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Postprandial Hepatic Lipid Metabolism Requires Signaling through Akt2 Independent of the Transcription Factors FoxA2, FoxO1, and SREBP1c

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SUMMARY

Under conditions of obesity and insulin resistance, the serine/threonine protein kinase Akt/PKB is required for lipid accumulation in liver. Two forkhead transcription factors, FoxA2 and FoxO1, have been suggested to function downstream of and to be negatively regulated by Akt and are proposed as key determinants of hepatic triglyceride content. In this study, we utilize genetic loss of function experiments to show that constitutive activation of neither FoxA2 nor FoxO1 can account for the protection from steatosis afforded by deletion of Akt2 in liver. Rather, another downstream target positively regulated by Akt, the mTORC1 complex, is required in vivo for de novo lipogenesis and Srebp1c expression. Nonetheless, activation of mTORC1 and SREBP1c is not sufficient to drive postprandial lipogenesis in the absence of Akt2. These data show that insulin signaling through Akt2 promotes anabolic lipid metabolism independent of Foxa2 or FoxO1 and through pathways additional to the mTORC1-dependent activation of SREBP1c.

INTRODUCTION

Insulin is the primary hormone responsible for coordinating the metabolic response to nutrient intake. Following a meal, insulin suppresses the hepatic glucose production that provides the brain substrate during fasting and directs ingested nutrients into long-term energy stores. In particular, insulin promotes triglyceride (TG) synthesis and storage utilizing dietary fatty acids and induces de novo lipogenesis in liver and adipose tissue. Much of this synchronized metabolic response is thought to be mediated by hormone-dependent reduction in the transcription of gluconeogenic genes, such as glucose-6-phosphatase, catalytic subunit (G6pc), and cytosolic phosphoenolpyruvate carboxykinase 1 (Pck1), and activation of lipogenic gene expression via the master regulator sterol regulatory element-binding transcription factor 1c (Srebp1c) (Argaud et al., 1996; Horton et al., 2002; O’Brien et al., 2001). Thus, the transcriptional targets of the insulin signaling pathway are of considerable interest.

The serine/threonine kinase Akt (also known as protein kinase B, PKB) is now well-established as a major mediator of the metabolic actions of insulin (Whiteman et al., 2002). Akt2 is the predominant isoform in the insulin-responsive tissues like liver, muscle, and adipose tissue (Cho et al., 2001). Akt2 knockout mice are “diabetic,” whereas liver-specific disruption of the Akt2 gene has mild effects on glycemia but more dramatic effects on lipogenic gene expression and steatosis in obese, insulin-resistant mice (Cho et al., 2001; Leavens et al., 2009). The canonical nuclear target of Akt, established in worms and flies as well as vertebrates, is the transcription factor Foxhead box O (FoxO) (Gross et al., 2009). Akt phosphorylates and inhibits the transcriptional activity of FoxO at least in part by promoting its exclusion from the nucleus (Durham et al., 1999; Guo et al., 1999; Nakae et al., 1999; Rena et al., 1999; Tang et al., 1999). There are now considerable data implicating FoxO1 as an intermediate in the pathway by which insulin through Akt suppresses hepatic gluconeogenic gene expression and glucose output (Haeusler et al., 2010b; Li et al., 2007; Liu et al., 2008; Matsumoto et al., 2007; Nakae et al., 2001; Puigserver et al., 2003; Qu et al., 2006).

In contrast to the consensus of opinion regarding the role of FoxO1 in the control of gluconeogenic gene expression, its contribution to regulation of hepatic lipid metabolism remains unclear. In some studies, expression of a constitutively active FoxO1 in liver induces Srebp1c expression and hepatic TG accumulation, though others have not found this response; in addition, FoxO1 inhibits TG secretion (Matsumoto et al., 2006; Zhang et al., 2006). In contrast, Kamagate et al. reported that FoxO1 is necessary and sufficient to promote hepatic very-low-density lipoprotein-associated TG (VLDL-TG) production and hypertriglyceridemia via its regulation of microsomal TG transfer protein (MTP), and further proposed that this pathway accounts for...
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elevated serum lipids in insulin-resistant states (Kamagate et al., 2008). Loss-of-function approaches to understand the contribution of FoxO1 to lipogenic gene expression have yielded few striking results, though its ablation in streptozotocin (STZ)-induced diabetes increases serum TG and VLDL-TG secretion (Haeusler et al., 2010a). Deletion of Foxf1 in insulin receptor substrate 1 and 2 (IRS1 and IRS2) double-knockout mouse livers partially rescues the deficit in VLDL-TG secretion (Dong et al., 2008). Ablation of all three FoxO isoforms in liver leads to hepatic steatosis, potentially through regulating the expression of nicotinamide phosphoribosyltransferase (Nampt) and consequently NAD⁺ levels (Tao et al., 2011). Thus, there persists considerable uncertainty concerning the physiological role of FoxO1 in controlling hepatic lipid metabolism.

