**Glucocorticoid-Induced Metabolic Disturbances are Exacerbated in Obesity**

Innocence Harvey, Erin J. Stephenson, JeAnna R. Redd, Quynh T. Tran, Irit Hochberg, Nathan Qi and Dave Bridges

**Abstract**

Obesity and chronically elevated glucocorticoids result in similar co-morbidities, but the effect of a combination of these ailments on metabolic outcomes is unclear. Measures of glucose homeostasis and markers of hepatic lipid accumulations were assessed to determine whether obesity exaggerated the effects of dexamethasone-induced metabolic disturbances. The combination of obesity and glucocorticoids resulted in synergistic elevations in hepatic steatosis and insulin resistance and this was matched with synergistic elevations in markers of lipolysis. These findings suggest lipolysis may be a key player in glucocorticoid-induced insulin resistance and fatty liver in people with obesity.

**Introduction**

Obesity has become an epidemic in the US and other developing countries, and though Cushing’s disease is rare, it is estimated that 1-3% of US, UK and Denmark populations are prescribed corticosteroids at any given time (1–4). Comparing the increased levels/amounts of corticosteroid prescription with the prevalence of overweight and obesity in America, it is likely that the combination of obesity and glucocorticoid excess is present in many individuals. Given the similar co-morbidities associated with obesity and chronically elevated glucocorticoids, we hypothesized that the combinations of these two conditions would lead to worse metabolic outcomes than either of them alone. This is supported by studies in rats showing that corticosterone and high-fat diets combine to cause worsened insulin resistance and non-alcoholic fatty liver disease (NAFLD; (5,6)).

Obesity is often accompanied by a multitude of metabolic complications, such as insulin resistance (7–9) and NAFLD (10,11). Similarly, chronically elevated glucocorticoids, such as is seen in Cushing’s disease or corticosteroid treatment, often causes impaired glucose tolerance or type 2 diabetes (12,13) and fatty liver (14,15) and changes in fat mass and distribution (16). Though these diseases and their co-morbidities are well characterized, underlying mechanisms caused by the disease subsequently leading to these metabolic complications have not been identified. Moreover, to our knowledge, the combined effect of obesity and elevated glucocorticoids on the severity of the aforementioned outcomes has yet to be investigated.

There is an array of physiological changes that occur as a result of elevated glucocorticoids including decreased lean mass (17–19), increased fat mass (18,20,21) and increased lipolysis (22–24), all of which have been associated with decreased insulin sensitivity (25–27). Likewise, obesity, insulin resistance and increased fatty acid flux are associated with NAFLD (10,28–30). It has also been demonstrated that inhibition of lipolysis promotes insulin sensitivity (25,31–33). Recent tissue-specific knockouts of glucocorticoid signaling molecules have implicated adipose tissue as a central node linking glucocorticoid action and lipolysis to systemic insulin resistance and NAFLD (34–37).

Here, we show that chronically elevated glucocorticoids in the presence of obesity have synergistic effects on lipolysis, insulin resistance and fatty liver disease. Obese glucocorticoid-treated mice have reduced fat mass compared to all other groups, yet have hyperglycemia and severe insulin resistance; therefore, we speculate that lipolysis drives insulin resistance in obese animals.

**Methods**

**Patient Recruitment and data collection**: Patients were recruited and data was collected as described in Hochberg et al. (18). But briefly,… Control patients were those that had non-secreting adenomas and Cushing’s patients were those that had ACTH-secreting adenomas.

