Dietary manipulation reveals an unexpected inverse relationship between fat mass and adipose 11β-hydroxysteroid dehydrogenase type 1

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Man TY, Michailidou Z, Gokcel A, Ramage L, Chapman KE, Kenyon CJ, Seckl JR, Morton NM. Dietary manipulation reveals an unexpected inverse relationship between fat mass and adipose 11β-hydroxysteroid dehydrogenase type 1. Am J Physiol Endocrinol Metab 300: E1076–E1084, 2011. First published March 15, 2011; doi:10.1152/ajpendo.00531.2010.—Increased dietary fat intake is associated with obesity, insulin resistance, and metabolic disease. In transgenic mice, adipose tissue-specific overexpression of the glucocorticoid-amplifying enzyme 11β-hydroxysteroid dehydrogenase type 1 (11β-HSD1) exacerbates high-fat (HF) diet-induced visceral obesity and diabetes, whereas 11β-HSD1 gene knockout ameliorates this, favoring accumulation of fat in nonvisceral depots. Paradoxically, in normal mice HF diet-induced obesity (DIO) is associated with marked downregulation of adipose tissue 11β-HSD1 levels. To identify the specific dietary fats that regulate adipose 11β-HSD1 and thereby impact upon metabolic disease, we either fed mice diets enriched (45% calories as fat) in saturated (stearate), monounsaturated (oleate), or polyunsaturated (safflower oil) fats ad libitum or we pair fed them (45% calories as fat) in saturated, monounsaturated (oleate), or polyunsaturated (safflower oil) fats ad libitum or we pair fed them a low-fat (11%) control diet for 4 wk. Adipose and liver mass and glucocorticoid receptor and 11β-HSD1 mRNA and activity levels were determined. Stearate caused weight loss and hypoinsulinemia, partly due to malabsorption, and this markedly increased plasma corticosterone levels and adipose 11β-HSD1 activity. Oleate induced pronounced weight gain and hyperinsulinemia in association with markedly low plasma corticosterone and adipose 11β-HSD1 activity. Weight gain and hyperinsulinemia was less pronounced with safflower compared with oleate despite comparable suppression of plasma corticosterone and adipose 11β-HSD1. However, with pair feeding, safflower caused a selective reduction in visceral fat mass and relative insulin sensitization without affecting plasma corticosterone or adipose 11β-HSD1. The dynamic depot-selective relationship between adipose 11β-HSD1 and fat mass strongly implicates a dominant physiological role for local tissue glucocorticoid reactivation in fat mobilization.

glucocorticoid; dietary fats

SPECIFIC DIETARY FATS affect insulin sensitivity and consequently have a major impact upon metabolic disease over and above their contribution to total calorie content (39, 49). Stearate, a long-chain saturated dietary fat (18:0), directly inhibits insulin signaling in muscle cells, whereas long-chain unsaturated fats (oleate 18:1) and shorter-chain saturated fats do not (8). Oleate enrichment can improve insulin sensitivity if overall fat content is low (49), whereas polyunsaturated fats improve insulin sensitivity (20).

High glucocorticoid levels (e.g., Cushing’s syndrome) cause insulin resistance and promote visceral fat accumulation, whereas adrenalectomy ameliorates obesity in rodents (18, 22). Substantial evidence links the disturbances of fatty acid and glucocorticoid metabolism in obesity. Fatty acids and high-fat diets can cause adrenal and pituitary activation in rodents (15, 42, 45, 53), suggesting that in the obese/diabetic state, a feed-forward effect of high-plasma free fatty acids and increased adrenal glucocorticoid production may exacerbate insulin resistance. Moreover, saturated fats and glucocorticoids may induce insulin resistance in tissues through a common ceramide-mediated mechanism (14).

Human idiopathic obesity is associated with high intraadipose glucocorticoid levels generated by the intracellular enzyme 11β-hydroxysteroid dehydrogenase type 1 (11β-HSD1) rather than high circulating glucocorticoids (31). Transgenic overexpression of 11β-HSD1 in mouse adipose tissue causes insulin-resistant diabetes, dyslipidemia, and hypertension (23, 24). 11β-HSD1-deficient mice resist high-fat diet-induced obesity (DIO) due to beneficial changes in fat distribution and insulin sensitivity of adipose tissue and liver (28, 29). Similar protective effects are found in mice overexpressing the glucocorticoid-inactivating enzyme 11β-HSD2 specifically in fat (16).

