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11β -Hydroxysteroid dehydrogenase type 1 is an important regulator at the interface of obesity and inflammation

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ABSTRACT

Systemic glucocorticoid excess, as exemplified by the Cushing syndrome, leads to obesity and all further symptoms of the metabolic syndrome. The current obesity epidemic, however, is not characterized by increased plasma cortisol concentrations, but instead comes along with chronic low-grade inflammation in adipose tissue and concomitant increased levels of 11 β -hydroxysteroid dehydrogenase type 1 (11 β -HSD1, gene *HSD11B1*), a parameter known to cause obesity in a mouse model. 11 β -HSD1 represents an intracellular amplifier of active glucocorticoid, thus enhances the associated effects on the inflammatory response as well as on nutrient and energy metabolism, and may therefore cause and exacerbate obesity by local increase of glucocorticoid concentrations. Obtained by extensive literature and database searching, the present review includes comprehensive lists of primary glucocorticoid-sensitive genes and gene products as well as of the thus far known regulators of *HSD11B1* expression with implication in inflammation and metabolic disease. Collectively, the data clearly show that, in addition to amplifying active glucocorticoid of multiple additional immunomodulatory and metabolic regulators. Hence, 11 β -HSD1 acts at the interface of inflammation and obesity and represents an efficient integrator and effector of local inflammatory and metabolic state.

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1. Introduction

The striking resemblances between symptoms of hypercortisolism (also known as Cushing syndrome) and symptoms of the metabolic syndrome have initiated intensive investigations on the potential aetiological role of glucocorticoids in the current obesity epidemic. Glucocorticoids (cortisol and cortisone in man, corticosterone and dehydrocorticosterone in rodents) are synthesized in and secreted from the *zona fasciculata* of the adrenal gland, under control of adrenocorticotropic hormone (ACTH, also known as corticotropin) which is secreted from the anterior pituitary gland. The secretion of ACTH in turn is regulated by vasopressin and corticotropin-releasing hormone (CRH), both peptide hormones that originate in the hypothalamus. This complex set of hormone interactions and regulations is often referred to as the hypothalamus-pituitary-adrenal (HPA) axis.

Serum glucocorticoids readily pass cell membranes and exert their intracellular functions by binding to the glucocorticoid receptor (GR), a ligand-activated nuclear receptor which regulates the expression of a plethora of genes involved in various physiological processes including energy metabolism and inflammation. However, this receptor only binds the reduced form, *e.g.* cortisol, with high affinity. Two microsomal enzymes collectively referred to as the 11 β -hydroxysteroid dehydrogenase (11 β -HSD) system interconvert receptor-active cortisol and inert cortisone and, through intracellular cortisol amplification or inactivation, represent an additional regulatory step prior to glucocorticoid action (Fig. 1).

Hence, glucocorticoid functions are subject to several levels of regulation, and an exaggerated glucocorticoid response – as observed in the metabolic syndrome – might be a result of excess glucocorticoid secretion by the HPA axis, increased intracellular GR density or deregulated intracellular glucocorticoid prereceptor metabolism by the 11 β -HSD system. During the last 10 years, evidence has accumulated that strongly argues for an aetiological role of 11 β -hydroxysteroid dehydrogenase type 1 (11 β -HSD1) in obesity and the metabolic syndrome [1–7]. At the same time, increasingly more studies support a function for 11 β -HSD1 in inflammation [8–15]. Interestingly, adiposity has

Abbreviations: ACTH, adrenocorticotropic hormone; AP-1, activator protein-1; C/EBP, CCAAT-enhancer-binding protein; CRH, corticotropin-releasing hormone; GH, growth hormone; GR, glucocorticoid receptor; GREs, glucocorticoidresponse elements; 11β-HSD, 11β-hydroxysteroid dehydrogenase; 11β-HSD1, 11β-hydroxysteroid dehydrogenase type 1; 11β-HSD2, 11β-hydroxysteroid dehydrogenase type 2; HPA, hypothalamus-pituitary-adrenal; IFN-γ, interferon γ; IGF-I, insulin-like growth factor-I; IL, interleukin; IRS1, insulin receptor substrate 1; LXR, liver X receptor; MAPK, mitogen-activated protein kinase; NF-κB, nuclear factor κB; PKA, protein kinase A; PKC, protein kinase C; PPAR, peroxisome proliferatoractivated receptor; SNP, single nucleotide polymorphism; TNF, tumor necrosis factor.

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Fig. 1. Interconversion of cortisone and cortisol by the 11β-HSD system and glucocorticoid responses. 11β-HSD1 reduces receptor-inactive cortisone to cortisol which can bind to the glucocorticoid receptor (GR). The hereby activated GR modulates expression of numerous genes involved in nutrient metabolism as well as inflammation. Physiological effects in terms of metabolism include the stimulation of lipolysis in adipose tissue, of protein degradation and amino acid mobilization from muscle, and of hepatic gluconeogenesis. During the normal inflammatory response, glucocorticoid suppress the initiation and promote the resolution of inflammation. In contrast, glucocorticoid excess can cause all symptoms of the metabolic syndrome including hyperglycaemia, insulin resistance, obesity and hypertension, as well as contribute to chronic inflammatory diseases.

been shown to associate with an increase of macrophage numbers and pro-inflammatory cytokines in adipose tissue [16–19]. Hence, 11β -HSD1 might function as an important regulator at the interface of inflammation and obesity.

Within this review, we will present support for this hypothesis in form of a comprehensive list of GR-regulated genes with implication in metabolic/inflammatory disease and a summary of the thus far published transcription factors/agonists with known implication in energy metabolism and inflammation that modulate intracellular 11 β -HSD1 activity.

2. Glucocorticoids and glucocorticoid receptor in metabolic and inflammatory disease

2.1. Glucocorticoids and glucocorticoid receptor in the aetiology of the metabolic syndrome

Glucocorticoid treatment of inflammatory diseases or excess secretion of cortisol by the adrenal cortex results in the Cushing syndrome, with symptoms closely reflecting the metabolic syndrome, *i.e.* obesity, insulin resistance, hypertension and an unfavourable lipid and lipoprotein profile [20]. Furthermore, monogenic rodent models for the metabolic syndrome, *e.g.* the leptin-deficient ob/ob mouse or the leptin-resistant Zucker rat, display overall increased secretion of glucocorticoids [21,22]. These observations have driven researchers to investigate whether increased adrenal cortisol secretion is a direct cause of the current global obesity epidemic. However, obese patients exhibit mostly unchanged or sometimes even decreased systemic cortisol levels [2]. Hence, common obesity, as usually caused by excess calorie intake and lack of physical activity, does not come along with an HPA-dependent increase in systemic glucocorticoid levels as Cushing syndrome suggests.

