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Fatty Acids in Meat

047 **Genetic association of delta-six fatty acid desaturase single nucleotide polymorphic molecular marker and muscle long chain omega-3 fatty acids in Australian lamb**

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For sustainable prime lamb production in the Australian sheep industry and a better understanding of the relationships between fat metabolism-related genes and sheep muscle long chain omega-3 polyunsaturated fatty acids, we investigated the genetic association between polyunsaturated fatty acids (PUFAs), delta-6 desaturase (FADS2) and fatty acid binding protein (FABP) gene clusters in crossbred sheep. Thirty-one single nucleotide polymorphisms (SNPs) were genotyped in *Longissimus dorsi* muscle samples from 362 crossbred prime lambs sired by five genetically divergent rams. Total intramuscular lipid long chain fatty acid levels were analysed using gas chromatography. Genetic association was tested for significance using mixed model analyses in SAS fitting genotype, sire breed and sex as fixed effects and sire as a random variable. FABP SNP was highly significantly associated ($P < 0.05$) with 18:4n-3 (stearidonic acid), while FADS2 SNP was significantly associated ($P < 0.05$) with intramuscular levels of eicosapentaenoic (C20:5n-3) and docosahexaenoic (C22:6n-3) acids. The results suggest that this SNP is in linkage disequilibrium with functional lipid synthesis pathway associated with higher delta-six desaturase activity. For the first time, this study provides evidence for an association between genetic variants of FADS2 and omega-3 PUFA in sheep muscle. This SNP could potentially be a novel marker of choice for prime lamb producers to effectively select for enhanced muscle omega-3 fatty acid content in their breeding flock.

048 **Effects of DGAT1, FABP4, FASN, PPARGC1A, SCD1, SREBP-1 and STAT5A gene polymorphisms on the fatty acid composition in Fleckvieh bulls**

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The objective of this study was to confirm the presence of previously reported allelic variants in diacylglycerol acyltransferase 1 (DGAT1; g.10433_10434delinsAA), fatty acid binding protein 4 (FABP4; c.220A>G), fatty acid synthase (FASN; g.16024G>A, g.17924A>G), peroxysome proliferator-activated receptor- γ coactivator-1 α (PPARGC1A; c.1790+514G>A, c.1892+19C>T), stearoyl-coenzyme A desaturase 1 (SCD1; c.878C>T), sterol regulatory element binding protein-1 (SREBP-1; 84-bp del), and signal transducer and activator of transcription 5A (STAT5A; g.9501G>A) in Fleckvieh cattle. In addition, we evaluated the single effects of these variants on the fatty acid (FA) composition of intramuscular and subcutaneous fat in a total of 602 bulls. Except for one (AA genotype for PPARGC1A, c.1790+514G>A), all the evaluated allelic variants were present in the analysed population but significant effects on FA composition ($P < 0.05$) were only determined for the SCD1 and both FASN polymorphisms. The SCD1 c.878C>T genotype was associated with concentrations of stearic, myristoleic and oleic acids. The FASN g.16024G>A and g.17924A>G genotypes did not explain the same part of FA variation and were mainly associated with concentrations of myristic, palmitic, myristoleic and oleic acids. It is concluded that the genetic variations in SCD1 and FASN genes contribute to the variability of FA composition in intramuscular and subcutaneous fat of Fleckvieh cattle.