**Animal Procedures:** C57BL/6J adult male mice were purchased from the Jackson Laboratory at nine weeks of age. Following a week of acclimation, mice were treated as described previously (18) or either remained on normal chow (NCD) or were provided a high fat diet (45% fat; 35% carbohydrate; 20% protein; cat# D12451) for either eight or twelve weeks. Mice remained on their respective diets for the duration of the study. Mice were treated with 1 mg/kg per day of dexamethasone (Sigma–Aldrich), provided in their drinking water (NCD n=12; HFD n=32), or used as controls (NCD n=12; HFD n=22) for 3-6 weeks, as indicated. For the six-week dexamethasone treatment and prior to sacrifice, sixteen HFD-fed, dexamethasone-treated mice appeared ill and died or were euthanized and thus removed from all analyses once symptoms were noticed. Animal body weight and composition was determined weekly using an EchoMRI 2100. Food was weighed weekly, with food intake determined as the decrease in food weight per mouse per week per cage. All mice were provided with access to food and water *ad libitum* throughout the study, unless otherwise noted. At the end of treatment, mice were fasted for 16 h and were sacrificed by cervical dislocation at ZT3 after isoflurane anesthesia. Following cervical dislocation, a sagittal incision was made along the medioventral surface of each mouse and the skin was carefully pulled back to expose the subcutaneous fat depots. The incision was extended along the anterior surface of each hind limb to allow careful dissection of the inguinal fat pads. A small incision was then made into the rectus abdominus muscle to expose the abdominal cavity. The epididymal fat pads were identified and carefully dissected out. The right fat pads from each mouse were weighed and snap frozen in liquid nitrogen for later analysis, along with a section of the left lateral lobe of the liver. Small pieces of tissues were fixed in 10% phosphate-buffered formalin for histology. All animal procedures were approved by both the University of Tennessee Health Science Center and University of Michigan Institutional Animal Care and Use Committees.

**Insulin Tolerance Tests and Hyperinsulinemic Euglycemic Clamp Experiments:** Insulin tolerance was assessed following five weeks of treatment (27 weeks of age). Following a six hour fast, mice were given an intraperitoneal (IP) injection of insulin (Humulin R, Lilly, Indianapolis, IN, USA)at a concentration of 2.5mU/kg . Blood was collected from a tail cut and blood glucose was determined using a One Touch Ultra Glucometer (Lifescan) prior to and every 15 minutes post injection. For the hyperglycemic euglycemic clamp experiments, C57BL/6J adult (70d) male mice were fed HFD ()for eight weeks and treated with dexamethasone for three weeks. Animals were anesthetized with an IPl injection of sodium pentobarbital (50−60 mg/kg). Indwelling catheters were inserted into the right jugular vein and the right carotid artery, respectively.  The free ends of catheters were tunneled subcutaneously and exteriorized at the back of the neck via a stainless-steel tubing connector (coated with medical silicone) that was fixed subcutaneously upon closure of the incision. Animals with healthy appearance, normal activity, and weight regain to or above 90% of their pre-surgery levels were used for the study. Experiments were carried out in conscious and unrestrained animals using techniques described previously (38–40). Briefly, the primed (1.0 Ci)-continuous infusion (0.05 Ci/min and increased to 0.1 µCi/min at t = 0) of [3-3H] glucose (50 µCi/ml in saline) was started at t = -120min. After a 5-hour fast, the insulin clamp was initiated at t = 0, with a prime-continuous infusion (16 mU/kg bolus, followed by 2.5 mU/kg/min) of human insulin (Novo Nordisk). Euglycemia (120~130 mg/dL) was maintained during the clamp by measuring blood glucose every 10 min and infusing 50% glucose at variable rates, accordingly.  Blood samples were collected at t = 80, 90, 100, and 120 min for determination of glucose specific activity.  Blood insulin concentrations were determined from samples taken at t = -10 and 120 min. A bolus injection of [1-14C]-2-deoxyglucose ([14C]2DG; PerkinElmer) (10 µCi) was given at t = 120 min. Blood samples weretaken at 2, 5, 10, 15, and 25 min after the injection for determination of plasma [14C]2DG radioactivity. At the end of the experiment, animals were anesthetized with an intravenous injection of sodium pentobarbital and tissues were collected and immediately frozen in liquid nitrogen for later analysis of tissue [1-14C]-2-deoxyglucose phosphate ([14C]2DGP) radioactivity. Blood glucose was measured using an Accu-Chek glucometer (Roche, Germany). Plasma insulin was measured using the Linco rat/mouse insulin ELISA kits.  For determination of plasma radioactivity of [3-3H]glucose and [1-14C]2DG, plasma samples were deproteinized with ZnSO4 and Ba(OH)2 and counted using a Liquid Scintillation Counter (Beckman Coulter LS6500 Multi-purpose Scintillation Counter). Glucose turnover rate, hepatic glucose production and tissue glucose uptake were calculated as described elsewhere (39–41).