Still, invariant blood glucocorticoid concentrations do not rule out an aetiological role for glucocorticoid excess in the metabolic syndrome. Other mechanisms than excess glucocorticoid secretion can trigger an exaggerated glucocorticoid response and might provide an explanation for the striking similarity between symptoms of the metabolic syndrome and the Cushing syndrome. Glucocorticoids exert their intracellular effects via the glucocorticoid receptor (gene name NR3C1), a ubiquitous ligand-activated nuclear receptor. There exist two alternative splice variants of the GR, termed GR α and GR β [23,24]. Whereas GR α is the classic GR, i.e. mediates glucocorticoid effects, GRB does not bind glucocorticoids and thus far its functions are a subject of controversy [25,26]. There is evidence that $GR\beta$ may act as a dominant negative inhibitor of GR α , apparently by the formation of GR α /GR β heterodimers which prevent GRα homodimerization [27,28]. Additionally, specific targets for GRβ-mediated transcriptional activity, independent of glucocorticoids and $GR\alpha$, have been identified recently [24,29]. Hence, not mere NR3C1 overexpression but also dysregulation of the intracellular $GR\alpha/GR\beta$ ratio could underlie altered tissue sensitivity to glucocorticoids in the metabolic syndrome, but this subject has not received much attention so far [30].

In absence of its cognate ligand cortisol, the $GR\alpha$ is retained in the cytoplasm in form of a heteromultimeric complex with chaperones and immunophilins, as e.g. the heat shock proteins HSP70 and HSP90 and FK506-binding proteins FKBP51 and FKBP52 [31,32]. Binding of cortisol leads to the dissociation of the complex and ultimately allows translocation into the nucleus, where the GR homodimer mediates its effects, inducing or repressing target gene transcription (cf. Table 1). Studies with rodent models have shown that selective downregulation of Nr3c1 expression in liver and adipose tissue by antisense oligonucleotides reduced hyperglycaemia and hyperlipidemia [33]. Hence, NR3C1 polymorphisms or altered intracellular GR density could contribute to the pathogenesis of obesity and its associated medical complications. But despite the discovery of several interesting NR3C1 gene polymorphisms their functional implication in the aetiology of the metabolic syndrome is still unclear as appropriate studies have generated conflicting results [34-36]. As to intracellular GR density, studies indicate that GR levels are unchanged or decreased in adipose tissue of obese individuals, thus in part even contrary to anticipated results [30,37]. However, for human skeletal muscle limited findings suggest a positive correlation between insulin resistance, body mass index and NR3C1 expression [38].

2.2. Glucocorticoids and glucocorticoid receptor in inflammation

Glucocorticoids are potent immunosuppressors and as such routinely used in the treatment of chronic inflammatory disease. In physiological concentrations, they exhibit various antiinflammatory effects and, overall, suppress initial events of the inflammatory process and promote the resolution of the inflammation at a later stage. In response to inflammation, the HPA axis is activated by the increase in circulating pro-inflammatory cytokines like tumor necrosis factor (TNF)- α , interleukin (IL)-1 β , IL-6 and the adipokine leptin [39,40]. HPA activation then leads to an increased production of serum glucocorticoids which, by virtue of their antiinflammatory properties, denotes a negative feedback loop for the inflammatory response. Hence, it is not surprising that a deregulation of HPA axis activation contributes to chronic inflammatory disease in several animal disease models [41]. Whether such a deregulation is an aetiological factor in human disease is plausible, but less well established [41-44].

Although deregulated *NR3C1* expression has the potential to contribute to chronic inflammatory disease, only few corresponding studies support this concept, *e.g.* in the context of rheumatoid arthritis [45–47]. Studies on patients suffering from inflammatory bowel disease have provided inconsistent results [48,49]. Hence, similar to observations regarding the metabolic syndrome, altered expression of *NR3C1* appears to be a less important factor in the aetiology of inflammatory disorders.

3. The contribution of 11β-HSD1 to glucocorticoid response

3.1. The 11 β -HSD system in glucocorticoid metabolism

The intracellular bioavailability of active glucocorticoids is modulated by the microsomal 11β-hydroxysteroid dehydrogenases which interconvert cortisol and cortisone in man, and corticosterone and 11-dehydrocorticosterone in rodents (Fig. 1) [50–52]. 11B-hydroxysteroid dehydrogenase type 1 mainly acts as an NADPH-dependent reductase, due to its colocalization with hexose-6-phosphate dehydrogenase in the endoplasmic reticulum [53,54]. In contrast, 11β-hydroxysteroid dehydrogenase type 2 (11β-HSD2) is an NAD⁺-dependent dehydrogenase which inactivates cortisol and corticosterone in man and mice, respectively [55]. As a result, the 11β -HSD1-dependent reaction generates active glucocorticoids which bind to the GR in glucocorticoid target tissues like liver, lung and adipose tissue, while the 11B-HSD2dependent reaction impedes binding of glucocorticoids to the non-selective mineralocorticoid receptor in mineralocorticoid target tissues as kidney and colon. Hence, glucocorticoid response depends not merely on systemic glucocorticoid levels and intracellular GR activity, but also on intracellular amplification or elimination of bioactive glucocorticoids by 11\beta-hydroxysteroid dehydrogenases.

The importance of 11β-HSD1 becomes apparent when considering concentrations of free cortisol relative to free cortisone in the blood. Both plasma cortisone and cortisol levels follow a pronounced circadian rhythm and vary from 5 to 100 nM and from 20 to 400 nM, respectively, with a peak in the morning and a nadir at night [56]. (11B-HSD1 expression itself is not subject to circadian rhythm [57].) However, as 85–95% of total plasma cortisol is bound to plasma proteins, particularly to cortisol-binding protein which does not bind cortisone, free plasma cortisone levels mostly exceed free plasma cortisol levels [58,59]. Hence, following diffusion of cortisone across the cell membrane, 11B-HSD1-mediated cortisone reduction can provide GR-activating cortisol against an unfavourable plasma free cortisol/cortisone ratio. Interestingly, 11β-HSD1 exhibits cooperative kinetics with cortisone, but not with cortisol, in a concentration range of 0.1 nM to 75 µM, suggesting that the enzyme is able to dynamically adapt its activity to fluctuating cortisone levels [51].

