7 ± 1.8	24.6± 2.6	62.1± 2.5
Wagyu (22)	25.5 ± 1.8	2.3 ± 0.6	40.2 ± 2.3	38.2 ± 1.7	21.6± 2.4	65.8± 2.5
Significance	0.04*	0.05”	0.21ns	0.01**	0.24ns	0.02*

*Figures in brackets are number of animals. Only the major fatty acids shown
*P<0.05, **P<0.01, ns=not significant
SFA= 14:0+16dma+16:0+17:0+18dma+18:0+20:0+22:0+24:0
MUFA= 14:1+16:1+17:1+18:1n-9+18:1n-7+20:1+22:1+24:1
PUFA= 18:2n-6+18:3n-3+18:3n-6+18:4n-3+20:2+20:3+20:4+20:5+22:5+22:6
Δ9-desaturase(C 18) enzyme activity index=(18: 1 n-9)/(18:0+18: 1 n-9) x 100

Wagyu x Hereford and Belgian Blue x Hereford breeds had the highest proportion of 18: ln-9 (25.5%) while purebred Herefords had the lowest (19.2%). Wagyu x Hereford also portrayed the highest Δ9-desaturase enzyme activity index of 65.8% compared to that of 55.2% in Herefords (Table 1). St. John et *al.* (1991) suggested that an alternative approach to modifying the fatty acid profiles in cattle to favour more of the 18-carbon atoms could be through selective breeding. Our data demonstrates that the proportion of 18: ln-9 in the phospholipid fraction can be increased by about 6% and total MUFA by 7% through crossbreeding Hereford dams with Wagyu and Belgian Blue sires.

Alpha-linolenate (18:3n-3) also significantly varied between breeds (Table 1). It is a fatty acid that abounds in forages. It is also an essential fatty acid that needs to be provided in the diet

since it cannot be synthesised by the animals. Purebred Hereford and Jersey x Hereford weaners had the most 18:3n-3 (3.9%) and Belgian Blue x Hereford the least (1.7%). Given the dietary source of 18:3n-3, this difference might reflect a variation in feed consumption per unit weight or the efficiency of ruminal saturation of fatty acids (Doreau and Ferlay 1994).

In conclusion, this study has demonstrated that Wagyu, Belgian Blue and Jersey crosses had higher proportions of monounsaturated fatty acids than all the other genotypes studied.

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