**Serum Determination** Following 11 weeks of dexamethasone treatment, 21 collected into heparin-coated capillary tubes bothprior tointraperitoneal , either ,- was collected

**Cell culture:** 3T3-L1 fibroblasts (pre-adipocytes) were cultured in 10% newborn calf serum (NCS), high glucose Dulbecco's Modification of Eagle's Medium (DMEM) with 1% penicillin, streptomycin and glutamine (PSG), until confluence. Cells were switched to a differentiation cocktail at two days post confluence (250nM dexamethasone, 500M 3-isobutyl-1-methylxanthine and 1g/mL insulin in 10% fetal bovine serum (FBS), in high glucose DMEM with 1% PSG) for four days (42). Media was replaced with differentiation medium containing only insulin for an additional three days. For the following three days, cells remained in FBS media with no additional treatment. To assess rates of lipolysis, cells remained in FBS media and were treated with ethanol (vehicle) or 250nM dexamethasone for five days before lysing.

**Assessment of Triglyceride Content in Cells and Tissue:** 3T3-L1 cells were grown and treated as described above. At the end of the treatment period, cells were lysed in homogenization buffer (50 mM Tris pH 8, 5 mM EDTA, 30 mM Mannitol, PI inhibitor) and subjected to three freeze thaw cycles. Frozen liver tissue was homogenized with 5mm stainless steel pellets in this buffer using a TissueLyser II (Qiagen). Lipids were extracted using KOH and a chloroform:methanol extraction. Triglyceride content was assessed using the Serum Triglyceride Determination Kit (Sigma) and absorbance was detected as described in (43).

**Histology:** Tissues were fixed in 10% phosphate-buffered formalin for 24 hours and then stored in 70% ethanol until further processing. Tissues were dehydrated, embedded in paraffin and sent to the Comprehensive Cancer Center Tissue Core where they were processed and stained with hematoxylin and eosin (H&E) to assess cell morphology.

**mRNA Extraction and Analysis:** Cells and tissues were lysed in TRIzol using the TissueLyser II, as decribed above, and RNA was extracted using a PureLink RNA kit (Life Technologies). cDNA was synthesized from 0.5-1g of RNA using the High Capacity Reverse Transcription Kit (Life Technologies). Primers, cDNA and Power SYBR Green PCR Master Mix (Life Technologies) were combined in accordance with the manufacturer’s guidelines and quantitative real-time PCR (qPCR) was performed as previously described (44). mRNA expression level was normalized to *Actb* after evaluation of several reference genes. qPCR primer sequences are listed in Table 1.

**Protein Extraction and Analysis:** Cells and tissues were lysed in RIPA buffer (50 mM Tris, pH 7.4, 0.25% sodium deoxycholate, 1% NP40, 150 mM sodium chloride, 1 mM EDTA, 100 uM sodium orthovanadate, 5 mM sodium fluoride and 10 mM sodium pyrophosphate), and clarified lysates were boiled into SDS-PAGE buffer (Life Technologies) transferred and blotted using ATGL (Cell Signaling Technologies), GAPDH (Fitzgerald Industries), and Actin (Invitrogen) antibodies. Antibody complexes were detected by anti-mouse and anti-rabbit fluorescent conjugated antibodies (Invitrogen) and visualized using an Odyssey CLx image scanner. Blots were quantified using Image Studio software version 5.2 (LiCOR).