It should be noted, as an aside, that 11 β -HSD1 belongs to the superfamily of short-chain dehydrogenases/reductases (SDR) for which recently a new gene nomenclature has been proposed [60]. According to that nomenclature, the gene encoding human 11 β -HSD1 is termed *SDR26C1* and the one encoding human 11 β -HSD2 *SDR9C3* [60]. But as this nomenclature currently does not go beyond human SDR enzymes and is not implemented in all common protein databases yet (*e.g.* UniProtKB), we will continue to use the conventional gene nomenclature in this review, *i.e.* HSD11B1 and HSD11B2 for human 11 β -HSD1 and 11 β -HSD2, respectively, and Hsd11b1 and Hsd11b2 for murine 11 β -HSD1 and 11 β -HSD2.

3.2. 11β -HSD1 in the aetiology of the metabolic syndrome

In contrast to little support for an aetiological role of the GR, compelling evidence has accumulated that argues for 11 β -HSD1 as a major aetiological factor in obesity [2–5]. Studies with transgenic rodents as well as clinical studies involving lean and obese humans lend strong support to this concept: 11β -HSD1^{-/-} mice are protected from hyperglycaemia, display an improved cardioprotective serum lipid profile and enhanced hepatic insulin sensitivity [61–63]. Disruption of *Hsd11b1* in an obesity/diabetes-prone strain results in a more favourable adipose tissue distribution as well as protection from diabetes and weight gain upon high-fat feeding [63]. Moreover, modest (about two-fold) upregulation of

Table 1

Primary glucocorticoid receptor (GR, gene NR3C1) target genes with implications in metabolic disease and/or inflammation. Direct GR-responsive genes were initially compiled using the "Build/Grow Pathway"-tool in Ingenuity Pathway Analysis (www.ingenuity.com), choosing metabolic disease and "inflammatory response/disease" from "Diseases". Data were then complemented with additional relevant data from the literature. They include interactions identified in human, mouse and rat.

GR target gene	Protein name	Type of interaction	Implications in metabolism, metabolic disease and/or inflammation	References (for the interaction)
AGT	Angiotensinogen	Transcriptional repression	Metabolic syndrome (regulation of blood pressure) Angiotensin-2 precursor (potent	[139]
AKAP12	A-kinase anchor protein 12	Transcriptional activation	pressor substance) Inflammatory response Strongly induced by lipopolysaccharide and the	[95]
ALOX5AP	Arachidonate 5-lipoxygenase-activating protein	Transcriptional activation	pro-inflammatory cytokine tumor necrosis factor (TNF)-α [140] <i>Inflammatory response</i> Activator of 5-lipoxygenase-mediated biosynthesis of leukotrienes	[93]
ANGPTL4	Angiopoietin-related protein 4	Transcriptional activation	(inflammatory mediators/chemotactic factors) <i>Metabolism</i> Regulator of glucose homeostasis, lipid metabolism, and insulin sensitivity	[93]
B3GNT5	UDP-GlcNAc:βGal β-1,3-N- acetylglucosaminyl-transferase	Transcriptional activation	Metabolism Glycosphingolipid synthesis	[93]
CCL2	5 C-C motif chemokine 2	Transcriptional repression	Inflammatory response Chemotactic factor, which regulates macrophage recruitment to sites of inflammation [141,142] including adiagese tissue [142]	[93]
CCL20	C-C motif chemokine 20	Transcriptional activation	Inflammatory response Chemotactic factor that attracts lymphocytes and neutrophils, but	[93]
CPS1	Mitochondrial carbamoylphosphate synthetase	Transcriptional activation	Metabolism Urea cycle: plays an important role in removing excess ammonia from	[144]
CRH	Corticotropin-releasing hormone	Transcriptional repression	the cell Feedback regulation Corticotropin-releasing hormone regulates the release of ACTH from the pituitary gland which results in the synthesis and secretion of	[145,146]
CYP27A1	Cytochrome P450 27A1	Transcriptional activation	Metabolism Metabolism of steroid and vitamin	[147]
СҮР2С9	Cytochrome P450 2C9	Transcriptional activation	Metabolism of steroids, fatty acids,	[148]
DNER	Delta/Notch-like epidermal growth factor-related receptor	Transcriptional activation	Inflammatory response Activator of the NOTCH1 pathway which regulates expression of genes involved in pro-inflammatory responses,	[88]
DUSP1	Dual specificity protein phosphatase 1	Transcriptional activation	through activation of NF-ĸB Inflammatory response Phosphatase which dephosphorylates and inactivates mitogen-activated protein kinases (MAPKs), notably including p38 MAPK, an important positive regulator of inflammatory gene	[87]
EKI2	Ethanolamine kinase 2	Transcriptional activation	Metabolism	[93]
FKBP51	FK506-binding protein 5	Transcriptional activation	Firesphorpho biosynthesis Feedback regulation Part of a heteromultimeric cytoplasmic complex with HSP90, HSP70 and GR; dissociates from the complex when GR binds glucocorticoid	[88,149]

Table 1 (Continued)

GR target gene	Protein name	Type of interaction	Implications in metabolism, metabolic disease and/or inflammation	References (for the interaction)
FOXO1	Forkhead box protein O1	Transcriptional activation	<i>Metabolism</i> Insulin-induced transcription factor	[88]
GCN2	eIF2α kinase	Transcriptional activation	Inflammatory response Phosphorylates eIF2 α which leads to induction of NF- κ B	[95]
GHRHR	Growth hormone-releasing hormone receptor	Transcriptional activation	transcriptional activity [150] Metabolism Increases growth hormone gene transcription and secretion which stimulates the liver and other tissues to secrete insulin-like	[151]
GLCCI1	Glucocorticoid-induced transcript 1 protein	Transcriptional activation	growth factor-IA Metabolism Function is unknown, but GLCC11-SNPs associate with diabetes mellitus type 2	[152]
GPR65	Psychosine receptor	Transcriptional activation	Inflammatory response Receptor for psychosine, a glycosphingolipid, which may activate the expression of inflammatory cytokines [153]	[95]
HSD11B1	11β-Hydroxysteroid dehydrogenase type 1	Transcriptional activation	Metabolism Catalyzes the conversion of inert cortisone to GR-binding cortisol, thus amplifying glucocorticoid	[131,134]
HSD11B2	11β-Hydroxysteroid dehydrogenase type 2	Transcriptional activation	Metabolism Catalyzes the conversion of cortisol to the inactive metabolite cortisone in mineralocorticoid target tissues, thus protecting the non-selective mineralocorticoid receptor from occupation by elucocorticoids	[154]
HTR1A	5-hydroxytryptamine receptor 1A	Transcriptional repression	Inflammatory response/metabolic syndrome (regulation of blood pressure) Receptor for 5-hydroxytryptamine (serotonin), a mediator of the early inflammatory response and regulator of vascular tone	[155]
IFNB1	Interferon β	Transcriptional activation	Inflammatory response Part of the innate immune response, has antiviral, antibacterial and anticancer activities	[156]
IGF1	Insulin-like growth factor-l	Transcriptional activation	Metabolism Growth factor, in structure and function related to insulin	[157]
IGFBP1	Insulin-like growth factor-binding protein 1	Transcriptional activation	Metabolism Prolongs the half-life of IGFs and thus modulates the growth promoting effects of IGFs	[88,158,159]
IL6	Interleukin 6	Transcriptional repression	Inflammatory response Inflammatory cytokine	[160–162]
IL7R	Interleukin-7 receptor subunit α	Transcriptional activation	Inflammatory response Receptor for interleukin-7, an inflammatory cytokine	[163]
IL8	Interleukin 8	Transcriptional repression	Inflammatory cytokine	[164,165]
IL11	Interleukin11	Transcriptional repression	Inflammatory response	[93]
INSR	Insulin receptor	Transcriptional activation	Metabolism Receptor that mediates the metabolic functions of insulin	[166]
ІР6КЗ	Inositol hexakisphosphate kinase 3	Transcriptional activation	Metabolic mitchins of insulin Metabolism Involved in the metabolism of inositol phosphates which may act as messengers of cellular energy status [167]	[88]
IRS1	Insulin receptor substrate 1	Transcriptional repression	Metabolism Key player in the insulin signalling pathway	[168]

