

Glucocorticoids and 11beta-Hydroxysteroid Dehydrogenase in Adipose Tissue

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ABSTRACT

The highly prevalent metabolic syndrome (insulin resistance, type 2 diabetes, dyslipidemia, hypertension, along with abdominal obesity) resembles Cushing's syndrome. However, in simple obesity, plasma cortisol levels are not elevated. 11beta-hydroxysteroid dehydrogenase type 1 (11 β -HSD1), at least in mature adipocytes and hepatocytes, converts inactive circulating 11-keto steroids into active glucocorticoids, amplifying local glucocorticoid action. 11 β -HSD1 is elevated in adipose tissue in obese humans and rodents, suggesting that adipose tissue glucocorticoid excess may explain the conundrum. Indeed, transgenic mice overexpressing 11 β -HSD1 in adipose tissue faithfully replicate the metabolic syndrome. Conversely, 11 β -HSD1^{-/-} mice resist the metabolic consequences of stress and high-fat feeding via insulin sensitisation and other advantageous effects in the liver and adipose tissue. Adipose 11 β -HSD1 deficiency contributes to a protective metabolic phenotype, supporting its role as a therapeutic target for the metabolic syndrome.

"I am resolved to grow fat and look young till forty, and then slip out of the world with the first wrinkle." — John Dryden, *The Maiden Queen*, 1668

I. Preamble

Dryden's witty 17th-century view of obesity as a convenient disguise for ageing reflects an era when the average life expectancy of a child surviving infancy was only half of today's eight decades or more in western countries. Millions of years of vertebrate evolution and most of human history are reflected in spectacular metabolic adaptations to periodic starvation. By the standards of the age, Dryden's woman was not only believed to be improving her complexion but also to be healthy and resistant to episodic famine and contagion. Today, in contrast, obesity itself has reached epidemic proportions for the world's affluent nations and, increasingly, for developing countries too. Excess fat contributes to early morbidity and mortality, bringing a latter-day irony to Dryden's line. While obesity's primary cause is a chronic imbalance between calorie intake and energy expenditure, underlying vulnerabilities within individuals modulate the likeli-

hood of its development and complications. The metabolic syndrome (Reaven's syndrome X; the insulin resistance syndrome) describes a constellation of cardiovascular risk factors — specifically, insulin resistance, type 2 diabetes, dyslipidemia, and hypertension (Reaven, 1993,2002). The relative risk of morbidities in the metabolic syndrome is increased by the co-occurrence of obesity — notably, visceral (abdominal, android, central) obesity. Despite debate about its definition, the metabolic syndrome is increasing rapidly in prevalence and represents a major burden upon health-care delivery organisations worldwide. Understanding the pathogenesis and potential treatments for visceral obesity and its cardiometabolic associations is a high priority.

Endocrinologists have long puzzled over the strong morphological and metabolic similarities between the rare Cushing's syndrome of endogenous or exogenous glucocorticoid excess and the metabolic syndrome (Walker and Seckl, 2001). Excessive cortisol secretion in Cushing's syndrome is a classic cause of secondary obesity. Effects of excess cortisol on adipose tissue are complex, with an increase in central (i.e., visceral, abdominal, facial, and nape of neck) fat deposition, while peripheral fat is reduced. This may result from opposing effects of glucocorticoids that, on the one hand, increase lipolysis and downregulate lipoprotein lipase — thereby liberating free fatty acids (FFAs) from peripheral fat — but, on the other hand, stimulate preadipocyte differentiation and enhance substrate flux in favour of gluconeogenesis and triglyceride synthesis in central fat (Samra *et al.*, 1998; Andrews and Walker, 1999). Additionally important in glucocorticoid-induced obesity is central stimulation of appetite (Udden *et al.*, 2003), mediated by complex interactions between hypothalamic responses to glucocorticoids, their effects upon target appetite-controlling neurotransmitters such as neuropeptide Y (NPY), and both central and peripheral effects upon adipose-derived endocrine mediators such as leptin and gut hormones (Solano and Jacobson, 1999). Other central effects of increased glucocorticoid action include depression (Cohen, 1980), which intriguingly is also linked specifically to idiopathic visceral obesity (Ahlberg *et al.*, 2002).

Raised plasma cortisol levels cause phenotypic changes in Cushing's syndrome. Against this background, the importance of glucocorticoids in obesity has been investigated in animal models and in humans. Many studies have focused on glucocorticoid secretion and circulating blood levels of steroids. This research has shown that cortisol levels are modestly, if at all, elevated in patients with the metabolic syndrome and even may be reduced in simple obesity (i.e., obesity without diabetes or other disease states complicating increased fat mass) (Walker and Seckl, 2001). This conundrum recently was readdressed and some progress made in disentangling the mechanisms and importance of altered tissue sensitivity to glucocorticoids. This, then, is a story of cellular corticosteroid receptors, and particularly of prereceptor metabolism by enzymes, notably by the hitherto-obscure 11 β -hydroxysteroid dehydrogenases (11 β -HSDs).

II. Blood Glucocorticoid Levels in Obesity

A. GLUCOCORTICOID CONTROL: THE HYPOTHALAMIC-PITUITARY-ADRENAL AXIS

Until recently, it was axiomatic that the major determinants of corticosteroid action were levels of steroid hormones in the blood, modified by binding to plasma proteins (notably, corticosteroid binding globulin (CBG)), and the densities of intracellular receptors in target organs. Plasma glucocorticoid levels are, of course, determined by the activity of the hypothalamic-pituitary-adrenal (HPA) axis, a classical short-term neuroendocrine feedback circuit. The HPA axis functions to restrict excursions of circulating glucocorticoid concentrations within fairly tight limits, with forward drive at the diurnal maximum or during stress rapidly attenuated by negative feedback of adrenal steroids upon pituitary corticotrophs, hypothalamic paraventricular nucleus (PVN) neurons that synthesise corticotropin-releasing hormone (CRH) and vasopressin (AVP), as well as a number of suprahypothalamic sites. Of the latter, the hippocampus, a part of the limbic system, has attracted much attention, as it contains a very high density of intracellular receptors for glucocorticoids and is a key locus for glucocorticoid effects upon memory and perhaps mood (de Kloet, 1991; McEwen, 1999). The hippocampus appears to act as a “brake” upon the HPA axis, since lesions interfere with glucocorticoid feedback control of HPA stress responses (Jacobson and Sapolsky, 1991). Increased HPA axis activity sufficient to cause raised blood cortisol levels would be a convenient mechanism to explain the Cushingoid aspects of the metabolic syndrome and simple visceral obesity. Data relating to glucocorticoid hypersecretion in the metabolic syndrome/visceral obesity continuum are described briefly in the following section.

B. THE HPA AXIS AND CORTISOL DYNAMICS IN OBESITY

A number of case-control studies have suggested that obesity is associated with increased urinary free cortisol (UFC) excretion (Strain *et al.*, 1980; Marin *et al.*, 1992; Pasquali *et al.*, 1993a). This association is particularly prominent in subjects with abdominal obesity, at least in women (Pasquali *et al.*, 1993b). A caveat is that UFC, though a useful marker of HPA axis activation, forms a very small fraction of total cortisol metabolite excretion. More convincingly, recent large studies confirm that total cortisol production rate is somewhat enhanced in obesity in men as well as women (Andrew *et al.*, 1998; Fraser *et al.*, 1999; Stewart *et al.*, 1999). This is further supported by evidence that HPA axis responsiveness to stimuli such as acute stress, CRH/AVP (Pasquali *et al.*, 1999), adrenergic manipulations (Pasquali *et al.*, 2000), hypoglycaemia, or a standard meal (Marin *et al.*, 1992; Hautanen and Adlercreutz, 1993) is enhanced in idiopathic obesity, particularly visceral obesity (Pasquali *et al.*, 2000). Moreover,

the cortisol response to particular types of food may differ with the locus of adiposity, as viscerally obese women show lower HPA axis responses to high-fat and protein but greater responses to high-carbohydrate meals, compared to peripherally obese and lean subjects (Vicennati *et al.*, 2002). However, in obesity, overall plasma cortisol levels are not consistently elevated. Indeed, peak plasma cortisol levels in the morning are typically *low* in the obese (Ljung *et al.*, 1996; Phillips *et al.*, 1998; Rosmond *et al.*, 1998; Walker *et al.*, 1999), though South Asians may be an exception (Ward *et al.*, 2003). While some data in humans suggest that plasma cortisol is higher during the evening nadir in obesity, flattening the diurnal variation (Ljung *et al.*, 1996; Rosmond *et al.*, 1998), evidence is lacking for marked elevations of basal plasma cortisol in obesity. The combination of increased secretion with low morning plasma levels suggests that the diurnal variation of cortisol secretion is disrupted and/or that peripheral metabolism of cortisol is enhanced.