Another forkhead family transcription factor, FoxA2, has been implicated in the control of hepatic lipid metabolism by insulin. Like FoxO, FoxA2 is phosphorylated by Akt, thereby leading to exclusion from the nucleus and inhibition of transcriptional activity, though some investigators have found that FoxA2 resides in nuclei constitutively and does not respond to different nutritional conditions (Wolfrum et al., 2004; Zhang et al., 2005). Expression of a constitutively active FoxA2 in liver of obese mice leads to a phenotype much like a deficiency of insulin signaling, i.e., increased fatty acid oxidation and TG secretion and reduced hepatic TG content (Wolfrum et al., 2004; Wolfrum and Stoffel, 2006). However, the role of FoxA2 in insulin action has been challenged; mice with liver-specific deletion of FoxA2 demonstrate impaired bile acid metabolism but no alterations in hepatic or serum TG (Bochkis et al., 2008). It has long been known that a major target of insulin signaling in the regulation of hepatic lipid metabolism is another transcription factor, SREBP1c, a member of the basic helix-loop-helix-leucine-zipper family (Ferre and Foufelle, 2010; Horton et al., 2002). Both transcription and posttranslational processing of SREBP1c to its transcriptionally active form are stimulated by insulin signaling through Akt, contributing to postprandial increases in de novo lipogenesis (Chakrabarti et al., 2010; Fleischmann and Iynedjian, 2000; Leavens et al., 2009; Li et al., 2010). SREBP1c translocates to the Golgi complex where it is proteolyzed, liberating an amino-terminal fragment that activates its own expression as well as that of a set of lipogenic enzymes including fatty acid synthase (Fasn), acetyl-Coenzyme A carboxylase (Acc), ATP citrate lyase (Acly), and glycerol-3-phosphate acyltransferase (Gpat) (Horton et al., 2002; Postic and Girard, 2008). Insulin’s ability to promote Srebp1c expression depends on the mammalian target of rapamycin complex 1 (mTORC1), as knockdown of an essential component of mTORC1, Raptor (regulatory-associated protein of mTOR), in multiple tissue culture cell lines significantly blunts insulin or Akt-stimulated expression of Srebp1c and its targets (Chakrabarti et al., 2010; Duvel et al., 2010; Porstmann et al., 2005, 2008). In primary hepatocytes, rapamycin prevents the insulin-dependent induction of Srebp1c, but not the reduction in Pck1, consistent with the idea that distinct transcriptional targets mediate the effect of insulin on gluconeogenic and lipogenic gene expression (Li et al., 2010).

The goal of the experiments reported herein is to test the dependency of these three transcriptional pathways as downstream targets linking insulin signaling to control of hepatic TG content and de novo lipogenesis in mice. We have taken a genetic approach to address the epistatic relationship between Akt and its downstream candidate nuclear targets. If inhibition of FoxO1 or FoxA2 were critical to insulin signaling, then the loss in hormone action that accompanies deletion of Akt2 in liver would be reversed by concomitant deletion of the target transcription factor. If Akt2 promotes de novo lipogenesis in liver via mTORC1, both its activity and Srebp1c expression would be decreased upon deletion of Akt2 in liver. Thus, we ablated Akt2 expression in liver by tissue-specific homologous recombination alone or simultaneously with either FoxA2 or FoxO1, and analyzed lipid metabolism. Neither FoxA2 nor FoxO1 is downstream of Akt2 in the control of hepatic lipid accumulation, but rather FoxO1 reduces hepatic TG content upstream of or via a parallel pathway to Akt2. We then tested the requirement and sufficiency of activation of mTORC1 for de novo lipogenesis. We found that mTORC1 was required for Srebp1c expression and de novo lipogenesis, but, when hepatic Akt2 was deleted, activation of mTORC1 and SREBP1c was insufficient to drive de novo lipogenesis following a high-carbohydrate meal.

