

HERITABILITIES OF TRIACYLGLYCEROL FATTY ACIDS FROM THE ADIPOSE TISSUE OF BEEF CATTLE AT WEANING AND SLAUGHTER

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SUMMARY

A first attempt at estimating the heritabilities of total saturated (SFA), monounsaturated (MUFA) and polyunsaturated (PUFA) fatty acids from the triacylglycerol fraction of adipose tissues is presented. The data were from subcutaneous fat biopsies of 324 weaner steers and heifers across 7 genotypes and 26 sires. These animals all went into the feedlot postweaning, but the carcasses of 150 at slaughter were sampled for fatty acid analysis. Results showed that weaner SFA, MUFA and PUFA had heritability estimates of 15, 16 and 0% respectively. At slaughter, estimates of heritabilities were 23, 57 and 15% for SFA, MUFA and PUFA respectively. Since monounsaturated fatty acids are highly desirable given their cholesterol-lowering ability, this study suggests that selective breeding for MUFA has a good prospect of making genetic progress given the high h^2 of 57%. A larger data set would shed more light on the precision and accuracy of the estimates presented since these are based on a small data set.

Keywords Heritability, fatty acids, triacylglycerols, adipose tissue, beef cattle.

INTRODUCTION

Genetic improvement demands that breed differences be established between the genotypes being selected and an estimation of the trait's heritability determined. Several studies on breed differences in cattle for fatty acid composition have been published (Malau-Aduli *et al.* 1995, Siebert *et al.* 1996; Kruk *et al.* 1997; Malau-Aduli *et al.* 1997). However, to our knowledge, there is no single published work on heritability estimates of fatty acids. Since genetic parameters are population attributes that require large data sets and given the lengthy laboratory procedures involved in fatty acid analysis, such large data sets are hard to come by. The major objective of this study was to estimate the heritabilities of total saturated, monounsaturated and polyunsaturated fatty acids in beef cattle at weaning and slaughter.

MATERIALS AND METHODS

Animals and management. Adipose tissues were biopsied from 324 weaner progeny of 26 sires (Angus, Belgian Blue, Hereford, Jersey, Limousin, South Devon and Wagyu) crossed to Hereford dams at the Southern Crossbreeding Project. After weaning and 90 days in the feedlot, the animals were slaughtered and adipose tissue from their carcasses analysed for fatty acids. A distribution of the animals by genotype is shown in Table 1. The lot-fed animals were all raised together while the weaners were grass-fed on two properties at the Struan Research Centre. The herd's location and management practices have been described in detail (Rutley *et al.* 1995).

Biopsy technique. Subcutaneous adipose tissues from the weaners were biopsied by a technique already described in detail (Malau-Aduli *et al.*, 1997).

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. Heritabilities were computed from between and within sire variance components by restricted maximum likelihood (REML) procedures of PROC MIXED (SAS 1989). For the weaner data, a univariate model that included the fixed effects of sex, location and genotype, and sire nested within genotype as a random effect was used. A similar univariate model was also utilised for the slaughter data except that sex was not included since the animals were all heifers.

Average number of progeny per sire for the weaner data was 13 (range of 5-16). At slaughter, the average was 6 (range of 1-9). Standard errors on the heritability estimates were calculated using the average number of progeny per sire as described by Cameron (1997).

Table 1. Distributions of cattle sampled by genotype

Genotype	No. of sires	No. of progeny at:	
		Weaning	Slaughter
Angus x Hereford	3	38	17
Belgian Blue x Hereford	4	56	27
Hereford	3	39	13
Jersey x Hereford	4	50	28
Limousin x Hereford	4	48	24
South Devon x Hereford	4	38	14
Wagyu x Hereford	4	55	27

RESULTS AND DISCUSSION

Estimates of heritabilities are essential in quantifying the superiority of parents over their contemporaries for a trait which on the average, is passed unto their offspring. The rate of genetic progress, genetic correlations and development of selection indices all depend on the heritability (h^2) of the trait. Estimates of variance components and h^2 of total saturated

(SFA), monounsaturated (MUFA) and polyunsaturated (PUFA) fatty acids are shown in Table 2.

Table 2. Between sire (σ_s^2), within sire (σ_w^2), phenotypic (σ_P^2), additive (σ_A^2) variance components and h^2 estimates (%) of fatty acids at weaning and slaughter*

	Weaning			Slaughter		
	SFA	MUFA	PUPA	SFA	MUFA	PUFA
σ_s^2	0.47	0.49	0.00	0.87	1.70	0.20
σ_w^2	11.81	11.41	3.64	14.50	10.24	5.11
σ_P^2	12.28	11.90	3.64	15.37	11.94	5.31
σ_A^2	1.88	1.96	0.00	3.48	6.80	0.80
h^2	15.00	16.00	0.00	23.00	57.00	15.00
s.e. (%)	6.00	6.00	9.00	15.00	15.00	14.00

* $\sigma_P^2 = \sigma_s^2 + \sigma_w^2$, $\sigma_A^2 = 4\sigma_s^2$, $h^2 = \sigma_A^2 / \sigma_P^2$

The heritability of SFA in the adipose tissue was moderately low. At weaning, it was 15% and this rose to 23% at slaughter (Table 2). This increase from weaning to slaughter was not limited to saturated fatty acids, but also monounsaturated and polyunsaturated fatty acids. Monounsaturated fatty acids at weaning had a heritability of 16%, and at slaughter, it was 57%. While the increase in SFA heritability may not be significant due to the high standard error (15%) at slaughter, the same cannot be said of MUFA: 57% is significantly higher than 16%. This comparatively high heritability at slaughter suggests that the proportion of additive genetic variance is such that genetic progress has a good prospect if selective breeding for MUFA is practised. It has been shown (Malau-Aduli et al. 1997) that there is a substitution of saturated fatty acids with monounsaturated fatty acids as age increases in yearling cattle. Perhaps this age factor (maturity pattern) is responsible for the high heritability obtained at slaughter compared to weaners.

Polyunsaturated fatty acids are the least in terms of quantity, in the adipose tissue, accounting for less than 4% of the total fatty acids (Siebert et al. 1998). This is because being long-chained, they are associated with the muscle tissue where they abound as structural phospholipids. It is therefore not surprising that at weaning, their heritability was 0% (Table 2). At slaughter, it increased to 15%, which is still moderately low. This indicates that it would be pointless trying to selectively breed cattle for PUFAs in the adipose tissue.

In conclusion, this study has shown that generally, the heritability of fatty acids in the adipose tissue of cattle is low to moderately low. SFA and PUFA are the least heritable, while MUFA

are moderately heritable, especially at slaughter (57%). Since MUFA are highly desirable given their cholesterol-lowering function in humans, there seems to be a good prospect of making genetic progress by selectively breeding cattle for this trait. However, it should be clearly borne in mind that these estimates were based on a small data set. This is the first attempt to estimate the heritability of fatty acids. Although the population size was relatively small, the estimates hold the promise that selection may be the key to genetic improvement of MUFA in cattle. A larger data set would shed more light on the precision and accuracy* of the estimates. On-going work in our laboratory is geared towards meeting this goal.

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