Table 1 (Continued)

GR target gene	Protein name	Type of interaction	Implications in metabolism, metabolic disease and/or inflammation	References (for the interaction)
JUN	Proto-oncogene c-jun, forms the heterodimeric transcription factor AP-1 with a member of	Inhibition by direct interaction	Inflammatory response AP-1 is a pleiotropic transcription factor involved in many biological	[169]
KITLG	Kit ligand (stem cell factor)	Transcriptional activation	Inflammatory response	[170]
MGAM	Intestinal maltase-glucoamylase	Transcriptional activation	Major mast cell growth factor Metabolism	[93]
MGMT	O ⁶ -methylguanine-DNA	Transcriptional activation	Metabolism	[172]
	methyl-transferase		Repairs alkylated guanine in DNA; MGMT expression is reduced in patients with both type 1 and type 2 diabetes [171]	
MIF	Macrophage migration inhibitory factor	Transcriptional activation	Inflammatory response Pro-inflammatory cytokine, counter-regulates anti-inflammatory glucocorticoid	[97]
МҮС	Myc proto-oncogene protein	Transcriptional activation	effects [98] Metabolic disease Trigger of apoptosis in β -cells, induced by hyperglycaemia; may thus play a role in β -cell	[175]
NFKBIA	$NF\kappa B$ inhibitor α	Transcriptional activation	dysfunction in diabetes [173,174] Inflammatory response Inhibits the activity of dimeric NFκB/REL complexes by	[176]
NOTCH4	Neurogenic locus notch homolog protein 4	Transcriptional activation	cytoplasmic sequestration Metabolic disease A SNP in the 5'-region of NOTCH4 is associated with type 1 diabetes risk [177]; an intronic SNP is a	[179]
PCK1	Phosphoenolpyruvate carboxykinase	Transcriptional activation	susceptibility marker for rheumatoid arthritis [178] <i>Metabolism</i> Catalyzes the conversion of oxaloacetate to phosphoenolpyruvate, the	[180]
PDE4B	cAMP-specific 3',5'-cyclic phosphodiesterase 4B	Transcriptional repression	rate-limiting step in gluconeogenesis Inflammatory response May be involved in mediating central nervous system effects of	[93]
PIK3R1	Phosphatidylinositol 3-kinase regulatory subunit α	Binding to promoter region	anti-inflammatory agents. <i>Metabolism</i> Necessary for the insulin-stimulated increase in glucose uptake and glycogen synthesis in insulin-sensitive	[181]
PLA2G4A	Cytosolic phospholipase A2	Transcriptional activation ^a	t issues Inflammatory response/metabolism Responsible for the liberation of arachidonic acid from membrane phospholipide	[182]
РОМС	Pro-opiomelanocortin	Transcriptional repression	Freedback regulation ACTH precursor; ACTH stimulates the adrenal glands to release cortisol	[145,183]
PPARA	Peroxisome proliferator-activated receptor α	Transcriptional activation	Metabolism Receptor that activates the transcription of the gene for acyl-CoA oxidase and therefore controls the peroxisomal B-oxidation pathway of fatty acids	[184]
PTGS2	Prostaglandin G/H synthase 2	Transcriptional repression	Inflammatory response/metabolism Catalyses the formation of prostaglandin H ₂ from arachidonic acid, the rate-limiting step in prostaglandin synthesis	[93]
PTPN22	Tyrosine-protein phosphatase non-receptor type 22	Transcriptional activation	Inflammatory response/metabolic disease A PTPN22 SNP is associated with diabetes type 1 and inflammatory/autoimmune disorders [185]	[95]

Table 1 (Continued)

GR target gene	Protein name	Type of interaction	Implications in metabolism, metabolic disease and/or inflammation	References (for the interaction)
RELA	Nuclear factor NF-кВ p65 subunit	Inhibition by direct interaction	Inflammatory response Pleiotropic transcription factor involved in many biological processes including inflammation. Crosstalk between GR and NF-κB leads to transcriptional repression of NF-κB-dependent pro-inflammatory genes as, <i>e.g.</i> <i>ICAM</i> or <i>TNF</i> (encoding intercellular adhesion molecule and TNF-α, respectively) [06]	[89]
SCNN1A	Amiloride-sensitive sodium channel subunit $\boldsymbol{\alpha}$	Transcriptional activation	Metabolic syndrome Sodium permeable non-voltage-sensitive ion channel which contributes to the regulation of blood pressure in the kidney	[186,187]
SERPINE1	Plasminogen activator inhibitor 1	Transcriptional repression	Inflammatory response/metabolic disease Involved in the regulation of fibrinolysis. Its overexpression correlates positively with BMI and is, among others, mediated by dietary factors and inflammatory cvtokines [188]	[189]
SGK1	Serine/threonine-protein kinase Sgk1	Transcriptional activation	Inflammatory response Protein kinase that may contribute to hypertension and diabetic nephropathy; associates with NF- κ B inhibitor kinase β leading to activation of the NF- κ B pathway [190]	[88,191]
SLC10A2	lleal sodium/bile acid cotransporter	Transcriptional activation	Metabolism Plays a key role in cholesterol metabolism	[192]
SPP1	Osteopontin (OPN)	Transcriptional activation	Inflammatory disease/metabolic disease Highly expressed in chronic inflammatory and autoimmune diseases; plays a major role in the recruitment of monocytes-macrophages, including in adipose tissue, and the regulation of cytokine production in macrophages, dendritic cells, and T-cells during the inflammatory response [103,193]	[194]
ΤΑΤ	Tyrosine aminotransferase	Transcriptional activation	Metabolism Catalyzes the reaction of L-tyrosine and 2-oxoglutarate to 4-hydroxyphenylpyruvate and L-glutamate and thus provides gluconeogenic substrates	[195–197]
THBD	Thrombomodulin	Transcriptional activation	Inflammatory response Endothelial cell receptor that in a complex with thrombin activates protein C which suppresses cytokine amplification by monocytes and attenuates pro-inflammatory intracellular signalling pathways in endothelial cells [198]	[88,93]
TLR2	Toll-like receptor 2	Transcriptional activation	Inflammatory response Mediator of innate immune response, entailing NF-κB activation, cytokine secretion and the inflammatory response	[199]
TSC22D3	TSC22 domain family protein 3	Transcriptional activation	Inflammatory response Plays a role in the anti-inflammatory and immunosuppressive effects of glucocorticoids and IL-10 in macrophages	[93]