RESULTS

Akt2 Regulates Hepatic TG Accumulation Independent of FoxA2

It has been proposed that insulin inhibits FoxA2 via Akt-dependent phosphorylation and nuclear exclusion, controlling lipid export, fatty acid oxidation, and accumulation of TG in the liver (Wolfrum et al., 2004, 2008; Wolfrum and Stoffel, 2006). We generated mice lacking both Akt2 and FoxA2 in liver by breeding Akt2(loxP/loxP);FoxA2(loxP/loxP) mice to AFP-Cre, which is expressed exclusively in liver (Zhang et al., 2005). As shown in Figure 1A, we achieved essentially complete deletion of Akt2 in both Akt2(loxP/loxP);FoxA2(loxP/loxP) and Akt2(loxP/loxP);FoxA2(loxP/loxP) mice. FoxA2 protein levels were also greatly reduced in both FoxA2 single-knockout and Akt2, FoxA2 double-knockout hepatocytes (Figure 1A). Mice of all four genotypes were submitted to glucose tolerance tests, which showed indistinguishable rates of glucose disposal (see Figure S1A available online). In addition, there were no significant changes in serum insulin or TG levels from either fed or overnight-fasted mice lacking Akt2, FoxA2, or both in liver (Figures S1B and S1C). Adipose tissue mass was the same among the mice of all four genotypes (Figure S1D).

The TG content in livers deficient in Akt2, FoxA2, or both was unchanged compared to wild-type controls when assayed in mice under chow-fed conditions (Figure 1B). Akt2 is required for accumulation of liver TG under some situations that induce hepatic steatosis, and expression of a constitutively active FoxA2 reduces hepatic TG accumulation in leptin-deficient (ab/ob) mice (Leavens et al., 2009; Wolfrum et al., 2004; Wolfrum and Stoffel, 2006). To address the question of whether endogenous FoxA2 is responsible for the reduction in hepatic TG in livers deficient in Akt2, mice lacking Akt2, FoxA2, or both in liver were fed a high-fat diet (HFD) for 3 months. Glucose tolerance tests were indistinguishable among the four genotypes (Figure S2A), as were serum insulin and TG levels under both fasting and fed conditions (Figures S2B and S2C). Loss of Akt2 in livers trended to a decrease of hepatic TG accumulation relative to wild-type controls after HFD feeding, and this was unaffected by deletion.
of FoxA2 (Figure 1C). These data show that, at least under conditions of diet-induced obesity (DIO), FoxA2 activity is unlikely to be the cause of the protection from steatosis rendered by removal of Akt2 from liver. These data are also consistent with previous findings challenging the notion of FoxA2 as a target of insulin signaling (Zhang et al., 2005).

### Loss of Akt2 Suppresses Hepatic TG Levels in FoxO1-Deficient Liver

FoxO1, a transcription factor negatively regulated by the insulin/Akt signaling pathway, promotes expression of gluconeogenic genes such as G6pc and Pck1 (Gross et al., 2009). To assess the function of FoxO1 as a downstream target of Akt2, we derived Akt2, FoxO1 and combined liver-specific double-knockout mice. Akt2 and FoxO1 protein levels were significantly reduced in Akt2 and FoxO1 single-knockout mice, respectively, and in Akt2, FoxO1 double-knockout mice (Figure 2A, left), and real-time PCR from either FoxO1 knockout livers or Akt2, FoxO1 double-knockout mice showed reduction of FoxO1 mRNA levels compared to either wild-type controls or Akt2 knockout livers (Figure 2A, right). Under conditions of normal chow feeding, both AFP > Cre;Akt2(loxP/loxP);FoxO1(loxP/loxP) and AFP > Cre;FoxO1(loxP/loxP) mice demonstrated normal glucose tolerance (Figure S3A). Moreover, serum insulin and TG levels were the same for all four genotypes when assayed under either fasting or fed conditions (Figures S3 B and S3C). When challenged with pyruvate, AFP > Cre;FoxO1(loxP/loxP) mice trended to lower levels of blood glucose, as did AFP > Cre;Akt2(loxP/loxP);FoxO1(loxP/loxP) mice. A FP > Cre;Akt2(loxP/loxP) mice did not differ...
from wild-type controls (Figures 2B and 2C). These data are consistent with previously published results that support a model in which FoxO1 regulates glucose output and is downstream of Akt (Matsumoto et al., 2007).

