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Nutrigenomics: a high fat diet influences gut gene expression in a mouse model

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A high fat level in a diet can cause local gut inflammation and leads to metabolic abnormalities, such as obesity and insulin resistance. This study aimed to investigate the effect of a high fat diet in C57BL/6 mice. Twenty-seven mice were divided into five groups. The experiment started at weaning (T0). Five mice were sacrificed at T0 (n=5), while high-fat-fed mice (n=11) and control-fed mice (n=11) were sacrificed after one (T1, n=5 for each treatment) and two weeks (T2, n=6 for each treatment) of such dietary regimens. Even though neither blood nor histological analysis gave evidence of a clear inflammatory state in the caecum after 1 or 2 weeks of treatment, we used 90K Combimatrix microarray technology to check if the expression level of genes was changed. A total of 29,435 probes in triplicates were considered, representing all the available mouse genes in database. After hybridization and scanning, the Cy5 signal intensities were analyzed using limma package from Bioconductor. Only 7 genes were detected differentially expressed between control and high fat diet mice, out of the whole transcriptome (q-value ≤ 0.05), with a range of log fold change between -2.06 and 1.22. Among statistically significant genes 4 were successfully validated by real time PCR. In conclusion, genes differentially expressed after two weeks of treatment all shared an involvement in the regulatory pathway of the circadian clock system, which was recently shown to affect lipid metabolism and inflammatory processes.

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Effect of whole linseed addition on the expression of some lipid metabolism genes in the adipose tissue of Italian Simmental and Holstein young bulls

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The objective of this trial was to determine the effect of breed and whole linseed addition on the expression of some genes involved in the lipid metabolism in subcutaneous adipose tissue of young bulls. Thirty-two young bulls were assigned to four groups following a factorial design 2 breeds (Italian Simmental, IS and Italian Holstein, IH) x 2 diets (containing 8% of DM of ground whole linseed, WL and without linseed, CON). At slaughter the 8th rib sample joint was taken and dissected with the aim to predict the carcass composition and samples of subcutaneous adipose tissue (head tail) were collected, from which RNA was extracted. The mRNA abundances of stearoyl-CoA desaturase (SCD), fatty acid synthetase (FAS), lipoprotein lipase (LPL), leptin (LEP), PPAR γ (Peroxisome proliferator-activated receptors) were detected by real-time PCR. Changes in gene expression were calculated using the delta-delta Ct method. Two-way ANOVA was used to determine the effects of diets and breeds. In the LEP mRNA expression analysis, the estimated carcass fat was used as a covariate. Results showed that the inclusion of linseed, rich in C18:3 n-3, decreased the expression of SCD gene (P<0.05), LPL gene (P<0.05), and tended to decrease the expression of FAS gene (P=0.056) without affecting the LEP and PPAR γ mRNA abundance in the adipose tissue of bulls. No breed effect was found on the gene expression, also the interaction diet x breed was considered, but it never reached a level of significance (P>0.05). In our trial the linseed supplementation reduces the gene expression of key lipogenic enzymes in subcutaneous adipose tissue of young bulls by a mechanism that does not involve the PPAR γ regulation.

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Specie-specific probiotic supplement in veal calves diet: effects on zootechnical and microbial parameters in standard rearing conditions

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The aim of the study was to evaluate the effects of the administration of a specie-specific probiotic supplement to veal calves on performance and microbial parameters in standard rearing conditions (SRC). Ninety-six male Friesian veal calves (49.31 \pm 1.38kg) were divided in two homogeneous groups of 48 animals each from the arrival in the farm and fed either a basal diet (C) or a basal diet plus 1.8x10¹⁰ CFU/head/day of a probiotic supplement containing