^a Transcriptional activation of *PLA2G4A* has so far only been detected in amnion fibroblasts. The classical glucocorticoid effect on *PLA2G4A* expression is the powerful inhibition of induction by pro-inflammatory cytokines, *i.e.* the opposite effect.

Hsd11b1 expression selectively in adipose tissue of mice leads to a phenotype that faithfully mimics all symptoms of the metabolic syndrome [1]. Finally, most clinical studies showed an increase of adipose tissue HSD11B1 expression and/or activity in human obesity (reviewed in Ref. [4]). 11 β -HSD1 has thus emerged as a major potential drug target for the treatment of obesity and its associated medical conditions [4,64-69]. To date, however, the regulation of HSD11B1 expression in adipose tissue and the mechanisms underlying the development of insulin resistance remain poorly understood. Interestingly, a recent report established a strong connection between a key player in insulin signalling, the insulin receptor substrate 1 (IRS1), and 11β-HSD1 [70]. According to the results of this study, glucocorticoid-induced insulin resistance in skeletal muscle is a result of downregulation of IRS1 gene expression and inactivation of IRS1 protein by serine phosphorylation, which collectively leads to disruption of the insulin signalling cascade. Notably, both events are dependent on 11β -HSD1, as they could be abolished by the addition of a selective 11β -HSD1-inhibitor [70]. Another recent study explored single nucleotide polymorphisms (SNPs) in this context, but no significant correlations between common SNPs and type 2 diabetes have been found [71].

3.3. 11β -HSD1 in inflammation

At least some of the immunomodulatory effects of glucocorticoids in the inflammatory response are dependent on 11β-HSD1 activity. For instance, 11β-HSD1-deficient mice suffering from experimental arthritis exhibit a delayed resolution of the inflammatory response, in part possibly due to attenuated macrophage phagocytosis of leukocyte apoptotic bodies [8,9]. As glucocorticoids regulate both the suppression of the early and the promotion of the late phase of the inflammatory response, it is conceivable that overall deregulated, *i.e.* both decreased and increased, glucocorticoid levels could contribute to chronic inflammatory disease. Although certainly not a characteristic feature for all, some chronic inflammatory conditions indeed have been associated with increased HSD11B1 expression, in particular inflammatory diseases of the digestive tract, e.g. inflammatory bowel disease and colitis [11,72-74], but also atherosclerosis [75,76] (Fig. 1). These observations are in line with numerous reports on induction of HSD11B1 expression by the pro-inflammatory cytokines TNF- α and IL-1 β in various cell types and lines including fibroblasts, adipocytes, osteoblasts and smooth muscle cells [12-14,77-85] (Table 2).

3.4. Primary GR α -target genes in metabolism and inflammation

Upregulation of 11β -HSD1 activity in adipose tissue of the obese and in inflammatory disease leads to intracellular amplification of cortisol and enhances activation of $GR\alpha$, expression of which is largely unchanged under the mentioned disease conditions, as already mentioned under Section 2. In other words, the ultimate effect of HSD11B1 overexpression is an increase in GR α -dependent regulation of gene expression. Two major mechanisms of GRamodulated gene transcription have been investigated intensely, namely direct DNA binding and antagonism of other transcription factors by direct protein-protein interactions [86]. For regulation through direct DNA binding, the conventional view is that the GR α dimer binds palindromic glucocorticoid-response elements (GREs) in promoter regions of primary GR α target genes, leading to transactivation or transrepression. However, it should be mentioned that recent reports have shown the $GR\alpha$ dimerization domain to be dispensable for transactivation of some glucocorticoid-responsive genes, as e.g. DUSP1 and IP6K3 [87,88]. The second mechanism relies on non-classic, so-called "tethering GREs": Here, GRa does not interact with the DNA itself but binds to other transcription factors, impedes binding to the promoters of their target genes and thus opposes their action. Important examples for this type of negative transcription factor crosstalk are activator protein-1 (AP-1) and nuclear factor κB (NF- κB), which both are crucial for the inflammatory process as they induce a wide range of genes involved in inflammation [89,90]. Traditionally, the antiinflammatory properties of glucocorticoids were to the largest part ascribed to the latter mechanism, *i.e.* antagonism of proinflammatory transcription factors, while glucocorticoid-induced transactivation of anti-inflammatory genes was considered to have relatively little importance for the inflammatory process. However, it becomes increasingly clear that this is not true as, in fact, several important anti-inflammatory mediators are glucocorticoidinduced [91,92]. For instance, the above mentioned DUSP1 has only recently been shown to contribute significantly to the antiinflammatory effects of glucocorticoids in mouse macrophages by deactivating mitogen-activated protein kinases (MAPKs), as e.g. p38 MAPK and c-Jun N-terminal kinase (JNK) [87].

