Genetic and phenotypic correlations between triacylglycerol fatty acids at weaning and slaughter in beef cattle

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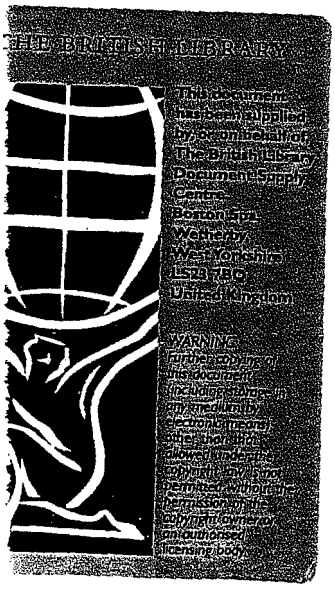
Predicting fatty acid composition of beef cattle at slaughter using weaner data would enable an early selection decision thereby saving time and costs associated with progeny testing. The aim of this study was to examine genetic and phenotypic correlations between triacylglycerol fatty acid composition at weaning and slaughter. Subcutaneous fat between the 12h and 13h rib interface was biopsied from 324 weaner calves sired by Angus, Belgian Blue, Hereford, Jersey, Limousin, South Devon and Wagyu. Fat from the same anatomical site was sampled from their carcasses at slaughter and analysed for fatty acids by gas-liquid chromatography. Statistical analysis was by Mixed Model and Maximum Likelihood Procedures of Harvey (1990) after adjusting for genotype, sire nested within genotype, sex and location. Results indicated strongly positive genetic correlations between biopsy and carcass stearate (18:0), oleate (18: ln-9), total monounsaturated fatty acids (MUFA) and $t.^{9}$-desaturase enzyme index of 0.84, 0.99, 0:93 and 0.82 respectively. However, biopsy and carcass palmitate (16:0) had a low genetic correlation of 0.15. Phenotypic correlations were relatively low and ranged from 0 to 0.67. The highly significant genetic correlations obtained suggest that selection decisions for fatty acid composition in the adipose tissue of cattle could be made at weaning.



Paper GC3.6

Mixture model approach to obtain unbiased estimates of QTL effects from a selectively genotyped outbred population

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A mixture model approach is employed for the mapping of quantitative trait loci (QTL) for the situation where individuals, in an outbred population, are selectively genotyped. Maximum likelihood estimation of model parameters is obtained from an Expectation-Maximization (EM) algorithm facilitated by Monte Carlo sampling using a Gibbs sampler. All individuals with phenotypes, whether genotyped or not, are included in the analysis where both putative QTLs and missing marker genotypes are sampled conditional on known marker information and phenotype. A simulation of a half-sib family structure demonstrates that this mixture model approach will yield unbiased estimates of the allelic effects of a QTL affecting the trait on which selective genotyping is based as well as for correlated traits. The procedure is also compared with a standard linear model approach. The applic tion of these methods is demonstrated for bovine chromosome *six,* the data arising from two Holstein-Friesian families selectively genotyped for prntein yield in a daughter design in New Zealand. The two families comprise 914 and 1018 daughters of which 34% and 29% were selectively genotyped. A QTL for protein yield was identified in one family near markers BM143 and.TGLA37.