

Concurrent Session 9: Animal Nutrition

Peri-renal and Subcutaneous adipose tissue gene expression in sheep

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Background – Many adipose tissue (AT) genes can regulate adipogenesis and lipolysis. Uncoupling protein (UCP2), common in white AT and involved in thermogenesis, peroxisome proliferator-activated receptor-gamma (PPAR γ), the master switch of adipogenesis, the feed regulatory gene leptin, and hormone sensitive (HSL) and lipoprotein (LPL) lipase which are involved in lipolysis, are some of these genes. It is important to evaluate AT gene expression in order to manipulate an animals lean to fat ratio, and target specific sites for obesity and diabetes research.

Objectives – To investigate the *in vivo* regulation of UCP2, PPAR γ leptin, HSL, and LPL mRNA expression in peri-renal (PR) and subcutaneous (SC) AT depots in sheep.

Design – 60 mixed sex lambs representing 5 breed combinations selected for their growth and muscling development potential were grown to 22 months of age. At slaughter, PR and SC AT samples were collected and carcasses were scanned by dual x-ray absorptiometry to determine carcass lean and fat content. Animals were ranked according to carcass fat % and both AT depots were analysed for adipogenic and lipolytic mRNA expression by reverse transcription polymerase chain reaction (RT-PCR).

Outcomes – UCP2, HSL and LPL expression was higher in PR than SC AT ($P \leq 0.005$) whereas leptin expression was higher in SC than PR AT ($P < 0.001$). PPAR γ expression was similar in both AT sites, with expression decreased as body fat % increased ($P = 0.002$).

Conclusion – These data suggest that mRNA expression differs between AT depots in sheep and PPAR γ expression decreases with increasing adiposity.