Since obesity in humans and monogenic rodent models is associated with high adipose 11β-HSD1 levels (31), it was unexpected that DIO caused a pronounced adipose-specific downregulation of 11β-HSD1 in rodents (11, 30). Furthermore, DIO-resistant mouse strains shut down adipose 11β-HSD1 expression to a greater extent than DIO-prone strains (27, 30), suggesting that this response might be an intrinsic mechanism invoked to counter insulin resistance.

Despite these findings, little is known about the impact of individual fatty acids upon tissue level glucocorticoid action and the cross-talk between these two key contributors to fat storage and insulin resistance. To address this, we selectively enriched dietary long-chain saturated, monounsaturated, and polyunsaturated fatty acids and investigated their effects on fat mass, adipose, and liver tissue 11β-HSD1 and glucocorticoid receptor (GR) levels in mice.

METHODS

Animals and diets. All experiments were approved by The University of Edinburgh ethics committee and were carried out according to the UK Animals (Scientific Procedures) Act of 1986. Age- and weight-matched C57BL/6J mice were housed in standard conditions on a 12:12-h light-dark cycle, lights on at 7 AM, and were randomly assigned to the diets. The experiment used singly housed adult age-matched (8 wk) male mice (n = 6) given one of
the following diets (Research Diets, New Brunswick, NJ): control diet (11% calories as fat with cornstarch; D12329), a stearate-enriched diet (stearate; 45% calories from ethyl stearate, 100%; D04070901), an oleate-enriched diet (oleate; 45% calories from high oleic acid, ~80% C18:1; D04070902), and a safflower oil-enriched diet (safflower; 45% calories as safflower oil, ~80% C18:2; D04070903). A positive control for the previously observed adipose 11β-HSD1 downregulation was used (58HF; 58% calories as fat, mainly hydrogenated coconut oil; 99.1% saturated with 7.7% C8, 5.9% C10, 47.6% C12, 18% C14, 8.7% C16, 10.6% C18, and traces of unsaturated fats at ~0.8% C18:1 and 0.03% C18:2; D12331). A further positive control that was matched to the singularly enriched diets was used in that 45% of the calories consisted of fat (45HF; 45% calories with hydrogenated coconut oil, with the same composition as the 58HF; D04070907). All diets contained the same amount of soybean oil (4% calories as fat; 14.2% saturated fat, 14.2% monounsaturated, C18:1 and 61.3% polyunsaturated with 53.5% 18:2, and 7.8% C18:3). For the pair-feeding experiment, the three singly enriched diets (stearate, oleate, and safflower) and a low-fat control diet that was enriched with sucrose (D12328) were used. Ad libitum consumption was monitored for 1 wk, and the low-fat control was found to be the limiting diet for calorie intake in this run-in period. Therefore, all other diets were provided as calorie-matched amounts with respect to measured food intake daily before lights out (7 PM) and the amount adjusted to the continuously monitored average daily intake for mice on the control diet throughout (starting intake: 0.23 ± 0.08 kcal·g body wt−1·day−1; final intake: 0.39 ± 0.08 kcal·g body wt−1·day−1). Note that calorie-matching diets by measured food intake of the limiting diet, although it is standard practice, cannot control for loss of calories through malabsorption. Results pertaining to this unexpected effect of the stearate diet are described in context in the RESULTS and DISCUSSION.

Tissue and plasma measurements. At the end of the experiment, mice were euthanized within 1 min of disturbing the home cage by cervical dislocation to avoid stress-induced changes in corticosterone. Blood was collected in EDTA-coated tubes (Sarstedt, Numbrecht, Germany). Plasma corticosterone was measured using an in-house RIA as described (28), insulin and leptin by ELISA (Crystal Chem, Downers Grove, IL), and glucose determined by automated (Bioxytech reagent, Sigma, Dorset, UK). Liver, kidney, and epididymal, subcutaneous (sc), and mesenteric adipose tissues were collected, weighed, and stored at −80°C.

