Identification of Adipocyte Genes Regulated by Caloric Intake
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Context: Changes in energy intake have marked and rapid effects on metabolic functions, and some of these effects may be due to changes in adipocyte gene expression that precede alterations in body weight.
Objective: The aim of the study was to identify adipocyte genes regulated by changes in caloric intake independent of alterations in body weight.
Research Design and Methods: Obese subjects given a very low-caloric diet followed by gradual reintroduction of ordinary food and healthy subjects subjected to overfeeding were investigated. Adipose tissue biopsies were taken at multiple time-points, and gene expression was measured by DNA microarray. Genes regulated in the obese subjects undergoing caloric restriction followed by refeeding were identified using two-way ANOVA corrected with Bonferroni. From these, genes regulated by caloric restriction and oppositely during the weight-stable refeeding phase were identified in the obese subjects. The genes that were also regulated, in the same direction as the refeeding phase, in the healthy subjects after overfeeding were defined as being regulated by caloric intake. Results were confirmed using real-time PCR or immunohistoassay.
Results: Using a significance level of $P < 0.05$ for all comparisons, 52 genes were down-regulated, and 50 were up-regulated by caloric restriction and regulated in the opposite direction by refeeding and overfeeding. Among these were genes involved in lipogenesis (ACYL, ACACA, FASN, SCD), control of protein synthesis (4EFP1, 4EFP2), β-oxidation (CPT1B), and insulin resistance (PEDF, SPARC).
Conclusions: Metabolic genes involved in lipogenesis, protein synthesis, and insulin resistance are central in the transcriptional response of adipocytes to changes in caloric intake.
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GH Response to Oral Glucose Tolerance Test: A Comparison between Patients with Acromegaly and Other Pituitary Disorders
Context: The cutoff value of nadir GH after an oral glucose tolerance test (OGTT) used to define disease remission in acromegaly is higher than that observed in healthy subjects. However, it is uncertain whether the impaired GH inhibition might be related to subtle abnormalities of GH secretion or to functional and/or anatomical hypothalamic-pituitary disconnection due to tumor per se or treatments.
Objective: The objective of the study was to evaluate the impact of pituitary disorders other than acromegaly on GH response to OGTT.

Design, Subjects, and Methods: Thirty-three patients (24 females and nine males, aged 50.1 ± 12.3 yr, 13 operated and two irradiated) with various hypothalamic-pituitary disorders (HPDs), 45 healthy subjects (controls), and 42 cured acromegalic patients matched for sex, age, and body mass index were investigated. All subjects were studied for IGF-I levels and GH levels before and during the OGTT.
Results: In HPD patients mean postglucose nadir GH levels were $0.11 ± 0.08 \mu g/liter$ without any difference between patients treated with neurosurgery and/or radiotherapy and untreated and between patients with and without pituitary stalk alterations and/or hyperprolactinemia. Mean nadir GH values were similar in HPD patients and controls ($0.11 ± 0.08$ vs. $0.08 ± 0.08 \mu g/liter, $P = 0.23$) and lower than those found in cured acromegalic patients ($0.18 ± 0.13 \mu g/liter, P = 0.02$), although there was an overlapping in about half of patients.
Conclusions: Hypothalamic control of glucose-mediated GH suppression is not perturbed in patients with HPD. These data indicate that defective GH suppression to glucose that is found in acromegaly is unlikely to reflect a lack of integrity of hypothalamic function.
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Altered Autophagy in Human Adipose Tissues in Obesity
Context: Autophagy is a housekeeping mechanism, involved in metabolic regulation and stress response, shown recently to regulate lipid droplets biogenesis/breakdown and adipose tissue phenotype.
Objective: We hypothesized that in human obesity autophagy may be altered in adipose tissue in a fat depot and distribution-dependent manner.
Setting and Patients: Paired omental (Om) and sc adipose tissue samples were used from obese and nonobese ($n = 65$, cohort 1); lean, sc-obese and intraabdominally obese ($n = 196$, cohort 2); severely obese persons without diabetes or obesity-associated morbidity, matched for being insulin sensitive or resistant ($n = 60$, cohort 3).
Results: Protein and mRNA levels of the autophagy genes Atg5, LC3A, and LC3B were increased in Om compared with sc, more pronounced among obese persons, particularly if with intraabdominal fat accumulation. Both adipocytes and stromal-vascular cells contribute to the expression of autophagy genes. The increased number of autophagosomes and elevated autophagic flux assessed in fat explants incubated with lysosomal inhibitors were observed in obesity, particularly in Om. The degree of visceral adiposity and adipocyte hypertrophy accounted for approximately 50% of the variance in Atg5 mRNA levels by multivariate regression analysis, whereas age, sex, measures of insulin sensitivity, inflammation, and adipose tissue stress were excluded from the model. Moreover, in cohort 3, the autophagy marker genes were increased in those who were insulin resistant compared with insulin sensitive, particularly in Om.