

The role of nutrient signaling in the regulation of pancreatic α -cell mass and glucagon secretion

by

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Dedication

This work is dedicated to my family. Thank you for your limitless love, support, encouragement, and for the sacrifices you made to give me the opportunity to pursue my career goals.

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I wish to thank my parents, Kalina Bozadjieva and Ivan Bozadjiev, for their limitless love, support, encouragement, and for the sacrifices they have made to give me many opportunities. My deepest appreciation goes to Mark Kramer who has lived through this experience with me and has patiently listened and supported me through numerous failed experiments and “great-data day” celebrations.

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Preface

Type 2 Diabetes (T2D) is characterized by defective adaptation of β -cells to insulin resistance. Most of the research effort has focused on elucidating the physiological, molecular, and genetic components that regulate β -cell mass and insulin secretion, presenting diabetes as a unihormonal disorder. Contrary to this current approach, clinical data and animal experiments have shown that increased glucagon secretion by pancreatic α -cells play a role in the pathogenesis of hyperglycemia in diabetes. Physiological and genetic models of obesity show an increase in α -cell mass and glucagon secretion, but the signaling mechanisms responsible for these changes are not completely understood. Glucagon secretion is regulated by nutrients (glucose, amino acids) and growth factors (insulin). Studies in mice with loss of the insulin receptor in α -cells and studies in glucagon-secreting cell lines demonstrate that insulin receptor signaling regulates α -cell mass and glucagon secretion through AKT activation. Alpha cell proliferation is reduced by treatment with the mTOR Complex 1 (mTORC1) inhibitor, rapamycin, suggesting that downstream of the insulin receptor, Tuberous Sclerosis Complex (TSC1/2) and mTORC1 are important candidates in regulating α -cell mass and glucagon secretion. Most recently, studies using glucagon receptor deficient mice report increased α -cell proliferation and this was associated with a significant increase of circulating amino acids (known activators of mTORC1) suggesting that certain amino acids could induce α -cell mass in this mouse model. However, how downstream nutrient or insulin signaling regulates α -cell mass and glucagon secretion *in vivo* is currently unknown.

We hypothesize that mTORC1 signaling plays an essential role in nutrient-dependent regulation of α -cell mass maintenance and glucagon secretion. The following projects will test the hypothesis:

Chapter 1: Determine how loss of mTORC1 signaling regulates α -cell mass, glucagon secretion and adaptation of α -cells to diabetogenic conditions. The hypothesis for this project is that mTORC1 signaling is necessary for the proper maintenance of α -cell mass and glucagon secretion. The approach used to test this hypothesis includes *in vivo* and *in vitro* experiments using a genetic model of loss of mTORC1 signaling by ablating *raptor* in α -cells.

Chapter 2: Establish the role of gain of mTORC1 function on the regulation of α -cell mass, glucagon secretion and adaptation of α -cells to diabetogenic conditions. The working hypothesis is that gain in mTORC1 in α -cells potentiates α -cell mass expansion and increases glucagon levels as observed in diabetic patients. The approach used to test this hypothesis includes *in vivo* and *in vitro* experiments using a genetic model of gain of mTORC1 signaling by ablating *TSC2* in α -cells.

Uncovering the roles of mTOR Complex 1 in the regulation of α -cell mass and function using animal models and further examining these mechanisms using *in vitro* approaches will expand our understanding of how this pathway contributes to regulation of glucose homeostasis during normal and diabetogenic conditions. Finally, these studies will provide novel potential targets for therapeutic approaches in the maintenance of normoglycemia in diabetes.

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Abstract

Increased α -cell mass and aberrant glucagon response play major roles in the pathogenesis and complications associated with diabetes. In these studies, we determined that mTOR Complex 1 (mTORC1) is a major regulator of α -cell mass and glucagon secretion. Using mice deficient of *raptor* exclusively in α -cells we revealed that mTORC1 signaling promotes glucagon secretion during fasting by positively regulating K_{ATP} channels and glucagon expression. A novel mTORC1/FoxA2 axis provided a link between mTORC1 and transcriptional regulation of key genes responsible for α -cell function. Furthermore, we also found that mTORC1 signaling positively modulates the maintenance of islet α -cells by an autophagy-mediated process. In proceeding studies, we demonstrated that activation of mTORC1 signaling in α -cells is sufficient to induce α -cell mass expansion and hyperglucagonemia as observed in diabetic patients. We increased mTORC1 activity in α -cells by deletion of *TSC2*, a negative mTORC1 regulator. Our results revealed that gain of mTORC1 signaling in α -cells leads to increased fed and fasting glucagon levels and increased α -cell mass. Despite hyperglucagonemia, these mice were normoglycemic and had improved glucose tolerance and decreased hepatic glucose production. The results of these studies support a role for increased mTORC1 signaling in promoting the increase in α -cell mass and glucagon secretion observed in diabetic patients. Overall, our results revealed a novel function of mTORC1 in nutrient-dependent regulation of glucagon secretion and support a role for mTORC1 in controlling α -cell mass and function in patients treated with rapamycin analogs.

INTRODUCTION*

The discovery of glucagon

In 1907, Michael Lane described his anatomical observations of the pancreatic islets of Langerhans as cells with distinctive anatomical properties versus the earlier theory as those of “exhausted acini” (Lane, 1907). In his characterization of stained hamster pancreatic sections, Lane described the existence of two distinct types of cells within the islet, which he referred to as the large α and smaller β -cells (Lane, 1907). Four decades later, Sutherland and de Duve established that the α -cells of the pancreatic islet are the primary source of glucagon (Sutherland and De Duve, 1948a, b). Initially labeled as a contaminant, the physiological role of glucagon was first described in 1921, when Banting and Best conducted their classical experiments of insulin’s actions. Banting and Best tested their first pancreatic extracts in depancreatized dogs and observed an initial transient rise in blood glucose followed by the insulin-induced hypoglycemia (Gromada et al., 2007). Several years later, Murlin and his colleagues credited this transient rise in blood glucose to a hormone they named “Glucagon” or “Hyperglycemic-Glycogenolytic Factor” (Foa PP, 1952; Gromada et al., 2007; Murlin JR, 1923). Insights into the regulation of glucagon release came from elegant cross-circulation experiments performed by Foa and his colleagues in the 1950s, showing that hypoglycemia triggered by the injection of insulin in a donor dog induces the release of glucagon, which secreted through the donor blood *via* a pancreatic-femoral anastomosis causes a hyperglycemic response in a recipient dog (Foa PP, 1952). Bensley and Woerner added to these observations with their suggestion that glucagon

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induces liver glycogenolysis and thereby promotes a rise in blood glucose levels (Bensley S.H., 1939).

Glucagon

Glucagon is a 29-amino acid peptide derived from the tissue-specific processing of proglucagon in pancreatic α -cells through cleavage by prohormone convertase 2 (PC2) (Figure 1) (Furuta et al., 2001). In contrast, processing of proglucagon to glucagon-like peptides (GLP-1, GLP-2), oxyntomodulin and glicentin occurs in intestinal enteroendocrine cells by prohormone convertase 1 (PC1) (Figure 1) (Lefebvre, 1995). Glucagon plays a major role in antagonizing the effects of insulin and maintaining glucose homeostasis by promoting hepatic gluconeogenesis and glycogenolysis and inhibiting glycogen synthesis. Therefore, the secretion of glucagon is normally induced in states of decreasing blood glucose, such as fasting and increased energy expenditure, to sufficiently induce a rapid, yet transient rise in blood glucose.

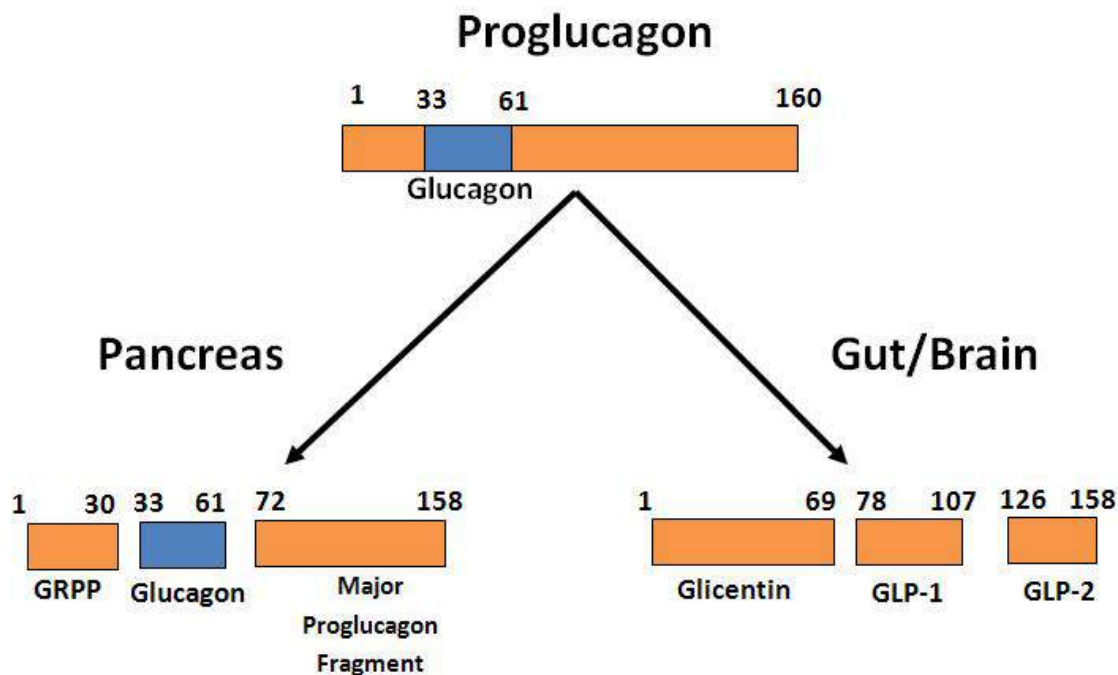


Figure 1. Diagram of differential processing of the proglucagon gene product in α -cells of the pancreas, gut (L-cells) and brain. Glucagon is a 29-amino acid peptide derived from the tissue-specific processing of proglucagon in pancreatic α -cells through cleavage by prohormone convertase 2 (PC2) In contrast, processing of proglucagon to glucagon-like peptides (GLP-1, GLP-2), oxyntomodulin and glicentin occurs in intestinal

enteroendocrine cells by prohormone convertase 1 (PC1) Only biologically active products are shown. For further details of cleavage sites and processing see reference (Lefebvre, 1995).

Glucagon and the endocrine pancreas

The pancreatic islet comprises five major types of polypeptide-secreting cells: insulin-secreting β -cells (65-80% of total islet cells), the glucagon secreting α -cells (15-20%), somatostatin-secreting δ -cells (3-10%) and pancreatic polypeptide-secreting cells (3-5%), along with ghrelin-positive cells which are mostly observed in early development (Wierup et al., 2004). The five major islet cell types are aligned on blood vessels at no particular order or structured organization within the human islet (Cabrera et al., 2006) (Figure 2A). In contrast, the rodent islet shows a more-defined architecture placing the β -cells in the core and the α , δ and PP-cells lying at the mantle of the islet (Figure 2B). This unique structure in the rodent islet suggests an organized system allowing paracrine interactions between the peptides released. This is supported by studies showing that arterial blood is directed from the core of the rodent islet (insulin-secreting β -cells) to the periphery (Bonner-Weir and Orci, 1982). Therefore, during a rise in blood glucose, the pancreatic α -cells are exposed to high levels of secreted insulin leading to the inhibition of glucagon secretion and glucagon gene transcription.

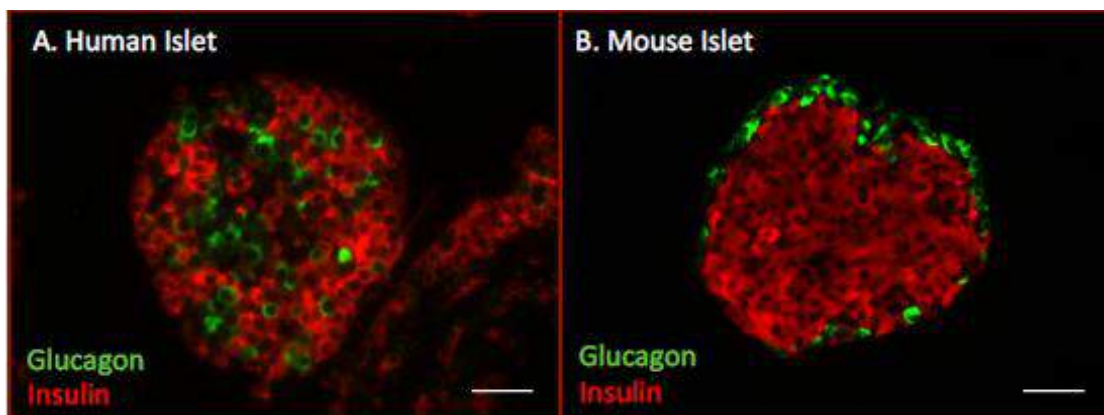


Figure 2. Immunofluorescent labeling of human and mouse islets. A. Human islet: glucagon-positive α -cells (green) are randomly dispersed among insulin-positive β -cells (red) within the human islet (scale 50 μ m). **B.** Mouse islet: glucagon-positive α -cells (green) are concentrated on the mantle and insulin-positive β -cells (red) make-up the core of the mouse islet (scale 50 μ m).

Transcriptional regulation of α -cell development, maintenance and glucagon gene transcription

A cascade of transcriptional factor regulators, starting from pancreatic progenitors expressing Pdx1, Ptf1a and Sox9, mediate the differentiation of α -cells. The pancreatic endocrine progenitors that give rise to islet cells express Neurog3 at embryonic day (E) 8.5. The newly formed endocrine cells accumulate along the ducts and blood vessels and undergo rapid expansion *via* self-replication during the neonatal period. The final committed α -cell lineage is defined by the expression of the transcription factors Arx, Foxa1/2, Pou3f4 (Brn4), MafB, Pax6 and Isl1. Glucagon is expressed at E12.5.

The loss of α -cell transcription factors Arx and Pax6 results in loss of α -cells and circulating glucagon levels. The specific loss of Arx is sufficient to promote the conversion of α to β -cells at any stage, and is independent of Pax4 expression (Courtney et al., 2013). Loss of Pax4 results in dramatic loss of β and δ -cells and increase in α -cells (Sosa-Pineda et al., 1997). In contrast, ectopic expression of Pax4 drives endocrine precursor cells and mature α -cells to adopt a β -cell fate by suppressing Pax6-mediated transcription (Collombat et al., 2003; Collombat et al., 2009; St-Onge et al., 1997). Pax6 also has been shown to play a key role in the regulation of proglucagon gene expression and processing, as well as glucagon biosynthesis and secretion (Gosmain et al., 2012; Katz et al., 2009; Ritz-Laser et al., 2002).

Foxa1 and Foxa2 play major roles in α -cell development and glucagon expression. Foxa1 null mice lack key islet genes, including glucagon, and die shortly after birth due to hypoglycemia (Kaestner et al., 1999; Shih et al., 1999). Ablation of Foxa2 in the gut endoderm leads to major reduction in the number of mature α -cells and proglucagon expression (Lee et al., 2005). Pou3f4 (Brn4) is dispensable for α -cell development and maintenance, but this transcription factor promotes the expression of glucagon by directly binding to the proglucagon promoter. Isl1 and MafB have also been shown to promote glucagon expression by directly binding to the proglucagon promoter (Artner et al., 2006; Conrad et al., 2015).

Regulation of glucagon release

The secretion of glucagon by the α -cells is regulated by the effects of paracrine and autocrine factors as well as neuronal inputs. Glucagon release is inhibited after carbohydrate-rich meal and the consequent rise in blood glucose (hyperglycemia) and insulin secretion. However, a meal rich in amino acids induces glucagon release. Parasympathetic (Adrenaline) and sympathetic (Epinephrine, Norepinephrine, Galanin, Neuropeptide Y) nerve stimulations induce the secretion of glucagon from the pancreatic α -cells.

Nutrients (Amino Acids and Glucose)

Nutrients play primary role in the regulation of glucagon secretion, in part by modulating cell mass and glucagon expression (reviewed in (Marroqui et al., 2014)). The amino acids arginine, alanine, glutamine and low levels of leucine potentiate glucagon secretion and it has been shown that this effect is suppressed during high glucose in an insulin-independent manner (Pipeleers et al., 1985). In turn, lysine and high levels of leucine inhibit glucagon release.

Glucagon is secreted by the pancreatic α -cells in states of decreasing blood glucose; however, whether changes in glucose concentrations alone can regulate glucagon secretion still remains unclear. Contrary to the regulation of glucagon release in the fed state, it has been strongly suggested that extrinsic paracrine signals (insulin/GABA, somatostatin) do not play a role in regulating glucagon secretion during fasting (1-6 mM glucose) (Walker et al., 2011).

Rat α -cells express glucokinase and glucose transporter GLUT1, an isoform with a lower capacity compared to GLUT2 - the predominant form in insulin-secreting mouse β -cells (Heimberg et al., 1996). Despite differences in metabolism of glucose by the two cells types, studies have shown that they share similar inherent mechanisms of activation (Olsen et al., 2005). Alpha cells have high ATP concentrations under low glucose, which rise further after stimulation with high glucose. In contrast to β -cells, net K_{ATP} -channel activity at low (1 mM) glucose is significantly inhibited (Rorsman et al.,

2014; Rorsman et al., 2008). This renders K_{ATP} -channel partly open, shifting the membrane potential enough to activate low-voltage-activated L-type Ca^{2+} -channels. Ca^{2+} influx activates Na^+ -channels to further depolarize membrane potential triggering Ca^{2+} entry through P/Q type channels (Leclerc et al., 2011; Rorsman et al., 2014; Rorsman et al., 2008; Zhang et al., 2013). Influx of Ca^{2+} triggers glucagon granule exocytosis. In contrast, glucose elevation inhibits remaining α -cell K_{ATP} channel activity causing further depolarization that partially inactivates voltage-dependent Na^+ -channels, decreases spike height and results in low P/Q Ca^{2+} channel activity. This depolarization ultimately results in inhibition of secretion (Leclerc et al., 2011; Rorsman et al., 2014; Rorsman et al., 2008; Zhang et al., 2013). Elegant studies have shown that K_{ATP} channels play an essential role in potentiating glucagon release and their activity is altered in diabetic islets (Gopel et al., 2000; MacDonald et al., 2007; Zhang et al., 2013). Also, these studies have shown that glucose-mediated regulation of glucagon secretion is dependent on K_{ATP} channel function (Rorsman et al., 2008; Zhang et al., 2013).