As explanation for the increased glucocorticoid production and exaggerated cortisol responses in obesity, both increased forward drive to the HPA axis — perhaps reflecting some form of primary meal-related abnormality of cortisol release — moderate chronic stress (Rosmond *et al.*, 1998), and/or reduced sensitivity to HPA axis feedback have been suggested (Ljung *et al.*, 1996; Di Blasio *et al.*, 2003; Jessop *et al.*, 2003). Indeed, obesity has been associated with reduced sensitivity to glucocorticoid feedback (Ljung *et al.*, 1996; Jessop *et al.*, 2003), an effect thought to be mediated via altered sensitivity of glucocorticoid receptor (GR). However, increased feedback sensitivity may not be applicable to obese men (Pasquali *et al.*, 2002), although this sex is typified by a more-android adipose distribution! Several studies suggest that individuals with common GR polymorphisms demonstrate HPA axis abnormalities in addition to a peripheral phenotype of increased adiposity, insulin resistance, and hypertension (Bjorntorp *et al.*, 1999; Rosmond *et al.*, 2000; Ljung *et al.*, 2002; Di Blasio *et al.*, 2003). Whether this GR genotype is a primary cause of obesity or whether obesity reflects HPA activation remains unclear but is the topic of ongoing investigations. An additional complexity stems from recent data showing that, in the nucleus, GR homodimers are part of a macromolecular complex with specific coactivator and corepressor proteins that, in combination, determine the actions of glucocorticoids-GR upon a target gene. Variation in density or function of coactivators and corepressors may underlie aspects of interindividual variation in glucocorticoid sensitivity (Li *et al.*, 2003).

For the metabolic syndrome, case-control and cross-sectional studies have suggested that high blood pressure associates with somewhat elevated cortisol concentrations (in blood, saliva, or urine) (Watt *et al.*, 1992; Filipovsky *et al.*, 1996; Stolk *et al.*, 1996; Rosmond *et al.*, 1998; Walker *et al.*, 1998; Fraser *et al.*, 1999; Brunner *et al.*, 2002). Similarly, insulin resistance and glucose intolerance are associated with higher circulating cortisol levels (Phillips *et al.*, 1998;

Reynolds *et al.*, 2001). Higher morning plasma cortisol concentrations and increased responsiveness to corticotropin (ACTH) occur in adults having the additional cardiovascular risk factor of low birth weight (Phillips *et al.*, 1998,2000; Levitt *et al.*, 2000; Reynolds *et al.*, 2001). However, all these associations between cortisol activity and hypertension/insulin resistance are *independent* of obesity. In such studies, obesity again is associated with lower (not higher) plasma cortisol, no change in (renal) 11 β -HSD2, and no difference in dermal sensitivity (vasoconstrictor responses) to glucocorticoids.

From these observational studies, it is not possible to dissect causality but they do not strongly favour a unifying hypothesis that ascribes the associations between obesity and other features of the metabolic syndrome to enhanced cortisol secretion. Rather, a primary or secondary increase in HPA axis activity may occur in subjects with hypertension and/or insulin resistance that do not directly predispose to obesity. Clearly, this syndrome cannot result from simple HPA activation or generalised alterations in tissue glucocorticoid sensitivity, yet the parallels with Cushing's remain persuasive.

Thinking this through, it is plausible that the observed combination of increased total cortisol secretion with lower plasma cortisol levels during peak secretion in obesity reflects increased peripheral cortisol clearance. More than 20 years ago, obesity was associated with increased cortisol clearance rates (Strain *et al.*, 1980; Lottenberg *et al.*, 1998). Increased glucocorticoid clearance could itself reduce plasma levels and lead to compensatory HPA axis activation. Any such activation would lead to adrenal hyperresponsivity to stress and other stimuli.

III. Corticosteroid Receptors and Obesity

Tissue sensitivity to glucocorticoids is determined by the density of receptors (and transcriptional cofactors and post-transcriptional mechanisms) in a particular cell type and, crucially, by tissue-specific metabolism by enzymes. In addition to evidence for altered sensitivity to glucocorticoids in HPA feedback sites, peripheral tissue sensitivity to glucocorticoids may be increased in the metabolic syndrome. For example, patients with essential hypertension or type 2 diabetes have enhanced tissue sensitivity to glucocorticoids, as measured by the intensity of dermal vasoconstriction following topical application of beclomethasone (Walker *et al.*, 1996,1998; Andrews *et al.*, 2002). In addressing tissue sensitivity to glucocorticoids, we will first review data on receptors and then concentrate upon enzymes.

Glucocorticoids act predominantly via nuclear receptors. There are two subtypes, GR and mineralocorticoid receptors (MR). These receptors are essential for life, since knockout (KO) of either by homologous recombination in mice is lethal at (for GR) or soon after (for MR) birth (Cole *et al.*,

1995; Berger *et al.*, 1998). GR are near ubiquitous, albeit their density varies considerably between cell types. MR are highly restricted to aldosterone target organs (i.e., distal nephron, distal colon, sweat and salivary glands) as well as some central nervous system (CNS) regions, notably, the hippocampus, and cardiovascular structures, including the heart. Metabolic effects associated with abdominal obesity are thought to originate in visceral adipose tissue and the liver, key sites determining hepatic glucose insulin and lipid homeostasis, as well as in skeletal muscle, the principal organ of glucose uptake. These tissues all highly express GR but have little or no MR. The importance of GR in obesity has been indicated by both its attenuation with adrenalectomy and GR antagonists in animal models and the effects on various mice bearing transgenic GR manipulations. However, the phenotypes are complex, since GR in the CNS also play a key role in HPA axis control such that a generalised transgenic reduction of GR causes obesity (Pepin *et al.*, 1989). This is probably because HPA axis overactivity and marked hypercorticonaeemia override the reduced density of GR in peripheral tissues. Such outcomes are predicted by the relatively low affinity of GR, which is little occupied by basal levels of glucocorticoids but fully occupied under conditions of glucocorticoid excess (e.g., severe stress) (de Kloet, 1991).

GR density in key metabolic cells, at least in skeletal muscle and adipose tissue, shows considerable interindividual variation. Importantly, in humans, GR mRNA levels in skeletal muscle correlate with insulin sensitivity and blood pressure (Reynolds *et al.*, 2002; Whorwood *et al.*, 2002). Moreover, dermal (vascular) sensitivity to GR agonists correlates with component disorders of the metabolic syndrome (Walker *et al.*, 1996,1998; Andrews *et al.*, 2002) and is associated with a common *bclI* restriction fragment length polymorphism (RFLP) of the GR gene (Panarelli *et al.*, 1998), though any functional implications of this particular polymorphism are unclear. Thus, it has been hypothesised that genetic and environmental variations in GR density in specific metabolic tissues underlie the metabolic syndrome. Moreover, a mechanistic basis for such tissue-specific variation in GR expression has been provided through demonstration that the GR gene has a number of alternate untranslated exon1/promoter sequences in the 5' region that, at least in lymphocytes and the brain, can drive tissue-specific expression under some circumstances (McCormick *et al.*, 2000). However, in obesity, GR mRNA is not consistently elevated in adipose tissue (Lindsay *et al.*, 2003; Wake *et al.*, 2003). This may reflect the fact that simple obesity and the metabolic syndrome can exist as discrete associated metabolic defects within a continuum of (visceral) obesity. Again, mechanisms pertaining to other features of the metabolic syndrome appear to differ from those that operate in obesity.

IV. Tissue Metabolism of Glucocorticoids

A. BASIC BIOCHEMISTRY

The enzymes directly metabolising cortisol include the steroid A-ring reductases (5 α - and 5 β -reductases), 6 β -hydroxylase, 20-reductase, and 11 β -HSDs. In rats and mice, which lack 17-hydroxylase in their adrenal cortex, the principal glucocorticoid is corticosterone, which is subject to analogous metabolism. This review will focus on the role of 11 β -HSDs.

