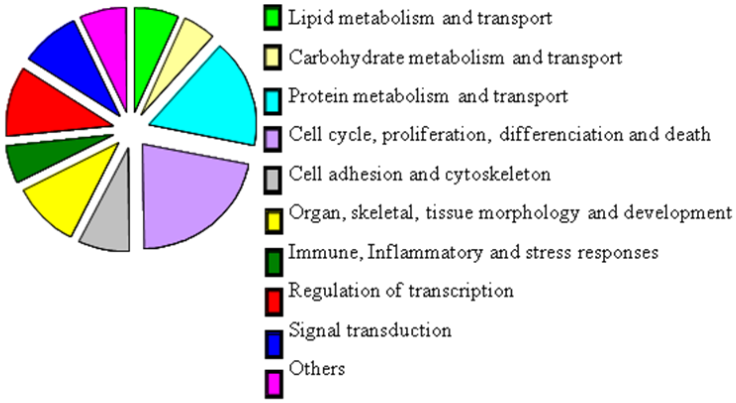
UR1213 Herbivores

Nutrition-Genomics-Lactation Team (AGL)

Adipose nutrigenomics in dairy animals



Distribution of differentially expressed genes in each of 10 biology process categories in omental and perirenal adipose tissues of 48h-feed deprived compared to control lactating goats.

The productivity of dairy females depends in part on the mobilisation of fat tissues when the animals undergo a negative energy balance (e.g. early lactation, feed restriction). When these animals are fasted, genes involved in lipid metabolism are under-expressed, while genes involved in inflammatory processes are over-expressed.

The productivity of dairy females depends in part on the mobilisation of AT during periods of negative energy balance (e.g. early lactation and feed restriction). Adipose tissue metabolism involves a large number of genes and the nutritional regulation of their expression is poorly documented in the ruminant. A transcriptomic study of AT was therefore performed in lactating goats under extreme nutritional conditions.

We examined the effect of food deprivation (48 h) on the expression of 8379 genes in caprine AT using a bovine oligonucleotide microarray. Feed deprivation altered the expression of 456 and 199 genes in omental and perirenal AT, respectively, with 97 genes identical in both sites. The differentially expressed genes were classified into 10 functional categories according to Gene Ontology annotation in both AT sites (Fig.1). Concerning lipid metabolism, we observed decreased expression of genes involved in fatty acid (e.g. ACACA) and triglyceride (e.g. GPAM) synthesis, desaturation (e.g. SCD), elongation and activation of fatty acids (e.g. ELOVL5, ACSL1, ACSS2) and lipid uptake (e.g. LPL) (Fig.2). By contrast, expression of several factors regulating transcription of these genes (e.g. SREBP1 & 2) was upregulated in omental tissue. This study also showed enhanced expression of genes involved in inflammation mechanisms (e.g. HIF1A, B2M, SPP1,…) in AT of feed-deprived animals.

This experiment is complementary to previous research at the mammary gland level. Follow-up studies will be performed in cattle and goats under different diets. Enzyme activities and blood composition will also be assessed. This research enhances our understanding of mechanisms regulating adipose function, and its role in ruminant adaptability to negative nutritional balance.

Partners: Plateforme d'Exploration du Métabolisme, Inra, Theix

References: Faulconnier Y, Chilliard Y, Torbati MB, Leroux C. 2011. Comp Biochem Physiol Part D Genomics Proteomics, 6, 139-49; Faulconnier Y., Domagalski J., Montazer Torbati M. B., Bany D., Chilliard Y., Leroux C., 2009. 3èmes Journées d'Animation Scientifique du Département Phase, Tours, p.145 ; Faulconnier Y., Domagalski J., Montazer Torbati M. B., Gaudron Y., Bany D., Chilliard Y., Leroux C., 2009. In Ruminant physiology. Digestion, metabolism, and effects of nutrition on reproduction and welfare. Proceedings XIth ISRP, Clermont-Ferrand, France. September 6-9 2009, p502-3.

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