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**Statistics**: For animal studies, two-way ANOVA analyses were performed to test for significance of diet and dexamethasone treatment, as well as their interaction. Pairwise comparisons, normality and equal variance were tested using Shapiro-Wilk and Levene’s tests, respectively. Pending those results, a Mann-Whitney, Welch’s or Student’s *t*-test were used. performed. P-values below p=0.05 were considered significant. All statistical tests were performed using the R software package version 3.30. All raw data and analysis scripts are available at https://github.com/BridgesLab/CushingAcromegalyStudy.

**Results**

# Dexamethasone-Induced Insulin Resistance is Worsened in the Presence of Obesity

We have previously published data suggesting differential gene expression in adipose tissue between those with Cushing’s disease and controls depending on their obesity status (18). Based on this finding, we speculated that the glucocorticoid responses may vary according to obesity status. Here, we have re-analyzed the data stratifying the Cushingoid and control groups by BMI (Figure 1A), classifying participants as either “Not obese” (BMI < 30) or “Obese” (BMI ≥ 30). We found no significant differences in BMI in the control group compared to the Cushing’s. However, there group; however, a near-significant interaction between obesity status and Cushing’s diagnosis for HOMA-IR score (p=0.057; Figure 1A-B) was observed. Furthermore, we observed a modest (17%) increase in HOMA-IR score when comparing non-obese subjects with and without Cushing’s disease, yet a 3.4-fold increase in the obese patients.

To investigate if obesity status influences insulin sensitivity in the presence of elevated glucocorticoids we performed an insulin tolerance test (ITT) on lean (NCD) and diet-induced obese (HFD) mice that were untreated (Control) or treated with glucocorticoids (Dexamethasone; Figure 1C). HFD-fed, dexamethasone-treated mice were significantly more resistant to insulin-stimulated glucose uptake when compared to all other groups (Figure 1D). Additionally, HFD dexamethasone-treated mice exhibited dramatic fasting hyperglycemia, with a significant interaction between diet and drug (p=0.00009; Figure 1E). While HFD animals had a 24% increase in fasting glucose when compared to NCD animals, in the presence of Dexamethasone, HFD-fed animals had a 122% increase in fasting glucose relative to NCD controls not treated with dexamethasone. In the lean, NCD-fed animals, dexamethasone caused an 18% decrease in fasting glucose.

To evaluate glucose homeostasis in more detail we performed a hyperinsulinemic-euglycemic clamp in obese mice (11 weeks of HFD) treated with dexamethasone for the three weeks. This shorter HFD/dexamethasone exposure still caused dramatic insulin resistance, and hyperglycemia (Supplementary Figure 1A-B) and reductions in lean mass, but no differences in fat mass between the groups (Supplementary Figures 1C-D). Animals were clamped while conscious and glucose levels during the clamp (Supplementary Figure 1E) as well as insulin turnover rate (Supplementary Figure 1F) were similar between groups. During the hyperinsulinemic phase, the glucose infusion rate was 39% lower in obese dexamethasone-treated mice when compared to obese controls indicating insulin resistance at euglycemia (Figure 1E). Basal endogenous glucose production (EGP) was 37% higher in the dexamethasone treated group (p=0.026). Moreover, in the control group, EGP was reduced to near zero by a high dose of insulin but only reduced 70% in the dexamethasone group (p=0.0091) resulting in glucose production being higher during the insulin phase in dexamethasone treated mice (p=0.014) when compared to controls (Figure 1F-G). Glucose turnover was slightly decreased in the presence of insulin (p=0.141; Figure 1H). In spite of these modest changes in glucose turnover, there were significant reductions in the obese, dexamethasone treated animals in 2-deoxyglucose uptake in heart (34% reduced, p=0.0003) and gastrocnemius tissues (68% reduced; p=0.00002; Supplementary Figures 1G-H). These data suggest that increased glucose production and impaired suppression by insulin are the primary causes of insulin resistance and hyperglycemia in obese, dexamethasone treated animals.