B. HISTORY OF 11 β -HSD

50 years ago, Amelung and colleagues (1953) discovered an enzyme that catalysed the interconversion of 11-hydroxy glucocorticoids (cortisol, corticosterone) and 11-keto forms (cortisone, 11-dehydrocorticosterone): 11 β -hydroxysteroid dehydrogenase (Figure 1). While 11-hydroxyglucocorticoids are active at receptors, 11-ketosteroids have very low affinity for GR and MR and appear to all intents and purposes inert. This 11 β -HSD activity subsequently was described in a broad range of cells and tissues (Monder and White, 1993). In the 1980s, Monder and his coworkers in New York purified an 11 β -HSD activity from rat liver (Lakshmi and Monder, 1988). Homogenates, microsomal preparations, and purified enzyme from rat liver catalysed both 11 β -dehydrogenation of cortisol to inert cortisone and, typically to a lesser extent, the 11 β -reduction of cortisone to active cortisol. Thus, 11 β -HSD was thought to represent one of several arcane pathways for glucocorticoid clearance, so no specific function was ascribed to it.

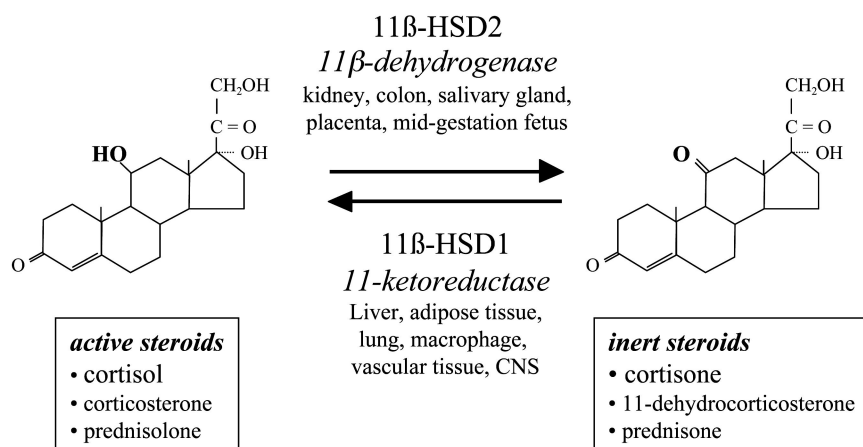


FIG. 1. 11 β -Hydroxysteroid dehydrogenase (11 β -HSD). CNS, central nervous system.

Subsequently, two 11β -HSD isozymes have been characterised, isolated, and their cDNAs cloned, the products of distinct and only distantly related genes (reviewed in White *et al.*, 1997; Stewart and Krozowski, 1999; Seckl and Walker, 2001).

C. 11β -HSD TYPE 2

11β -HSD type 2 is a high-affinity (low nM K_m for cortisol), nicotinamide adenine dinucleotide (NAD)-dependent dehydrogenase that rapidly converts active cortisol to inert cortisone (Albiston *et al.*, 1994; Brown *et al.*, 1996b). Although expressed in many tissues during fetal life, including the placenta (Brown *et al.*, 1996a), in adults, 11β -HSD2 is expressed principally in tissues where aldosterone induces its classical effects on sodium excretion, including distal nephron, sweat glands, salivary glands, and colonic mucosa (Smith *et al.*, 1996; Hirasawa *et al.*, 1997). There is some expression in other epithelial cells, such as in lung (Page *et al.*, 1994) and endothelium (Brem *et al.*, 1998; Hadoke *et al.*, 1998; Christy *et al.*, 2003). 11β -HSD2 functions predominantly to exclude glucocorticoids from intrinsically nonselective MR *in vivo* (Edwards *et al.*, 1988; Funder *et al.*, 1988). In an analogous action, 11β -HSD2 in placenta and fetal tissues appears to exclude glucocorticoids from GR *in utero* (Benediktsson *et al.*, 1997; Seckl *et al.*, 2000). Inhibition of this enzyme with liquorice (Stewart *et al.*, 1987) or disruption of the 11β -HSD2 gene in mice (Kotelevtsev *et al.*, 1999) or humans (Mune *et al.*, 1995; Dave-Sharma *et al.*, 1998) leads to the syndrome of apparent mineralocorticoid excess (AME). In AME, glucocorticoids illicitly occupy renal MR, causing sodium retention, hypertension, and hypokalemia. 11β -HSD2 inhibition also reduces fetal growth and alters tissue maturation (Lindsay *et al.*, 1996a,b).

D. 11β -HSD TYPE 1

1. Biochemistry and Distribution

In contrast to the well-defined functions of 11β -HSD2, although 11β -HSD1 was the first isoform to be identified and characterised, it remained until recently the Cinderella of this story. 11β -HSD1 has a much-lower affinity (i.e., low μ M K_m) for cortisol and corticosterone, is a nicotinamide adenine dinucleotide phosphate (NADP(H))-dependent enzyme, and is widely distributed. In cell homogenates or microsomal preparations, 11β -HSD1 readily converts cortisol to cortisone. Thus, for several years, it was thought to be responsible for inactivation of cortisol in the kidney. However, more-recent data in intact cells either transfected with 11β -HSD1 cDNA or in primary cells in culture show that in most, if not all, intact cells and organs, this enzyme is a predominant 11-ketoreductase, reactivating inert cortisone into cortisol (Low *et al.*, 1994a;

Hundertmark *et al.*, 1995; Jamieson *et al.*, 1995; Rajan *et al.*, 1996). The preponderant reductive direction *in vivo* appears to be due more to the intracellular redox context of 11 β -HSD1 in the inner leaflet of the endoplasmic reticulum than to any structural feature, such as glycosylation (Agarwal *et al.*, 1995). The mechanisms determining reaction directionality have not been elucidated fully. Nonetheless, 11 β -HSD1 co-precipitates with the NADPH-generating enzyme, hexose-6-phosphate dehydrogenase (Ozols, 1995), which may dictate the predominant 11-ketoreductase action of 11 β -HSD1 *in vivo* (Draper *et al.*, 2003). Short-term, post-translational changes such as enzyme phosphorylation also may be important, particularly to explain the apparent instability of the 11-ketoreductase activity in homogenates despite plentiful NADPH, but remain to be clarified. Biochemical investigation of expressed 11 β -HSD1 suggests that the reductase reaction has cooperative rather than Michaelis-Menten kinetics, unlike the dehydrogenase, ensuring cortisol generation across a wide range of substrate concentrations (Maser *et al.*, 2002), as observed *ex vivo* in perfused liver (Jamieson *et al.*, 2000).

In a few studies (e.g., in Leydig cells), 11 β -dehydrogenase activity has been reported in apparently intact cell preparations (Gao *et al.*, 1997; Ge and Hardy, 2000). Others have found predominantly 11-ketoreduction in similar preparations (Leckie *et al.*, 1998). The discordance of reported reaction direction in intact cells, largely involving Leydig cells and preadipocytes (Bujalska *et al.*, 2002), remains unresolved but is an important issue, given the current enthusiasm to decrease/inhibit 11-ketoreductase as a therapeutic target. It has been suggested that some 11 β -HSD1 may have been liberated from possible damaged cells in studies reporting 11 β -dehydrogenase activity (Seckl and Walker, 2001), since this direction is more stable in homogenates and broken-cell preparations. More plausibly, adipose tissue dissociation and culture lead to early induction of adipocyte cytokine synthesis and release (Ruan *et al.*, 2003). Cytokines have potent effects upon 11 β -HSD1 and other adipocyte products, which may explain some discordances in the human adipose 11 β -HSD1 activities between freshly isolated tissue and cultured cells.

11 β -HSD1 is expressed in kidneys of rats but negligible expression occurs in adult human kidney (Stewart *et al.*, 1994). However, 11 β -HSD1 is widely expressed in other tissues in humans (Ricketts *et al.*, 1998) and rodents (Moisan *et al.*, 1990b), including liver (Agarwal *et al.*, 1989; Tannin *et al.*, 1990), adipose tissue (Bujalska *et al.*, 1997; Napolitano *et al.*, 1998), lung (Hundertmark *et al.*, 1993), skeletal muscle, cardiac and vascular smooth muscle (Walker *et al.*, 1991; Brem *et al.*, 1995; Christy *et al.*, 2003), anterior pituitary gland, brain (including hippocampus) (Moisan *et al.*, 1990a,b; Lakshmi *et al.*, 1991; Sakai *et al.*, 1992), and adrenal cortex (Shimojo *et al.*, 1996). Notably, these locations have high GR rather than MR expression, with the exception of hippocampus and heart, where MR act as high-affinity sites for physiological glucocorticoids rather than aldosterone *in vivo* (Whorwood *et al.*, 1991).