Gene expression. RNA was extracted using 800 μl of TRIzol reagent (Invitrogen, Paisley, UK) per 50 mg of tissue. Briefly, 200 μl of chloroform was added to the homogenate and then centrifuged at 12,000 rpm for 1 min to remove cell debris. The supernatant was then vortexed for 15 s and centrifuged at 12,000 rpm for 15 min at 4°C. The upper (aqueous) layer was removed, mixed with 30 μl of RNAaid+ matrix (Anachem, Luton, UK), and agitated for 5 min before centrifugation at 12,000 rpm for 1 min. The supernatant was removed and washed three times with 500 μl of RNA wash (Anachem), resuspended in 20 μl of diethyl pyrocarbonate-treated water with 10 mM DTT and 1 U/ml RNasin, and eluted by incubation at 55°C for 10 min. Concentration and purity of RNA were assessed using a GeneQuant RNA/DNA calculator before Northern blot or real-time PCR analysis. For Northern blotting, 5 μg of RNA was denatured at 65°C for 15 min in a mixture of MOPS, denatured formamide, and formaldehyde as described (28) and run on denaturing MOPS-formaldehyde 0.8% agarose gels. Briefly, RNA was transferred using capillary action on a nylon membrane for hybridization, using 20× saline-sodium citrate (SSC) as the transfer buffer. RNA was cross-linked by UV exposure (power at 1,200 × 100 μW/cm²; Spectronics). Membranes were prehybridized at 65°C for 3 h with 18 ml of phosphate buffer and 9 ml of 20% SDS in a hybridization bottle. One milliliter of salmon testes DNA (10 mg/ml) was denatured at 100°C for 10 min and added to the prehybridization mix. Radiolabeled cDNA probes were made for genes of interest using a Rediprime 2 random prime labeling kit (Amersham). Twenty-five nanograms of DNA template (PCR fragment) was diluted to 45 μl with Tris-EDTA buffer. The probe was then denatured at 100°C for 15 min and immediately cooled on ice for an additional 10 min. Denatured DNA was then added to the reaction tube together with 5 μl of [32P]dCTP. The reaction was incubated at room temperature for 2 h, and then labeled cDNA was purified through a Nick column (GE Healthcare, Buckinghamshire, UK). The hybridization mixture was then incubated overnight at 55°C. Three 15-min, 50-ml washes were performed; an initial wash at room temperature with 2× SSC and 0.1% SDS was followed by two washes at 65°C with 1× SSC and 0.1% SDS and then 0.5× SSC and 0.1% SDS. The washed membrane was wrapped in Saran wrap and exposed to a phosphorimager screen (Fuji imaging plate) for 10 min and scanned using a Fuji BAS phosphorimager. Transcript levels were quantified using Aida software (Advance Image Data Analyzer, version 3.4.035).

Real-time PCR. cDNA was synthesized from 2 μg of RNA using the Reverse Transcription system (Promega, Southampton, UK) with oligo(dT) primer according to the manufacturer’s instructions. Liver GR mRNA levels were measured using the LightCycler 480 Real-Time PCR system (Roche Diagnostics, West Sussex, UK) with light cycler 480 probe master (Roche Diagnostics) and TaqMan Gene expression Assays (Applied, Cheshire, UK). Samples were analyzed in triplicate with each PCR reaction containing 4.5 μl of cDNA, 5 μl of master mix, and 0.5 μl of primer/probe. Results are expressed as the ratio of liver GR to actin and/or TATA box-binding protein mRNA levels, which act as internal controls. TaqMan Gene expression Assays were nuclear receptor subfamily 3, group C, member 1 (mous GR) Mm00433832_m1, actin, β-cytosplasm (actin) Mm00607939_s1, and TATA box-binding protein, mouse 11β-HSD1 Mm00476182.