# HFD-Induced Liver Steatosis in Dexamethasone-Treated mice

Obesity and chronic elevations in glucocorticoids are associated with increased liver fat and NAFLD (10,14). We observe increases in plasma ALT, a liver enzyme associated with liver disease, in obese Cushing’s patients (38% increase in non-obese subjects versus a 2.8 fold increase in obese subjects, p=0.13 for the interaction of disease and obesity status; Figure 2A). In our mouse model of HFD-fed, dexamethasone-treated mice, we observe drastically elevated liver triglycerides when compared to all other groups with a significant interaction of drug and diet (p=0.000068; Figure 2B). In support of this, H&E staining of hepatic tissue clearly depicts exacerbated lipid levels in the obese, glucocorticoid-treated group when compared to HFD-fed or dexamethasone-treated controls (Figure 2C).

We used qPCR to measure the expression of genes involved in hepatic *de novo* lipogenesis, *Srebf1* and *Fasn*, in liver lysates (Figure 2D). We observe a significant effect of diet and drug on *Fasn* expression (p=0.014), and alt). hough both transcripts were somewhat elevated in response to HFD alone, no synergism in expression levels was observed with dexamethasone. This finding indicates that lipid accumulation in response to dexamethasone treatment is likely occurring via mechanisms other than accelerated glucocorticoid-dependent activation of *de novo* lipogenesis.

# Dexamethasone Causes Decreased Fat Mass in HFD-Fed Mice

To understand the overall changes in these animals, we evaluated body composition in mice via EchoMRI. We observed reductions in fat mass in the HFD-fed dexamethasone treated group (Figure 3A-B). These reductions do not appear to be depot-specific, as we observe reductions in both inguinal (65% reduced) and epididymal adipose mass (59% reduced) in the HFD-fed animals treated with dexamethasone (Figure 3C). There were no significant reductions in fat mass, either by MRI or gross tissue weights of inguinal or epididymal adipose depots in response to dexamethasone treatment in the chow-fed groups (Figure 3B-C). To determine if changes in body composition could be explained by changes in food consumption throughout this study (Figure 3D), we compared food intake between the groups. Surprisingly, we found that the dexamethasone-treated HFD animals ate slightly more food, even though they lost substantial fat mass throughout the study (11% increase, p=0.032). These data suggest that the weight loss in obese animals provided dexamethasone is not due to reductions in food intake.

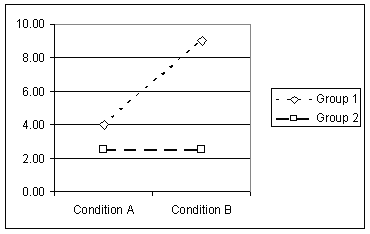
Dexamethasone Treatment Results in Increased Lipolysis

One potential mechanism that could explain reduced adiposity, increased insulin resistance and NAFLD is accelerated adipocyte lipolysis. Lipolysis has previously been associated with insulin resistance (25,31), is known to be elevated in patients with NAFLD(28), and has been shown to increase with glucocorticoid treatment (18,22–24). First we assessed whether there was a direct effect of dexamethasone on adipocyte lipolysis in cultured adipocytes. 3T3-L1 fibroblasts were undifferentiated (pre-adipocytes), differentiated and treated with vehicle (mature adipocytes) or dexamethasone following differentiation (mature adipocytes +dexamethasone) over a 15-day period. Dexamethasone treatment following differentiation led to decreased lipid content (50% reduction, p=) and a 71% increase in the amount of glycerol in the media (p=0.001), suggesting increased lipolysis (Figure 4B). In order to identify a potential GR-dependent lipolytic target, we evaluated the levels of ATGL, the rate limiting enzyme in lipolysis. Expression of ATGL (encoded by the *Pnpla2* gene) was enhanced following dexamethasone treatment in 3T3-L1 cells at both the transcript (2.7 fold, p=0.002; Figure 4C) and protein (8.4 fold; Figure 4D-E) levels. These data show that glucocorticoids elevate both ATGL levels and lipolysis in cultured adipocytes.