These observations in cells suggested a novel role for 11β -HSD1 involving reactivation rather than inactivation of glucocorticoid. This, indeed, occurs in intact organs, at least in the liver. Isolated perfused cat (Bush *et al.*, 1968) or rat (Jamieson *et al.*, 2000) liver models suggest that 11β -HSD1, which is the only isozyme expressed in liver, is a predominant 11β -reductase with a high capacity for reactivating 11 -ketosteroid substrate over a broad range of substrate concentrations. These findings can be extrapolated to human liver *in vivo*, since historical work suggests that, on oral administration, cortisone (the first pharmacological glucocorticoid used in man) is rapidly activated to cortisol. Indeed, recent studies confirm that very little oral cortisone reaches the systemic circulation (A. Jamieson *et al.*, 1999) and that hepatic vein cortisol/cortisone ratios are very high (Walker *et al.*, 1992). 11 -ketoreductase activity has been shown in other human tissues *in vivo*, including subcutaneous adipose tissue (Katz *et al.*, 1999).

2. Substrate Levels

For 11 -ketoreductase to play a physiological role in regulating receptor exposure to active glucocorticoids (as opposed to a pharmacological role when cortisone is administered), there must be a substantial pool of substrate inert 11 -ketosteroids in the circulation and tissues. *In vivo*, the main source of 11 -ketosteroid is 11β -HSD2 dehydrogenation of cortisol and corticosterone, which predominantly occurs in the kidney (Whitworth *et al.*, 1989). In humans, cortisone circulates at levels approximating 50–100 nmol/l (Walker *et al.*, 1992). While this level is lower than diurnal peak cortisol of 400–600 nmol/l, cortisone is largely unbound, while $\approx 95\%$ of cortisol is sequestered by binding to plasma proteins such as CBG (Dunn *et al.*, 1981). Moreover cortisone, unlike cortisol, shows no pronounced diurnal rhythm and so is constantly available for conversion to active glucocorticoid (Walker *et al.*, 1992). Estimates of “free” cortisol levels are rather imprecise but approximate 0.5–1 nmol/l at the diurnal nadir. In the rat, plasma concentrations of 11 -dehydrocorticosterone are also ≈ 50 nmol/l, though in the mouse, levels are lower (≈ 3 –5 nmol/l) (Kotelevtsev *et al.*, 1997). Thus, for at least the quiescent part of the diurnal cycle, circulating cortisone levels equal or exceed free cortisol levels and similar ratios pertain in rodents.

E. FUNCTIONAL STUDIES OF 11β -HSD1 IN LIVER

Initial findings suggesting that 11β -HSD1 increases effective intracellular glucocorticoid action were obtained in liver. Here, glucocorticoids oppose the actions of insulin, for example, by upregulating expression of the key enzyme for gluconeogenesis, phosphoenolpyruvate carboxykinase (PEPCK). In male rats, estradiol potently downregulates 11β -HSD1 expression (Low *et al.*, 1993) and, only in the presence of glucocorticoids, downregulates PEPCK expression (P.M. Jamieson *et al.*, 1999). Such indirect studies, as well as the use of relatively

nonselective, liquorice-based inhibitors (Walker *et al.*, 1995; Andrews *et al.*, 2003), indicate that impaired activity of 11 β -HSD1 in liver is associated with features of reduced glucocorticoid action and increased insulin sensitivity in hepatocytes. This has been supported by recent studies with selective 11 β -HSD1 inhibitors (Alberts *et al.*, 2002,2003) (see below).

To explore this further, 11 β -HSD1 KO mice have been generated (Kotelevtsev *et al.*, 1997). These mice appear to develop normally and are viable, fertile, and apparently normotensive. This model shows that 11 β -HSD1 is the sole major 11 β -reductase, at least in mice, since adrenalectomised 11 β -HSD1 KO mice cannot convert administered 11-dehydrocorticosterone to active corticosterone. Plasma corticosterone levels are modestly elevated at the diurnal nadir, presumably due to somewhat deficient feedback upon the HPA axis (11 β -HSD1 is expressed in hippocampus, PVN, and anterior pituitary) (Harris *et al.*, 2001). However, despite slightly elevated basal plasma corticosterone levels, 11 β -HSD1^{-/-} mice have a phenotype compatible with impaired intracellular glucocorticoid regeneration and reduced antagonism of insulin action. They show impaired induction of the key glucocorticoid-inducible hepatic enzymes PEPCK and glucose-6-phosphatase on fasting and an attenuated hyperglycemic response to novel environment stress or chronic high-fat feeding (Kotelevtsev *et al.*, 1997). Importantly, the mice have more-than-adequate, stress-induced HPA axis responses (Harris *et al.*, 2001) and do not exhibit hypoglycaemia with prolonged fasting (Kotelevtsev *et al.*, 1997). Further aspects of the 11 β -HSD1 null phenotype affect hepatic metabolic control and cardiovascular risk factors (Morton *et al.*, 2001). *Ad lib*-fed 11 β -HSD1^{-/-} mice have lower plasma triglyceride and elevated “cardioprotective” high-density lipoprotein (HDL) cholesterol levels (Morton *et al.*, 2001). This appears to be due to increased hepatic β oxidation of lipids, rather than to altered lipogenesis. Indeed, hepatic expression of peroxisome proliferator-activated receptor alpha (PPAR α), a key glucocorticoid-sensitive transcription factor driving lipid metabolism, is elevated in fed 11 β -HSD1^{-/-} mice. The major murine HDL carrier, apolipoprotein AI, is increased in the null mice, whereas serum apolipoprotein CIII, which increases plasma triglycerides by inhibiting hepatic lipolysis and interfering with transfer of triglycerides to the liver, is reduced. Additionally, preliminary data suggest favourable effects upon haemostasis, as in liver, glucocorticoid-inducible A α -fibrinogen transcript levels are reduced (Morton *et al.*, 2001).

F. 11 β -HSD1 IN ADIPOSE TISSUE

1. Isozymes and Directionality

Glucocorticoids play a key role both in the regulation of adipose tissue metabolism and in the differentiation of preadipocytes into adipocytes (Gaillard

et al., 1991). 11 β -HSD expression in adipose tissue was noted in the 1980s and thought to be a dehydrogenase (Monder and White, 1993). Studies in adipose cells derived from the mammary gland confirmed the presence of 11 β -dehydrogenase activity *in vitro* (Quirk *et al.*, 1991). More recently, 11 β -HSD in adipose tissue has been re-examined in light of the 11-ketoreductase predominance of this isozyme in intact hepatocytes and whole liver.

In terms of isozymes, 11 β -HSD1, but not 11 β -HSD2, mRNA is expressed in rat white (epididymal) adipose tissue (WAT) (Napolitano *et al.*, 1998) and in human adipose tissue (Bujalska *et al.*, 1997; Sun *et al.*, 1997; Paulmyer-Lacroix *et al.*, 2002). The enzyme appears to be expressed similarly in adipocytes and the stromal vascular fraction (enriched with preadipocytes and vascular cells) in the rat, though perhaps is more highly concentrated in adipose stromal cells in humans (Bujalska *et al.*, 1997). 11 β -HSD also is expressed in murine fibroblast-adipocyte 3T3-F442A and 3T3-L1 cell lines, which closely reproduce preadipocyte differentiation *in vitro* when cultured in the presence of inducing agents, including dexamethasone. These respond to glucocorticoids in a similar manner to adipose tissue *in vivo* (MacDougald *et al.*, 1994; MacDougald and Lane, 1995). 3T3 cells exclusively express the 11 β -HSD1 isozyme and, in intact cells, the reaction direction is solely 11-ketoreduction (Napolitano *et al.*, 1998). 11 β -HSD1 mRNA and activity in 3T3 cells increases markedly with differentiation of cells from their preadipocyte to mature adipocyte state. 11 β -HSD1 appears to be a late-differentiation gene in 3T3 cells. 3T3 cell *in vitro* differentiation is promoted by insulin and glucocorticoids. However, the increase in 11 β -HSD1 with differentiation does not appear to be mediated directly by these hormones, since, at least in differentiated 3T3 cells, insulin and glucocorticoids reduce 11 β -HSD1 expression. By contrast, intact human adipose stromal cells cultured in the presence of insulin and cortisol have been reported to show bi-directional 11 β -HSD1 activity, although 11-ketoreductase activity predominates in cells derived from omental fat, with further induction by glucocorticoids in mature cells (Bujalska *et al.*, 1997).