Paracrine Regulation by Insulin and GABA

Pancreatic α -cells are exposed to high levels of insulin secreted from the β -cells in the islet. Insulin is a potent inhibitor of glucagon secretion and glucagon gene transcription (Asplin et al., 1981; Maruyama et al., 1984; Philippe, 1989; Weir et al., 1976; Zhang et al., 2012). Data have shown that the diminished insulin release during hyperglycemia associated with diabetes paradoxically stimulates the release of glucagon (Dinneen et al., 1995; Reaven et al., 1987; Yoon et al., 2003). It has also been shown that chronic high glucose induces glucotoxicity increasing glucagon secretion by reducing the insulin-mediated activation of phosphatidylinositol 3-kinase (PI3K)-AKT activity in rat islets and glucagon-secreting cell line (Shen et al., 2012). Studies utilizing *in vitro* approaches have shown that insulin receptors are very abundant on pancreatic α -cells and activate the PI3K/AKT pathway leading to inhibition of glucagon gene transcription and secretion (Schinner et al., 2005; Shen et al., 2012; Xu et al., 2006). Insulin has been shown to induce the AKT-dependent $GABA_A$ receptor translocation to the plasma membrane (which can be activated by GABA (co-released with insulin) and PI3K-dependent opening of K_{ATP} channels, culminating in hyperpolarizing the plasma

membrane and inhibiting glucagon secretion (Xu et al., 2006). Although, the precise mechanisms responsible for changes in the α -cell function in diabetes remain unclear, a recent study by Kawamori and colleagues showed that inhibiting insulin signaling in the pancreatic α -cells of mice through genetic ablation of insulin receptors in α -cells leads to altered glucose metabolism including mild glucose intolerance, hyperglycemia, and mild hyperglucagonemia (Kawamori and Kulkarni, 2009).

GABA (γ -Aminobutyric acid) is produced from the excitatory amino acid glutamate and co-released with insulin from the pancreatic β -cells by high glucose and glutamate stimulation. GABA can diffuse within the islet interstitium to activate GABA_A receptors present on the cell-surface of α -cells (Wendt et al., 2004). This nonpeptidal neurotransmitter has been shown to act as a suppressor of amino acid-stimulated glucagon release in the mouse and isolated α -cells via GABA_A receptors (Gilon et al., 1991). Data have suggested that glucose-stimulated insulin release and the subsequent activation of the Insulin Receptor-PI3K-AKT pathway induce the activation and translocation of GABA_A receptors to the plasma membrane (Xu et al., 2006). The GABA co-released with insulin from the β -cells can activate the newly translocated cell-surface GABA_A receptors and increase Cl⁻ inhibitory currents, subsequently hyperpolarizing the plasma membrane (Wendt et al., 2004). The hyperpolarization of the membrane closes the voltage-dependent Ca²⁺ channels, which lowers the free cytoplasmic Ca²⁺ levels and reduces glucagon exocytosis (Rorsman et al., 1989; Wendt et al., 2004).

Paracrine Regulation by Somatostatin

Somatostatin, secreted by the islet δ -cells, has been long accepted as a glucagon-suppressing peptide. Exogenous somatostatin inhibits glucagon release in isolated α -cells, as well as in healthy and diabetic patients (Chen et al., 2011; Gerich et al., 1974). In addition, islets isolated from somatostatin-deficient mice have reduced glucose-suppression of glucagon release (Hauge-Evans et al., 2009). Somatostatin-suppressed glucagon secretion is regulated through the somatostatin receptor type 2 (SS2R) and genetic disruption of the receptor leads to an increased glucagon secretion (Yue et al., 2013).

Autocrine Regulation: Glucagon and Glutamate

Perfusion experiments in the human and rat pancreas have shown that glucagon suppresses insulin and somatostatin release (Brunicardi et al., 2001; Stagner et al., 1989). Glucagon receptor knock out mice exhibit α -cell hyperplasia and hyperglucagonemia, which has been suggested to be due to a lack of autocrine signals of glucagon on the α -cell (Gromada et al., 2007). Contrary to this theory, a recent study has shown that transplantation of wild type islets into mice with liver-specific deletion of the glucagon receptor also develop α -cell hyperplasia (Longuet et al., 2013). These data suggest that a circulating factor generated after the disruption of glucagon signaling in the liver can increase α -cell proliferation independent of direct pancreatic input.

Glutamate is a major excitatory neurotransmitter in the central nervous system, which has also been implicated in the regulation of glucagon release. An elegant study published by Cabrera and colleagues described the positive autocrine signal of glutamate in the human, monkey and mouse islets (Cabrera et al., 2008). The authors proposed a mechanistic model where glutamate co-released with glucagon potentiates glucagon secretion through acting on the ionotropic glutamate receptors on the α -cell membrane and creating a positive autocrine loop (Cabrera et al., 2008).

Regulation of α -cell mass

Although the mechanisms of modulating α -cell mass are not fully understood, several hypotheses have been developed based on animal models with increase in α -cell mass. Mice fed with high protein diet or high fat diet exhibit increased α -cell hyperplasia and hypertrophy suggesting that nutrient environment and/or insulin resistance could regulate α -cell mass expansion (Ellingsgaard et al., 2008; Morley et al., 1982). Studies using liver-specific glucagon receptor knock out mice suggest that a circulating factor generated after the disruption of glucagon signaling in the liver can increase α -cell proliferation independent of direct pancreatic input (Gromada et al., 2007; Longuet et al., 2013). Metabolomic profile in glucagon receptor knock out mice suggest that significant increase in circulating amino acids and their derivatives could be responsible for induction of α -cell mass in these mice (Yang et al., 2011). These studies support the

concept that α -cell mass is a dynamic process and responds to extracellular signals including nutrients (amino acids, glucose), growth factors (insulin) and potentially uncharacterized factors from the liver.

Physiological actions of glucagon at target tissues

Glucagon exerts its physiological action on target tissues *via* the G-protein coupled glucagon receptor. The principle target tissues for glucagon signaling are liver and adipose tissue. However, the glucagon receptor is found on multiple other tissues including intestine, kidney and brain (Jiang and Zhang, 2003).

In the liver, glucagon counteracts the anabolic properties of insulin by promoting gluconeogenesis and glycogenolysis and inhibiting glycolysis resulting in a net increase in hepatic glucose production. The hepatocyte is exposed to high levels of glucagon released by the pancreas *via* the portal vein. The mechanistic actions of glucagon on the hepatocyte are mediated by glucagon's binding and activation of the G-protein coupled glucagon receptors on the cell membrane. The subsequent activation of adenylate cyclase leads to the increase in intracellular cyclic adenosine monophosphate (cAMP) levels and the activation of protein kinase A (PKA) (Jiang and Zhang, 2003). The second messenger cAMP can activate cyclic nucleotide-gated ion channels, Exchange Proteins Activated by cAMP (EPAC) and Protein Kinase A (PKA). Activated PKA leads to glycogen breakdown (glycogenolysis) by the activation of the PKA-glycogen phosphorylase kinase-glycogen phosphorylate cascade and increased expression of glucose-6-phosphatase (*G6Pase*), which converts glucose-6-phosphate to glucose (Jiang and Zhang, 2003). Glucagon's activation of the liver's glucagon receptor leading to hepatic glucose output has been shown to act through the gluconeogenic process is also promoted by the activity of additional transcription factors. The activated CREB binds to the promoter region of the transcriptional coactivator *PGC-1* gene, increasing its transcription. PGC-1 and the nuclear transcription factor Hepatocyte Nuclear Factor-4 (HNF-4) further promote gluconeogenesis by increasing the transcription of *PEPCK* gene and therefore PEPCK activity (Jiang and Zhang, 2003).

Glucagon signaling in adipose tissue is relevant during periods of starvation and stress and in particular when insulin is suppressed. In the adipocyte, glucagon binds to the glucagon receptor to activate the cAMP-PKA pathway, leading to the phosphorylation and activation of hormone-sensitive lipase and the subsequent breakdown of triglycerides (lipolysis) and release of diacylglycerol and free fatty acids into the circulation. The liver can further utilize glycerol and free fatty acids for gluconeogenesis or re-esterification of free fatty acids to form ketone bodies.

Glucagon's physiological effects on the heart and kidney have also been described, although glucagon's actions in these tissues are less understood mechanistically compared to those in the liver and adipose tissue. Glucagon stimulates Ca^{2+} currents *via* increased cAMP thus increasing heart contractility (Gonzalez-Munoz et al., 2008; Mery et al., 1990). Glucagon increases glucose utilization and lipid oxidation in the heart, but decreases cardiomyocyte survival (Campbell and Drucker, 2015). Glucagon has been described as a vasodilator, which lowers blood pressure by decreasing the vascular resistance in the liver and spleen. Glucagon has diuretic effects on the kidney, increasing glomerular filtration and electrolyte/water excretion (Farah, 1983).

Glucagon receptors are expressed in the brain and data has suggested that circulating glucagon can pass the blood-brain barrier to modulate its effects in the central nervous system (CNS). Glucagon is expressed in the brainstem and hypothalamus, but glucagon receptors are widely expressed in the CNS. Glucagon infused in the CNS has shown to cause a transient drop in blood glucose, followed by hyperglycemia (LaPierre et al., 2014). The initial drop in blood glucose was abolished in vagotomized dogs and in pancreatectomized dogs, demonstrating that the parasympathetic system and the pancreas are both essential in the central regulation of blood glucose by glucagon (LaPierre et al., 2014). Glucagon infused in the central nervous system has also shown anorexigenic effects in rats, chicks and sheep. In addition, intravenous infusion of glucagon has been shown to suppress appetite in humans; however, the direct link between glucagon and central food intake regulation in humans is unclear. Although the mechanisms of glucagon's activity on the brain remain largely unclear, the involvement

of the hypothalamic corticotropin-releasing factor (CRF) and the activation of the hypothalamic-pituitary-adrenal (HPA) axis are implicated in modulating glucagon's suppression of food intake (Filippi et al., 2013).

The role of glucagon in diabetes

Type 1 (T1D) and Type 2 (T2D) Diabetes are characterized by uncontrolled hyperglycemia associated with progressive decrease in insulin. Glucagon, insulin's counterregulatory hormone, plays a major role in maintaining glucose homeostasis by promoting glucose production *via* hepatic glycogenolysis and gluconeogenesis. Paradoxically, glucagon levels are elevated in insulin-resistant non-diabetic, T1D, and T2D patients, leading to enhanced hepatic glucose output and thereby exacerbating hyperglycemia (Dinneen et al., 1995; Mezza et al., 2014; Orci et al., 1976; Rahier et al., 1983; Sherwin et al., 1976; Yoon et al., 2003). Increase in glucagon levels in T1D and T2D patients can be explained in part by increase in α -cell mass, but the mechanisms for the increase in α -cell mass in diabetes remain unclear (Orci et al., 1976; Rahier et al., 1983; Yoon et al., 2003).

A major complication in the management of T1D diabetes or advanced T2D is the failure to secrete glucagon in response to hypoglycemia. This results in recurrent hypoglycemia, referred as Hypoglycemia-Associated Autonomic Failure (HAAF), and presents a major limiting factor for optimal glucose control in insulin-dependent diabetic patients (Cryer, 2002; Gerich et al., 1973; Segel et al., 2002). Unfortunately, as T1D and advanced T2D progresses insulin administration becomes increasingly necessary and the glucagon response to hypoglycemia could become greatly attenuated.

Insulin Receptor/mTOR signaling and its role in metabolic tissues

The AKT/mTOR signaling pathway

The mammalian/mechanistic target of rapamycin (mTOR) couples the growth of the cell to its nutritional status (Efeyan et al., 2012; Murakami et al., 2004). The mammalian TOR is associated with two distinct complexes (mTORC1 and 2) that differ in upstream inputs and downstream targets (Dowling et al., 2010; Laplante and Sabatini, 2012; Lee et al., 2007; Shimobayashi and Hall, 2014; Soulard et al., 2009). mTORC1 constitutes the rapamycin sensitive arm of mTOR signaling and contains at least 3 distinct proteins: Raptor, mLST8 and PRAS40 (Dowling et al., 2010; Laplante and Sabatini, 2012; Lee et al., 2007; Shimobayashi and Hall, 2014; Soulard et al., 2009). mTORC1 activity is regulated by growth factors, amino acids, energy state, stress and oxygen levels of the cell. mTORC1 activity is negatively regulated by Tuberous Sclerosis Complex (TSC1/2), which functions as a GTPase-activating protein for the Ras homolog enriched in brain GTPase, Rheb (Figure 3). TSC1/2 negatively regulates mTORC1 by keeping Rheb in its inactive GDP-bound state (Inoki et al., 2003). Activation of the Insulin Receptor/IRS1/2 by growth factors leads to phosphorylation and activation of AKT (Protein Kinase B). Upon phosphorylation and inactivation by AKT, TSC1/2 releases its inhibition on Rheb, allowing Rheb's direct activation of mTORC1 (Dan et al., 2002; Inoki et al., 2002; Inoki et al., 2003; Manning et al., 2002). AKT can also directly activate mTORC1, by phosphorylating, inhibiting and allowing the release of PRAS40 from mTORC1. TSC2 exists in a complex with TSC1, but the major function of TSC1 in mTORC1 signaling is to stabilize TSC2 and prevent its ubiquitin-mediated degradation. In contrast, phosphorylation and activation of TSC2 by AMPK and GSK3 β inhibits mTOR signaling (Inoki et al., 2006; Inoki et al., 2003). Amino acid-activation of mTORC1 is activated by the subcellular localization of mTOR and Raptor by Rag GTPases, Ragulator complex (LAMTOR1-3) and vacuolar H⁺-ATPase (v-ATPase) to the lysosomes and late endosomes (Bar-Peled et al., 2012; Sancak et al., 2010; Sancak and Sabatini, 2009). The Ragulator complex is a pentameric protein complex, consisting of five subunits, p18 (LAMTOR1), p14, MP1, HBXIP, and C7orf59 (Sancak et al., 2010; Sancak et al., 2008). Rapamycin directly inhibits mTORC1 by forming a complex with FK506-binding protein

(FKBP12) (Brown et al., 1994).

mTORC1 controls growth (cell size) and proliferation (cell number) by modulating mRNA translation through phosphorylation of 4E-BP1, 2, and 3 and the ribosomal protein S6 kinases (S6K1 and 2) (Figure 3) (Dowling et al., 2010; Laplante and Sabatini, 2012; Lee et al., 2007; Shimobayashi and Hall, 2014; Soulard et al., 2009). Phosphorylation of the 4E-BPs triggers their release from eIF4E and initiates cap-dependent translation. Thus, activated mTORC1 downstream substrates promote mRNA translation initiation, and progression and control of the rate of protein synthesis.

mTORC1 inhibits autophagy by phosphorylation and activation of the kinase ULK1/2 and subcellular localization of transcription factor EB, TFEB (Figure 3). mTORC1/Raptor directly interact with ULK complexes by phosphorylating and inhibiting their kinase activity to suppress autophagy (Hosokawa et al., 2009; Jung et al., 2009). In turn, the inhibition of mTORC1 activity, such as starvation, suppresses the phosphorylation and therefore inactivates ULK complexes to increase autophagy (Hosokawa et al., 2009). mTORC1-dependent ULK1 phosphorylation induces the dissociation of AMPK from the ULK1 complex, thereby attenuating AMPK-dependent ULK1 phosphorylation and activation (Kim et al., 2011). Nutrient depletion triggers the shuttling of TFEB from cytosol to nucleus, where TFEB initiates transcription of autophagy-mediated genes. Interestingly, it has been also reported that ULK-silenced cells have increased S6K1 activity and that ULK negatively regulates mTORC1 activity to promote increase in cell size (Jung et al., 2009).

mTOR Complex 2 (mTORC2) is insensitive to rapamycin and contains Rictor, mLst/GbL, and mTOR (Dowling et al., 2010; Laplante and Sabatini, 2012; Lee et al., 2007; Shimobayashi and Hall, 2014; Soulard et al., 2009). mTOR Complex 2 phosphorylates AKT on Ser473, suggesting that this pathway indirectly could be linked to proliferation (Sarbasov et al., 2005).

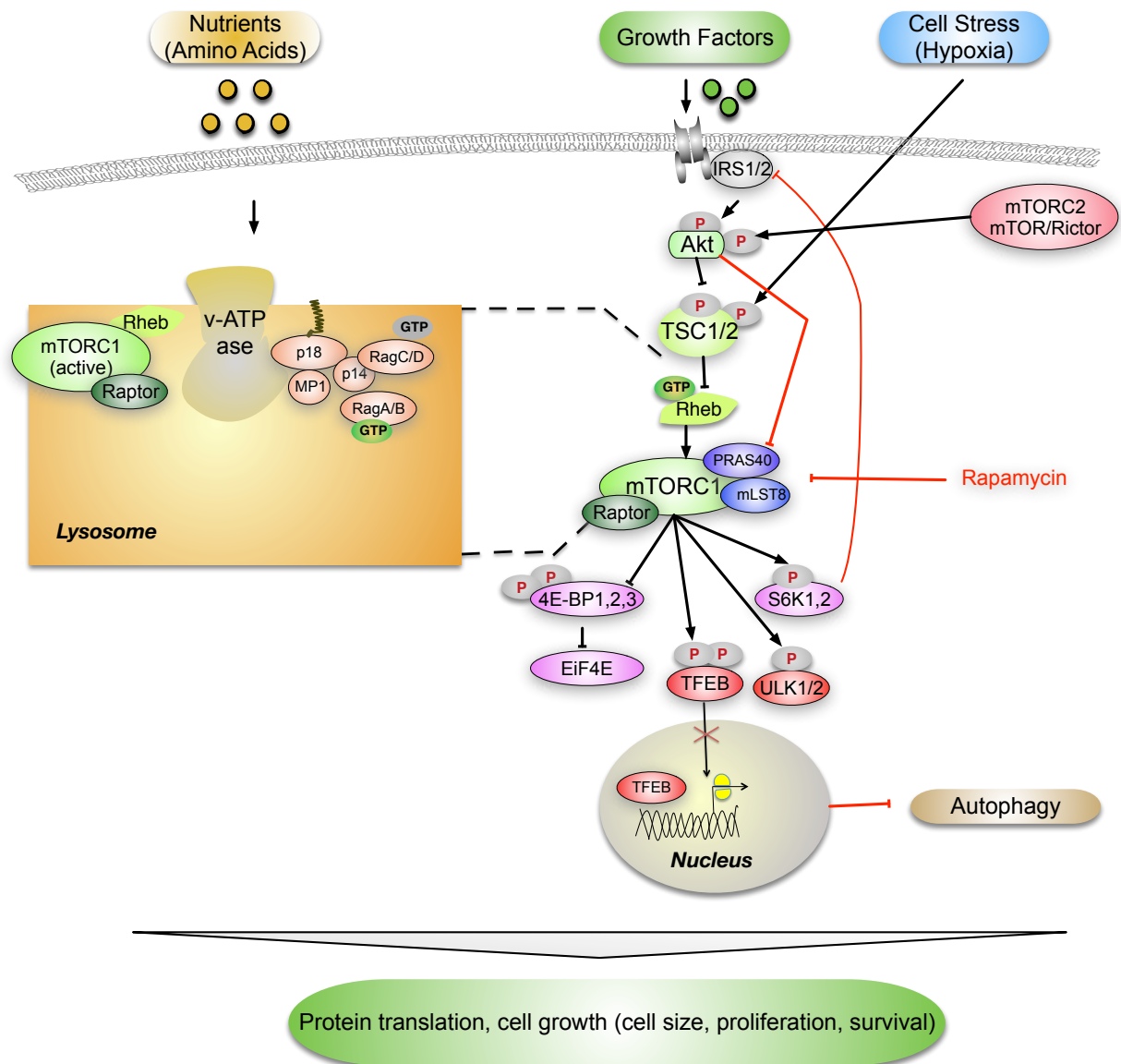


Figure 3. Diagram of the mTOR signaling pathway The mammalian target of rapamycin (mTOR) is essential for cell growth and proliferation. mTOR activity is regulated by growth factors and nutrients, as well as the redox state of the cells. The mammalian TOR is associated with two distinct complexes (mTORC1 and 2). Activation of the Insulin Receptor/IRS1/2 by growth factors, leads to phosphorylation and activation of AKT (Protein Kinase B). mTORC1 activity is negatively regulated by Tuberous Sclerosis Complex (TSC1/2). TSC2 phosphorylation and inactivation by AKT releases the inhibition of small G-protein Rheb, leading to activation of mTORC1. Amino acid-activation of mTORC1 is activated by the subcellular localization of mTOR and Raptor by Rag GTPases, Ragulator complex (LAMTOR1-3) and vacuolar H⁺-ATPase (v-ATPase) to the lysosomes and late endosomes. mTORC1 is rapamycin sensitive and controls cell growth (cell size) and proliferation (cell number) by modulating mRNA translation through phosphorylation and inhibition of 4E-BPs and the phosphorylation

and activation of ribosomal protein S6 kinases. mTORC1 inhibits autophagy by phosphorylation and activation of ULK1/2 and TFEB. mTORC2 is insensitive to rapamycin and can phosphorylates and activate AKT.