A number of studies have been performed to identify GRa target genes at a larger scale, including some with bias towards primary target genes [88,93-95]. In order to compile these target genes we took advantage of a bioinformatic tool, the Ingenuity Pathways Analysis (www.ingenuity.com), which allows for assessing and building comprehensive molecular networks based on an extensive knowledge database. We selected only direct interactions and genes and gene products known to be implicated in metabolism and/or the inflammatory process. The results obtained were complemented and curated by manual literature research and are listed in Table 1. In efforts to confine the list to primary GRa targets we included only genes or gene products exhibiting direct interactions with $GR\alpha$ and GR targets derived from the above mentioned studies with bias towards the detection of primary target genes. Hence we excluded target genes known to be regulated via a tethered mechanism, as e.g. TNF and ICAM1, as they are already covered by including NF-κB as direct interaction partner into the table [96]. In total, we obtained 59 direct target genes and gene products. Of those, 24 exert functions related to the metabolic syndrome, e.g. hypertension (AGT, HTR1A, SCNN1A, and SGK1), hyperglycaemia (MGAM, PCK1, and TAT) and insulin resistance (ANGPTL4, FOXO1, GHRHR, GLCCI1, HSD11B1, IGF1, IGFBP1, INSR, ISR1, MGMT, MYC, NOTCH4, PCK1, PIK3R1, PPARA, PTPN22, and SERPINE1). Other affected metabolic pathways include glycosphingolipid and phospholipid synthesis (B3GNT5 and EKI2), the urea cycle (CPS1), cholesterol, steroid, prostaglandin and xenobiotic metabolism (CYP27A1, CYP2C9, HSD11B1, HSD11B2, PLA2G4A, PTGS2, and SLC10A2) and the metabolism of inositol phosphates (IP6K3). As to genes associated with the inflammatory response, our database search yielded 28 target genes and gene products, including a subset involved in the metabolism and signal transduction of inflammatory mediators (ALOX5P, GPR65, HSD11B1, HSD11B2, HTR1A, PDE4B, PLA2G4A, and PTGS2), a subset involved in the NF-κB (DNER, GCN2, RELA, NFKBIA, and TLR2) and the AP-1 pathway (JUN), as well as chemotactic factors (CCL2 and CCL20), inflammatory cytokines/cytokine receptors (IFNB1, IL6, IL7R, IL8, IL11, KITLG, and MIF) and a subset providing other immunomodulatory functions (AKAP12, DUSP1, SPP1, THBD, and TSC22D3). Notably, several target genes were found that provide glucocorticoid feedback regulation on four distinct levels: First, feedback regulation of glucocorticoid secretion under the HPA axis involves CRH and POMC. Second, augmented expression of FKBP51 might contribute to increased cytoplasmic sequestration of the GR. Third, induction of HSD11B2 may result in enhanced glucocorticoid inactivation and finally, the glucocorticoid-inducible gene MIF encodes a macrophage cytokine that counter-regulates anti-inflammatory effects of glucocorticoids such as transcriptional repression of pro-inflammatory cytokines [97,98].

Table 2

Regulation of 11 β -HSD1 expression by cytokines/hormones/kinase activators/transcription factor agonists with implication in inflammatory or metabolic disease in different cell types and lines. Upwards arrows depict upregulation, downwards arrows downregulation of *HSD11B1* expression/11 β -HSD1 activity.

Regulator	Implication in inflammatory or metabolic disease	Effect on <i>HSD11B1</i> expression	References
Adrenergic receptor agonists (salbutamol, clonidine)	Adrenergic receptors are targets of catecholamines (<i>e.g.</i> noradrenaline, adrenaline) and thus implicated in mobilization of energy in response to stress	↑ Activity (salbutamol) ↓ Activity (clonidine)	[78]
Eicosanoids (15-Deoxy- Δ 12,14-PGJ2, prostaglandin F2 α)	15-Deoxy- Δ 12,14-PGJ2 is a putative (albeit disputed) endogenous PPARγ agonist [200] (also see PPARγ agonists below). Prostaglandin F2α belongs to the pro-inflammatory prostaglandins, which activate the inflammatory response	↑ Protein and activity	[14,201]
Growth hormone (GH)	Stimulates synthesis of IGF-I (see below); regulator of muscle mass and body growth	↓ Activity [109] - No effect [78]	[14,50,78,106,108–110,202–208]
Glucocorticoid receptor (GR) agonists (cortisol/corticosterone, dexamethasone)	GR regulates a multitude of genes involved in inflammation and metabolic disease (cf. Table 1). Glucocorticoids are potent inflammatory mediators, they suppress the initiation and promote the resolution of inflammation. Glucocorticoid excess can contribute to chronic inflammatory disease and leads to all symptoms of the metabolic syndrome	↑ mRNA and activity ↑↑↑ (in synergy with TNF-α/IL-1β) [85,138] ↔ Can antagonize induction by insulin	[38,75,79,80,85,107,109–112,131,132,138,204,209–215]
Interferon γ (IFN-γ)	Cytokine with important modulatory functions in the inflammatory response; potent activator of macronhages	↔ Antagonizes induction by IL-4 and II -13	[15]
Interleukin (IL) 1α, IL-1β	Pro-inflammatory cytokine; induces acute phase reaction and fever	↑ mRNA and activity ↑↑↑ (in synergy with dexamethasone or cortisol) [85,138]	[12-15,77-81,85,109,115,138,216]
IL-4	Inflammatory cytokine with major functions in allergic inflammation	↑ mRNA and activity	[15]
IL-6	Pro-inflammatory cytokine; induces acute phase reaction	↑ Activity	[14,217]
IL-13	Anti-inflammatory cytokine; inhibits the production of macrophage inflammatory cytokines	↑ mRNA and/or activity	[15,135]
Insulin	Crucial regulator of blood sugar; increases uptake of glucose in liver, muscle, and fat tissue, stimulates glycogen synthesis and glycolysis in the liver	↓ mRNA and/or activity ↑ mRNA and activity ↔ Can antagonize induction by TNF-α	[79,82,107–112]
Insulin-like growth factor-I (IGF-I)	Crucial regulator of muscle mass; stimulates protein synthesis and inhibits protein degradation in skeletal muscle [218]	↓ Activity	[14,106]
Leptin	Regulator of body weight; controls food intake and stimulates energy expenditure, but has also pro-inflammatory functions [219]	↑ Activity	[14,220]
Liver X receptor (LXR) agonist (T0901317)	The nuclear receptor LXR, activated by oxysterols and intermediates of cholesterol biosynthesis, regulates cholesterol homeostasis and hepatic lipogenesis [125]; also modulates inflammatory signalling in macrophages by <i>e.g.</i> repressing pro-inflammatory genes [126–128]	\downarrow mRNA and activity	[121]
Tumor necrosis factor α (TNF- α)	Pro-inflammatory cytokine, induces acute phase reaction, activates; NF-κB and AP-1	↑ mRNA and activity ↑↑↑ (in synergy with dexamethasone or cortisol) [85,138]	[12–15,77–79,81–85,138]

Table 2 (Continued)