Some recent findings suggest that 11 β -HSD1 reaction direction may alter in adipose tissue with differentiation state (Bujalska *et al.*, 2002), although this was not apparent in a clonal 3T3 cell model (Napolitano *et al.*, 1998). Thus, primary cultures of human stromal and mature adipocytes taken from patients undergoing elective abdominal surgery showed predominant 11 β -dehydrogenase activity in freshly isolated stromal cells from the omental compartment, whereas intact mature adipocytes had predominantly 11-ketoreductase activity. Following culture for 2 weeks, 11-ketoreductase activity predominated, despite no significant changes in 11 β -HSD1 mRNA. The authors speculated that since glucocorticoids inhibit cell proliferation, dehydrogenase in immature preadipocytes facilitates proliferation. However, once

differentiation is initiated, 11-ketoreductase amplifies glucocorticoid levels, promoting adipogenesis. While these findings might be explained by cell breakage leading to liberation of enzyme into a homogenate-like state in the early phases of cell culture and/or by cytokine-inductive effects of adipose tissue dissociation and early culture *in vitro*, an intriguing biochemical mechanism for shifts in 11 β -HSD1 directionality has been advanced. This advocates varying developmental expression of hexose-6-phosphate dehydrogenase, which co-precipitates with 11 β -HSD1 and acts to generate NADPH inside the lumen of the endoplasmic reticulum in adipose tissue (Stegeman and Klotz, 1979). Intriguingly, while polymorphisms in the 11 β -HSD1 gene (HSD11B1) correlate rather poorly (Draper *et al.*, 2002; Gelernter-Yaniv *et al.*, 2003), if at all (Caramelli *et al.*, 2001), with adipose distribution in humans, changes in the hexose-6-phosphate dehydrogenase gene may be key. Thus, in three patients with rare cortisone reductase deficiency (Phillipov *et al.*, 1996), null mutations in the HSD11B1 gene have not been found. Recent data suggest that such individuals have more-subtle mutations in both HSD11B1 and in hexose-6-phosphate dehydrogenase, resulting in both low 11 β -HSD1 expression and low endoplasmic reticulum NADPH generation, with consequent loss of 11 β -HSD1 reductase activity (Draper *et al.*, 2003). It remains to be established whether or not this mechanism applies to more-common cases of 11 β -HSD1 dysregulation in adipose tissue with obesity and associated insulin-resistance states, such as the polycystic ovary syndrome, which phenotypically most closely resembles cortisone reductase deficiency.

2. Depot Differences

Fat depots may differ in 11 β -HSD1 activity, although no clear consensus exists. Discrepancies may reflect species differences or assay conditions employed. Thus, in humans, cultures of omental stromal cells have more 11 β -HSD1 than subcutaneous stromal cells (Bujalska *et al.*, 1999). In contrast, in various nonobese strains of mice, 11 β -HSD1 mRNA expression and activity are higher in freshly isolated peripheral than visceral fat depots (Morton *et al.*, 2003). This is consistent with the idea that increased glucocorticoid reactivation correlates with increased differentiation potential of this depot. These interspecies differences may reflect the conditions of assay; *ex vivo* cultures in high glucocorticoid concentrations employed in humans perhaps favour increased activity in visceral fat because this depot has more GR (Masuzaki *et al.*, 2001) and/or has greater capacity for glucocorticoid-induced differentiation of immature to mature (i.e., higher 11 β -HSD1-expressing) adipocytes.

3. Molecular Regulatory Mechanisms

Several studies have examined regulation of 11 β -HSD1 expression in adipose tissue. Insulin appears to reduce 11 β -HSD1 gene expression in fat cells. Although glucocorticoids reduce adipose 11 β -HSD1 expression in some systems, in others, they stimulate its activity, with effects reflecting the assay conditions and perhaps species. Proinflammatory cytokines such as tumor necrosis factor alpha (TNF α) and interleukin-1 (IL1) increase and anti-inflammatory cytokines reduce 11 β -HSD1 in adipose cells *in vitro* (Handoko *et al.*, 2000; Friedberg *et al.*, 2003). As detailed earlier, both glucocorticoids and insulin exert effects, albeit *in vitro*. However, regulation by other nuclear receptors remains less certain. Thus, while PPAR γ ligands such as thiazolidinediones downregulate 11 β -HSD1 in 3T3 cells *in vitro* and in epididymal fat in mice *in vivo* (Berger *et al.*, 2001), the same was not observed in lean or obese Zucker rats (Livingstone *et al.*, 2000b). Liver X receptor (LXR) agonists also partially downregulate 11 β -HSD1 *in vitro* and *in vivo* (Stulnig *et al.*, 2002). The mechanism may be indirect, which may explain the discrepancies observed in such studies. In terms of more-direct effects, CCAAT/enhancer binding protein alpha (C/EBP α) binds to several sites on the 11 β -HSD1 promoter and, when transfected into human hepatoma hepG2 cells, increases 11 β -HSD1 promoter activity (Williams *et al.*, 2000). In contrast, C/EBP β acts as a dominant-negative repressor of 11 β -HSD1 transcription when added to C/EBP α , although alone, it is a weak inducer. Electrophoretic mobility shift assays (EMSA) using nuclear extracts from undifferentiated and differentiated 3T3-F442A cells suggest that C/EBP α also may regulate 11 β -HSD1 expression in adipocytes (Williams *et al.*, 1993). These data suggest the possibility that 11 β -HSD1 regulation in the adipocyte by insulin and glucocorticoids may be mediated indirectly through changes in C/EBP-related proteins. Since under many circumstances, 11 β -HSD1 regulation in liver and adipose tissue is discordant, as with other well-characterised C/EBP-regulated genes such as PEPCK, the fine details of control are likely to be tissue specific. 11 β -HSD1 mRNA regulation in 3T3-F442A cells parallels glycerol-3-phosphate dehydrogenase, a key enzyme in triglyceride synthesis and a well-characterised marker of adipocyte differentiation (Moustaid *et al.*, 1990).

G. AP2-11 β -HSD1 ADIPOSE OVEREXPRESSING TRANSGENIC MICE: A MODEL OF THE METABOLIC SYNDROME

The preponderance of data suggest that 11-ketoreductase activity is increased in adipose tissue in obese rodent models and humans (see below). The key question is whether increased adipose 11 β -HSD1 is a cause or a consequence of obesity and any associated metabolic syndrome. To dissect this, mice over-

expressing 11 β -HSD1 selectively in adipose tissue have been generated, exploiting the adipocyte fatty acid binding protein (aP2) promoter (Masuzaki *et al.*, 2001). Two lines have been selectively developed to exhibit 2- to 3-fold overexpression of 11 β -HSD1 in adipose tissue, which represents the degree of enzyme increase found in obese humans and animals. These aP2–11 β -HSD1 mice are viable and appear developmentally normal. The transgene is expressed in all adipose depots examined and in brown adipose tissue (BAT) but is absent from other 11 β -HSD targets such as the brain, liver, skeletal muscle, and kidney. The effect of the transgene is to approximately double corticosterone levels within adipose tissue, while circulating glucocorticoid levels are unaltered, at least under basal conditions. As a consequence of local intra-adipose glucocorticoid excess, aP2–11 β -HSD1 mice are modestly obese. Strikingly, the obesity is predominantly intra-abdominal, with a > 3-fold increase in the mesenteric fat depot, whereas peripheral fat depots are significantly, but much less spectacularly, increased. The visceral adipose expansion in these animals (which overexpress 11 β -HSD1 similarly in all adipose beds) may relate to much-greater levels of GR α in visceral adipose than peripheral depots in mice (Masuzaki *et al.*, 2001). Indeed, the transgenics show increased expression of the glucocorticoid target gene lipoprotein lipase, particularly in mesenteric adipose tissue that could drive lipid accumulation in this adipose depot. It is interesting that GR α is not downregulated in the transgenic animals. Glucocorticoid autoregulation of GR is highly tissue specific and is only seen acutely in many tissues.