The role of mTOR Complex 1 in metabolic cells

The excess nutrient intake associated with obesity increases the activity of mTORC1/S6K signaling. The chronic activation of the pathway and specifically, the S6K arm of the mTORC1 activation, leads to a negative feedback inhibition of IRS/IRS2 and AKT signaling and insulin resistance (Figure 3) (Khamzina et al., 2005; Shigeyama et al., 2008; Um et al., 2004). Therefore, the regulation of mTORC1 activity plays a major role in insulin-sensitive tissues, however mTORC1 does have tissue-specific roles. Raptor, regulatory associated protein of mTOR, plays an essential role in the nutrient-dependent regulation of mTORC1 and the regulation of cell size by mTORC1 activity (Kim et al., 2002). The conditional deletion of *raptor* in adipocytes improves glucose tolerance, insulin sensitivity and resistance to high fat feeding (Polak et al., 2008). In turn, deletion of *raptor* in muscle results in mice that are glucose intolerant and have decreased mitochondrial biogenesis and associated proteins (Bentzinger et al., 2008). In the liver, loss of mTORC1 signaling by conditional deletion of *raptor* has major implications to the liver's adaptation to fasting by a defect in ketogenesis (Sengupta et al., 2010). Overall, the role of mTORC1 signaling is tissue-specific and additional studies are needed to understand the contribution of this pathway in pancreatic endocrine cells, which play a major role in the maintenance of normoglycemia.

Insulin receptor signaling regulates α -cell mass and glucagon secretion

Insulin has been shown to be one of the most potent regulators of glucagon synthesis and secretion (Franklin et al., 2005; Ishihara et al., 2003; Kawamori et al., 2009; Philippe, 1989; Schinner et al., 2005; Xu et al., 2006). Mice with loss of the insulin receptor in α -cells have increased fed glucagon levels demonstrating that insulin receptor signaling regulates insulin-mediated suppression of glucagon secretion at the fed state (Kawamori et al., 2009). These findings can be translated to explain the

increased glucagon levels associated with insulin resistance and T2D. Moreover, mice with pancreatic deletion of the Insulin Receptor Substrate 2 (IRS2) have a decreased α -cell mass and glucagon levels, implicating the Insulin-Receptor signaling pathway in promoting α -cell mass and glucagon content (Cantley et al., 2007).

The role of mTOR Complex 1 in the regulation of α -cell mass and glucagon secretion

mTOR Complex 1/Raptor (mTORC1) emerge as prime candidates in the regulation of α -cell mass and glucagon secretion, as mTORC1/Raptor integrates signals from growth factors and nutrients to regulate cell growth, survival and function of insulin-sensitive metabolic tissues (Bentzinger et al., 2008; Cota et al., 2006; Polak et al., 2008; Sengupta et al., 2010). Alpha cell proliferation is reduced by treatment with the mTOR Complex 1/Raptor (mTORC1) inhibitor, rapamycin (Liu et al., 2011; Solloway et al., 2015), suggesting that downstream of the insulin receptor, Tuberous Sclerosis Complex (TSC1/2) and mTORC1 could be important candidates to mediate the effects of insulin on α -cell mass and glucagon secretion. Most recently, studies using glucagon receptor deficient mice report increased α -cell proliferation (Gromada et al., 2007; Longuet et al., 2013) and this was associated with a significant increase of circulating amino acids (known activators of mTORC1) suggesting that certain amino acids could induce α -cell mass in this mouse model (Solloway et al., 2015; Yang et al., 2011). These findings support the concept that α -cell mass and glucagon secretion are sensitive to extracellular signals including nutrients (amino acids, glucose) and growth factors (insulin) and that the mTORC1 pathway may be involved in this process. However, how nutrients or downstream targets of the insulin receptor signaling regulate α -cell mass and glucagon secretion *in vivo* is currently unknown.

CHAPTER 1

Experimental Methods

Animals

Mice were housed in pathogen-free environment and maintained on 12-hour light/dark cycle at the University of Michigan Brehm Center Animal Facility. All protocols are approved by the University of Michigan Animal Care and Use Committee and are in accordance to NIH guidelines. We utilized the *Cre/lox P* system to generate mice with loss of *raptor* expression in α -cells. The Glucagon-Cre mice (generous gift from Dr. G. Gittes at the University of Pittsburg)(Shiota et al., 2013), expressing *Cre* recombinase driven by the glucagon promoter were crossed with *Raptor*^{flox/flox} (generous gift by Dr. M. Hall and Dr. M. Rüegg at the University of Basel, Switzerland) (Polak et al., 2008).

We generated three experimental groups for all described experiments in Chapter 1: controls (*Raptor*^{flox/flox}, *Raptor*^{flox/+} and Glucagon-Cre), α *Raptor*^{KO} (Glucagon-Cre; *Raptor*^{flox/flox}) and α *Raptor*^{HET} (Glucagon-Cre; *Raptor*^{flox/+}). All animals were *C57BL/6* background. The animals were born in expected Mendelian ratios and expected lifespans.

We generated three experimental groups for all described experiments in Chapter 2: controls (*TSC2*^{flox/flox}, *TSC2*^{flox/+}, Glucagon-Cre), α *TSC2*^{KO} (Glucagon-Cre; *TSC2*^{flox/flox}) and α *TSC2*^{HET} (Glucagon-Cre; *TSC2*^{flox/+}). These mice had mixed background between *C57BL/6* and *129X1*. All animals were born in expected Mendelian ratios, but had a reduced lifespan due to decreased body weight and observed seizure episodes of unknown origin (but not due to hypoglycemia).

Reporter transgenic animals CAG-tdTomato, Ins1-EGFP and CAG-YFP were purchased from Jackson Labs and generously provided to us by Drs. Martin Myers and Peter Arvan (University of Michigan). Reporter transgenic mice, GFP-LC3#53 were obtained from RIKEN with the permission of the depositor, Dr. Noboru Mizushima (Mizushima et al., 2004). All metabolic (2 or 8 months) and *ex vivo* islet secretion (2 months) studies were performed with aged-matched male mice. Islet morphometric analysis utilized age-matched cohorts with male and female mice.

Metabolic Studies

Body weight and random blood glucose was monitored monthly for total of 4 months. Fed (9 AM) and fasting (12 hours; 9 PM) glucose, insulin and glucagon levels were evaluated in 2 and 8-month old males. Blood was obtained from the tail vein and blood glucose was measured with Accu-Chek blood glucose meter. Glucagon and insulin levels were measured with ELISAs (Mercodia and AlpcO, respectively). IPGTT (2 g/kg), ITT (1 U/kg) and 2 deoxy-D-glucose (2g/kg) were performed by intraperitoneal (IP) injections of respective agents in 4-6 hour fasted male mice. Hepatic glucose production was measured by IP injection of pyruvate (2g/kg) in 16-hour fasted male mice. Active GLP-1 levels were measured by oral administration of glucose (2g/kg) and plasma levels of active GLP-1 were measured with STELLUX Chemiluminescent Assay (AlpcO). Prior to measuring active GLP-1 levels, DPP-IV Inhibitor (Millipore) was added to plasma (20 μ L per 1 mL of plasma) before storing the samples in -80°C. Food intake and activity levels were recorded for the duration of 3 days using CLAMS metabolic chamber (Columbus Instruments).

Preparation and Treatment with Agents

Rapamycin

Rapamycin (LC Laboratories) was dissolved in 100% ethanol and stored at -20°C. The stock solution was further diluted in an aqueous solution of 5.2% Tween 80 and 5.2% PEG 400 with a final concentration of ethanol of 2% (Mori et al., 2009a; Mori et al., 2009b). Wild-type mice were injected with Rapamycin (2 mg/kg) every other day for 9

days. ITT was performed on day 8 between injections. Necropsy was performed on day 9 after last injection.

Chloroquine

α Raptor^{KO} mice were treated with chloroquine diphosphate (Sigma, St. Louis, MO) in 0.9% saline administered at 7 mg/kg body weight. The mice were treated starting at 2 weeks of age and were treated twice weekly for the duration of 2 weeks.

Streptozotocin

Mice were treated with Streptozotocin (150 mg/kg Sigma) by a single intraperitoneal injection at 2 months of age (Zhang et al., 2012). The mice were fasted for 6 hours and Streptozotocin was injected in the late afternoon on day 0. Morning (fed) glucose levels were monitored for a week post-STZ treatment. Fed insulin and glucagon levels were measured at 0 and 8 days post-STZ treatment. Pancreata was collected for immunohistochemical analysis of α and β -cell mass on day 8.

Total Pancreatic Glucagon Extraction

Pancreata was dissected, cleaned in cold PBS and blotted on filter paper before weighting. The pancreata was placed in 3 mL ice-cold acid ethanol in polypropylene falcon tubes and homogenized using a tissue polytron for 2 minutes. Acid ethanol was prepared by adding 1 mL of 12N hydrochloric acid to 110 mL of 95% ethanol. After homogenizing the tubes were closed and placed in rotating rack at 4°C for 72 hours. The tubes were centrifuged at 2500 rpm for 30 minutes and the supernatant was placed in a new tube. Glucagon was measured using the supernatant at 1:10 dilution using Glucagon Elisa (R&D Duoset). The glucagon values were divided by the pancreas mass and final supernatant volume to calculate the final pancreatic glucagon content.

Liver Glycogen Content

Liver was dissected and immediately frozen in liquid nitrogen. Liver glycogen content was measured with Glycogen Content Kit (Sigma-Aldrich) using ~5 mg of liver sample and following the manufacturer's instructions.

Free Fatty Acids (NEFA) Measurement

Plasma free fatty acids (NEFA) were measured using NEFA-HR(2) Microtiter Procedure Kit (Wako Diagnostics) and following the manufacturer's instructions.

Islet Studies

Islet Isolation Procedure

Islet isolation was accomplished by collagenase digestion as described previously (Bernal-Mizrachi et al., 2010; Bernal-Mizrachi et al., 2004). Briefly, 1 mg/mL of collagenase (Roche) was dissolved in Hank's Buffer. The junction of the common bile duct to the duodenum was closed using a clamp. Approximately 5 mL of collagenase solution was injected slowly into the common bile duct of each mouse. Glucagon secretion *ex vivo* was assessed using isolated islets by static incubation. After injecting the collagenase solution, the pancreas was dissected and placed in a tube and incubated in water bath at 37°C for 12-16 minutes for further digestion. The digested pancreas was washed multiple times with Hanks's Buffer supplemented with 10% FBS and passed through a strainer to eliminate undigested parts. Finally, the digested pancreas was passed through 70µm filter to collect islets. The islets collected in the filter were washed onto a 100 mm cell culture plate (untreated) and incubated overnight in a cell culture incubator at 37°C.

Islet Secretion Studies

After overnight culture in RPMI containing 5 mM glucose, islets were pre-cultured in Krebs-Ringer (KRBB) medium containing 6 mM glucose and 0.2% BSA for 1 hour. Groups of 15 islets/mouse were placed in 8 µm cell culture inserts (Millicell), pre-incubated in HG KRBB (6 mM glucose) for 1-2 hours and incubated subsequently for 1 hour in each of the following conditions: LG KRBB (1 mM glucose; with a brief wash with LG between HG KRBB and LG KRBB) and LG KRBB + Arginine (20 mM) or KCl (30 mM). Experiments measuring glucagon response to increasing dose concentrations of diazoxide and tolbutamide had incubation time of 30 minutes per condition. Experiment assessing short-term rapamycin treatment on glucagon release was performed using wild-type islets and following the same experimental design with the

addition of +/- rapamycin (30 nM) at increasing concentrations for glucose (1, 6, 12, 24 mM) for 30 minutes per condition. Assessment of glucagon content of the islets was performed by extraction in 0.5 mL acid-alcohol per 15 islets/insert after each assay. All assays represent results from 2-3 independent experiments. Secreted glucagon levels and islet glucagon content were measured with an ELISA (Glucagon DuoSet Elisa from R&D Systems). All data is represented as secreted glucagon in the culture medium normalized to islet glucagon content for each insert of islets and presented as fold change compared to control.

Fluorescent-Activated Cell Sorting (FACS)

Control (Glucagon-Cre) and α Raptor^{HET} mice were crossed to reporter mice Ins1-EGFP and CAG-tdTomato. The islets from 2 month-old Glucagon-Cre^{Ins1GFP; tdTomato} and α Raptor^{HET;Ins1-EGFP;tdTomato} were isolated and incubated overnight in RPMI containing 5 mM glucose. The islets were dispersed into a single-cell suspension and filtered. Sorting was performed on FACS Aria III (BD Biosciences) at the University of Michigan and Moflo Astrios EQ (Beckman Coulter) at the University of Miami. Dead cells were excluded with 4'6-diamidino-2-phenylindole (Sigma) or Ghost Dye Red 780 (Tonbo). Cells expressing CAG-tdTomato (glucagon and insulin) and cells expressing Ins1-EGFP (all insulin) were sorted in separate collection tubes, representing Tomato Gate and GFP Gate, respectively. Hormone content in each gate was analyzed in 4 Control animals by ELISAs for glucagon (DuoSet, R&D Systems) and insulin (Alpco) and normalized to the number of cells sorted. Glucagon data is presented as fold change from glucagon content in Tomato Gate. Insulin data is presented as fold change from insulin content in GFP Gate.

Flow Cytometry

Islets were isolated and incubated overnight in RPMI containing 5 mM glucose. The islets were dispersed into a single-cell suspension with trypsin-EDTA and fixed with BD Pharmingen Transcription Factor Phospho Buffer Set (BD Biosciences). The fixed cells were incubated with conjugated antibodies overnight, at 4°C and gentle rotation. Dead cells were excluded by Ghost Dye Red 780 (Tonbo). Glucagon, foxA2, pS6 (Ser240)

expression was analyzed by mean fluorescent intensity (MFI) per glucagon-positive cells using BD LSR II (BD Biosciences). The size of live glucagon positive cells was analyzed by forward scatter area (FSC-A) and glucagon mean fluorescent intensity (MFI).

Immunofluorescence and Cell Morphometry

Pancreata were fixed in 3.7% formaldehyde, embedded in paraffin and sectioned (5 μm). Fluorescent images were acquired using a microscope (Leica DM5500B) and a motorized stage using a camera (Leica DFC360FX) (Leica Microsystems). Cell mass was determined in 5 stained sections (5 μm) separated by 200 μm as described (Bernal-Mizrachi et al., 2004; Bernal-Mizrachi et al., 2001). The area of insulin, glucagon, somatostatin and pancreatic polypeptide and the area of each section were quantified with Image Pro Software (version 7; Media Cybernetics). The ratio of the five hormone stained area to the total pancreatic section area for each mouse were averaged and multiplied by the pancreas weight.

Dispersed cell stainings were performed by gently dispersing isolated islets with trypsin-EDTA (0.25% trypsin, 1 mM EDTA). The cells were cytofuged using StatSpin Cytofuge 2 (Beckman Coulter) on slides pre-coated with poly-L-lysine. The cells were immediately fixed with 3.7% formaldehyde for 20 minutes and incubated with TBS-Triton (0.1%) for 10 minutes at room temperature. For FoxA2 stains, the cells were additionally permeabilized with cold methanol at 4°C for 10 minutes (after fixation with formaldehyde). Analysis for nuclear FoxA2 and DAPI signal intensity was done on 16-bit images acquired at using a microscope (Leica DM5500B) and a motorized stage using a camera (Leica DFC360FX) (Leica Microsystems). FoxA2 and DAPI levels were determined by measuring pixel intensity using Adobe Photoshop (Adobe Systems).

Islet cell size was calculated by immunostaining dispersed islets from 1-month old mice for glucagon and DAPI and measuring the area of glucagon positive cells using NIH Image J Software (v1/49d available free at <http://rsb.info.nih.gov/ij/index.html>).

Assessment of *Cre*-mediated recombination was measured by counting the number of Glucagon+/Reporter+ cells in dispersed islets from Glucagon-Cre^{YFP} and Glucagon-Cre^{tdTomato} mice (2 months-old). Assessment of autophagy was assessed in Control and α Raptor^{KO} mice bred to GFP-LC3 mice (Mizushima et al., 2004). Islets from 1 month-old Control^{GFP-LC3} and α Raptor^{KO;GFP-LC3} mice were isolated, dispersed and cytofuged on slides and stained for glucagon, GFP and DAPI.

Assessment of cell death was measured by Immunofluorescent-based apoptosis TUNEL assay (Millipore) in 3-5 stained sections (5 μ m) separated by 200 μ m and co-stained for glucagon and DAPI. Assessment of cell proliferation was measured by staining and counting ki67⁺/glucagon⁺ cells (Sigma) in 3-5 stained sections (5 μ m) separated by 200 μ m and co-stained for glucagon and DAPI.

All antibodies used are summarized in Table 1.