After an overnight fast, AFP > Cre;Akt2(loxP/loxP), AFP > Cre; FoxO1(loxP/loxP) and AFP > Cre;Akt2(loxP/loxP);FoxO1(loxP/loxP) mice had hepatic TG levels indistinguishable from that in wild-type controls (Leavens et al., 2009; Matsumoto et al., 2007) (Figure 2D). Fed AFP > Cre;FoxO1(loxP/loxP) mice displayed increased hepatic TG levels compared to controls and AFP > Cre;Akt2(loxP/loxP);FoxO1(loxP/loxP) mice, though TG secretion was unaltered (Figure 2E and Figure S4). Surprisingly, the accumulation of liver TG in the AFP > Cre;FoxO1(loxP/loxP) mice was suppressed by concomitant deletion of Akt2 (Figure 2E). Though deletion of FoxO1 leads to a phenotype opposite to that of deletion of Akt2, these data are inconsistent with a model in which Akt2 regulates lipid accumulation through suppression of FoxO1 activity.

Akt2 Regulates Hepatic TG Levels Independent of FoxO1 upon HFD Feeding

Suppression of FoxO1 by shRNA in livers from DIO mice decreases blood glucose and insulin levels and improves insulin sensitivity as assessed by the euglycemic, hyperinsulinemic clamp (Samuel et al., 2006). To investigate the role of FoxO1 as a downstream mediator of Akt’s role in metabolism under pathological conditions, we placed the wild-type controls, AFP > Cre; Akt2(loxP/loxP), AFP > Cre; FoxO1(loxP/loxP) and AFP > Cre; Akt2(loxP/loxP); FoxO1(loxP/loxP) mice, on a HFD for 3 months. Glucose tolerance tests were indistinguishable in mice of all four genotypes (Figure 3A). Fasting and fed serum insulin and TG levels were also similar among these same mice (Figures 3B and 3C). However, under fed conditions, loss of hepatic Akt2 in HFD-fed mice trended to a lower TG level in liver, whereas liver TG upon ablation of FoxO1 did not differ from wild-type controls (Figure 3D). Deletion of FoxO1 concomitant with Akt2 did not reverse the protection from steatosis in AFP > Cre; Akt2(loxP/loxP) mice (Figure 3D), again militating against the idea that FoxO1 regulates lipid metabolism downstream of Akt2.

Loss of Akt2 Decreases Hepatic TG Levels in FoxO1 Knockout Mice after Aurothioglucose Treatment

In DIO, deletion of Akt2 in liver reduces hepatic TG without altering lipogenesis, whereas in ob/ob mice protection from steatosis is accompanied by a concomitant reduction in lipogenesis and lipogenic gene expression (Leavens et al., 2009). To study the AFP > Cre; Akt2(loxP/loxP); FoxO1(loxP/loxP) mice under conditions that mimic ob/ob mice, we injected mice with aurothioglucose (goldthioglucose, GTG), which causes hypothalamic damage, hyperphagia, and weight gain (Brecher et al., 1965; Marshall and Mayer, 1954). As shown in Figure 4A, 8 weeks after GTG injection, mice of all genotypes displayed significantly increased body weight and hepatic TG levels compared to age-matched controls (compare Figure 4B to Figure 2E). AFP > Cre; Akt2(loxP/loxP) mice trended to lower hepatic TG, while AFP > Cre; FoxO1(loxP/loxP) mice had significantly elevated TG in liver (Figure 4B). Interestingly, concomitant deletion of Akt2 and FoxO1 concomitant with Akt2 did not reverse the protection from steatosis in AFP > Cre; Akt2(loxP/loxP) mice (Figure 3D), again militating against the idea that FoxO1 regulates lipid metabolism downstream of Akt2.
feeding suppressed insulin-induced gene 2a (INSIG2a) expression for at least 6 hr independent of the presence of hepatic Akt2 (Figure 5E).

To test whether unrestrained activity of FoxO1 is the major factor responsible for the lack of postprandial de novo lipogenesis and hepatic weight gain in AFP > Cre;Akt2(loxP/loxP) mice, we measured fatty acid synthesis in livers from AFP > Cre;Akt2(loxP/loxP);FoxO1(loxP/loxP) mice. Elimination of FoxO1 in liver was without effect on the increase in blood glucose evident after ingestion of a HCD (Figure 6A). However, deletion of FoxO1 in liver appeared to reverse the prevention in hepatic weight gain evident in the AFP > Cre;Akt2(loxP/loxP) livers, much like the suppression of a similar defect in livers lacking IRS1 and IRS2 (Figure 6B) (Dong et al., 2008). Deletion of FoxO1 alone in liver led to a trend for increased de novo lipogenesis following a meal, consistent with the increase in hepatic TG under several conditions (Figures 2E, 4B, and 6C). Unlike liver size, the decrease in lipid synthesis in livers lacking Akt2 was not reversed by concomitant removal of FoxO1; instead, AFP > Cre;Akt2(loxP/loxP);FoxO1(loxP/loxP) livers demonstrated rates of de novo lipogenesis virtually identical to those in AFP > Cre;FoxO1(loxP/loxP) livers (Figure 6C). Delivery by adenovirus of a dominant-negative form of FoxO1 (Nakae et al., 2001) into AFP > Cre;Akt2(loxP/loxP);FoxO1(loxP/loxP) livers also failed to reverse the decreased lipogenesis in Akt2 null livers (data not shown). These data are consistent with those presented above in which Akt2 is epistatic to FoxO1 regarding the control of liver TG content.