In association with this localised change in glucocorticoid exposure and the consequent increased visceral fat mass, aP2–11 β -HSD1 mice develop all major features of the metabolic syndrome. The animals are markedly glucose intolerant and insulin resistant, features exacerbated by high-fat feeding. The animals do not show obvious fasting hyperglycemia but this becomes markedly manifest after a glucose load, suggesting the deficit is in peripheral glucose uptake rather than a predominant increase in hepatic glucose production. They also show dyslipidemia with elevated FFA and triglyceride levels (Masuzaki *et al.*, 2001). Glucocorticoids are potent secretagogues of leptin from adipose tissue. Serum leptin levels are elevated in the transgenic animals disproportionately to their degree of obesity, suggesting leptin resistance, as observed in human obesity.

aP2–11 β -HSD1 transgenic mice show adipocyte hypertrophy but not hyperplasia (Masuzaki *et al.*, 2001). This is perhaps not surprising, as aP2 is a late differentiation gene in adipocytes, so expression and effects in preadipocytes would not be expected. Within adipocytes themselves, aP2–11 β -HSD1 mice show changes concordant with decreased sensitivity to insulin and/or increased corticosterone levels. Thus, transgenic adipose tissue has decreased expression of the insulin-sensitising factor adiponectin (acrp30, adipoQ) (Yamauchi *et al.*, 2002) and increased expression of TNF α , an adipose cytokine that causes insulin

resistance (Hotamisligil *et al.*, 1993). Both are commensurate with the effects of glucocorticoid excess (Fasshauer *et al.*, 2002; Viengchareun *et al.*, 2002). Serum TNF α levels also are elevated. In contrast, adipose mRNA-encoding resistin, which may lead to insulin resistance (Steppan *et al.*, 2001), is reduced in transgenic adipose tissue, perhaps as a consequence of glucocorticoid excess (Viengchareun *et al.*, 2002). Intriguingly, angiotensinogen mRNA, which normally is expressed at low levels in adipose tissue, is strikingly elevated in aP2-11 β -HSD1 transgenic mouse fat. This glucocorticoid-regulated transcript may underpin the marked hypertension seen in these animals. The hypertension is associated with renin-angiotensin-aldosterone system (RAAS) activation and is strikingly sensitive to low doses of an angiotensin II receptor antagonist (Masuzaki *et al.*, 2003). Finally, the animals show intriguing hyperphagia, indicating the potential for a novel pathway, other than leptin deficiency (though leptin resistance is not excluded), of signalling between the adipocyte and CNS appetite centres. The aP2-11 β -HSD1 transgenic mouse faithfully models the major features of the metabolic syndrome.

The aP2-11 β -HSD1 transgenic mouse permits speculation about the subtle but important phenotypic differences between Cushing's syndrome and the metabolic syndrome. If the metabolic syndrome is, indeed, generated by local glucocorticoid excess inside adipose tissue and/or liver but with normal circulating cortisol levels, then tissue without the adipose-hepatic axis will be unaffected. We would not necessarily expect Cushingoid skin thinning, vascular fragility, delayed wound healing, myopathy, or CNS effects, which may well reflect the actions of *systemic* glucocorticoid excess upon skin, blood vessels, skeletal muscle, and brain without the compass of *local* adipose and hepatic glucocorticoid excess seen in the 11 β -HSD1 transgenic models.

H. LIVER GLUCOCORTICOID EXCESS: APOE-11 β -HSD1 TRANSGENIC MICE

Blood from visceral adipose tissue drains via the hepatic portal vein to the liver. Unsurprisingly, therefore, aP2-11 β -HSD1 transgenic mice have elevated levels of corticosterone and FFA in the portal plasma, implying that the liver is exposed to excess glucocorticoids. To address this and to examine whether excess 11 β -HSD1 in the liver *per se* can cause the metabolic syndrome, transgenic mice overexpressing 11 β -HSD1 in the liver have been generated under the ApoE promoter. These mice are viable and appear normal. As adults, the mice show modest insulin resistance and hypertriglyceridemia, along with substantially increased fat deposits in the liver. However, ApoE-11 β -HSD1 transgenic mice have normal weight with normal distribution and mass of fat depots and show normal glucose tolerance. Intriguingly, the animals are hypertensive, with activation of the RAAS, in this case due, apparently, to overex-

pression of angiotensinogen in the liver but not adipose tissue. Overexpression of 11 β -HSD1 in liver produces an attenuated metabolic syndrome phenotype *without* visceral obesity. This might be of pathogenic relevance in cases such as patients with the insulin resistance of myotonic dystrophy (Johansson *et al.*, 2001), in which liver 11 β -HSD1 activity is raised.

I. DEFICIENCY OF 11 β -HSD1 IN ADIPOSE TISSUE: LESSONS FROM THE KO MOUSE

11 β -HSD1 expression in adipose tissue produces a striking metabolic syndrome phenotype. But what about enzyme deficiency (Figure 2)? Inhibitors have provided some conflicting data that may relate to difficulties in access of carbenoxolone to adipose tissue *in vivo*, at least in the doses administered to rodent models (Livingstone and Walker, 2003) and perhaps humans (Andrews *et al.*, 2003). Adiposity in 11 β -HSD1 KO animals has been examined on both intrinsically obesity-resistant and obesity-prone genetic backgrounds. Intra-adipose corticosterone levels are lowered substantially in the 11 β -HSD1^{-/-} animal

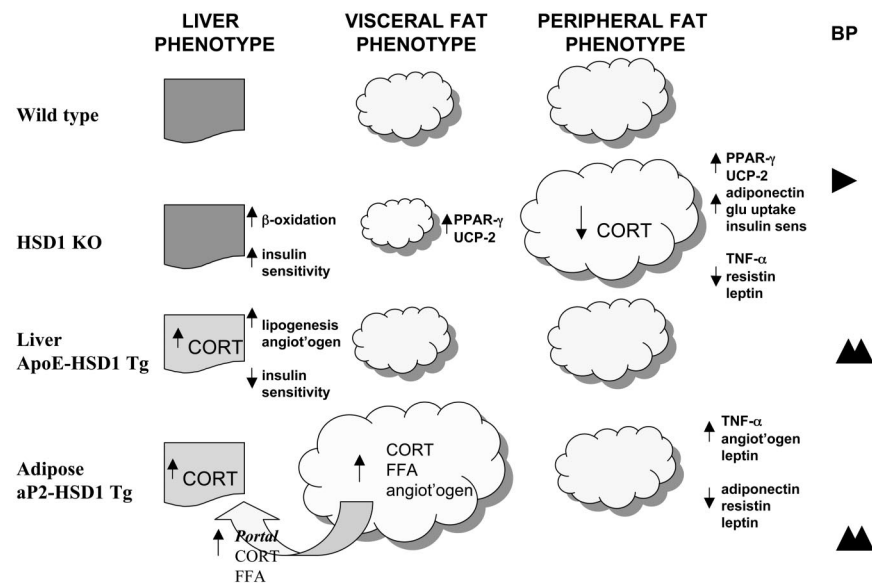


FIG. 2. Schematic of the phenotypes of mice lacking or overexpressing 11 β -HSD1 in metabolic tissues. The size of the representations of fat depots reflects the mass observed. Paler liver colours represent fat accumulation. Abbreviations: BP, blood pressure; KO, knockout; Tg, transgenic; PPAR γ , peroxisome proliferator-activated receptor gamma; UCP-2, uncoupling protein 2; TNF α = tumor necrosis factor alpha; HSD, hydroxysteroid dehydrogenase; FFA, free fatty acid; CORT, corticosterone.

in the face of modestly elevated plasma corticosterone concentrations (Morton *et al.*, 2003). On the obesity-prone C57Bl/6J genetic background, high-fat diet-fed 11β -HSD1 KO mice gain significantly less weight than controls, despite relative hyperphagia. This appears due to an enhanced metabolic rate, as judged by increased core body temperature (Morton *et al.*, 2002). With high-fat diet on either genetic background, 11β -HSD1 KO mice preferentially gain adipose tissue in the "metabolically safer" peripheral depots rather than in the "metabolically disadvantageous" visceral sites. While the explanation of fat redistribution in 11β -HSD1^{-/-} animals is uncertain, these mice show higher expression of the thiazolidinedione target adipogenic transcription factor PPAR γ receptor in all adipose tissue beds. Furthermore, 11β -HSD1^{-/-} mice show a greater increase of adipose PPAR γ receptors with high-fat feeding than wild-type (WT) mice. PPAR γ ligands cause fat redistribution to the periphery, which may underpin the favourable morphology seen (Kelly *et al.*, 1999; Sewter *et al.*, 2002). Additionally, 11β -HSD1 null animals show greater induction of uncoupling protein-2 (UCP-2) in mesenteric adipose tissue than WT mice (Morton *et al.*, 2002), which may allow local calorie wastage rather than storage as fat (Digby *et al.*, 2000). UCP-2 is downregulated by glucocorticoids (Udden *et al.*, 2001) and upregulated by PPAR γ activation (Kelly *et al.*, 1998), so its induction in the 11β -HSD1 null mouse adipose tissue is not unexpected.