K_{ATP} Channel Activity

Islets from Glucagon-Cre^{tdTomato} and α Raptor^{HET;tdTomato} mice, expressing a fluorescent reporter in α -cells mice, were dispersed to single cells and plated overnight on 35-mm dishes as described previously (Dai et al., 2011). Cells were patch-clamped in the whole-cell voltage-clamp configuration in a heated bath at 32-35°C using a HEKA EPC10 amplifier and PatchMaster Software (Heka Elektronik, Germany) and patch pipettes with resistances of 5 ~ 6 MOhm after fire polishing. Whole-cell currents of K_{ATP} channel are recorded in response to voltage steps going to -60 and -80 mV from a holding potential of -70 mV. For the K_{ATP} current measurement, the bath solution contained: 138 mM NaCl, 5.6 mM KCl, 1.2 mM MgCl₂, 2.6 mM CaCl₂, 5 mM HEPES, 1 mM glucose (pH 7.4). The pipette solution for these experiments contained: 125 mM KCl, 30 mM KOH, 1 mM MgCl₂, 10 mM EGTA, 5 mM HEPES, 0.3 mM Mg-ATP and 0.3 mM K-ADP (pH 7.15).

Following the experiments, α -cells were positively identified by immunostaining for glucagon (guinea pig anti-glucagon, 1:5,000; Linco, St Charles, MO, USA), and

appropriate secondary antibody (Alexa Fluor 594 goat anti-guinea pig 1:200; Invitrogen, Eugene, OR, USA). Data were analyzed using FitMaster (Heka Elektronik) and Prism (v6).

Single Cell Analysis by Fluidigm

Islets from Control (Raptor f/f^{Ins1-GFP;tdTomato} and Ins1-GFP;tdTomato (n=6) and α Raptor^{KO;Ins1-EGFP;tdTomato} (n=3) were isolated, dispersed and sorted to enrich an α -cell population and sorted based on viability. The cells were sorted into complete islet medium (RPMI; 10%FBS; 5mM Glucose). The viability (87-97%) and concentration (250-300 cells/ μ L) of cells were measured by Countess Automated Cell Counter and mixed with C1 Cell Suspension Reagent (Fluidigm) in 3:2 ratio. The cells were captured into a small (5-10 μ m) or middle (10-17 μ m)-sized IFC before undergoing cell lysis, reverse transcription and cDNA amplification in the C1 Single-Cell Auto Prep instrument. Capture sites containing a single cell were identified by careful examination of the IFC using an Olympus CK2 inverted microscope. Quantitative RT-PCR of 96 Delta Gene Assays was performed by BiomarkHD (Fluidigm) using pre-amplified cDNA from single cells, positive (bulk cell) and negative (no template) controls from each IFC capture. Glucagon cells were identified as single cells with detectable levels of glucagon gene expression in the Biomark HD data (Control n=10, α Raptor^{KO} n=19 cells). Delta Gene Assays were validated for single cell gene expression analysis on Biomark HD using mouse pancreatic total islet mRNA serially diluted over 12 two-fold dilutions (512pg to 0.25pg) and 7 replicates.

Quantitative Real-Time PCR

For mRNA expression, total RNA was extracted from islets, α TC-1 cells and liver samples using the RNeasy isolation kit (Qiagen). Gene expression was performed by quantitative real time RT-PCR using Power SYBR Green PCR Mix (Applied Biosystems) using StepOnePlus detection system (Applied Biosystems) with a standard protocol including a melting curve. Relative abundance for each transcript was calculated by a standard curve of cycle thresholds and normalized to 18S (α TC-1 cells

and liver) and β -actin (islets). Primers were purchased from IDT Technologies, with the exception of Arx1, MafB and Nkx2.2 purchased from Operon.

All primer sequences are available in Table 2.

Single Cell RT-PCR

The following methods were adapted and modified from Liss *et al.* and Shiota *et al.* (Liss *et al.*, 1999; Shiota *et al.*, 2005). Red-fluorescent, dispersed islet cells from 1 month-old Control^{tdTomato} and α Raptor^{KO;tdTomato} were individually picked under an inverted phase-contrast microscope (Leica DMI 3000B). Each cell was collected with a pipette adjusted to 1.5 μ L in individual tube with 3.5 μ L water and 5 μ L of a mix containing: 1 μ L 10X RT Buffer (Applied Biosystems), 0.5 μ L RNase inhibitor (10 Units; Applied Biosystems) and 0.5 μ L dithiothreitol (10 mM; DTT). The tubes were immediately frozen on dry ice. The first strand of cDNA was performed by using High-Capacity Reverse Transcription cDNA Kit and following the manufacturer's directions (Applied Biosystems). Each cell was treated as separate reaction yielding a final volume of 20 μ L. Reverse Transcription (RT) reaction was carried for 60 minutes at 42°C, followed by incubation at 75°C for 15 minutes. All cells underwent PCR amplification for glucagon and 18S. Only glucagon-positive cells were further analyzed.

Single Cell-Nested PCR for *SUR1* and *raptor*

SUR1: The first round of PCR contained 8 μ L of RT reaction, outside primers for SUR1 (0.5 μ M), MgCl₂ (2 mM), dNTPs (0.4 mM) and 2 Units Platinum Taq (Invitrogen), in a total volume of 20 μ L. The first PCR was performed under the following conditions: 3 minutes at 94°C, 35 cycles (94°C for 30 seconds, 58°C for 60 seconds, 72°C for 3 minutes), final elongation at 72°C for 7 minutes using MasterCycler proS (Eppendorf). The second round of PCR for SUR1 was performed using 1 μ L of first-PCR product and 19 μ L of a mix containing Power SYBR Green PCR Mix (Applied Biosystems), inside primers and water, and was performed using StepOnePlus detection system (Applied Biosystems). The final product for SUR1 was visualized in an ethidium bromide-stained agarose gel (2%) by electrophoresis. The results were analyzed by the presence or

absence of a positive band. Positive (whole islets) and negative (water) controls were used in every experiment. Primers were purchased from IDT Technologies.

Raptor: The first round of PCR was contained 4 μ L of RT reaction, outside primers for *raptor* (0.6 μ M), $MgCl_2$ (2 mM), dNTPs (0.4 mM) and 2 Units Platinum Taq (Invitrogen), in a total volume of 20 μ L. The first PCR was performed under the following conditions: 4 minutes at 94°C, 35 cycles (94°C for 30 seconds, 55°C for 30 seconds, 72°C for 30 seconds), final elongation at 7°C for 4 minutes using MasterCycler proS (Eppendorf). The second PCR product for *raptor* was performed using 2 μ L of the first PCR product and inside primers under the same conditions.

All primer sequences are available in Table 2.

Cell Culture Studies

The glucagon-secreting cell line, α TC-1 cells clone #6, was purchased from ATCC and maintained according to company's instructions. For rapamycin experiments, the cells were cultured in 12-well plates and incubated in complete media +/- rapamycin (30nM) for 48 hours.

Western Blotting

α TC-1 cells and primary cells were collected and lysed in lysis buffer (125 mM Tris, pH7; 2% SDS, 1 mM DTT) containing a phosphatase (Roche Diagnostics) and protease (Sigma) inhibitor cocktails. Cell lysates were boiled for 10 minutes, loaded and electrophoresed on 12% SDS-PAGE and transferred to polyvinylidene fluoride membranes. All antibodies used are listed in Supplemental Table 1. Images were acquired using Western Bright Sirius kit (BioExpress). Band densitometry was determined by measuring pixel intensity using NIH Image J software (v1/49d available free at <http://rsb.info.nih.gov/ij/index.html>) and normalized to actin in the same membrane.

Electron Microscopy

Islets were isolated and fixed with 2% glutaraldehyde overnight at 4°C, dehydrated and embedded in Epon by the Microscopy & Image Analysis Laboratory Core (MiCORES). Ultrathin sections were stained with uranyl acetate and lead citrate. Images were recorded digitally using electron microscope (JEM-1400 Plus).

Statistical Analysis

Data are presented as means \pm S.E.M. The statistical significance of differences between the various conditions/animal groups was determined by nonparametric *U* test (Mann-Whitney) using Prism version 6.0d (GraphPad Software). Results are shown as significant when *P* value was ≤ 0.05 . Analysis of Fluidigm single-cell data identified 55 gene assays (Supplemental Table 3) that qualified for statistical analysis by t-test (≥ 3 data points/group). Principle Component Analysis (PCA) was performed using gene expression from 55 genes to evaluate whether the groups were separated distinctively. Heat map represents mean Ct of differentially expressed genes ($p > 0.05$) from t-test analysis. We applied a second method of statistical analysis to the dataset using R based MAST (Model-based Analysis of Single-cell Transcriptomics) package (Finak et al., 2015). . Additional gene (*GCG*) was identified as significantly different between the groups using MAST analysis.

Table 1. List of Antibodies

Antibody	Specie	Source	Application
Glucagon	Mouse	Abcam	IFC
Glucagon	Rabbit	Chemicon	IFC
Glucagon-BV421	Human/Mouse	BD Biosciences	FC
Insulin	Guinea Pig	Dako	IFC
Insulin-APC	Human/Mouse/Bovine	R&D	FC
GFP	Chicken	Abcam	IFC
pS6 (S235)	Rabbit	Cell Signaling	IFC
pS6 (S240)	Rabbit	Cell Signaling	IFC
pS6 (S240)-PE	Mouse	BD Biosciences	FC
FoxA2	Rabbit	Cell Signaling	IFC
FoxA2	Mouse	Abcam	WB
FoxA2-Dylight488 (conjugated in house)	Mouse	Abcam	FC
KIR6.2	Rabbit	Alamo Labs	WB
SUR1	Rabbit	Show-Ling Shyng	WB
Somatostatin	Rabbit	Santa Cruz	IFC
Pancreatic Polypeptide	Guinea Pig	Millipore	IFC
Actin	Mouse	Sigma	WB
Ghost Dye Red 780		Tonbo	FC
Ki67	rabbit	Sigma	IFC

WB = Western Blot

IFC = Immunofluorescent Chemistry

FC=Flow Cytometry

Table 2. Primer Sequences***αTC-1 Cells and Primary Islet Cells***

Gene	Forward	Reverse
FoxA2	CAGCTACTACGCGGAGCC	GCTCATTCCAGCGCCCAC
SUR1	CTGGTGGCCATCGACACAA	TGTACAGGAGCCAGCAGAAT
KIR6.2	GCTGCATCTTCATGAAAACG	TTGGAGTCGATGACGTGGTA
MafB	GAACGAGAAGACGCAGCTCT	CGAGTTTCTCGCACTTGACCT
Nkx2.2	TCGCTCTCCCCTTTGAACTTT	GTTAACGTTGGGATGGTTTGG
Pou3f4	TTCCTCAAGTGTCCCAAGCC	TAA ACCTCGTGTGGCTGCTG
FoxP1	CGAATGTTTGCTTACTTCCGA	GCCAGGCTGTGA AAGCATATGTGA
FoxP2	GCCAGGCTGTGAAAGCATAT GTGA	CATTTGCACTCGACATTGGGCAGT
FoxP4	GTCAGCCTGCAGCCCAAGCC AAGCCTC	GGAGCTGTCTCTCCGAGATGTGAGCA C
18S	GCAATTATTCCCATGAACG	GGGACTTAATCAACGCAAGC

Single Cell Analysis

Gene	Forward	Reverse
SUR1 (inside)	CTGGTG GCCATCGACACAA	TGTACAGGAGCCAGCAGAAT
SUR1 (outside)	GTCTACTTCCAACCTGTCAA T	ACCCTCGAGCAGAAGATGTT
Raptor (inside; exon 6)	CCTCTGTCCATATACGACCT	CTCTGCAGTGCAAAGTGT
Raptor (outside; exons 5&7)	CCTACTGTGGATGAAGTCAA G	CACTCCCATCAAGATTGCTC

Liver Analysis

Gene	Forward	Reverse
GCGR	ACGGTACAGCCAGAAGAT	CTACCAGCAACCAGCAATAG
PEPCK	ATCATCTTTGGTGGCCGTAG	ATCTTGCCCTTGTGTTCTG
G6Pase	CCGGTGTTTGAACGTCATCT	CAATGCCTGACAAGACTCCA
Gck	CTGTTAGCAGGATGGCAGCT	TTT CCTGGAGAGATGCTGTGG
FAS	AGAAGCCATGTGGGGAAGAT	AGCAGGGACAGGACAAGACAA

Table 3. Fluidigm Gene Targets Included in Analysis

CCNB1	NOTCH1	ABCC8	CCND1	FOXO1	LAMP1	PAX6
EIF4E	SNAP25	HSP90AB1	CCND2	FOXP1	LAMTOR2	PCSK2
CHRM3	ULK2	CACNA1S	CDKN1A	FOXP4	LAMTOR3	PTF1A
NEUROG3	MAFB	XBP1	CDKN1B	GCG	MAFA	RFX6
LAMTOR1	FOXA2	ARX	CPE	GIPR	NKX6-1	TM4SF4
NKX2-2	POU3F4	CACNA1A	CRYBA2	GLP1R	NOTCH2	UCP2
ULK1	KCNJ11	CASP3	DDIT3	HSPA5	OGT	VAMP2
GATA4	RBPJ	CCNA2	ERN1	IRS2	PAX4	

CHAPTER 2

Nutrient signaling maintains alpha cell mass and promotes K_{ATP} channel-dependent regulation of glucagon secretion

Introduction

Type 1 (T1D) and Type 2 (T2D) Diabetes are characterized by uncontrolled hyperglycemia associated with the progressive decrease in insulin. Glucagon, insulin's counterregulatory hormone, plays a major role in maintaining glucose homeostasis by promoting glucose production *via* hepatic glycogenolysis and gluconeogenesis. Paradoxically, glucagon levels are elevated in insulin-resistant non-diabetic, T1D and T2D patients, leading to enhanced hepatic glucose output and thereby exacerbating hyperglycemia (Dinneen et al., 1995; Mezza et al., 2014; Sherwin et al., 1976). On the contrary, On the contrary and much less understood is the failure of α -cells to secrete glucagon in response to hypoglycemia. This presents a major limiting factor for optimal glucose control in insulin-dependent T1D diabetes or advanced T2D patients (Cryer, 2002; Gerich et al., 1973; Segel et al., 2002). Thus, a better understanding of the molecular mechanisms governing glucagon levels could have major implications in understanding abnormal responses to hypoglycemia in diabetes and provide novel avenues for diabetes management.

Mice with loss of the insulin receptor in α -cells have increased fed glucagon levels suggesting insulin signaling mediates the suppression of glucagon secretion in the fed state (Kawamori et al., 2009). In addition, mice with pancreatic deletion of the Insulin Receptor Substrate 2 (IRS2) exhibit decreased α -cell mass and lower glucagon protein

and RNA levels, implicating IRS signaling in the control of α -cell mass and glucagon expression (Cantley et al., 2007). Insulin inhibits glucagon gene transcription and secretion and promotes α -cell proliferation by activation of IRS2/PI3K/Akt signaling (Schinner et al., 2005; Xu et al., 2006). Alpha cell proliferation is reduced by treatment with the mTOR Complex 1 (mTORC1) inhibitor, rapamycin (Liu et al., 2011; Solloway et al., 2015), suggesting that downstream of the insulin receptor, mTORC1 mediates the effects of insulin on α -cell mass and glucagon secretion.

Arginine, alanine and glutamine potentiate glucagon secretion and this effect is suppressed by high glucose in an insulin-independent manner (Pipeleers et al., 1985). Most recently, studies using glucagon receptor deficient mice report increased α -cell proliferation associated with a significant increase of circulating amino acids, known activators of mTORC1, suggesting that certain amino acids could induce α -cell mass in this mouse model (Longuet et al., 2013; Solloway et al., 2015; Yang et al., 2011). These findings support the concept that α -cell mass and glucagon secretion are sensitive to extracellular signals including nutrients (amino acids, glucose) and growth factors (insulin) and that the mTORC1 pathway may be involved as a downstream regulator of one or both of these processes. However, how downstream targets of nutrient or insulin receptor signaling regulate α -cell mass and glucagon secretion *in vivo* is unknown.

To investigate the importance of endogenous mTORC1 function on α -cell mass and glucagon secretion, we generated mice with a conditional deletion of *raptor* in α -cells. Our data uncovered a novel role of mTORC1 in maintenance of postnatal α -cell mass and identify a previously unknown function of this pathway on glucagon secretion during fasting and hypoglycemia by modulation of K_{ATP} channel subunit expression (*SUR1* and *KIR6.2*) and channel activity. We also discovered that mTORC1 positively regulates *KIR6.2* and *SUR1* expression by regulation of *FoxA2* levels, a critical transcription factor dysregulated in diabetes. This work provides new insights into how nutrient-dependent glucagon secretion and α -cell mass are regulated and suggests that pharmacologic inhibition of this pathway using immunosuppressant medications, such as everolimus or rapamycin, could alter glucagon levels and glucose homeostasis.

Results

Lack of mTORC1 signaling after deletion of *raptor* in α -cells

Alpha cell-specific deletion of *raptor* was achieved by crossing Glucagon-Cre and *Raptor*^{flox/flox} mice (α Raptor^{KO}) (Polak et al., 2008; Shiota et al., 2013). Single α -cells were isolated from control and α Raptor^{KO} mice. Single cell RT-PCR followed by nested PCR was performed for *raptor* in single α -cells from control and α Raptor^{KO} mice. Tissue-specific and single cell mRNA expression showed a lack of *raptor* expression exclusively in α -cells from α Raptor^{KO} mice (Figure 4A). Expression of *raptor* was preserved in the liver, hypothalamus, total pancreas and kidney in control and α Raptor^{KO} mice (Figure 4A). Loss of mTORC1 signaling was confirmed by lack of phospho-S6 (Serine240/44) immunofluorescent staining only in glucagon-positive cells from 1 month-old α Raptor^{KO} mice (Figure 4B). Phospho-S6 (Serine240) staining by flow cytometry of dispersed islets showed that phospho-S6 levels were nearly lost in glucagon-positive cells, but preserved in the insulin-positive cells from 1 month-old α Raptor^{KO} mice (Figure 4C,D). Recombination efficiency of Glucagon-Cre assessed by crossing these mice to reporter mice showed that Cre-mediated recombination was achieved in the majority of α -cells (84.2% +/- 6.4, n=4). These data demonstrate that we have successfully generated a mouse model with conditional deletion of *raptor* and loss of mTORC1 signaling in α -cells.