mTORC1 Is Required for De Novo Lipogenesis in Mouse Liver

We next turned to the question: since FoxO1 and FoxA2 do not appear to function downstream of Akt2 in lipid homeostasis, what pathway could mediate Akt2’s effect on lipogenic gene expression? The most likely answer lies in the recent observation that in primary hepatocytes, insulin utilizes a pathway dependent on mTORC1 to stimulate the processing and expression of SREBP1c, a transcription factor that drives coordinated lipogenic gene transcription (Azzout-Marniche et al., 2000; Chakrabarti et al., 2010; Duvel et al., 2010; Fleischmann and Iyedjian, 2000; Li et al., 2010; Porstmann et al., 2008). To test the requirement for this pathway in vivo, we injected raptor(loxP/loxP) mice with an adeno-associated virus expressing liver-specific Cre recombinase (AAV > Cre) or green fluorescent protein (AAV > GFP), thus generating hepatic raptor knockout mice or controls. As shown in Figure 7A, raptor protein levels were substantially reduced in AAV > Cre; raptor(loxP/loxP) mice, and the phosphorylation of an mTORC1 target, ribosomal protein S6 (S6), was not detected, as assayed by reactivity with a phosphospecific antibody (Figure 7A). Expression of the lipogenic genes Srebp1c, Fas, Acly, and Gpat were reduced in AAV > Cre; raptor(loxP/loxP) mice, though Acc and Gck were unchanged under fed conditions (Figure 7B). Most notably, de novo lipogenesis following a high-carbohydrate meal was largely abrogated in liver from AAV > Cre; raptor(loxP/loxP) mice (Figure 7C).

Having established the critical role of mTORC1 in de novo lipogenesis, we then asked whether defects in its expression and posttranslational processing of SREBP1c explained the disturbed lipid metabolism in AFP > Cre;Akt2(loxP/loxP) mice. Following a high-carbohydrate meal, there was an increase in
the phosphorylated form of protein S6 and eukaryotic translation initiation factor 4E-1A-binding protein 1 (4EBP1), which reflects activation of mTORC1 by nutrients and insulin. Surprisingly, this was unchanged in AFP > Cre;Akt2(loxP/loxP) mice (Figure 7D). Both the precursor and the processed form of SREBP1c increased 6 hr after HCD feeding; induction of these
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the latter a precursor for fatty acid synthesis. The activity of ACLY is regulated transcriptionally as a target of SREBP1c as well as at the posttranslational level by Akt and protein kinase A phosphorylation (Berwick et al., 2002; Horton et al., 2002; Potapova et al., 2000). Insulin injection stimulated phosphorylation of Akt and ACLY, and phosphorylation of both was blunted in livers from AFP > Cre;Akt2(loxP/loxP) mice (Figure S7A). To study this in more detail, hepatocytes were isolated from control and Akt2 KO livers. Again, insulin promoted Akt and ACLY phosphorylation in a dose-dependent manner. Phosphorylation of both was reduced in primary hepatocytes from Akt2-deficient livers, particularly at low concentrations of insulin (Figure S7B). Those data provide an additional pathway potentially dependent on Akt2 for the increase in de novo lipogenesis in liver.