11β-HSD enzyme activity assays. 11β-HSD1 is bidirectional in homogenates in vitro, with oxidative (dehydrogenase) more stable than dehydrogenase activity (19). Hence, dehydrogenase activity was measured routinely, which in the linear range of product formation gives an accurate reflection of total 11β-HSD1 protein levels. Tissues were homogenized in 10% glycerol, 300 mM sodium chloride, 1 mM EDTA, and 50 mM Tris, pH 7.7, and activity was measured as described (15). The protein concentration of each homogenate was determined colorimetrically by the Bradford method, using the Bio-Rad assay kit with bovine serum albumin protein standards (Bio-Rad, Hemel Hampstead, UK). Briefly, reactions (160 μl) containing 0.2 mg/ml protein, 10 nM [3H]corticosterone, and an excess (400 μM) of nicotinamide adenine dinucleotide phosphate with homogenization buffer were incubated in a shaking water bath at 37°C. After 1 h (adipose) or 10 min (liver) of incubation, steroids were extracted with ethyl acetate, separated by thin-layer chromatography, identified by comparison with the migration of unlabelled corticosterone and 11-dehydrocorticosterone standards, and quantified with a phosphorimagertritium screen (Fujiﬁlm, Tokyo, Japan). Under these conditions, product formation was linear with respect to protein concentration and time (data not shown).

Fecal fat extraction. Mice (n = 6) were housed individually in metabolic cages, and fecal matter was collected over a 1-wk period. Feces were dried at 40°C for 72 h in a preweighed 35-ml glass tube. Feces were sonicated in 1 ml water/0.1 g feces and rehydrated for 24 h. Chloroform-methanol (2:1) was added to the mixture (1:1), the homogenate was vortexed and left for 48 h, and layers were separated by centrifugation for 10 min at 2,000 g. Duplicate 2.5-ml aliquots of the organic layer were removed into preweighed fresh glass 12-mm tubes and dried under nitrogen. Fecal fat was assessed gravimetrically and presented as a percentage of the dry weight of the feces.

Statistical analysis. Data were analyzed by one-way ANOVA using the SigmaStat program (Systat software) with post hoc Holm-Sidak
tests to determine significance for multiple comparisons at a threshold of \( P < 0.05 \). Linear regression and multiple linear regression were used to determine correlations.

**RESULTS**

Effects of dietary fats on weight gain, food intake, and fat mass. Ad libitum feeding with stearate for 4 wk led to pronounced weight loss (starting weight: \(25.9 \pm 0.4\) g; final weight: \(22.9 \pm 0.7\) g), although caloric intake was higher than for all other diets (Fig. 1A). Monounsaturated oleate (starting weight: \(25.4 \pm 0.6\) g; final weight: \(31.5 \pm 0.9\) g) and, to a lesser extent, polyunsaturated safflower oil (starting weight: \(25.6 \pm 0.8\) g; final weight: \(29.0 \pm 1.0\) g) led to weight gain, although there was no difference in caloric intake. The most pronounced weight gain was with the 58HF (starting weight: \(24.3 \pm 1.0\) g; final weight: \(31.6 \pm 0.7\) g), which was included as a positive control for DIO-mediated \(11\beta\)-HSD1 downregulation (30). Mice fed 45HF gained less weight (starting weight: \(24.8 \pm 0.6\) g; final weight: \(27.6 \pm 0.8\) g) but consumed a similar number of calories compared with those fed the 58HF diet. The 45HF diet had the same mixture of fats as the 58HF diet but had a lower overall percent fat content that matched the other diets. Adipose tissue weights correlated with body weight.
An additional pair-feeding experiment was carried out to determine whether altered food intake and, therefore, total calorie intake could account for the dietary fat-dependent differences in adiposity. All diets were calorie matched to the low-fat control (see METHODS). With this paradigm (Fig. 1, D–F), stearate caused a pronounced and significant body weight increase (starting weight: 23.1 ± 0.4 g; final weight: 19.66 ± 0.7 g) and fat mass loss (ANOVA, \( P < 0.01 \) all fat depots). Mice fed the safflower diet did not gain weight (starting weight: 23.6 ± 0.4 g; final weight: 25.4 ± 0.4 g) and showed a reduction in mesenteric fat pad weight (Fig. 1D). Oleate increased weight gain (starting weight: 21.9 ± 0.3 g; final weight: 24.3 ± 0.6 g) but not fat pad weight (Fig. 1D). Fasting insulin correlated positively with fat mass (\( P < 0.001 \)) as expected (Fig. 1C).

Given the unexpected weight loss with stearate despite the highest caloric intake we tested for malabsorption. Fecal fat was higher in the stearate fed group (30.4 ± 2.8% of fecal dry weight, \( P < 0.001 \) vs. 45HF and control) compared with control diet (0.8 ± 0.02% of fecal dry weight) and the comparator 45HF diet (7.8 ± 0.7% of fecal dry weight), consistent with stearate malabsorption.