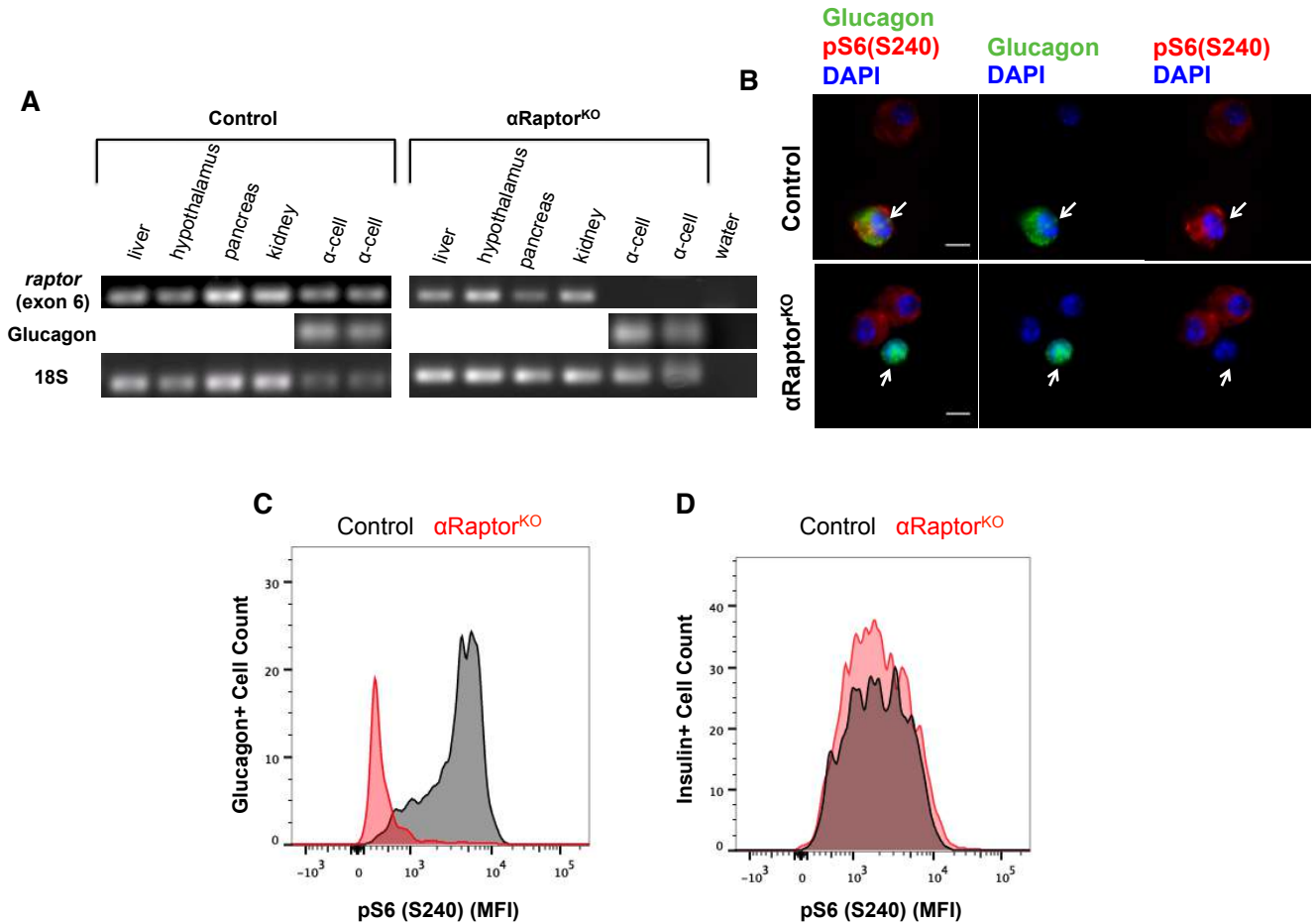


Figure 4. Loss of *raptor* and mTORC1 activity in α -cells of α Raptor^{KO} mice. **A.** Single α -cells were isolated from control and α Raptor^{KO} mice. Single cell RT-PCR followed by nested PCR was performed for *raptor* in single α -cells from control and α Raptor^{KO} mice. Tissue-specific and single cell analysis show lack of *raptor* expression exclusively in α -cells from α Raptor^{KO} mice. **B.** Immunofluorescent staining showing positive mTORC1 activity shown by pS6 (S240) stain in the control and lack of mTORC1 activity in the glucagon positive-cells of the α Raptor^{KO} mice in dispersed islets from 1 month-old mice (scale 10 μ m). **C.** Flow cytometry analysis showing loss of mTORC1 activity by pS6 (S240) in glucagon positive-cells of the α Raptor^{KO} mice (n=3-4). **D.** Flow cytometry analysis showing preserved mTORC1 activity by pS6 (S240) in insulin positive-cells of the α Raptor^{KO} mice (n=3-4). Data are shown as means \pm S.E.M. * $p \leq 0.05$; Nonparametric *U* test (Mann Whitney).

Low fed and fasting glucagon levels in mice with loss of mTORC1 signaling in α -cells

Body weight and random fed blood glucose were not different between control mice and mice with homozygous (α Raptor^{KO}) and heterozygous (α Raptor^{HET}) deletion of *raptor* (Figure 5A,B). Glucose tolerance at 2 and 8 months of age was not different between the three groups (Figure 5C,G). Assessment of the adaptation to the fasting state showed that control mice exhibited a decrease in glucose levels after 12 hours of fasting (Figure 5D,H). Compared to controls, 2 month-old α Raptor^{HET} mice had lower blood glucose after 6 hours of fasting, but this difference disappeared after 12 hours (Figure 5D). In contrast, α Raptor^{KO} mice were able to maintain blood glucose levels during the first 12 hours of fasting (Figure 5D). Glucose levels during fasting were similar among all the groups at 8 months (Figure 5H). Glucagon levels in the fed state were reduced in α Raptor^{KO} mice at 2 and 8-months of age (Figure 5E,I). Interestingly, α Raptor^{HET} mice exhibited fed glucagon levels that were reduced, but not to the level observed in the α Raptor^{KO} at 2 and 8 months (Figure 5E,I). Glucagon secretion is induced in states of decreasing blood glucose, as seen in 2 and 8 month-old control mice in response to fasting (Figure 5E). Compared to controls, glucagon levels decreased after 12-hour fasting in young and old α Raptor^{KO} and α Raptor^{HET} mice suggesting that the adaptation of glucagon secretion to fasting was compromised in these mice (Figure 5E,I). No differences were observed in fed or fasting insulin levels between controls, α Raptor^{KO} and α Raptor^{HET} mice at 2 and 8 months (Figure 5F,J).

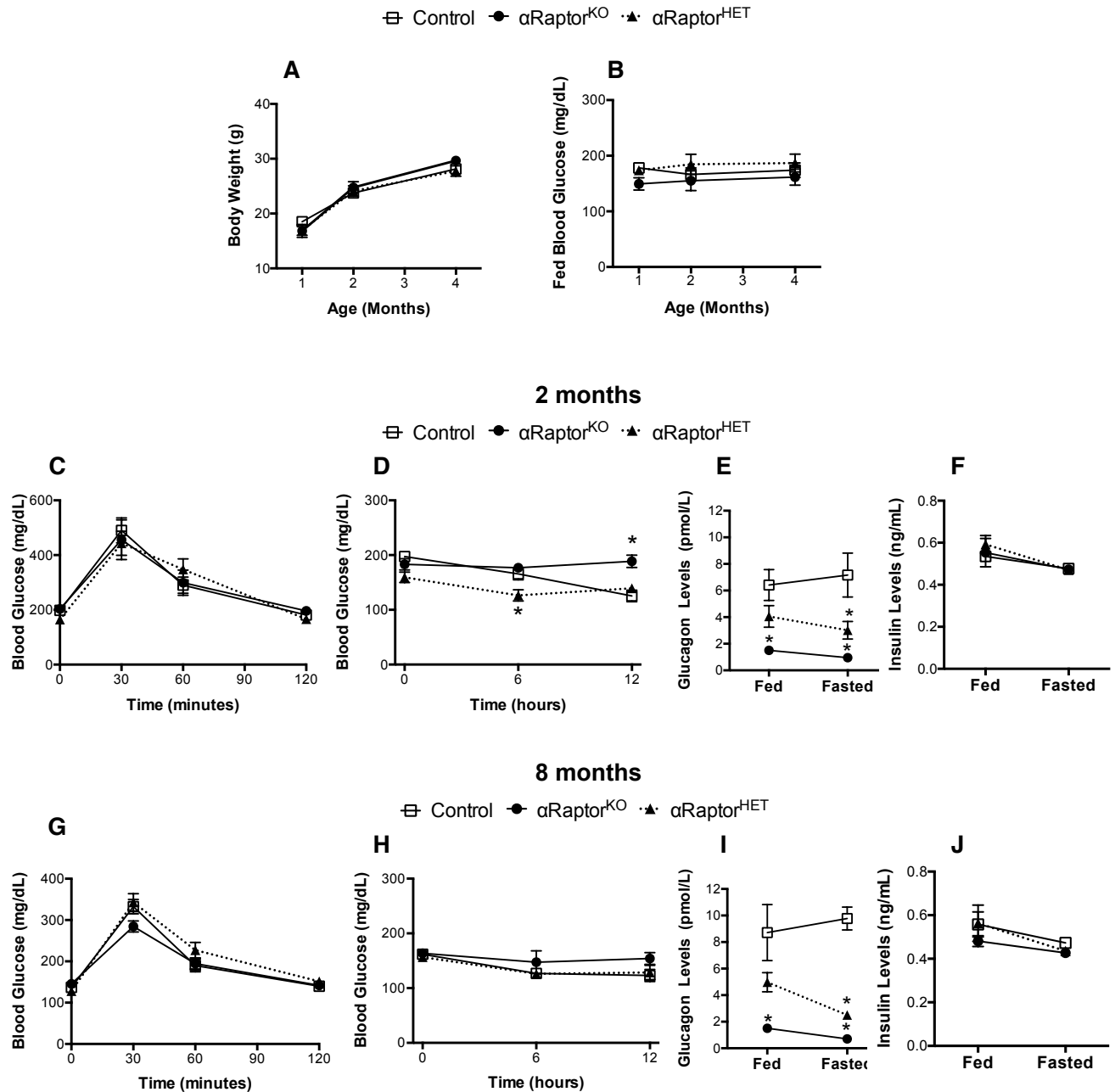


Figure 5. Mice with loss of mTORC1 signaling in α -cells exhibit low fed and fasting glucagon levels. **A.** Body weight and **B.** Random-fed blood glucose of control, α Raptor^{KO} and α Raptor^{HET} mice (n=8-9). Intraperitoneal glucose tolerance tests, IPGTT (2g/kg) of **C.** 2 months (n=3-4) and **G.** 8 months-old mice (n=5-8). Fasting blood glucose of **D.** 2 months (n=7-9) and **H.** 8 months-old mice (n=3-4). Fed and fasted glucagon levels of **E.** 2 months (n=5-6) and **I.** 8 months-old mice (n=5-6). Fed and fasted insulin levels of **F.** 2 months (n=3-4) and **J.** 8 months-old mice (n=3-4). Data are shown as means \pm S.E.M. * $p \leq 0.05$; Nonparametric *U* test (Mann Whitney).

The adaptation of fasting during physiological conditions involves multiple metabolic adjustments to maintain glucose levels. We showed that fasting glucose levels in 2 month-old α Raptor^{KO} mice were maintained at 12 hours, but returned to the levels of controls at 24 hours (Figure 6A). The lack of drop in glucose levels after 12 hours of fasting in α Raptor^{KO} mice was interesting as these mice exhibited very low glucagon levels. Assessment of liver weight and glycogen content showed that both were reduced after 12 hours of fasting, but fasting glycogen levels were higher in α Raptor^{KO} mice (Figure 6B,C). This suggested that gluconeogenesis could be upregulated in α Raptor^{KO} mice. Consistent with this, glucose levels after pyruvate tolerance testing were higher in α Raptor^{KO} mice suggesting that hepatic gluconeogenesis was increased (Figure 6D). The results of these studies suggest that α Raptor^{KO} mice were more resistant to a decrease in glucose during the first 12 hours of fasting by an increase in gluconeogenic pathways, but these mechanisms were not sufficient to maintain glucose after prolonged fasting (24 hours).

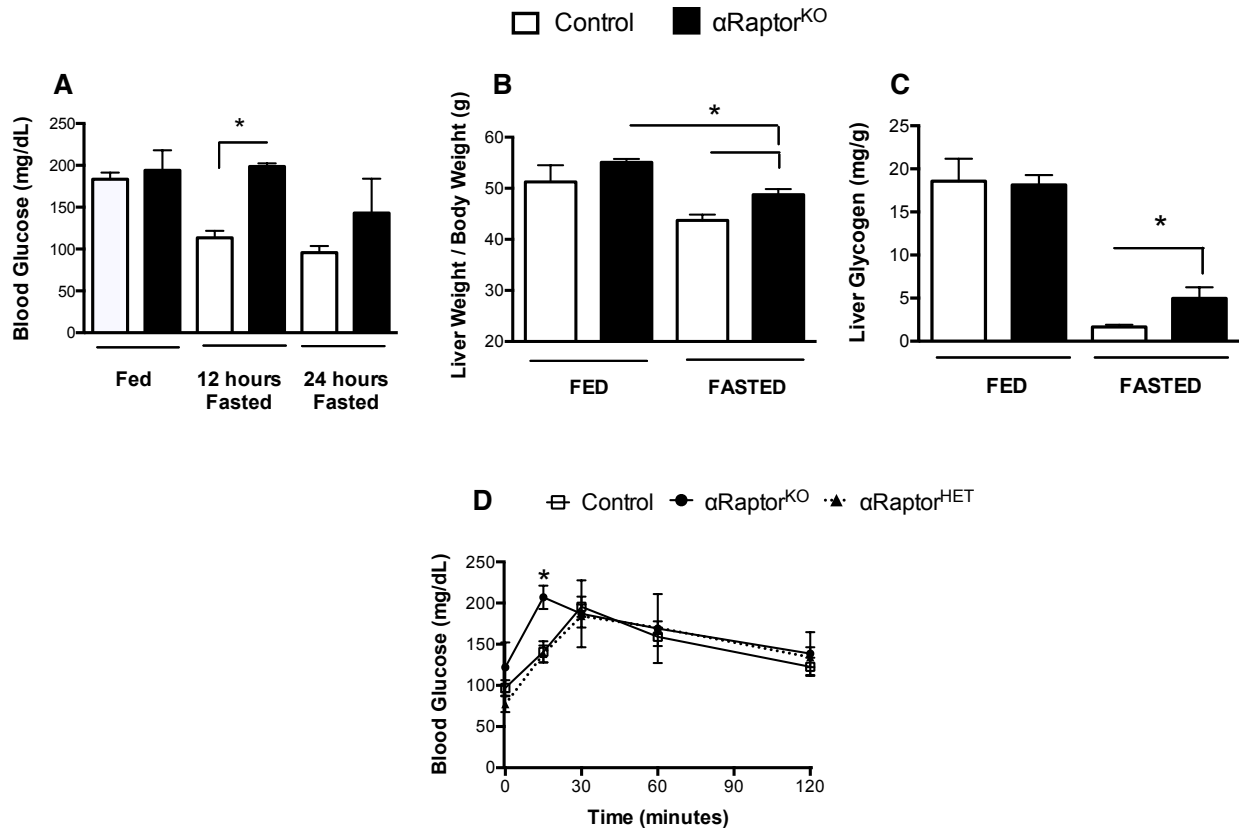


Figure 6. α Raptor^{KO} mice have increased gluconeogenesis. **A.** Fasting blood glucose (n=3-4). **B.** Fed and fasted liver weight (n=3-4) and **C.** Liver glycogen content (n=3-6) in 8 months-old control and α Raptor^{KO} mice. **D.** Pyruvate tolerance test (2 g/kg) in 2-months old mice (n=3-6). Data are shown as means \pm S.E.M. * $p \leq 0.05$; Nonparametric *U* test (Mann Whitney).

mTORC1 signaling is necessary for the maintenance of postnatal α -cells

Morphometric analysis at postnatal day 1 demonstrated that α Raptor^{KO} mice were born with normal α -cell mass (Figure 7B). At 2 weeks of age, α Raptor^{KO} mice exhibited normal α -cell mass, lower levels of proliferation and no changes in apoptosis (Figure 7C and Figure 8A,B). α Raptor^{KO} mice displayed a loss of α -cells as evidenced by a reduction in α -cell mass and pancreatic glucagon content at 2 and 8 months (Figure 7D-G). In contrast, β , δ (somatostatin) and PP (pancreatic polypeptide)-cell mass at 2 months mass was not altered in newborn and 2-month old α Raptor^{KO} mice (Figure 7H,I and Figure 8C-E). There was no difference in α -cell mass and pancreatic glucagon content in α Raptor^{HET} mice compared to controls at 2 months of age (Figure 7D,E).

However, by 8 months α Raptor^{HET} mice showed a reduction in α -cell mass and pancreatic glucagon content (Figure 7F,G). A decrease in the number of α -cells, but not the cell size or cellular glucagon content analyzed by flow cytometry in dispersed islets from α Raptor^{HET} mice, was responsible for the reduction in the α -cell mass of older α Raptor^{HET} mice (Figure 8F-H). Interestingly, β -cell mass was increased in 8 month-old α Raptor^{KO} mice with an intermediate increase in the 8 month-old α Raptor^{HET} mice (Figure 7J). In addition, pancreas weight was increased in 2 month-old α Raptor^{KO} mice (Figure 7K).

Morphologic evaluation by electron microscopy in 1 month-old α Raptor^{KO} showed a reduction in α -cell size (Figure 7L). Reduced cell size was confirmed by independent cell size measurements by immunohistochemistry using dispersed islets from 1 month-old control and α Raptor^{KO} (Figure 7M). In addition, the number of glucagon granules appeared reduced in α -cells from α Raptor^{KO} mice and was independently validated by reduced intracellular glucagon levels using flow cytometry (Figure 7N). To investigate the mechanisms of loss of α -cells in α Raptor^{KO} mice, we examined the role of decreased mTORC1 signaling in autophagy-mediated cell death (Egan et al., 2011; Kim et al., 2011; Sanchez et al., 2012). To test this, we crossed α Raptor^{KO} mice to an *in vivo* reporter of autophagy (GFP-LC3 mice) (Mizushima et al., 2004). Our results showed that at 1 month, α Raptor^{KO} mice have increased GFP-LC3 punctate in α -cells, suggesting that the loss in α -cell mass was mediated by autophagy (Figure 7O). Inhibition of autophagy by treatment of 2 week-old α Raptor^{KO} mice with chloroquine for 2 weeks showed that α -cell mass in α Raptor^{KO} mice treated with chloroquine was slightly improved (Figure 7P). These results are consistent with a role of autophagy in the loss of α -cell mass in α Raptor^{KO} mice.