Atypical PKCs (aPKCs) have been reported to be activated by several mechanisms, e.g., stimulating the expression of mTORC1 inhibitors such as Sestrin3, Raptor independent companion of mTOR (Rictor), and possibly Tuberous sclerosis complex 1 (TSC1) (Chen et al., 2010; Harvey et al., 2008). To ask whether such a mechanism accounts for the suppression of lipid accumulation by FoxO1, we assessed mTORC1 activity in animals lacking hepatic FoxO1. Six hours after ingesting a high-carbohydrate meal, hepatic phospho-S6 was not altered in AFP > Cre;FoxO1(loxP/loxP) or AFP > Cre;Akt2(loxP/loxP); FoxO1(loxP/loxP) mice (Figure 7E). The expression of Srebp1c, Gck, Fasn, Acc, Acly, and Sestrin3 was also unchanged in livers from AFP > Cre;FoxO1(loxP/loxP) mice after HCD refeeding (Figure S5). These data argue against mTORC1 as the mediator of hepatic TG accumulation induced by deletion of FoxO1.

**Insulin-Stimulated Phosphorylation of ATP Citrate Lyase Is Blunted in Akt2-Deficient Livers**

To explore other potential mechanisms utilized by Akt2 to regulate lipid metabolism, we examined two other pathways known to modulate hepatic lipogenesis activity responding to insulin signaling. ATP-citrate lyases (ACLY) catalyze the cleavage of cytosolic citrate to oxaloacetate and acetyl-CoA,
accumulation more closely resemble a state of augmented insulin sensitivity. The simplest, though by no means only, explanation for this phenomenon is that insulin resistance occurs at a step distal to a bifurcation in insulin signaling, resulting in selective inhibition of the hormone’s effect on glucose output, while permitting signaling to lipid metabolism. Work from our laboratory as well as others suggests that this divergence occurs downstream of Akt, and thus the identification of the specific pathways that Akt2 utilizes to regulate metabolism has achieved particular importance (He et al., 2010; Leavens et al., 2009). In this study, we investigated the roles of two proposed Akt target transcription factors, FoxO1 and FoxA2, and an indirect route for control of a third, SREBP1c, which is regulated by mTORC1. Our data show that, whereas suppression of FoxO1 activity is downstream of Akt in the inhibition of hepatic glucose output, phosphorylation of neither FoxO1 nor FoxA2 is likely to mediate insulin’s effects on de novo lipogenesis and TG accumulation in liver. Our data also support the notion that mTORC1 is required for maintenance of Srebp1c expression and de novo lipogenesis, but its activation is not sufficient to reverse the reduction of de novo lipogenesis coincident with deletion of Akt2. Moreover, it is likely that the mechanism by which Akt2 induces lipogenesis after a high-carbohydrate meal is not based on regulation of gene expression by any of the three transcription factors assessed in this study.

Considerable data support a role for FoxO1 in the control of hepatic gluconeogenic genes expression, though there is much less clarity regarding its importance for glycemia and hepatic lipid metabolism. As has been reported, we found that under normal conditions, hepatic deletion of FoxO1 resulted in an impaired pyruvate tolerance test, in this study independent of Akt2 (Figures 2B and 2C) (Matsumoto et al., 2007). Inhibition of FoxO1 activity by various techniques in genetically obese and DIO mouse models decreases blood glucose and insulin levels, and reduces hepatic glucose production as assayed by hyperinsulinenic-euglycemic clamp; loss of hepatic FoxO1 ameliorates fasting hyperglycemia in the STZ-induced diabetic mouse (Altomonte et al., 2003; Haeusler et al., 2010a; Kamagate et al., 2008). However, others (Matsumoto et al., 2007; Zhang et al., 2006). Fasting hepatic and serum TG levels were not changed in AFP > Cre;FoxO1fl/fl FoxA2loxP/loxP mice under normal conditions in this study and others (Figure 2D and Figure S3C) (Matsumoto et al., 2007), and no change was found on the rate of TG secretion in AFP > Cre;FoxO1fl/fl FoxA2loxP/loxP mice (Figure S4). There were no alterations in AFP > Cre; FoxO1fl/fl FoxA2loxP/loxP mice of serum TG under obese conditions, and MTP expression was not changed in AFP > Cre;FoxO1fl/fl FoxA2loxP/loxP mice during hypothalamic obesity (Figure 3 and Figure S6). These data suggest that changes in TG secretion are not responsible for hepatic TG accumulation in AFP > Cre;FoxO1fl/fl FoxA2loxP/loxP mice. FoxO1 also modulates mTORC1 activity, which regulates Srebp1c levels and lipogenesis (Chen et al., 2010; Duvel et al., 2010; Harvey et al., 2008). However, deletion of Akt2, FoxO1, or both did not alter phosphorylation of ribosomal protein S6 after HCD refeeding (Figure 7E), suggesting that the pathway by which FoxO1 normally suppresses lipid accumulation is independent of mTORC1.