**Effects of dietary fats on glucose homeostasis.** To assess the effects of the diets on glucose homeostasis, we measured fasting glucose and insulin levels in the ad libitum-fed groups (Fig. 1D). Note that, although insulin sensitivity was not formally measured in our studies, the glucose/insulin ratio was entirely consistent with the expected insulimimetic state found with the respective dietary effects on insulin sensitivity and the altered fat mass (8, 20, 39, 49).

Stearate caused relative hypoglycemia and hypoinsulinemia, whereas safflower oil and 45HF caused moderate fasting hyperglycemia. Oleate and 58HF caused marked fasting hyperglycemia and hyperinsulinemia, consistent with impaired glucose homeostasis and insulin resistance (Fig. 1D). Body weight was strongly correlated with fasting plasma insulin levels (\( P < 0.001, r = 0.78 \))

With pair-feeding, all mice ate their calorie-matched food parcels within a few hours of lights out. Therefore, to avoid a potentially confusing prolonged fast we measured morning glucose/insulin without a further defined fasting period. Glucose levels were unchanged between the groups (Fig. 1G). Plasma insulin was still markedly reduced in the stearate group, whereas the hyperinsulinemia caused by ad libitum oleate feeding was corrected (Fig. 1G). Safflower oil caused a significant reduction in insulin levels (Fig. 1G) rather than the moderate increase seen with ad libitum feeding (Fig. 1D).

**Effects of dietary fats on plasma corticosterone level.** Ad libitum feeding of oleate, safflower, 45HF, and 58HF diets for 4 wk suppressed nadir (morning) plasma corticosterone levels compared with control diet (Fig. 2A). In contrast, stearate significantly increased (2-fold) plasma corticosterone levels (Fig. 2A). There was a weak negative correlation of body weight with morning plasma corticosterone (\( P = 0.044, r = -0.31 \)).

Pair-feeding accentuated the effect of stearate, causing a pronounced (∼7-fold) increase in corticosterone (Fig. 2B). Oleate maintained significant suppression of corticosterone levels, but safflower had no effect (Fig. 2B).

**Effects of dietary fats on adipose 11β-HSD1 levels.** With ad libitum feeding, stearate increased adipose 11β-HSD1 mRNA and activity levels in subcutaneous adipose tissue (Fig. 3, A and B). In contrast, all other (45%) high-fat diets caused a marked and comparable reduction in adipose 11β-HSD1 mRNA levels in sc adipose tissue (Fig. 3A). Notably, 58HF caused a greater suppression of subcutaneous 11β-HSD1 activity (Fig. 3B) than the other high-fat diets.

Effects on mesenteric adipose were less pronounced; only 45HF and 58HF diets caused significant and similar reductions in adipose 11β-HSD1 mRNA levels (Fig. 3C). 58HF caused a pronounced downregulation of mesenteric adipose 11β-HSD1 activity (Fig. 3D), again disproportionately greater than its effect on 11β-HSD1 mRNA levels (Fig. 3C). Mesenteric adipose 11β-HSD1 activity (Fig. 3D) was threefold higher with stearate despite no significant effect on 11β-HSD1 mRNA (Fig. 3C).

Across all diets, body weight was strongly and negatively correlated with 11β-HSD1 activity in both subcutaneous (\( P < 0.001, r = -0.67 \)) and mesenteric adipose tissue (\( P < 0.001, r = 0.57 \)). Consistent with this being due to altered fat mass (Fig. 1B), leptin levels (in ng/ml: control 4.7 ± 0.7, stearate 14.1 ± 0.3, oleate 14.2 ± 1.9, safflower 10.1 ± 2, 45HF 6.4 ± 1.3, 58HF 19.7 ± 2) strongly and negatively correlated with subcutaneous (\( P < 0.001, r = 0.65 \)) and mesenteric 11β-HSD1 activity (\( P < 0.001, F = 15.512 \)). Adipose mass showed a negative correlation with 11β-HSD1 activity in sc (\( P < 0.001, r = -0.57 \)) but not mesenteric fat (\( P = 0.097, r = -0.26 \)).