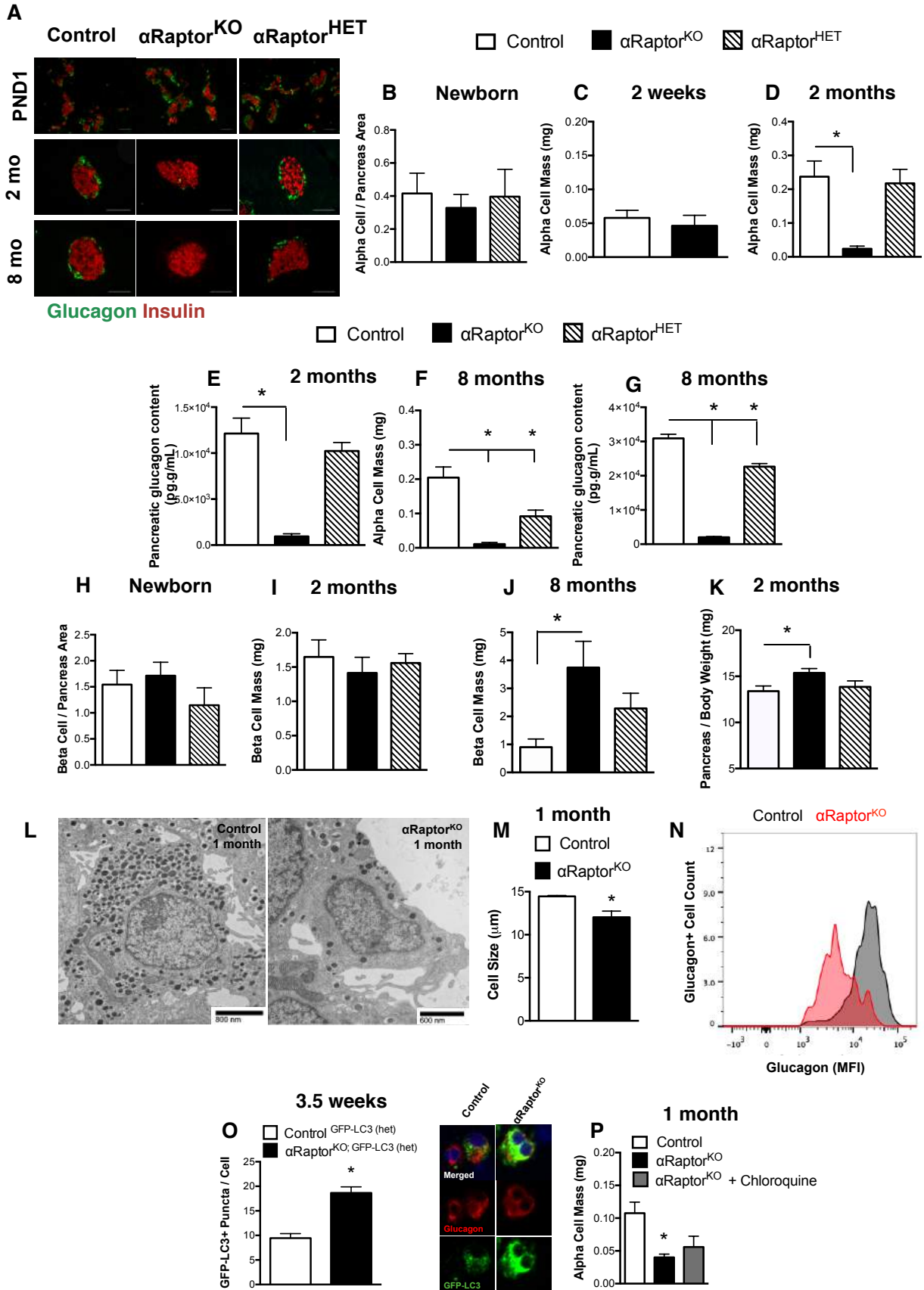


Figure 7. mTORC1 signaling is necessary in the maintenance, and not development of α -cells. **A.** Immunofluorescent images (scale 50 μ m) and **B.** Quantification of α -cell fraction at postnatal day-1 (newborn). Quantification of α -cell mass at **C.** 2 weeks (n=4). Quantification of **D.** α -cell mass (n=4-5) and **E.** Pancreatic glucagon content (n=4-6) in 2 month-old mice. Quantification of **F.** α -cell mass (n=3-4) and **G.** Pancreatic glucagon content (n=3-4) in 8 month-old mice. **H.** Quantification of β -cell fraction at postnatal day-1 (newborn), **I.** β -cell mass in 2 month-old mice (n=4-5) and **J.** β -cell mass in 8 month-old mice (n=3-4). **K.** Pancreas weight normalized to total body weight in 2 month-old mice (n=5-6). **L.** Electron microscopy images from 1 month-old Control and α Raptor^{KO} mice. **M.** Analysis α -cell size of control and α Raptor^{KO} mice at 1 month of age by immunohistochemistry using dispersed islets (n= 3-4) and **N.** Flow cytometry analysis of cell glucagon content of control and α Raptor^{KO} mice at 1 month (n=3-4). **O.** GFP-LC3 puncta in α -cells and representative immunofluorescent images (n=50-51 cells) in 3.5 week-old mice. **P.** Quantifications of α -cell mass at 1 month of age +/- chloroquine treatment in α Raptor^{KO} mice from 2-4 weeks of age (n=3-4). Data are shown as means \pm S.E.M. *p \leq 0.05; Nonparametric *U* test (Mann Whitney).

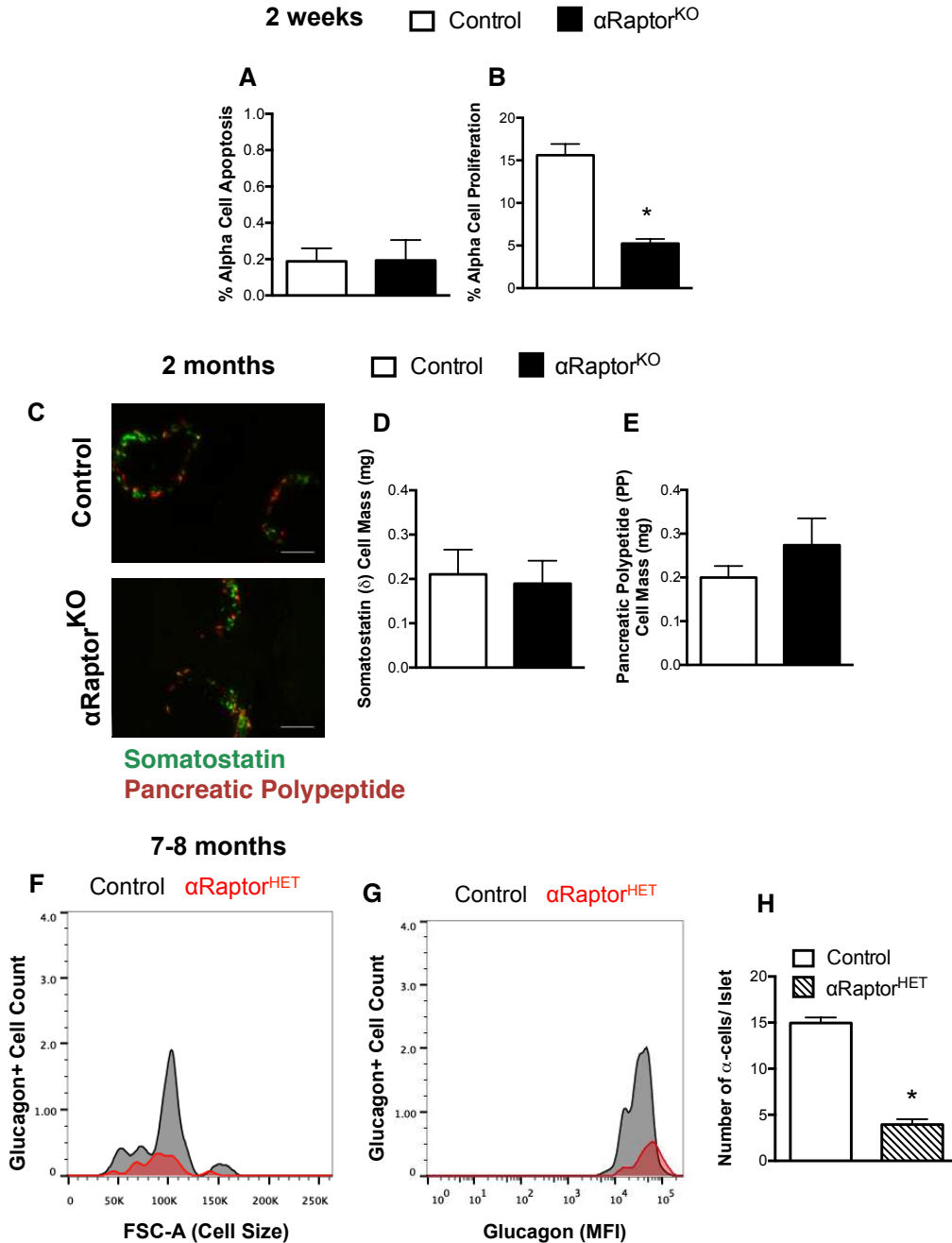


Figure 8. Loss of mTORC1 signaling in α -cells leads to decreased cell number and proliferation in α Raptor^{KO} and older α Raptor^{HET} mice. **A.** Quantifications of α -cell apoptosis and **B.** Proliferation at 2 weeks of age (n=4). **C.** Immunofluorescent images (scale 50 μ m) and quantification of **D.** δ (somatostatin) and **E.** PP (pancreatic polypeptide) cell mass in 2 month-old mice (n=3-4). **E.** Flow cytometry analysis of α -cell size and **F.** Glucagon content in older α Raptor^{HET} mice (n=3). **G.** Quantifications of number of α -cells/islet of older control and α Raptor^{HET} mice by immunohistochemistry using pancreatic sections (n=4). Data are shown as means \pm S.E.M. *p \leq 0.05; Nonparametric *U* test (Mann Whitney).

α Raptor^{KO} mice have increased active GLP-1 levels from intestinal origin

Interestingly, β -cell mass was increased in 8 month-old α Raptor^{KO} mice with an intermediate increase in the 8 month-old α Raptor^{HET} mice (Figure 7J). Analysis of incretin levels showed an increase in fed circulating active GLP-1 levels in α Raptor^{KO} mice at 2 months of age, associated with an improved oral glucose tolerance and increased active GLP-1 levels at zero and 10 minutes post oral glucose administration (Figure 9A-C). At 8 months of age, fed circulating GLP-1 levels in α Raptor^{KO} were further increased, with an intermediate rise in fed active GLP-1 levels in the α Raptor^{HET} mice (Figure 9E). However, analysis of pancreatic active GLP-1 levels at 2 and 8 months of age showed a reduction in α Raptor^{KO} mice, suggesting that the increased circulating active GLP-1 in these mice is not of pancreatic origin (Figure 9D,F). We measured active GLP-1 levels in intestinal extracts from 2-month old mice, and our data showed that α Raptor^{KO} mice have increased active GLP-1 levels (Figure 9G). Therefore, we concluded that the increase in circulating active GLP-1 levels α Raptor^{KO} mice is of intestinal origin.

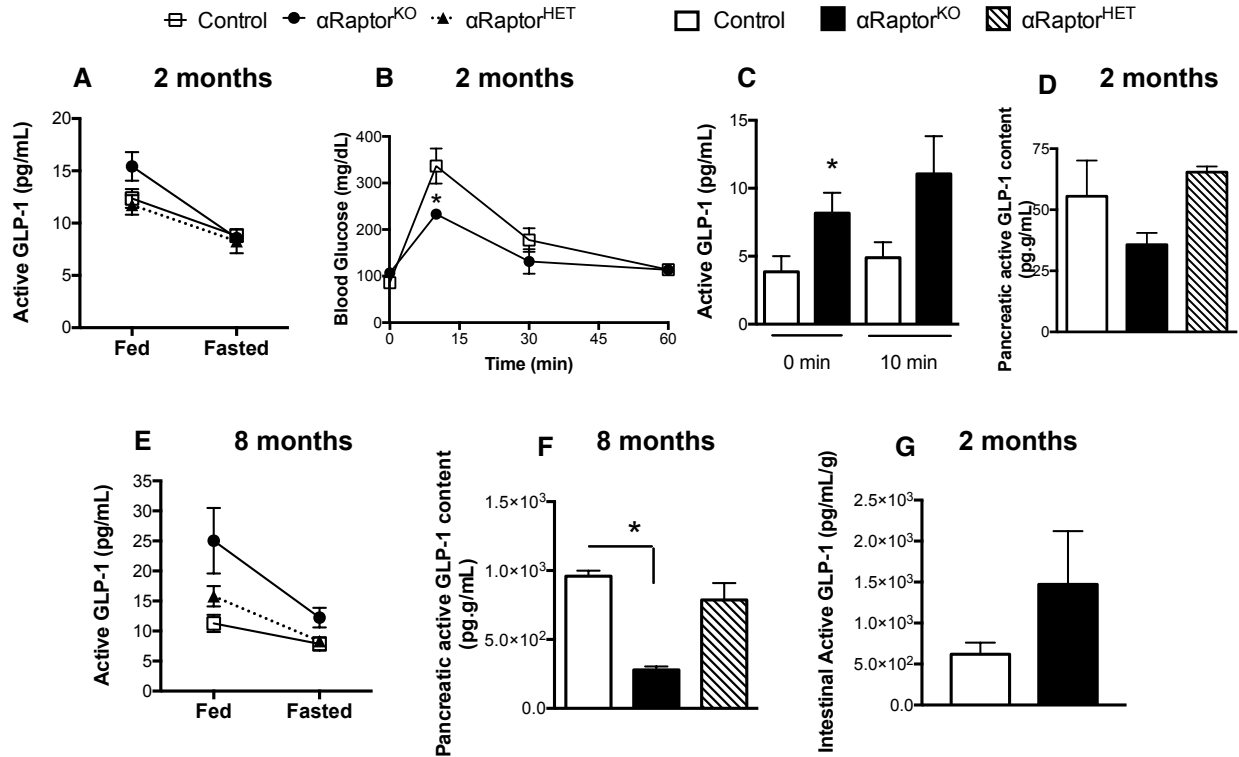


Figure 9. Improved oral glucose tolerance and increased active GLP-1 levels in α Raptor^{KO} mice. **A.** Fed and fasted active GLP-1 levels in 2 month-old mice (n=4). **B.** Blood glucose response to oral glucose tolerance test (2g/kg.bw) and **C.** Circulating active GLP-1 levels at zero and 10 minutes post oral glucose administration (n=6-7). **D.** Total pancreatic active GLP-1 levels in 2 month-old mice (n=4-5). **E.** Fed and fasted active GLP-1 levels in 8 month-old mice (n=3-4). **F.** Total pancreatic active GLP-1 levels in 8 month-old mice (n=3-4). **G.** Total intestinal active GLP-1 levels in 2 month-old mice (n=2-3). Data are shown as means \pm S.E.M. * $p \leq 0.05$; Nonparametric *U* test (Mann Whitney).

Glucagon secretion in response to fasting, hypoglycemia and neuroglycopenia is impaired in α Raptor^{HET} mice

The reduction in glucagon levels in α Raptor^{KO} could be explained in part by a marked reduction in α -cell mass. However, lower fasting glucagon levels with normal α -cell mass in 2-month-old α Raptor^{HET} mice suggested a defect in glucagon secretion. We investigated mTORC1 activity in α -cells from mice that were fasted for 6 hours and re-fed for 2 hours and mice fasted for 6 hours followed by administration of exogenous insulin (1 Unit/kg). Our data showed that mTORC1 is not active in α -cells in the fed pancreas; however, insulin-induced hypoglycemia significantly increased mTORC1

activity in α -cells (Figure 10A,B). To further investigate the role of mTORC1 on glucagon secretion, we subjected these mice to different stimulatory conditions *in vivo*. Examination of glucagon secretion by insulin-induced hypoglycemia in 2 month-old mice showed that insulin induced similar decreases in blood glucose in α Raptor^{KO}, α Raptor^{HET} and control mice (Figure 10C). However, glucagon secretion after insulin-induced hypoglycemia was compromised in α Raptor^{KO} mice, explained by the severe loss of α -cell mass (Figure 10D). In contrast, α Raptor^{HET} mice were able to respond, but showed reduced glucagon secretion after 30 minutes of insulin injection (Figure 10D). Next, we examined glucagon secretion under neuroglycopenic conditions induced by 2-deoxy-D-glucose (2DG) injection, a non-metabolizable glucose analog that inhibits phosphorylation of glucose by hexokinase. 2DG-induced neuroglycopenia triggers counterregulatory responses including glucagon secretion by activation of the autonomic nervous system (Karlsson and Ahren, 1987; Marty et al., 2005). As expected, control mice exhibited increased glucose levels at 60 and 120 minutes after 2DG glucose injection (Figure 10E). Glucose levels were higher at 120 minutes after 2DG injection in α Raptor^{KO} mice compared to those of control mice, explained by increased gluconeogenic mechanisms in these mice (Figure 10E). α Raptor^{HET} mice displayed higher glucose levels at 30 minutes after 2DG glucose injection, but glucose levels were not different than controls after 60 minutes (Figure 10E). Assessment of glucagon secretion after 2DG injection showed that α Raptor^{KO} failed to respond to neuroglycopenia, also likely due to the severe loss of α -cell mass. (Figure 10F). Although α Raptor^{HET} mice had a higher response in blood glucose output at 30 minutes, these mice displayed impaired glucagon responses compared to the controls (Figure 10F).