FoxA2 has been reported to stimulate fatty acid oxidation, increase TG secretion, and reduce hepatic TG accumulation in obese animals (Wolfrum et al., 2004, 2008; Wolfrum and Stoffel, 2006). Much of the data supporting this model are derived from experiments involving expression of constitutively active FoxA2 in mouse liver, and thus have the potential of off-target effects. Other experiments took advantage of the reduction in nuclear FoxA2 associated with the obese state, during which the liver is likely to have numerous uncharacterized, complicating metabolic alterations. However, other studies found no change to the nuclear localization of FoxA2, even in the extreme case of elevated insulin levels in ob/ob mice (Zhang et al., 2005). In loss-of-function studies, liver-specific FoxA2 knockout mice displayed no abnormality in hepatic TG levels, consistent with the current results (Bochkis et al., 2008). Under normal chow feeding or in mice with DIO, loss of hepatic FoxA2 did not affect serum glucose and insulin or hepatic TG levels (Figures 1B and 1C and Figures S1 and S2). These data are compatible with a model in which inhibition of FoxA2 is not required for Akt2 to regulate hepatic TG accumulation. These results are qualified by the possibility that, in other mouse strains, the requirements for hepatic steatosis might be different.

Recently, mTORC1 has been shown to enhance de novo lipogenesis by regulating Srebp1c expression and processing (Chakrabarti et al., 2010; Duvel et al., 2010; Li et al., 2010; Porstmann et al., 2008). The full activation of mTORC1 requires both nutrients and growth factor signaling, which determine cellular location and Akt-dependent activation of the mTORC1 complex, respectively (Sancak et al., 2008, 2010; Sengupta et al., 2010b). In tissue culture cells and primary hepatocytes, insulin/Akt regulates Srebp1c expression and processing and de novo lipogenesis in an mTORC1-dependent manner (Azzout-Marniche et al., 2000; Chakrabarti et al., 2010; Duvel et al., 2010; Fleischmann and Iynedjian, 2000; Li et al., 2010; Porstmann et al., 2008). However, the model of an obligate role for mTORC1 in hepatic lipogenesis has not been tested genetically in vivo. Herein we report that conditional deletion of raptor in liver abolished mTORC1 activity, leading to a reduction in the expression of Srebp1c and its targets and decreased de novo lipogenesis (Figures 7A–7C). Interestingly, even though AFP > Cre;Akt2fl/fl mice during fasting by accelerating TG secretion through increases in MTP (Kamagate et al., 2008). However, others have suggested FoxO1 inhibits VLDL-TG secretion in pathological
and AFP > Cre;Akt2loxP/loxP;FoxO1loxP/loxP mice exhibit significantly decreased de novo lipogenesis following a high-carbohydrate meal, activation of mTORC1 and SREBP1c were largely unaffected (Figures 5D, 7D, and 7E). These data indicate that mTORC1 activation is not sufficient to induce lipogenesis under these conditions. During the revision of this paper, Yecies et al. reported an mTORC1-independent pathway by which Akt2 signals through INSIG2a to promote SREBP1c processing (Yecies et al., 2011). We found no change in the normal decrease in hepatic INSIG2a mRNA in AFP > Cre;Akt2loxP/loxP mice after HCD refeeding and only a modest reduction in the nuclear form of SREBP1c or expression of its target genes (Figures 5E and 7E). Thus, the mTORC1-independent pathway revealed in this study by liver-specific deletion of Akt2 does not represent induction of INSIG2a and is unlikely to be related to SREBP1c processing or expression. Rather, we propose that the requirement for Akt2 is linked to its role in the posttranslational control of other targets such as ACLY.

Taking these data in aggregate, we suggest that Akt2 promotes hepatic lipid accumulation and de novo lipogenesis independent of FoxA2 and FoxO1. Moreover, activated mTORC1 and SREBP1c and increased lipogenic gene expression is required but not sufficient for postprandial lipogenesis. Thus, our data provide strong support for the notion that nutrients have a direct role in the liver to promote anabolic lipid metabolism by a process dependent on the presence of a functional mTORC1 complex as well as other Akt-dependent signaling pathways.