In terms of adipose endocrine changes, adipose leptin mRNA and plasma leptin levels are reduced in 11β -HSD1^{-/-} mice, particularly in peripheral adipose. On the obesity-prone C57Bl/6J genetic background, 11β -HSD1 null animals are clearly insulin sensitised and resist hyperglycaemia that occurs with high-fat feeding in WT mice. This occurs at least partly at the adipocyte level, since isolated primary adipocytes show increased basal and insulin-stimulated glucose uptake (Morton *et al.*, 2003). Adipocyte resistin and TNF α mRNAs are reduced, whereas adiponectin is increased, again compatible with an adipose-mediated, insulin-sensitised phenotype. Thus, overall, the mouse shows improved glucose tolerance, increased insulin sensitivity, and reduced intratissue glucocorticoid levels in the face of modest hypercortisteronaemia (Harris *et al.*, 2001). These beneficial effects of deletion in 11β -HSD1 in adipose tissue are accompanied by changes in hepatic gene expression consistent with increased β oxidation of lipids in the liver (Morton *et al.*, 2001).

Although the relative importance of liver and adipose tissues in contributing to this beneficial phenotype remains to be determined, it is clear that loss of 11β -HSD1 has few, if any, deleterious metabolic effects, at least as assessed in this mouse model. Indeed, the lifespan of this model is apparently normal and the animals resist the normal glucocorticoid-associated decline of memory and other cognitive processes with ageing (Yau *et al.*, 2001). Thus, loss of this enzyme appears to be beneficial.

1. Why Might 11 β -HSD1 Exist?

However, the phenotype of the 11 β -HSD1^{-/-} mouse and the various transgenic and pharmacological manipulations detailed here raise the evolutionary question of the overall biological purpose of such an apparently virtueless enzyme. It cannot exist merely as a convenient target for therapy. We can only speculate. Given that our vertebrate biological antecedents had to suffer considerably more starvation than plenty, perhaps the boost of glucocorticoid from local tissue reactivation, particularly during the diurnal nadir, provided an extra lift to metabolic processes underpinning calorie generation. This might well have assisted survival during periods of starvation. Even during relative nutritional plenty, the sustenance of some key metabolic organs, while others, including the HPA system, were quiescent (i.e., during sleep), may have had an advantage. However, in modern westernised existence with an excess of calorifically rich foods available at every street corner, perhaps such activity becomes redundant, particularly as obesity and its metabolic consequences become the problem. It is an intriguing notion that an enzyme putatively required to help survive starvation becomes a metabolic “appendix” in the presence of nutritional plenty and a target for therapy of the consequences of calorific excess.

V. 11 β -HSD1 and Glucocorticoid Metabolism in Obesity

The combination of increased total cortisol secretion with lower plasma cortisol levels during peak secretion suggests that peripheral cortisol clearance may be increased in obesity. Any such activation would lead to adrenal hyperresponsivity to stress and other stimuli, as observed in obesity. In the 2 decades since excess cortisol production and clearance rates were first noted in obesity (Strain *et al.*, 1980), the observation has been repeated many times (Andrew *et al.*, 1998,2002; Lottenberg *et al.*, 1998). Increased glucocorticoid clearance could reduce plasma levels and lead to compensatory HPA axis activation. The enzymes responsible for increased glucocorticoid clearance in obesity have been identified through analysis of cortisol metabolites in urine. Increased relative excretion of A-ring reduced metabolites of cortisol has been reported that is attributed to activation of the hepatic A-ring reductases (Andrew *et al.*, 1998; Fraser *et al.*, 1999). A-ring reductases (5 α - and - β) are activated in both animal (Livingstone *et al.*, 2000a) and human obesity (Andrew *et al.*, 1998,2002). The underlying cause of increased enzyme activity is unknown but these enzymes may be regulated by insulin, lipids, and substrate availability. However, here, we concentrate upon another pathway, the 11 β -HSDs.

A. 11β -HSD1 IN OBESITY

Measurement of 11β -HSD1 *in vivo* in humans is not straightforward (Walker, 2000). The original assessment relied upon measuring ratio of the most-abundant urinary metabolites of cortisol and cortisone (i.e., 5α - and 5β -tetrahydrocortisols/ 5β -tetrahydrocortisone). However, this ratio also is influenced by activities of other enzymes, including 11β -HSD2, 5α -reductase, 5β -reductase, and 3α -HSDs. For example, carbenoxolone, which inhibits both renal 11β -HSD2 and hepatic 11β -HSD1, does not alter the ratio of cortisol/cortisone metabolites (Stewart *et al.*, 1990). In obesity, the urinary cortisol/cortisone metabolite ratio has been reported to be increased (Andrew *et al.*, 1998; Rask *et al.*, 2002; Tiosano *et al.*, 2003), unchanged (Fraser *et al.*, 1999; Reynolds *et al.*, 2001), or decreased (Stewart *et al.*, 1999; Rask *et al.*, 2001). This inconsistency may depend in part upon variations — for example, with sex — in 5α - and 5β -reductase activity. Recent findings suggest that increased fat content of the liver, which constitutes a risk factor for insulin resistance over and above the effect of obesity, is associated with increased urinary excretion of 5β -reduced cortisol metabolites. Liver fat content was shown to be a more-powerful determinant of cortisol/cortisone metabolite ratios than the degree of obesity (Westerbacka *et al.*, 2003). However, this important confounder has not been accounted for in most studies in which liver fat content was not measured. Another source of inconsistency of cortisol/cortisone metabolite ratio in obesity is the possible influence of tissue-specific disruption of 11β -HSD1 activity. It is this last crucial point that turns out to be the key issue in obesity.

Studies in leptin-resistant obese Zucker rats revealed that obesity was associated with decreased 11β -HSD1 expression and activity in liver but increased 11β -HSD1 in omental adipose tissue (Livingstone *et al.*, 2000a). This led to dissection of potential tissue-specific differences in obese humans. In humans, conversion of cortisone after oral administration to cortisol in peripheral plasma, reflecting first-pass metabolism by hepatic 11β -HSD1, is impaired in obesity (Stewart *et al.*, 1999; Rask *et al.*, 2001,2002). In contrast, in subcutaneous abdominal adipose tissue, 11β -HSD1 activity is increased both *in vivo* and *in vitro* (Rask *et al.*, 2001,2002; Lindsay *et al.*, 2003; Wake *et al.*, 2003). Further studies have confirmed that the increased 11β -HSD1 activity in biopsies is accompanied by increased 11β -HSD1 mRNA (Paulmyer-Lacroix *et al.*, 2002; Lindsay *et al.*, 2003; Wake *et al.*, 2003; Westerbacka *et al.*, 2003). By analogy with the transgenic mouse having 3-fold overexpression of 11β -HSD1 in adipose tissue (Masuzaki *et al.*, 2001,2003), one would expect a Cushingoid phenotype to result from the similar magnitude of increase in adipose 11β -HSD1 documented in human obesity. Interestingly, while increased subcutaneous adipose 11β -HSD1 is associated with insulin resistance in obesity, it is not linked specifically with visceral adiposity or hypertension. In these respects, mice and

men may differ but it remains to be determined whether 11 β -HSD1 mRNA or activity is increased in intact *omental* adipose tissue in obese subjects (Tomlinson *et al.*, 2002).

The mechanisms underlying increased adipose 11 β -HSD1 in obesity are uncertain. 11 β -HSD1 transcription is highly regulated, including by many factors that are altered in obesity (e.g., cytokines, sex steroids, growth hormone (GH), insulin, PPAR α and - γ agonists). In obese Zucker rats and ob/ob mice, down-regulation of hepatic 11 β -HSD1 is reversible with other manipulations that induce weight loss (Livingstone *et al.*, 2000b; Liu *et al.*, 2003). Attempts to link the 11 β -HSD1 genotype with obesity have not been successful (Caramelli *et al.*, 2001; Draper *et al.*, 2002), although arguably the intermediate phenotypes (i.e., anthropometric measurements or urinary cortisol/cortisone metabolite ratios) employed are too insensitive to allow clear inferences about the influence of known polymorphisms in the 11 β -HSD1 gene.