Regulator	Implication in inflammatory or metabolic disease	Effect on <i>HSD11B1</i> expression	References
PPARα agonists (fenofibrate, bezafibrate, WY14,643)	The nuclear receptor PPARα, activated by polyunsaturated and some medium-chain saturated fatty acids, regulates intracellular lipid transport and metabolism; transrepresses activities of pro-inflammatory transcription factors including NF-κB and AP-1 [127–129]	↓ mRNA	[117,123,124]
PPARγ agonists (bezafibrate, rosiglitazone, TZD2, L-805645, COOH)	PPARy, activated by polyunsaturated fatty acids and 15-deoxy-Δ12,14-PGJ2, regulates intracellular lipid transport and metabolism; transrepresses activities of pro-inflammatory transcription factors including NF-κB and AP-1 [127–129]	↓ mRNA and activity ↑ mRNA (COOH)	[118–123]
Protein kinase A (PKA) activators (Forskolin, 8-bromo-cAMP, Dibutyryl-cAMP)	Activated by cAMP, PKA acts as a central switch from anabolic to catabolic pathways including glycolysis and β -oxidation [221–223]; also phosphorylates proteins with central functions in inflammation such as the NF- κ B subunit RelA [224] and 5-lipoxygenase, an enzyme involved in the biosynthesis of leukotrienes [225]	↑ mRNA and activity [115,133] ↓ Activity [107,110]	[107,110,115,133]
Protein kinase C (PKC) activators (Phorbol 12-myristate 13-acetate, 6-[N-decylamino]-4-hydroxy- methylinole)	Activated endogenously by diacylglycerols, protein kinase C mediates inhibition of components of the insulin signalling cascade by phosphorylation, most importantly of insulin receptor substrate 1 (IRS1) [113,114]	↑ mRNA [115] ↓ Activity [116]	[115,116]
Retinoic acid, RARγ agonist ER36009	Participates in the direct and indirect regulation of a number of genes involved in inflammation and energy metabolism, including genes encoding key mediators such as IL-1β, OPN, IL-6, insulin, AP-1, leptin, PPARα, PPARγ, and more [130]	\downarrow mRNA and activity	[121,136]
(1,25-Dihydroxy-) Vitamin D3	Vitamin D3 may protect from type 2 diabetes; the underlying mechanisms are poorly understood [226,227]	\uparrow mRNA and activity	[15,228]

Normal weight

Obesity



Fig. 2. Correlation between weight gain and adipose tissue levels of 11β-HSD1. In the course of weight gain, nutrient excess leads to ER stress and microhypoxia, provoking an inflammatory response which manifests itself in the recruitment of macrophages to adipose tissue. 11β-HSD1 is induced upon differentiation of monocytes to macrophages. Adipose tissue macrophages secrete pro-inflammatory cytokines, particularly TNF-α, and thus can entail induction of *HSD11B1* expression in adipocytes. Local 11β-HSD1 levels increase as a combined result of enhanced macrophage and adipocyte *HSD11B1* expression. This leads to local glucocorticoid excess which in turn can sustain and/or exacerbate obesity, reflecting a local Cushing syndrome-like effect.

3.5. 11β -HSD1 at the interface of inflammation and the metabolic syndrome

Several pieces of evidence argue for an important role of chronic "low grade" adipose tissue inflammation during the development of diet-induced visceral obesity and insulin resistance [99]. It was established more than 15 years ago that obesity is accompanied by an induction of TNF expression in white adipose tissue as well as an increase of systemic TNF- α protein, depletion of which leads to increased insulin sensitivity [17]. By now macrophages have been identified as the main origin of adipose tissue-secreted TNF- α and it is well acknowledged that weight gain is associated with increasing macrophage recruitment to adipose tissue [16,19,100]. HSD11B1 gene expression is induced in monocytes during differentiation to macrophages [15] and moreover, in adipocytes and adipose stromal cells, HSD11B1 gene expression is induced by TNF- α and IL-1 β [14,78,82] and correlates strongly and positively with adipocyte size [1,101]. This increase of both macrophage and adipocyte 11β-HSD1 activity in adipose tissue probably raises local tissue and hepatic portal vein cortisol concentrations entailing a Cushing syndrome-like effect, i.e. inducing hyperglycaemia and insulin resistance followed by exacerbation of obesity, without affecting overall systemic glucocorticoid concentrations (Fig. 2).

Although an attractive hypothesis, it raises questions regarding the well-known immunosuppressant effects of glucocorticoids in contrast to the persistent inflammatory state in adipose tissue in obesity. Glucocorticoids repress the expression of macrophage cytokines, like TNF- α and IL-1 β , and chemotactic factors like *CCL2* and *ICAM1*, both involved in macrophage recruitment to sites of inflammation. The activated glucocorticoid receptor physically interacts with two major inflammatory transcription factors, NF- κ B and AP-1, counteracting induction of their target genes [89,90]. Should not visceral glucocorticoid production contribute to the resolution of the inflammatory state rather than sustain or even exacerbate it?

In fact, there are actually some inflammatory mediators expression of which is induced by glucocorticoids rather than suppressed. Two important examples are the pro-inflammatory cytokines macrophage migration inhibitory factor (MIF) and osteopontin (OPN, gene name *SPP1*) (Table 1). MIF, for instance, can override

anti-inflammatory glucocorticoid effects, including the repression of TNF, IL1, IL6 and PTGS2 gene expression [97,98]. Similar to HSD11B1, MIF expression correlates positively with adipocyte size and hepatic insulin resistance [102]. The secreted matrix glycoprotein OPN has recently been recognized as a major determinant in macrophage infiltration of adipose tissue [103]. SPP1 $^{-/-}$ mice fed a high-fat diet display decreased macrophage and pro-inflammatory cytokine content in adipose tissue and reduced insulin sensitivity [103]. In comparison, the gene encoding C-C motif chemokine 2 (gene name CCL2), repressed by cortisol, appears not to be critical in the recruitment of macrophages as CCL2^{-/-} mice on a high-fat diet showed no reductions in adipose tissue macrophages [104]. Genes encoding other inflammatory mediators which are positively regulated by cortisol include ALOX5AP, an activator of leukotriene synthesis and *DNER*, an activator of NF-κB-dependent signal transduction pathways [88,93]. On the whole, it appears that cortisol can to some extent counter-balance or overrule its immunosuppressant effects by inducing other pro-inflammatory feed-forward mechanisms. This offers a possible partial explanation to the chronic low-grade nature of the inflammatory state in adipose tissue observed in obesity, but maybe chronic inflammatory states associated with increased HSD11B1 expression in general.