**EXPERIMENTAL PROCEDURES**

**Animals**

The AFP > Cre;Akt2loxP/loxP, AFP > Cre;FoxO1loxP/loxP, and RaptorloxP/loxP mice have been described previously (Leavens et al., 2009; Matsumoto et al., 2007; Sengupta et al., 2010a; Zhang et al., 2005). All animals were raised and treated with approval from the University of Pennsylvania IACUC in accordance with National Institutes of Health (NIH) guidelines. Mice were of a 129/FVB/C57BL/6 background and male littermates were used for all studies. In the FoxA2 experiments, the wild-type control group included mice of genotypes AAV-TBG-Cre; Akt2loxP/loxP; FoxA2loxP/loxP; and Akt2loxP/loxP; FoxA2loxP/loxP. Mice labeled as AFP > Cre;Akt2loxP/loxP included the genotypes AFP > Cre;Akt2loxP/loxP; and FoxA2loxP/loxP. Mice labeled as AFP > Cre;FoxA2loxP/loxP included the genotypes AFP > Cre; FoxA2loxP/loxP; and FoxA2loxP/loxP. Mice labeled as AFP > Cre;Akt2loxP/loxP and FoxA2loxP/loxP included the genotypes AFP > Cre;Akt2loxP/loxP; FoxA2loxP/loxP; and FoxA2loxP/loxP. In the FoxO1 experiments, wild-type controls included genotypes AFP > Cre;Akt2loxP/loxP; FoxO1loxP/loxP; and Akt2loxP/loxP; FoxO1loxP/loxP. Mice indicated as AFP > Cre; Akt2loxP/loxP included the genotypes AFP > Cre;Akt2loxP/loxP; FoxO1loxP/loxP; and FoxO1loxP/loxP. In all cases there were no metabolic phenotypes among the pooled genotypes including Cre expressed alone. Mice were main-
tained on a normal chow diet (laboratory rodent diet 5001, LabDiet) unless otherwise noted under 12 hr light/dark cycle (7 a.m./7 p.m.) in a barrier facility. When fed with HFD (D12331i, Research Diets), mice were started at an age of 1 month and remained for 3 months.

For aurothioglucose (GTG, A0606, Sigma Aldrich) treatment, mice were maintained on normal chow. At 5–6 weeks old, mice were fasted for 24 hr and then injected intraperitoneally (i.p.) with one dose of 0.3 g/kg GTG in PBS. After injection, mice were kept fasted for another 20 hr before normal chow diet was freely accessible for the following 2 months. This protocol has been suggested to reduce mortality caused by GTG injection in mice (Brecher et al., 1965).

For acute excision of Raptor in liver, the adeno-associated virus was generated by Viral Vector Core at University of Pennsylvania. GFP or Cre recombinase was driven by a liver-specific promoter, thyroxine-binding globulin (TBG) promoter. Mice were injected postpartum at a dosage of 1.0 x 10^{11} gc virus diluted in PBS at 6 weeks of age and maintained on normal chow for another 2 weeks before analysis.

**Metabolic Measurement**

Blood glucose, serum insulin, and hepatic and serum TG levels were measured as described before (Leavens et al., 2009). For experiments involving fasting, mice were deprived of food overnight. For "fed" measurements, mice were reared on designated diet ad libitum before blood and liver samples were taken during the morning between 8 and 10 a.m. For glucose and pyruvate tolerance test, mice were fasted overnight followed by i.p. injection of 2 g/kg glucose or pyruvate, and then blood glucose levels were taken at designated time points.

**De Novo Lipogenesis**

For de novo lipogenesis assay, mice were fed with HCD (D12450B, Research Diets) for 2 days, and then treated as described in the text. Whole blood and liver samples were taken 3 hr after D2O injection and frozen in liquid nitrogen. Palmitate was isolated and analyzed by using gas chromatography-electron impact ionization mass spectrometry by the Stable Isotope Tracer Kinetic Service Center in the Institute of Diabetes, Obesity, and Metabolism, University of Pennsylvania. The absolute amount of newly made palmitate was assumed equivalent to the de novo lipogenesis rate.

**TG Secretion Assay**

TG secretion assay was performed as described previously (Millar et al., 2005). Mice were fasted overnight and then injected i.p. with 1 g/kg poloxamer 407 (kindly provided by Dr. John S. Millar, University of Pennsylvania). Blood samples were collected at indicated time points and assayed for serum TG.

**Statistics**

All data are presented as mean ± SEM. As noted in the figure legends, data were analyzed by using unpaired Student’s t test with two-tailed analysis, one-way ANOVA followed by Tukey’s post test, or two-way ANOVA followed by Bonferroni’s post test.

**SUPPLEMENTAL INFORMATION**

Supplemental Information includes seven figures, one table, Supplemental Experimental Procedures, and Supplemental References and can be found with this article online at doi:10.1016/j.cmet.2011.09.001.
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