Notably, in the ad libitum feeding experiment, multiple linear regression showed that fasting insulin was strongly negatively correlated with sc (\( P < 0.001, r = -0.54 \)) and mesenteric 11β-HSD1 activity (\( P = 0.012, r = -0.44 \)).
With pair-feeding, sc adipose 11β-HSD1 mRNA levels (Fig. 4A) and activity (Fig. 4B) were increased with stearate and suppressed with oleate (Fig. 4, A and B), whereas safflower had no effect. As with ad libitum feeding, increased mesenteric adipose 11β-HSD1 activity (Fig. 4D) but not mRNA levels were observed with stearate, highlighting the discordance seen with ad libitum feeding in this depot (Fig. 3). Oleate and safflower had no effect on mesenteric adipose 11β-HSD1 (Fig. 4, C and D).

Linear regression showed corticosterone, but not insulin, correlated with sc (P = 0.013, r = 0.81) and mesenteric 11β-HSD1 activity (P = 0.007, r = 0.76) with pair-feeding.

To test whether changes in adipose 11β-HSD1 might precede and drive weight change, we performed a 1-wk ad libitum feeding experiment. Body weight did not change significantly (stearate before: 23.1 ± 0.8 g; stearate after: 20.1 ± 0.8 g; 45HF before: 20.6 ± 0.7 g; 45HF after: 20.9 ± 0.6 g) over 1 wk, as in our original study. Stearate caused a small but
significant increase in subcutaneous but not mesenteric adipose 11β-HSD1 activity (Fig. 5). Similarly, 45HF caused a small but significant reduction in sc but not mesenteric adipose tissue (Fig. 5).

Effects of dietary fats on adipose GR mRNA levels. A major determinant of glucocorticoid action is GR density. There was no significant effect of any diet on sc or mesenteric adipose tissue mRNA with ad libitum or pair-feeding (data not shown).

Effects of dietary fats on hepatic 11β-HSD1 and GR levels. Altered hepatic 11β-HSD1 (28, 36) and GR (34) affect glucose homeostasis. Therefore, we determined the effects of dietary fats on indices of glucocorticoid action in liver. Ad libitum feeding of 45HF and 58HF diets increased hepatic 11β-HSD1 mRNA levels (Fig. 6A). However, there was no effect of any diet on either hepatic 11β-HSD1 activity (Fig. 6B) or GR mRNA levels (data not shown).

DISCUSSION

Our data show that the changes in fat mass caused by distinct dietary fat enrichment associate specifically with changes in adipose tissue but not liver 11β-HSD1 activity. Although causation cannot be implied from associations, we show that changes in subcutaneous fat 11β-HSD1 preceed weight change with short-term diet exposure. Moreover, the strong inverse correlations between fat mass and adipose 11β-HSD1 activity, rather than corticosterone, suggest that this local tissue mechanism of glucocorticoid regeneration is dominant over the HPA axis in fat mass regulation in response to dietary manipulation (15, 42, 45, 53). As discussed below, this is based on the known effects of glucocorticoids to drive lipolysis or fat accretion in the appropriate nutritional context. Moreover, the strong negative correlation of insulin with adipose 11β-HSD1, particularly in subcutaneous fat, vs. the strong positive correlation between corticosterone with adipose 11β-HSD1, particularly in visceral (mesenteric) fat, indicates a potential mechanistic basis for the depot-specific physiological regulation of fat mass through local glucocorticoid regeneration.

Elevated adipose 11β-HSD1 activity drives insulin resistance and metabolic disease (31). Therefore, we hypothesized that DIO-mediated downregulation of adipose 11β-HSD1 was a beneficial response counteracting insulin resistance in adipose tissue (11, 27, 30). However, the current findings challenge this view. First, of the two unsaturated fats, oleate, was the most potent in increasing fat mass and insulin resistance but also in suppressing corticosterone and adipose 11β-HSD1. Second, pair-feeding of the safflower diet accentuated its relatively (39) protective metabolic effects by reducing mesenteric fat mass and preserving apparent insulin sensitivity while failing to suppress corticosterone and adipose 11β-HSD1.

