

GlcPase was not inhibited under euglycemic hyperinsulinic conditions (group I), and was significantly inhibited under hyperglycemic conditions (G1 and G2). Our data strongly suggest that hyperglycemia, but not hyperinsulinemia, could account for the inhibition of liver Glc6Pase activity during the postprandial period. This phenomenon might play an important role in the suppression of HGP in this situation.

The expression of ob gene is not acutely regulated by insulin and fasting in human abdominal subcutaneous adipose tissue.

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In rodents, the expression of leptin, the product of ob gene, is increased by insulin and decreased by fasting [Saladin et al (1995), *Nature* 377, 527-529; Trayhurn et al (1995), *FEBS Lett* 368, 488-490; Frederich et al (1995), *J Clin Invest* 96, 1658-1663]. In the present work, we investigated the regulation of ob gene expression in human abdominal subcutaneous adipose tissue using a reverse transcription-competitive PCR method to quantify the mRNA level of leptin. Leptin mRNA level was highly correlated ($r = 0.9$) with the body mass index of 26 subjects (12 lean, seven non insulin-dependent diabetic and seven obese patients). The effect of fasting on ob gene expression was investigated in ten subjects maintained on a hypocaloric diet (250 Kcal/day) for 5 days. While their metabolic parameters significantly changed (decrease in insulinemia, glycemia and resting metabolic rate and increase in plasma ketone bodies), the caloric restriction did not modify significantly the leptin mRNA

level in the adipose tissue. To verify whether insulin acutely regulates ob gene expression, six lean subjects underwent a 3 h euglycemic hyperinsulinemic (846 ± 138 pmol/L) clamp. Leptin and Glut 4 mRNA levels were quantified in adipose tissue biopsies taken before and at the end of the clamp. Insulin infusion produced a significant 3-fold increase in Glut 4 mRNA while leptin mRNA was not affected. It is concluded that ob gene expression is not acutely regulated by insulin or by metabolic factors related to fasting in human abdominal subcutaneous adipose tissue. Our data question therefore the role of leptin as a tightly controlled satiety factor in human but rather suggest that leptin signals the size of the adipose tissue deposit.

Glucose inhibits expression of the cytosolic aspartate aminotransferase gene in 3T3-F442A adipocytes: involvement of the promoter-regulatory region.

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Aspartate aminotransferase (AspAT) is an ubiquitous enzyme involved in the malate-aspartate shuttle, urogenesis, gluconeogenesis and amino-acid metabolism. Two isoforms of the enzyme have been described: a cytosolic one (cAspAT) and a mitochondrial one (mAspAT). Although cAspAT is expressed at similar levels in all tissues, it is specifically regulated by glucocorticoids and glucagon in liver [Pavé-Preux et al (1988), *J Biol Chem* 263, 17459-17466] in which the enzyme is involved in gluconeogenesis. Regulation of cAspAT gene expression has been extensively studied in Fao hepatoma cells. In such cells, the rate of cAspAT gene transcription is increased by

glucocorticoids and cAMP and inhibited by insulin and phorbol esters [Aggerbeck et al (1993), *Biochemistry* 32, 9065-9072]. The role of cAspAT in the metabolism of adipocytes is not clear. Adipose tissue is not gluconeogenic and the urea cycle is not functional in this tissue. Like cytosolic phosphoenolpyruvate carboxykinase (PEPCK), cAspAT could be implicated in glyceroneogenesis in adipose tissue in situations of hypoglycemia (starvation, hyperproteic and hyperlipidic diets).

We used the 3T3-F442A cell line to study the regulation of cAspAT gene expression in cultured adipocytes. Cells were grown and differentiated as described previously [Plee-Gautier et al (1996), *Biochem J* 318, 1057-1063] cAspAT mRNA content was measured by Northern blot using a rat cDNA fragment. 3T3-F442A adipocytes maintained in serum-free medium responded to an 18 h glucose deprivation by a 4-fold increase in cAspAT mRNA, whereas mAspAT mRNA remained unchanged. cAspAT activity was also increased in a weaker (1.5-fold in 48 h) but reproducible manner. Glucose addition to 24 h glucose-deprived adipocytes produced an 80% reduction in cAspAT mRNA in 8 h. This effect occurred under a physiological range of glucose concentrations (EC50 = 1.25 g/L). In Fao or H4IIE hepatoma cells, C2 muscle cells and 293 kidney cell, no regulation of cAspAT mRNA could be detected, demonstrating that glucose effect was cell-specific. The glucose analogue 2-deoxyglucose mimicked, at least partially, the glucose effect, suggesting that glucose-6-phosphate or glucose itself is the effector. We co-transfected 3T3-F442A adipoblasts as previously described [Antras-Ferry et al (1994), *Biochem J* 302, 943-948], with the region of the cAspAT gene from -2405 to -26 base pairs relative to the translation initiation site, fused to the chloramphenicol acetyltransferase (CAT) gene and the construct containing the SV2 promoter of the SV40 genome fused to the NEO gene. The latter confers resistance to

the antibiotic neomycin (G418). Twelve individual G418-resistant clones were isolated and analysed for CAT expression and regulation by glucose. After differentiation, stable transfectants responded to a 24 h glucose deprivation by a mean of 3.5-fold increase in CAT activity. Hence, glucose action is, at least partially, transcriptional and a negative glucose response region is located between -2405 and -26 bp of the cAspAT gene.

Experiments aimed at elucidating the mechanism of glucose-induced inhibition of cAspAT gene expression are underway and should help clarifying the role that cAspAT plays in adipocytes and the physiological significance of its regulation by glucose.

Glutamine contribution to gluconeogenesis in healthy adults fasted for 13 h, and 37 h. R Hankard, MW Haymond, D Darmaun (*Nemours Children's Clinic, Jacksonville, FL, USA*).

Other authors have shown that upon infusion of ^{14}C glutamine (gln), ^{14}C appears in plasma glucose (glc) in post-absorptive humans. Labeled carbon arising from glutamine's carbon skeleton might appear into glucose either through glutamine entering Krebs cycle or through mere fixation of labeled CO_2 arising from glutamine oxidation. These two pathways were quantitated in eight healthy adults (5 M, 3 F, age: 29 ± 2 years, weight: 76 ± 4 kg, means \pm SD) using 4-h-intravenous infusion of L-[3,4- $^{13}\text{C}_2$]gln, D-[6,6- D_2]glc, et L-[1- ^{14}C]leucine after 13 h, and 37 h of fasting. Carbon transfer from glutamine to glucose through the non-specific CO_2 pathway was estimated from CO_2 pool labeling resulting from ^{14}C -leucine oxidation and measurement of glucose specific activity (SA) in plasma and SACO_2 . Total carbon flux from glutamine to glucose measured after glucose combustion using gas-chromatogra-