To assess the effects of glucocorticoid-induced lipolysis *in vivo,* we determined glycerol levels in animals chronically exposed to glucocorticoids in basal and stimulated conditions (Figure 4E). Stimulation of lipolysis was achieved via isoproterenol, a -adrenergic receptor agonist, or by a 16-hour fast. Dexamethasone treatment led to significant increases in glycerol in the fed (2.9 fold), fasted (1.5 fold) and isoproterenol-stimulated (1.4 fold, all groups p<0.05) conditions, indicating that dexamethasone enhances basal and stimulated lipolysis *in vivo* in chow-fed mice, as has been previously reported (45). Consistent with these findings, mRNA analysis from inguinal white adipose tissue (iWAT) of these mice showed an upregulation of *Pnpla2* transcripts in the dexamethasone-treated mice compared to controls (2.1 fold, p=0.016; Figure 4F).

Since the HFD-fed, dexamethasone-treated mice have more severe insulin resistance and hepatic lipid accumulation than the chow fed mice, we measured serum glycerol concentrations following a 16-hour fast (Figure 5A) to determine if fasting lipolysis might be elevated. We observed a nearly two-fold increase in serum glycerol levels by dexamethasone in the HFD-fed animals, compared with only a 18% increase in chow-fed mice. There was a significant interaction between dexamethasone exposure and diet (p=0.017) on glycerol levels, suggesting synergistically elevated lipolysis.

We quantified mRNA and protein expression of the lipolytic enzyme ATGL, in the iWAT of these mice (5B-D). Consistent with the hypothesis that ATGL activation could drive increased lipolysis in HFD and dexamethasone treated mice, expression of ATGL was elevated in both dexamethasone-treated groups, with a significant synergistic effect of glucocorticoids and obesity at both the transcript (p=0.02 for the interaction) and protein (p=0.003) levels. These data support the hypothesis that glucocorticoid-stimulated lipolysis is augmented in the context of obesity, potentially via increased transactivation of *Pnpla2*/ATGL.



For example, this graph would represent the *Pnpla2I* expression level nicely. Condition A (NCD), condition B (HFD), Group 2: control, Group 1: Dex. The difference in *Pnpla2l* expression level between Dex and Control is at least 3 times more in the HFD condition than in the NCD condition.

**Discussion**

Chronic glucocorticoid elevations are associated with many co-morbidities such as increased fat mass (18,20,21), decreased muscle mass (17–19), insulin resistance (12,13) and non-alcoholic NAFLD; (14,15). These adverse effects are similar to those seen in obesity; however, the combination of chronically elevated glucocorticoids in the context of pre-existing obesity has not been assessed. Here, we show that the effects of glucocorticoid-induced insulin resistance and NAFLD are exacerbated when paired with obesity.-so

We previously reported that obese patients with Cushing’s disease have a tendency for increases in HOMA-IR score, suggesting increased insulin resistance; and increases in the liver enzyme ALT, a marker of liver disease. In line with these findings, increases central adiposity, as is frequently observed in people with obesity, has been associated with enhanced fatty acid flux (i.e. lipolysis) when compared to lower body fat stores (46), which is thought to contribute to insulin resistance and fatty liver (25,47). There are two limitations to these :interpretations: one is the small sample size, and two, that it is not possible to determine the physiological status of Cushing’s patients before they develop a tumor; therefore, we could not discern whether obesity was present prior to or after development of Cushing’s disease. To address the question of whether the obese state modulates the effects of glucocorticoid excess, we designed mouse studies that assess the metabolic outcomes frequently associated with both obesity and exposure to elevated glucocorticoid concentrations.