The most pronounced effect on weight gain and indices of glucocorticoid action was seen with the 58HF diet, which was used as a positive control to recapitulate our original observations (30). 58HF and the lower 45% HF diets contain almost exclusively saturated fats (99%), but these are of mixed chain length, and there are significant other minor constituents (see METHODS). To specifically address the role of saturated fats, we enriched with stearate alone. Unfortunately, given weight loss despite the highest calorie intake, it seemed likely that the stearate diet was malabsorbed. We confirmed this by detecting a high fecal fat content in stearate-fed mice. Nevertheless, the weight loss, hypoinsulinemia, and high plasma corticosterone with stearate unexpectedly provided us with an insight into both the regulation of and an unexpected physiological role for elevated adipose 11β-HSD1 in fat mass regulation. Clearly, rather than promoting obesity and adipose insulin resistance (31) in this metabolic context, the strikingly elevated adipose 11β-HSD1 was associated with pronounced loss of fat mass. With fasting, glucocorticoids increase lipolysis by transcriptional upregulation of hormone-sensitive lipase (43) and the
adipose tissue triglyceride lipase (desnutrin) in adipocytes (50) while suppressing lipoprotein lipase activity through induction of angiopoietin-like 4 (17). Our present work supports low while suppressing lipoprotein lipase activity through induction adipose tissue triglyceride lipase (desnutrin) in adipocytes (50).

Increased subcutaneous but not mesenteric adipose 11\(-HSD1\) precedes significant weight loss. Conversely, if this scenario is correct, high-fat-mediated downregulation of adipose 11\(-HSD1\) should attenuate glucocorticoid-mediated lipolysis and promote fat mass gain. It follows that downregulation of adipose 11\(-HSD1\) in response to high fat can only be considered beneficial if, by sequestering lipid away from muscle and liver, it prevents a state of more profound insulin resistance (4, 48).

High adipose 11\(-HSD1\), insulin, and free fatty acid levels coassociate in human and rodent (monogenic) obesity (31). In this case, increased adipose mass and, therefore, obesity may be maintained despite increased 11\(-HSD1\)-dependent lipolytic activity because the adipocyte lipogenic pathway remains selectively sensitive to the high circulating insulin levels (4, 48). Furthermore, 11\(-HSD1\) (glucocorticoid-dependent stimulation of de novo lipogenesis (6, 54) and lipid uptake from diet-derived chylomicrons through lipoprotein lipase (33, 35) will favor a net increase in fat mass. Selective hyperinsulinemia-driven lipogenesis (4, 48) may work in concert with the attenuated 11\(-HSD1\)-mediated lipolysis to drive exaggerated adipose lipid accumulation.

Superficially, this analysis of the in vivo role of 11\(-HSD1\) in adipose tissue contradicts some of our previous in vitro findings. We showed that total 11\(-HSD1\) gene deficiency led to insulin sensitization of adipocytes (29), which indeed led us to believe that adipose 11\(-HSD1\) downregulation in DIO would be directly beneficial in this tissue (30). However, this was based on evidence of enhanced glucose uptake (29), consistent with the effect of glucocorticoids to impair glucose uptake in adipocytes (7, 40). Downregulation, deficiency (29), or pharmacological inhibition of adipose 11\(-HSD1\) clearly protects against this manifestation of insulin resistance and also appears to promote fat oxidation and suppress lipogenesis (3).

However, the contribution of the lipolytic effects of glucocorticoids within the context of pathway-selective insulin resistance (4, 48) has not been elucidated, and the contribution of fat oxidation to overall fat mass is small (12). Our current data suggest that suppression of glucocorticoid (11\(-HSD1\))-mediated lipid mobilization could be a major physiological and depot-selective driver of increased fat mass. Consistent with this, 11\(-HSD1^{-/-}\) mice accumulate fat preferentially in metabolically protective nonvisceral depots (29) where the enzyme is most highly expressed (30), reflecting the increased sensitivity of subcutaneous and visceral depots to insulin and glucocorticoids, respectively (1, 37, 38, 55).

The question of what mediates dietary fat regulation of adipose 11\(-HSD1\) is important. Likely candidates include catecholamines (stearate-induced weight loss), leptin, and the direct actions of the free fatty acids (or their metabolites). However, we have been unable to show any direct regulation of 11\(-HSD1\) in differentiated mouse adipocytes (3T3-L1) across a range of relevant concentrations of these factors (CL316242 1–100 nM, 1–100 nM leptin, 0.5–500 \(\mu\)M stearate, palmitate, and oleate; unpublished observations). This leaves corticosterone and insulin, which show strong relationships with adipose 11\(-HSD1\) in the current study, as prime regulatory candidates.