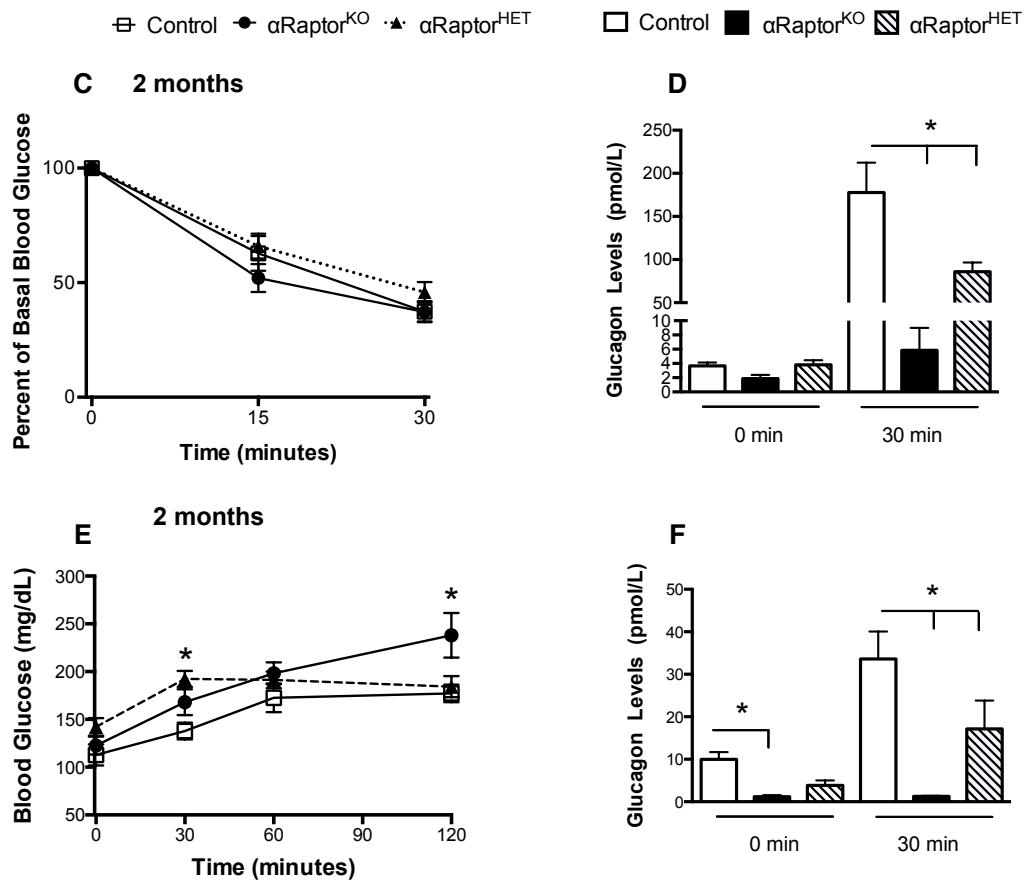
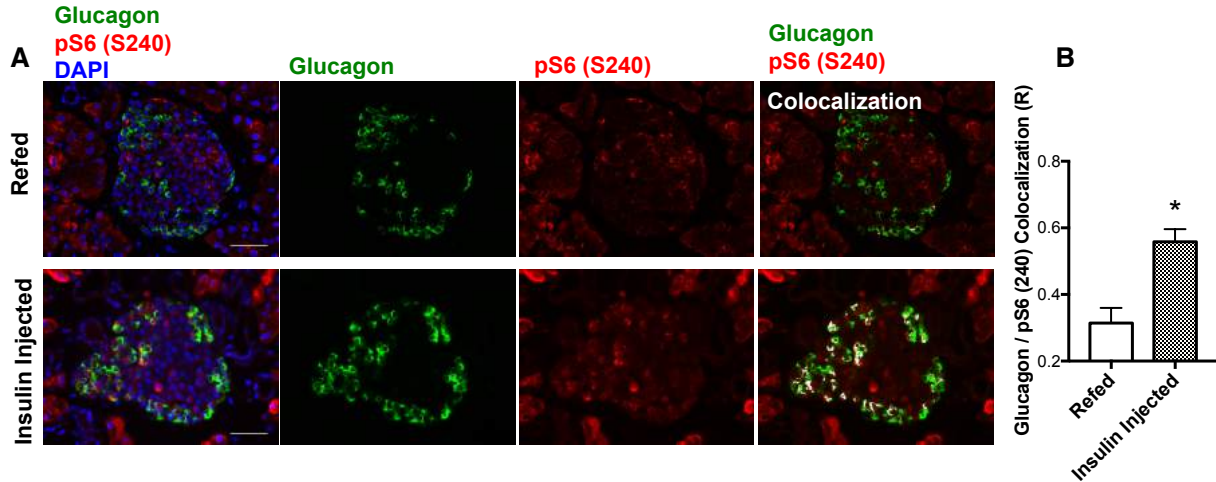


Figure 10. α Raptor^{HET} mice have decreased glucagon^{HET} response to hypoglycemia and neuroglycopenia. **A.** Immunofluorescent images (scale 50 μ m) of glucagon (green) and pS6 (S240; red) and **B.** Glucagon and pS6 colocalization (white) quantification by Pearson's Correlation Coefficient (R) in α -cells from mice fasted for 6 hours and refed for 2 hours or after administering exogenous insulin (1 Unit/kg). **C.** Blood glucose response and **D.** Glucagon response to Insulin Tolerance Test, ITT (1 U/kg.bw) at 2 months (n=5-6). **E.** Blood glucose response and **F.** Glucagon response to

2-deoxy-D-glucose (2 g/kg) at 2 months (n=4-5). Data are shown as means \pm S.E.M. * $p \leq 0.05$; Nonparametric *U* test (Mann Whitney).

Streptozotocin (STZ)-induced diabetes leads to increase in mTORC1 signaling in α -cells

In order to assess the role of mTORC1 on α -cell mass expansion we assessed the responses to Streptozotocin (STZ)-induced diabetes (Plesner et al., 2014; Zhang et al., 2012). mTORC1 signaling assessed by phospho-S6 (Serine 235/236) staining was enhanced in α -cells from control mice treated with STZ (Figure 11A) and therefore, we hypothesized that the α -cell mass expansion in this model is mTORC1-dependent. We administered a single, high-dose STZ (150 mg/kg) to controls, α Raptor^{KO} and α Raptor^{HET} mice. Insulin levels were greatly reduced a week after STZ injection (Figure 11B). All groups had a rapid increase in fed blood glucose levels and by 6 days post-injection the control mice had above-detectable fed blood glucose (Figure 11C). Compared to controls, α Raptor^{KO} mice restored their blood glucose to normal as early as 6 hours under fasting (Figure 11D). Examination of glucagon levels after STZ-treatment showed a significant increase in control mice (Figure 11E). A trend to a decreased glucagon levels was observed in α Raptor^{HET} mice post-STZ treatment (Figure 11E) and α Raptor^{KO} mice had no response in glucagon levels as a result of STZ (Figure 11E). As expected, controls showed increased α -cell mass after STZ injection (Figure 11F). The expansion of α -cell mass was partially reduced in α Raptor^{HET} mice and no response to STZ was observed in α -cell mass of α Raptor^{KO} mice (Figure 11F,G).

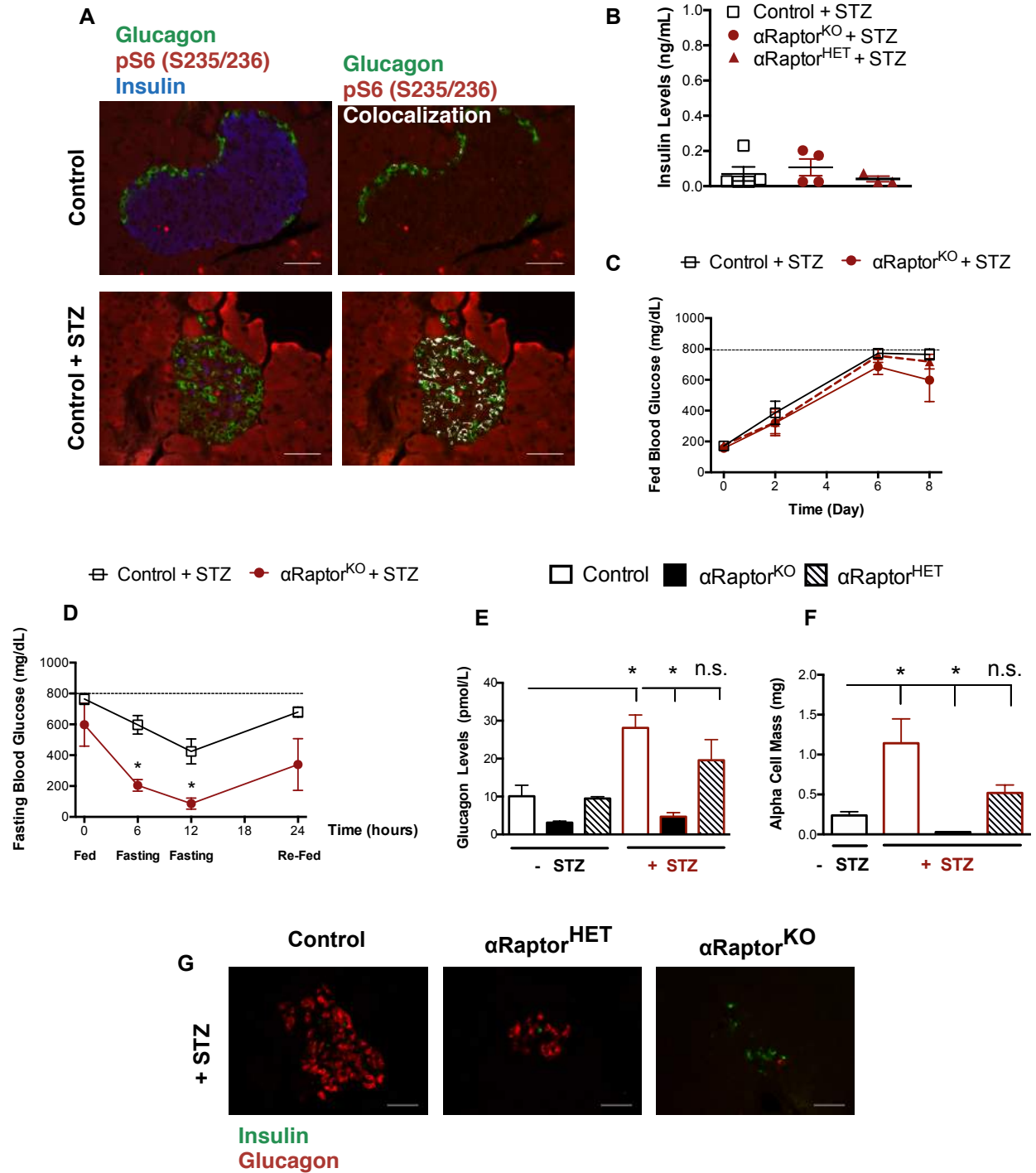


Figure 11. Streptozotocin (STZ)-induced diabetes leads to increase in mTORC1 signaling in α -cells. **A.** Immunofluorescent images representing glucagon (green), insulin (blue), pS6 (S235/36; red) and glucagon+pS6 colocalization (white) in control and control mice treated with STZ (150 mg/kg) (scale 50 μ m). **B.** Circulating insulin levels 8-days post single IP dose of 150 mg/kg STZ (n=3-5). **C.** Fed blood glucose from day 0 to day 8 post STZ (n=3-5). **D.** Fasting and re-fed blood glucose on day 8 post

STZ (n=4-5). **E.** Glucagon levels before and 8-days post STZ (n=3-5). **F.** Alpha cell mass of mice treated with STZ (150 mg/kg) for 8 days (n=3-5); data is represented as fold change from α -cell mass in non-treated mice. **G.** Immunofluorescent images representing insulin (green) and glucagon (red) in pancreas sections from control, α Raptor^{KO} and α Raptor^{HET} mice treated with STZ (scale 50 μ m). Data are shown as means \pm S.E.M. * $p \leq 0.05$; Nonparametric *U* test (Mann Whitney).

Rapamycin treatment *in vivo* reduces glucagon secretory response to hypoglycemia

In order to assess the role of mTORC1 signaling inhibition on glucagon secretion using a more clinically relevant model, we assessed the effects of systemic administration of rapamycin on glucagon secretion. Rapamycin (2 g/kg) was administered in wild type male mice by intraperitoneal injection every other day for total of five injections (Figure 12A). Body weight and fed blood glucose were not affected in all the groups at the end of rapamycin treatment (Figure 12B,C). After insulin injection, rapamycin-treated mice achieved similar drop in blood glucose levels during the first 60 minutes and lower glucose levels were observed at 120 minutes post insulin injection, suggesting an impairment in glucose counterregulation (Figure 12D). Evaluation of glucagon secretion showed that although rapamycin-treated mice had comparable baseline glucagon levels to those of control mice, the glucagon secretory response to hypoglycemia was blunted (Figure 12E). Glucagon content in isolated islets was also reduced in rapamycin-treated mice (Figure 12F). To determine if rapamycin treatment acutely alters glucagon secretion independently of glucagon content we assessed glucagon secretion in isolated control islets after short exposure to rapamycin (30 minutes at each glucose condition, for total of 2 hours). As expected, glucagon secretion decreased with increase in glucose concentrations (Figure 12G). However, 30 minutes of rapamycin treatment decreased glucagon secretion at 1mM glucose and had no additional effect under increasing glucose conditions, confirming *in vivo* data that rapamycin inhibits glucagon secretion in response to hypoglycemia (Figure 12G). The reduction in glucagon secretion induced by acute treatment with rapamycin was not explained by alterations in glucagon content suggesting that short-term rapamycin treatment can

affect glucagon secretion during states of low-glucose independently of alterations in glucagon content (Figure 12H).

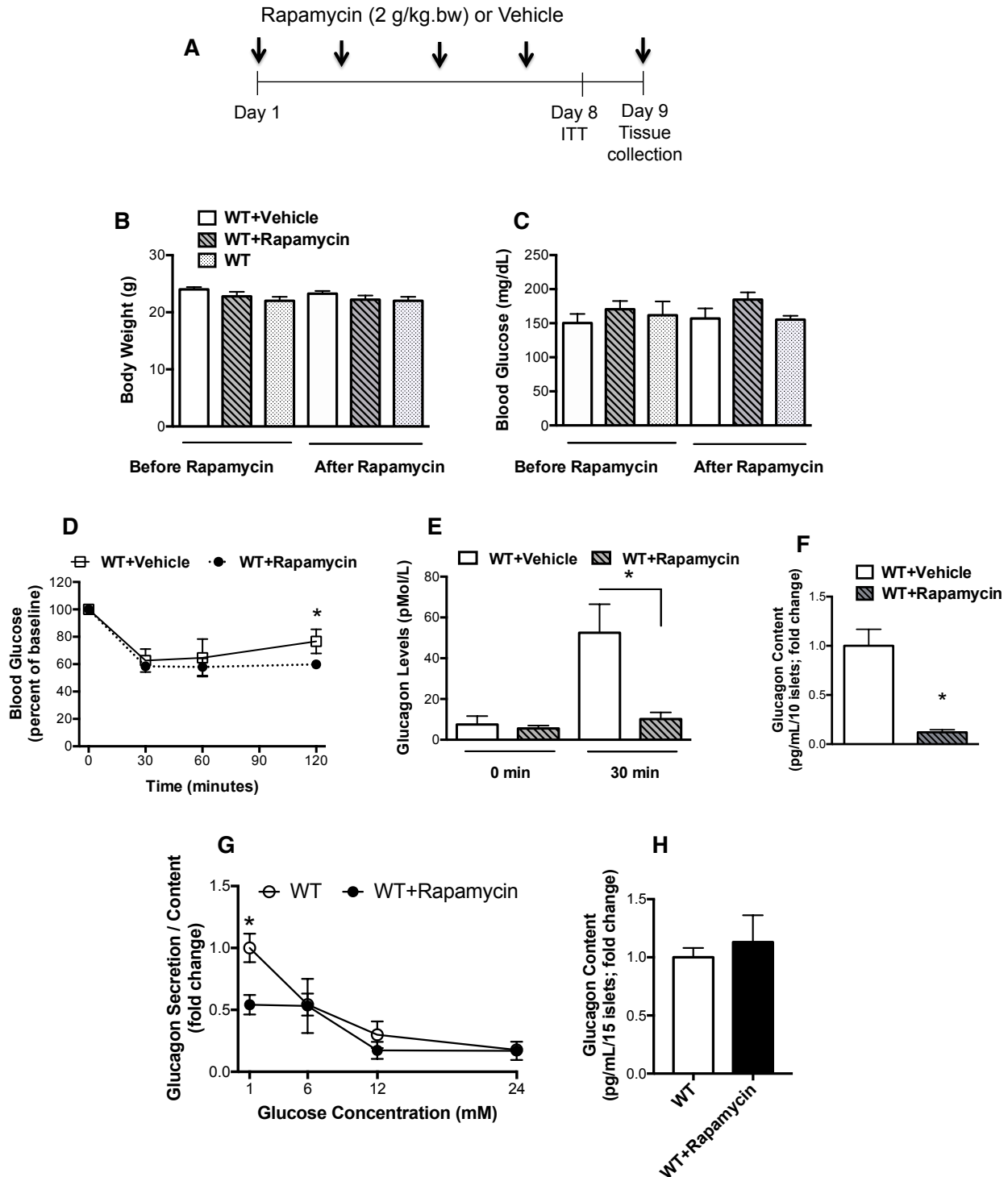


Figure 12. Rapamycin treatment *in vivo* recapitulates decreased glucagon secretory response to hypoglycemia and leads to decreased islet glucagon content. **A.** Experimental design for administering rapamycin to wild type, 2 month-old male mice. Arrows indicate intraperitoneal administration of rapamycin (2g/kg) every other day for 9 days. **B.** Body weight and **C.** Blood glucose levels on day 8 (n=4-5). **D.** Insulin Tolerance Test, ITT (1 U/kg) and **E.** Glucagon response at day 8 (n=4-5). **F.** Islet

glucagon content (n=4; presented as fold change from WT+Vehicle). **G.** Glucagon secretion and **H.** Islet glucagon content from isolated control islets treated with +/- rapamycin (30nM; n= 3-4 mice/treatment). Data are presented as fold change from control at 1 mM Glucose. Data are shown as means \pm S.E.M. * $p \leq 0.05$; Nonparametric *U* test (Mann Whitney).