We found that HFD-fed, dexamethasone-treated mice exhibited hyperglycemia and severe insulin resistance. This was primarily due to increased endogenous glucose production in these animals. HFD and dexamethasone also led to significant elevations in liver fat, consistent with a trend towards elevated ALT levels seen in the obese Cushing’s patients. Cushing’s disease is often paired with increased fat mass, which has been proposed to contribute to fatty liver (48,49). Indeed, obesity is a known risk factor of NAFLD (10,11). Previous work from our lab shows increased fat mass, following 12 weeks of dexamethasone treatment (18) in chow-fed mice, in accordance with what others have reported (50). However, to our surprise, the glucocorticoid treatment in obese mice led to an overall reduction in adiposity. Therefore, when comparing HFD control mice to HFD dexamethasone-treated mice, increased fat mass is not the the major mechanism behind the observed exacerbations in insulin resistance and increased liver fat.

Lipolysis has been linked to increased gluconeogenesis by several studies (51–54). One potential mechanism is that the increased flux of fatty acids, oxidized in the liver to acetyl-CoA, activate pyruvate carboxylase and gluconeogenesis (53,54). Glucocorticoids are known to stimulate lipolysis (18,22–24), possibly as a way to promote gluconeogenesis to maintain blood glucose levels, a key function of these hormones. Lipolysis has been implicated in insulin resistance (25,31) and NAFLD (28) and there is evidence that it is enhanced in the obese state (55). We found synergistic elevations in glycerol, indicative of enhanced lipolysis, as well as in hepatic fat accumulation in the HFD-fed dexamethasone-treated mice, but no data supporting enhanced hepatic *de novo* lipogenesis. These findings suggest that lipolysis may drive enhanced hepatic lipid accumulation in these mice.

There is some debate as to which genes glucocorticoids are acting on to promote lipolysis. Downregulation of *Pde3b* (56) and upregulation of -adrenergic receptors (57) and ATGL transcripts (35,58,59) have been proposed as possible mechanisms. We assessed all of the previously proposed targets and found adipose triglyceride lipase (ATGL), the rate limiting enzyme for adipose triglyceride lipolysis, to be synergistically activated by obesity and glucocorticoid-treatment. These findings bear a resemblance to elevations in glycerol levels in obese, dexamethasone-treated mice when compared to diet or glucocorticoids alone. The mechanisms by which obesity and glucocorticoids synergize to activate ATGL expression are not clear at this time, nor are the relative contributions of other glucocorticoid receptor-dependent targets.

Further research is needed to determine whether the insulin resistance observed is due to obesity or the high fat content of the diet. We evaluated glucocorticoid treatment in obesity; however, Riddell and colleagues have reported similar findings when giving HFD and glucocorticoids in concert to rats, prior to the onset of obesity (5,6,60). Further studies are needed to determine whether diet or obesity status or both are the source of this elevated metabolic risk to glucocorticoids, and whether these mechanisms are similar.

In summary, glucocorticoids are commonly prescribed drugs used to treat a multitude of health issues, but are known to induce a variety of adverse metabolic effects. Their actions in persons with obesity are not yet clear, even though there are a huge number of obese individuals routinely taking prescription glucocorticoids. The data presented here show that the obese state exaserbates several co-morbidities associated with chronically elevated glucocorticoids. These effects should be considered by physicians when determining glucocorticoid treatment options for patients with obesity. Future studies will determine whether blocking glucocorticoid/lipolytic action in the fat tissue is beneficial for preventing or enhancing recovery from glucocorticoid-induced metabolic disturbancescomorbidities.

# Acknowledgements

This study was supported by funds from NIH Grant R01-DK107535 (DB). This study also utilized the University of Michigan Metabolism, Bariatric Surgery and Behavior Core (U2C-DK110768), the Michigan Nutrition Obesity Research Center (P30-DK089503) and the University of Michigan Comprehensive Cancer Center Core (P30-CA062203). Erin Stephenson is partially supported by funding from Le Bonheur Children’s Hospital, the Children’s Foundation Research Institute and the Le Bonheur Associate Board . We would like to thank Jennifer DelProposto and Carey Lumeng for assistance with imaging liver sections, and Melanie Schmitt for assistance with glucose clamp studies. We would like to thank the other members of the Bridges laboratory, Thurl Harris (University of Virginia) and Edwards Park (UTHSC) for insights on this work.

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