Regulation of adipose 11\(-HSD1\) by insulin is a contentious issue and is influenced by dose, diet, and degree of adiposity (2, 32, 41, 51, 52). Although correlative, our results suggest that insulin acts as a negative regulator of adipose 11\(-HSD1\) under these in vivo dietary conditions. This fits with observations of reduced insulin and elevated adipose 11\(-HSD1\) in humans undergoing weight loss (46). Therefore, elevated adipose 11\(-HSD1\) in obesity may reflect resistance from a suppressive effect of insulin. Similarly, glucocorticoids can inhibit (2, 32) or increase 11\(-HSD1\) activity (6, 47) in vitro. In vivo, glucocorticoid administration increases adipose 11\(-HSD1\) (2, 25), whereas adrenalectomy reduces the elevated adipose 11\(-HSD1\) levels in obese Zucker rats (21). The positive correlation between corticosterone and adipose 11\(-HSD1\), accentuated by pair-feeding, suggests that it is a predominant (positive) regulator of adipose 11\(-HSD1\) levels when insulin action is low. Accordingly, elevated adipose 11\(-HSD1\) is found in genetically obese rodents with adipose insulin resistance (low insulin action) and high circulating corticosterone (21). Finally, association of pronounced visceral fat 11\(-HSD1\) activity in obesity (6, 9, 21, 26) may be due to this depot being intrinsically less sensitive to insulin (1, 55) and having higher levels of GR (24, 37, 38). In agreement with a depot-specific and insulin/glucocorticoid-sensitive role for 11\(-HSD1\), we found that shorter exposure to stearate and 45HF diets did not affect visceral mesenteric adipose 11\(-HSD1\) activity but did differentially affect activity in subcutaneous fat. The lack of an early effect in mesenteric fat suggests that a longer exposure with consequent effects on body weight, insulin, and corticosterone is required to change 11\(-HSD1\) activity in this depot. In contrast, in subcutaneous depots that are more responsive to insulin, changes in 11\(-HSD1\) activity are rapid and may immediately drive altered fat mass. Similarly, increases in hypothalamic 11\(-HSD1\) activity have been noted within 2 days of exposure (10), with possible implications in appetite regulation. It is notable that these early diet-induced changes in 11\(-HSD1\) in subcutaneous adipose tissue and hypothalamus precede any effects on body weight. Therefore, 11\(-HSD1\) may be key in driving body weight change at several levels.

Intriguingly, pronounced induction (stearate: high corticosterone, low insulin) or suppression (58HF: high insulin, low corticosterone) of 11\(-HSD1\) activity occurs despite more muted effects on 11\(-HSD1\) mRNA. Similar discrepancies between 11\(-HSD1\) activity and mRNA levels have been noted in intact visceral adipose preadipocytes (9) and in human visceral adipose tissue (13). Our current data suggest that a posttranscriptional mechanism is engaged at the extremes of physiological weight change that accentuates the effects on local glucocorticoid generation.
CONCLUSIONS

Our dietary interventions strongly implicate adipose 11β-HSD1 in the regulation of fat mass, which is likely subject to the opposing influence of glucocorticoids and insulin (44). Tissue GR and plasma corticosterone levels are of lesser importance in this dynamic physiological regulatory mechanism. In contrast to its pathophysiological role in obesity (31), high adipose 11β-HSD1 likely facilitates mobilization of adipose triglycerides in the presence of low insulin/weight loss. Contrary to our previous view, the main effect of diet-induced, adipose-specific 11β-HSD1 downregulation may be to promote fat accumulation (depot selectively), which, although initially protective of other metabolic tissues, ultimately leads to obesity and may worsen metabolic outcomes.

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DISCLOSURES

The authors declare that they have no competing interests.

REFERENCES

32. Napolitano A, Voice MW, Edwards CR, Seckl JR, Chapman KE. 11beta-hydroxysteroid dehydrogenase 1 in adipocytes: expression is dif-
Dietary fats and glucocorticoid action.