3.6. Regulation of HSD11B1 expression by immunomodulatory and metabolic factors

During the last 15 years, numerous studies have assessed the regulation of *HSD11B1* expression by cytokines, hormones, kinase activators, and transcription factor agonists in mammalian cells [105]. Overall, these studies have established that *HSD11B1* expression is subject to regulation by a remarkable number of immunomodulatory and metabolic regulators (Table 2). These include a range of inflammatory cytokines, *e.g.* interferon γ (IFN- γ), interleukins IL-1, IL-4, IL-6, IL-13, and TNF- α , which, with the exception of IFN- γ , mostly upregulate *HSD11B1* expression, albeit in a highly tissue-specific manner (extensively reviewed in Ref. [105]). For instance, TNF- α and IL-1 β induce *HSD11B1* expression in human adipocytes, adipose stromal cells, smooth muscle cells, osteoblasts and fibroblasts, but not in human monocytes and pri-



Fig. 3. 11β-HSD1 as an integrator of local metabolic and inflammatory state. Intracellular 11β-HSD1 activity is subject to regulation by multiple metabolic and inflammatory messengers, including components of the insulin signalling pathway, the GH/IGF-I axis, glucocorticoids, and inflammatory cytokines. Increased or decreased intracellular 11β-HSD1 activity leads to the corresponding change in the glucocorticoid response, with impact on the expression and activity of numerous key players in inflammation and metabolism including abundant possibilities in feed-forward or feedback mechanisms. Upwards arrows depict upregulation, downwards arrows downregulation of *HSD11B1* expression/11β-HSD1 activity. GH: growth hormone; IGF-I: insulin-like growth factor-I, and PKC: protein kinase C.

mary hepatocytes [12-15,78,80,81,85]. As to metabolic regulators, 11β-HSD1 activity is inhibited by the growth hormone/insulinlike growth factor-I (GH/IGF-I) axis in adipocytes, but again not in primary hepatocytes [14,78,106]. Diverse effects of insulin have been reported: Insulin alone may exhibit no effect, an inhibitory effect, or a stimulatory effect on HSD11B1 expression/11β-HSD1 activity, insulin can antagonize TNF- α -mediated induction and induction by insulin can be counteracted by dexamethasone [79,82,107-112]. Activators of protein kinase C, which inhibits components of the insulin signalling cascade by phosphorylation, also variably affect 11β-HSD1 activity [113-116]. Moreover, a role of catecholamines like adrenaline and noradrenaline is likely, as adrenergic receptor agonists can modulate HSD11B1 expression [78]. Furthermore, several key regulators of lipid metabolism and transport including peroxisome proliferator-activated receptor $(PPAR)\alpha$, PPAR γ , and liver X receptor (LXR) participate in the regulation of HSD11B1 expression [117–124]. It is striking that many regulators of HSD11B1 expression are involved in the regulation of both inflammatory and metabolic processes, as e.g. glucocorticoids, leptin, LXR, PPAR α , PPAR γ , and retinoic acid (Table 2) [125-130]. To complete the circle, many of these factors are encoded or regulated by glucocorticoid-sensitive genes, including IGF-I (encoded by IGFI, regulated by IGFBP1), growth hormone (regulated by GHRHR), insulin (effects mediated via INSR and ISR1), interleukin 6 (encoded by IL6), PPAR α (encoded by PPARA), TNF- α (encoded by *TNF*), and, of course, 11 β -HSD1 itself (cf. Table 1). Hence, a complex molecular network composed of a multitude of inflammatory and metabolic factors with abundant possibilities of feed-forward or feedback regulation mechanisms underlies the regulation of HSD11B1 expression. 11β-HSD1 could thus act as an efficient intracellular integrator and effector of the local inflammatory and metabolic state (Fig. 3).

The underlying mechanisms for the emerging tissue-specific expression pattern are poorly understood. Relatively few studies have addressed the implicated transcription factors in cytokinemediated induction of *HSD11B1* expression. According to these studies, CCAAT-enhancer-binding proteins (C/EBPs) appear to assume a basal role in the regulation of *HSD11B1* expression, as they contribute to TNF- α -, IL-1 β -, cAMP-, and glucocorticoid-induction, the latter being additionally mediated by the GR [80,81,83,84,131–134]. Further studies suggest a significant role of the transcription factor activator protein-1 (encoded by *JUN*, see Table 1) in mediating upregulation by IL-13 and TNF- α [79,84,135]. A role for the nuclear receptors PPAR α and PPAR γ was suggested, as corresponding agonists affect *HSD11B1* expression [14,117–124]. Finally, retinoic acid receptor γ (RAR γ) appears to mediate downregulation of *HSD11B1* expression in response to retinoic acid or other RAR γ agonists [118,136,137].

It should be noted that the studies cited in Table 2 only rarely considered the complex mixture of interacting hormones and growth factors that regulates *HSD11B1 in vivo*. Only few studies have assessed combined effects of pro-inflammatory cytokines, components of the insulin signalling pathway, and glucocorticoids. For instance, dexamethasone and insulin show no effect on *HSD11B1* expression in the hepatocyte line HuH7 when given separately, but lead to a more than two-fold induction in combination [79]. Also TNF- α /IL-1 β and glucocorticoids can function in synergy to increase *HSD11B1* expression in fibroblasts and osteoblasts [79,85,138]. Therefore it is likely that studies addressing glucocorticoid-sensitive genes in the context of obesity and insulin resistance would profit from being conducted in a controlled background of TNF- α and/or insulin excess to better mimic an inflammatory state and/or hyperglycaemic conditions.

4. Conclusions

For a long time, glucocorticoid excess has been known to cause obesity. From all possible regulatory levels of glucocorticoid action including the HPA axis, intracellular GR α density, and prereceptor metabolism, the latter, in the form of the enzyme 11β -HSD1, has emerged as the most convincing determinant. 11B-HSD1 is thus nowadays recognized as a promising drug target in the current obesity epidemic. Through amplification of receptor-active glucocorticoid, 11B-HSD1 enhances the glucocorticoid response with far-ranging consequences for the expression of genes with implication in metabolic disease and inflammation. At the same time, expression of HSD11B1 itself is subject to multifactorial control, e.g. by cortisol, insulin, pro-inflammatory cytokines and many more regulatory factors with central functions in inflammation and nutrient/energy metabolism. Hence, 11β-HSD1 can act as an intracellular processor of multiple metabolic and inflammatory signals and subsequently modulate both processes profoundly. In conclusion, considering the widely accepted concept of an inflammatory element in the aetiology of obesity, this enzyme is likely to play an important causative role in the development of the metabolic syndrome at the interface of inflammation and obesity.

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