B. 11 β -HSD1 AND GH

In addition to dysregulation in patients with idiopathic obesity, the central adiposity of GH deficiency and hypothalamic obesity may be associated with changes in cortisol metabolism and 11 β -HSD1 activation. 11 β -HSD1 is inhibited by GH and insulin-like growth factor-1 (IGF-1) *in vitro* (Napolitano *et al.*, 1998; Tomlinson *et al.*, 2001). In humans with hypopituitarism and acromegaly, this effect may be important (Moore *et al.*, 1999; Trainer *et al.*, 2001; Tiosano *et al.*, 2003). Indeed, GH therapy reduces cortisol:cortisone metabolite ratios in patients with hypopituitarism (Weaver *et al.*, 1994) and in idiopathic obesity (Tomlinson *et al.*, 2003). As in studies of idiopathic obesity, the difficulty is in the interpretation of urinary cortisol:cortisone metabolite ratios, which do not reflect any tissue-specific changes. *In vivo* animal studies have shown that GH regulates liver 11 β -HSD1, with the direction of change dependent upon sex-specific patterns of pulsatile GH release (Low *et al.*, 1994b). These findings may not explain changes in adiposity but may give a mechanism for improvements in insulin sensitivity in liver alone when GH is administered at the constant levels typical of female patterns that downregulate hepatic 11 β -HSD1. Whether such effects pertain to humans is not fully known.

C. 11 β -HSD IN THE BRAIN IN OBESITY

While not the main object of this review (for details of 11 β -HSDs in the CNS, see Seckl, 1997; Yau and Seckl, 2001), specific CNS changes in 11 β -HSDs in obese rodents have been reported that add to the complexity of tissue-specific dysregulation. In particular, obese Zucker rats have reduced 11 β -HSD1 mRNA in the hippocampus (Mattsson *et al.*, 2003). The enzyme functions as a reductase in hippocampal neurons (Rajan *et al.*, 1996). The reduced expression of 11 β -

HSD1 may, in part, underlie the reduced sensitivity to glucocorticoid feedback inhibition of the HPA axis and consequent hypercorticonsteronaemia of Zucker rats. Moreover, the feedback defect appears linked more to MR than GR, both in obese rodents (Mattsson *et al.*, 2003) and humans (Jessop *et al.*, 2003). Therefore, studies with GR-selective agonists like dexamethasone may be misleading (Weyer *et al.*, 1997). Whether such effects occur in obese humans is unknown (and is probably unknowable) but 11β -HSD1 is expressed in the human hippocampus (Sandeep *et al.*, 2002) and may be targeted by 11β -HSD inhibitors (Jellinck *et al.*, 1993).

VI. 11β -HSD1 as a Drug Target for Therapy in the Metabolic Syndrome

While the various mouse models described here represent a major series of advances in understanding the role of tissue (intracrine) glucocorticoid levels in generating visceral obesity and aspects of the metabolic syndrome, several discordances in human pathophysiology remain to be adequately accounted for.

First, studies showing increased 11β -HSD1 activity in adipose tissue in humans mainly have investigated abdominal subcutaneous fat. While this is not necessarily as distinct from visceral adipose as other subcutaneous depots — and subcutaneous fat is perhaps the major source of adipose hormones and cytokines — this depot is not the same as visceral fat and probably contributes little, if anything, to the portal venous influx to the liver.

Second, mice are not humans in key aspects of their biochemistry. Thus, murine HDL cholesterol represents the majority of total cholesterol, while in humans, the preponderance is reversed, with most cholesterol transported in low-density lipoprotein (LDL) particles. Mice have corticosterone as their sole glucocorticoid, whereas in humans, cortisol predominates. Corticosterone has a higher affinity for GR and MR. Mice do not spontaneously get atheroma without a specific mutation (e.g., ApoE^{-/-}), whereas humans do.

Third, while human subcutaneous adipose 11β -HSD1 correlates with obesity and increased insulin resistance, it does not correlate closely with the *distribution* of body fat, notably in the visceral compartment (Westerbacka *et al.*, 2003).

Fourth, it remains unclear whether 11β -HSD1 activity is also increased in omental adipose tissue in obese humans and drives a Cushingoid phenotype of central obesity (Bujalska *et al.*, 1997). One study has reported that 11β -HSD1 in omental adipose obtained during surgery is not correlated with obesity. Indeed, when adipocytes were cultured, there was an inverse correlation between 11β -HSD1 and obesity (Tomlinson *et al.*, 2002), although the effects of anaesthesia and/or stress on the subsequent pattern of gene expression and 11β -HSD1 activity and direction are difficult to anticipate. Attempts to demonstrate a close association between increased 11β -HSD1 and intra-adipose cortisol levels or

glucocorticoid-dependent gene transcription have been inconclusive (Lindsay *et al.*, 2003; Wake *et al.*, 2003). It has been proposed that the level of 11 β -HSD1 mRNA expression and total protein may not be the most-important determinant of net cortisol generation from cortisone, since the balance between reductase and dehydrogenase activities may be crucially dependent upon cofactor generation by hexose-6-phosphate dehydrogenase (Draper *et al.*, 2003). While this hypothesis has not been tested definitively, it is notable that subjects with combined 11 β -HSD1 and hexose-6-phosphate dehydrogenase mutations putatively conferring impaired conversion of cortisone to cortisol are not universally lean (Phillipou *et al.*, 1996; A. Jamieson *et al.*, 1999; Draper *et al.*, 2003).

Fifth, understanding the molecular mechanisms regulating 11 β -HSD1 is key. While insulin and other hormones exert indirect effects in rodents, the mechanisms in humans are poorly understood. However, recent data suggest that patients with glucose intolerance have paradoxically normal cortisol secretion, which is perhaps inappropriately high, given enhanced central and peripheral tissue sensitivity to glucocorticoids (Andrews *et al.*, 2002). In these subjects, "normal" 11 β -HSD1 activity in adipose tissue with reduced hepatic activity suggests that tissue-specific changes in 11 β -HSD1 in hyperglycemia differ from those in primary obesity (Andrews *et al.*, 2002). Thus, increased adipose 11 β -HSD1 appears to relate specifically to obesity, rather than to hyperglycaemia or insulin resistance (Westerbacka *et al.*, 2003) *per se*.

Despite these caveats, 11 β -HSD1 inhibition is a tempting target for treatment of the metabolic syndrome and its complications. In this line, at least one selective inhibitor has been formulated and doubtless others will be developed.

A. INHIBITOR STUDIES: OLD AND NEW AGENTS

Carbenoxolone, the hemisuccinate of glycyrrhetic acid, which is the main active derivative of liquorice, has been a prototype, though nonselective, 11 β -HSD1 inhibitor (Stewart *et al.*, 1990). Carbenoxolone enhances insulin sensitivity, as measured by a euglycaemic hyperinsulinaemic clamp (Walker *et al.*, 1995), an effect attributed to enhanced hepatic insulin sensitivity. Stable isotope glucose tracers have been used to demonstrate that, in lean patients with type 2 diabetes, carbenoxolone inhibits hepatic glucose production (Andrews *et al.*, 2003). However, in contrast with enhanced adipose insulin sensitivity and glucose disposal in 11 β -HSD1 KO mice, carbenoxolone has no effect on glucose disposal, perhaps because carbenoxolone poorly inhibits adipose 11 β -HSD1 (Livingstone and Walker, 2003). Moreover, liver 11 β -HSD1 is downregulated in obesity, so that the incremental effect of inhibition may be smaller in the obese (Stewart *et al.*, 1999; Rask *et al.*, 2001,2002). Whether inhibition in liver alone, and resulting enhancement of hepatic insulin sensitivity, is sufficient to confer clinically useful metabolic benefits is uncertain.

Recently, a new, potent, nonsteroidal class of selective inhibitors of 11 β -HSD1 has been described, the arylsulfonamidothiazoles (Barf *et al.*, 2002). These agents inhibit 11 β -HSD1 and enhance insulin action in liver, decreasing PEPCK and glucose-6-phosphatase expression and lowering blood glucose concentrations in KKA^Y diabetic and ob/ob obese mice (Alberts *et al.*, 2002,2003). However, euglycaemic hyperinsulinaemic clamps in mice suggested that the selective 11 β -HSD1 inhibitor did not increase peripheral glucose uptake (Alberts *et al.*, 2003). What remains to be established for 11 β -HSD1 inhibitors is whether their effects extend beyond the liver and include benefits in adipose tissue, where the most-beneficial target is likely to be.

VII. Summary

Close phenotypic similarities exist between rare Cushing's syndrome, caused by excess circulating glucocorticoids, and the much more-common visceral obesity (with or without the metabolic syndrome), although plasma cortisol levels in the latter typically are normal. This chapter reviews recent data suggesting that this paradox may be explained by increased local tissue activity of glucocorticoids in simple obesity syndromes. In particular, we concentrate on the emerging role of 11 β -HSD1, an enzyme that catalyses the regeneration of active glucocorticoids in adipose tissue and liver as both a cause and a therapeutic target in this increasingly prevalent group of disorders.

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