Glucagon secretory responses induced by pharmacologic manipulation of K_{ATP} channels in α Raptor^{HET} islets is abnormal

In vivo data showed that α Raptor^{HET} mice exhibited impaired glucagon secretion in response to fasting and hypoglycemia. To uncover the mechanisms responsible, we examined the secretory responses of isolated islets. Glucagon secretion in response to depolarization induced by a strongly depolarizing concentration of potassium chloride (KCl; 30 mM) was similar between control and α Raptor^{HET} islets (Figure 13A). Next, we examined the glucagon response to arginine, a secretagogue that induces glucagon secretion in part by modulating K_{ATP} channels (Shiota et al., 2005). Glucagon secretion induced by arginine was blunted in α Raptor^{HET} islets (Figure 13B). Taken together these data suggested that the defect in glucagon secretion in α Raptor^{HET} mice resided in steps prior to cell depolarization and possibly at the level of the K_{ATP} channel. We further evaluated glucagon secretion during pharmacological modulation of K_{ATP} channel activity with increasing concentrations of tolbutamide (K_{ATP} channel antagonist) and diazoxide (K_{ATP} channel agonist). Under low glucose conditions, when a relatively larger fraction of K_{ATP} channels are open, tolbutamide treatment of control islets induces glucagon secretion up to concentrations of 10 μ M, whereas glucagon secretion was inhibited at higher concentrations as previously described (MacDonald et al., 2007; Rorsman et al., 2008; Walker et al., 2011). In contrast, tolbutamide treatment of α Raptor^{HET} islets failed to induce glucagon secretion and suppressed glucagon release at lower concentrations of tolbutamide (Figure 13C). Next we tested the effects of diazoxide-mediated opening of K_{ATP} channels at high glucose, where most K_{ATP} channels should be closed. Increasing concentrations of diazoxide (0–10 μ M) relieved the suppression of glucagon secretion in control islets (Figure 13D). In contrast, islets from α Raptor^{HET} mice were unresponsive to diazoxide and this agent failed to induce glucagon secretion (Figure 13D). Conversely, under low-glucose (1 mM) conditions

when at least some K_{ATP} channels are open, diazoxide further induced glucagon secretion at 1 mM followed by a dose-dependent suppression at 10 and 100 mM in control islets (Figure 13E). Under this condition, α Raptor^{HET} islets still failed to respond to diazoxide (Figure 13D,E). Taken together, these studies suggest that K_{ATP} channel function is altered in α -cells with reduced mTORC1 signaling.

mTORC1 regulates glucagon secretion by modulating K_{ATP} channel activity and expression

Next, we tested whether the changes in glucagon secretion obtained by pharmacologic manipulation of K_{ATP} channels in α Raptor^{HET} mice resulted from alterations in K_{ATP} channel activity. Whole-cell patch clamp was performed on α -cells at low glucose from Glucagon-Cre^{tdTomato} and α Raptor^{HET;tdTomato} mice expressing a fluorescent reporter in α -cells. Following establishment of the whole-cell patch-clamp, and subsequent washout of intracellular ATP, K_{ATP} channel current was significantly reduced in α Raptor^{HET} α -cells compared to controls (Figure 13F, G). To test the hypothesis that these results could be explained by alterations in K_{ATP} subunit expression, we measured the expression of K_{ATP} channels subunits *KIR6.2* and sulfonylurea receptor subunit 1 (*SUR1*) in α -cells. We isolated an enriched population of α -cells by FACS sorted dispersed islets from α Raptor^{HET} and control mice crossed to Ins1-EGFP and CAG-tdTomato reporter mice (approximately 60-70% glucagon). Our data showed that the enriched α -cell population from α Raptor^{HET} exhibited a decrease in *SUR1* and *KIR6.2* mRNA expression (Figure 13H) and a lower protein level of SUR1 (Figure 13I). We were unable to assess KIR6.2 levels due to a lack of antibody detection. Single cell mRNA expression for *SUR1* in α -cells showed that young α Raptor^{KO;tdTomato} mice had less positive α -cells for *SUR1* (Figure 13J). Unfortunately, we were unable to detect mRNA expression of *KIR6.2* in single cells using this methodology. Lastly, we measured mRNA and protein in α TC-1 cells, a glucagon-expressing cell line, treated with rapamycin (30 nM) for 48 hours. These studies showed that inhibiting mTORC1 signaling leads to decreased KIR6.2 and SUR1 protein and RNA expression (Figure 13K,L). Overall, our data showed that mTORC1 regulates the expression and activity of K_{ATP} channels in α -cells.

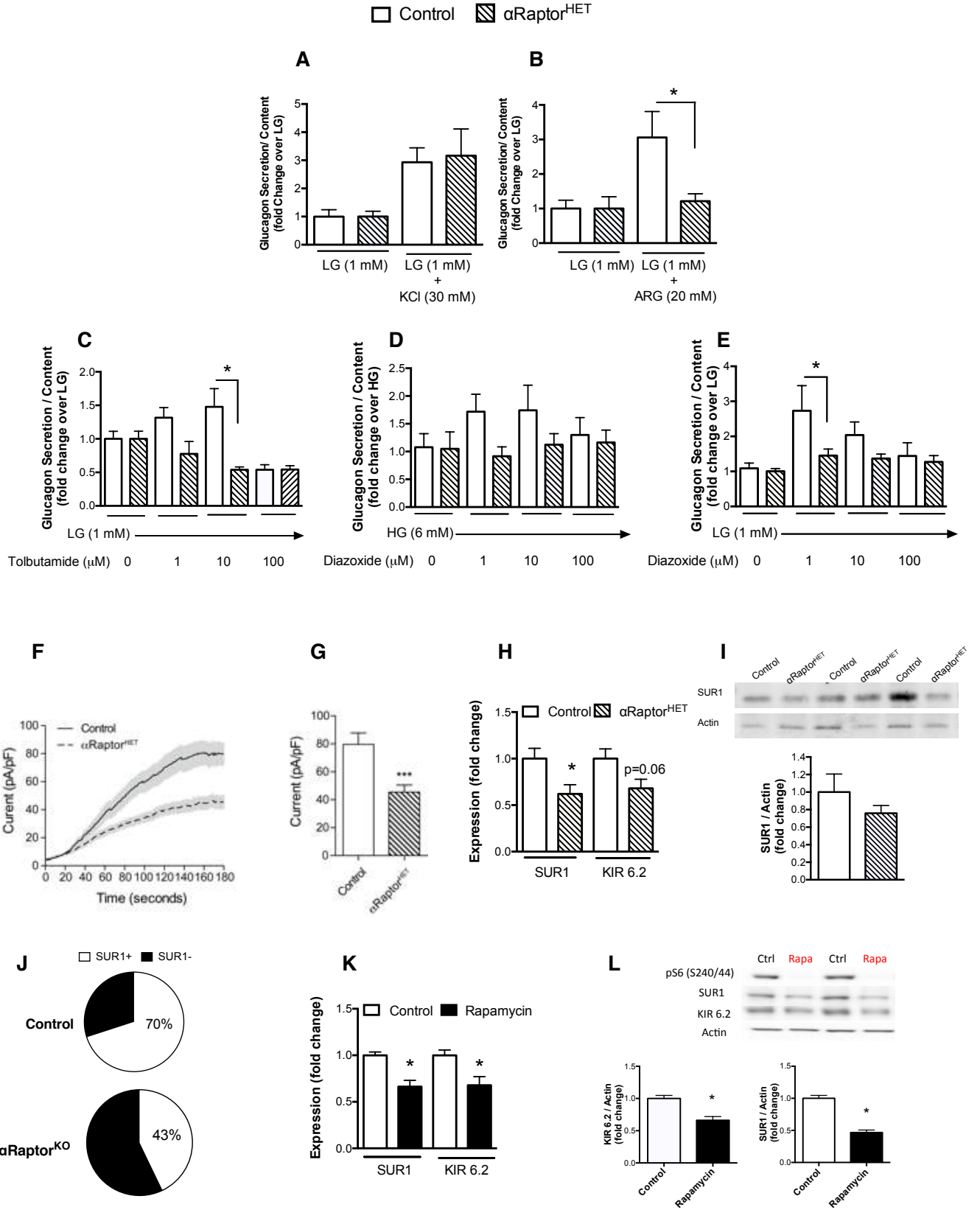


Figure 13. mTORC1 regulates glucagon response by alterations in K_{ATP} channel expression and activity. Glucagon response from isolated islets to **A.** KCl (30 mM) (n=8 mice) and **B.** Arginine (20 mM) (n=5-7 mice) under low-glucose Krebs Buffer (LG 1 mM). Glucagon response from isolated islets to increasing concentrations of **C.** Tolbutamide (0-100 μ M) under low-glucose conditions (1 mM; n=3-4 mice); **D.** Diazoxide (0-100 μ M) under high-glucose conditions (6 mM; n=5-7 mice); and **E.** Diazoxide (0-100 μ M) under low-glucose conditions (1 mM; n=5-6 mice). **F.** K_{ATP} channel activity during washout of intracellular ATP and **G.** Current amplitude quantification at 180 seconds in α -cells from control and α Raptor^{HET} mice (n=30-41 cells from 3-4 mice). **H.** RNA expression of *SUR1* and *KIR6.2* (n=6) and **I.** protein expression of SUR1 (n=3) in enriched α -cell population from control and α Raptor^{HET} mice. **J.** Single-cell analysis of *SUR1* expression frequency in α -cells from 1 month-old control and α Raptor^{KO} mice (n=20-21 cells from 3-4 mice). **K.** RNA expression and **L.** Protein levels of SUR1 and KIR6.2 from α TC-1 cells treated +/- rapamycin (30 nM) for 48 hours (n=7-8). Data are presented as fold change from control and shown as means \pm S.E.M. * $p \leq 0.05$; Nonparametric *U* test (Mann Whitney).

mTORC1 regulates K_{ATP} channel expression via the regulation of FoxA2 expression

To validate the expression studies and further explore the mechanisms linking mTORC1 to regulation of α -cell function and mass, we assessed expression of critical α -cell genes using Fluidigm C1 platform for RNA expression of single pancreatic islet cells (Table 3 in Experimental Methods for complete list of genes included in analysis). Single-cell gene analysis validated the decrease in *SUR1* and *KIR6.2* expression in α Raptor^{KO} and further showed reduced glucagon gene expression in these mice (Figure 14A,B). Autophagy-associated genes *ULK1* and *ULK2* were decreased in α Raptor^{KO} confirming a known role of this pathway in autophagy. Importantly, gene expression of key transcription factors involved in α -cell development and maintenance, such as *FoxA2*, *Neurogen3*, *Gata4*, *MafB*, *Pou3f4*, *Notch1*, *RBPJ* and *Nkx2.2*, were lower in α Raptor^{KO} compared to control α -cells (Figure 14A,B). Decreased expression of *CCNB1* (Cyclin B) and *EIF4E* suggest that these genes could be involved on the alteration of α -cell proliferation in α Raptor^{KO}. Single-cell gene analysis also identified targets involved in exocytosis and glucagon secretion, such as *SNAP25* (Synaptosomal-associated protein 25), *CACNA1S* (L-type voltage-dependent calcium channel) and *CHRM3* (muscarinic acetylcholine M3 receptor). Endoplasmic-reticulum stress-associated

genes, *XBP1* and *HSP90AB1*, were also decreased in α Raptor^{KO}. Reduced *FoxA2*, *MafB*, *Nkx2.2*, *Pou3f4* mRNA expression was also decreased in α TC-1 cells treated with rapamycin (30 nM) for 48 hours, validating the results obtained by the single cell analysis (Figure 14C).

The reduction in *Foxa2* expression in α -cells from α Raptor^{KO} was particularly interesting, as *FoxA2* has been shown to directly regulate glucagon, *SUR1* and *KIR6.2* gene expression in α -cells (Gao et al., 2007; Heddad Masson et al., 2014; Lantz et al., 2004; Lee et al., 2005; Philippe et al., 1994; Wang et al., 2002). Therefore, we hypothesized that mTORC1 modulates glucagon and K_{ATP} channel subunit expression through modulation of *FoxA2* expression. Flow cytometry analysis confirmed that *FoxA2* protein levels were also reduced in α -cells from α Raptor^{KO} mice (1 month old) (Figure 14D,E). In addition, nuclear *FoxA2* levels were decreased, as measured by the ratio of signal intensity of nuclear *FoxA2* over DAPI in the α -cells from α Raptor^{KO} mice (Figure 14F,G).

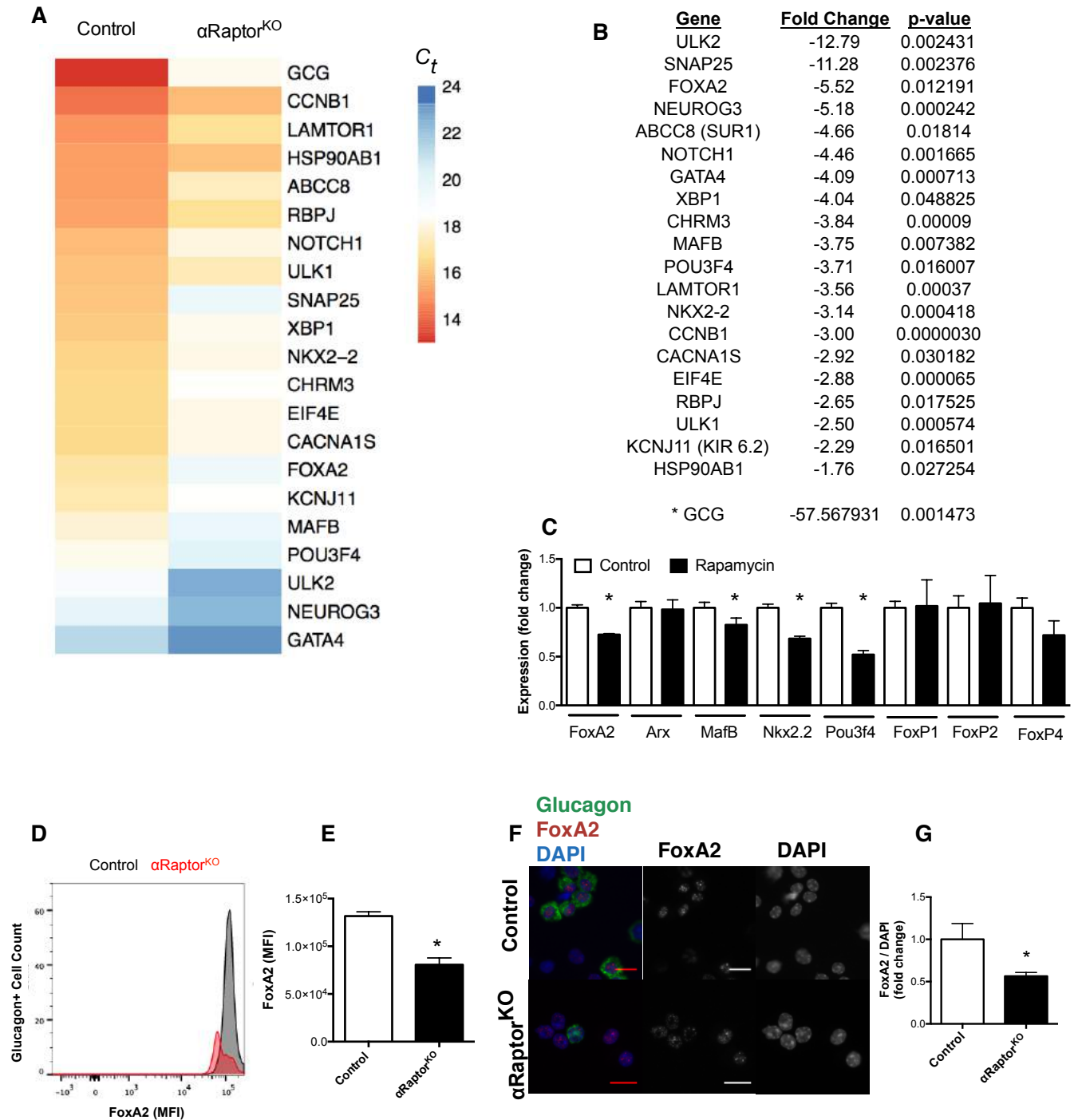


Figure 14. mTORC1 regulates the expression of genes involved in glucagon synthesis and regulation of glucagon secretion. A. Heat map represents mean C_t of differentially expressed genes ($p > 0.05$) from Fluidigm single-cell analysis. **B.** Fold change and p-value of differentially expressed genes identified in single-cell by t-test and *MAST analysis. **C.** RNA expression of genes from α TC-1 cells treated +/- rapamycin (30 nM) for 48 hours ($n = 4-8$ /group). **D.** Flow cytometry analysis and **E.**

quantification of FoxA2 protein in α -cells from 1 month-old control and α Raptor^{KO} mice (n=3-4). **F.** Immunofluorescent images representing FoxA2 (red), glucagon (green) and DAPI (blue) stain of isolated and dispersed islets from 1 month-old control and α Raptor^{KO} mice (scale 10 μ m). **G.** Quantification of the ratio of the signal intensity of nuclear FoxA2 over DAPI in dispersed α -cells from 1 month-old control and α Raptor^{KO} mice (n=4). Data are presented as fold change from control and shown as means \pm S.E.M. * $p \leq 0.05$; Nonparametric *U* test (Mann Whitney).

Discussion

The current studies provide new insights into the regulation of glucagon secretion and α -cell mass. Our studies were designed to examine signaling events controlling α -cell mass and glucagon secretion by characterizing mice with a conditional deletion of *raptor* in α -cells. This work demonstrated that mTORC1 signaling positively regulates α -cell mass maintenance and glucagon secretion during fasting. Our data also show that mTORC1 is dispensable for α -cell development and plays a role in the maintenance of α -cells after weaning. Importantly, these experiments uncover a novel role of mTORC1 signaling on regulation of glucagon secretion by transcriptional regulation of K_{ATP} channel subunit expression. We also present a novel role of mTORC1 on controlling critical transcription factors in α -cells and identified *FoxA2* as a novel mTORC1 target that mediates transcriptional regulation of K_{ATP} channel subunit and glucagon expression. More importantly, the decrease in glucagon secretion by lack of mTORC1 activity was recapitulated by administration of the clinically-used immunosuppressant and mTORC1 inhibitor, rapamycin. Our data suggest that these mechanisms could negatively regulate glucagon levels *in vivo* and thus inhibiting glucagon responses to hypoglycemia in patients taking these medications.

Morphologic studies showed that the decrease in glucagon levels observed in α Raptor^{KO} mice resulted from a loss of α -cells. Given the importance of mTORC1 signaling in autophagy, we hypothesized that the loss in α -cell mass in the α Raptor^{KO} mice was caused by increased autophagy-mediated failure of proper cell maintenance (Egan et al., 2011; Kim et al., 2011; Sanchez et al., 2012). This hypothesis was confirmed by crossing control and α Raptor^{KO} mice with mice expressing a molecular

marker of autophagy (LC3-GFP) and the partial restoration of α -cell mass at 1 month by 2-week treatment of the autophagy inhibitor, chloroquine. The lack of complete rescue could be explained by the concomitant decrease in α -cell proliferation observed in α Raptor^{KO} mice at 2 weeks of age. In addition to increased autophagy, smaller α -cells also contributed to the decrease in α -cell mass in α Raptor^{KO} mice. Increase in mTORC1 inhibits autophagy by phosphorylating ULK1/2 and the current studies showed that this kinase could also regulate *ULK1/2* mRNA levels. Interestingly, α Raptor^{HET} mice also showed reduction in α -cell mass only at 8 months suggesting that long-term reduction of mTORC1 activity could have an impact on controlling α -cell mass. Together, our data suggest that the loss in α -cell mass is mediated by an increased rate of autophagy in α Raptor^{KO} mice and that mTORC1 is essential for proper α -cell maintenance, α -cell size and glucagon content.

Glucose-dependent regulation of glucagon release is a complex process and much less understood than that of glucose-induced insulin secretion. Glucagon secretion is decreased by high glucose and paracrine factors released from neighboring insulin-secreting β -cells, somatostatin-secreting δ -cells and is also regulated by neural control (Bloom et al., 1978; Franklin et al., 2005; Gerich et al., 1973; Ishihara et al., 2003; Rorsman et al., 1989). α Raptor^{KO} and α Raptor^{HET} mice have abnormal glucagon response to fasting at 2 and 8-months of age. The decrease in glucagon levels could be explained by a marked reduction in α -cell mass observed in α Raptor^{KO} mice. In contrast, α Raptor^{HET} mice exhibited normal α -cell mass at 2 months, but impaired glucagon secretion during fasting, insulin-induced hypoglycemia and neuroglycopenia. These studies are consistent with the concept that mTORC1 is required for increase in glucagon secretion during fasting and hypoglycemia. Interestingly, suppression of glucagon secretion in the fed states appears to not be regulated by Insulin/Insulin Receptor/mTORC1 axis.

The current studies demonstrated that reduction of mTORC1 signaling decreases glucagon secretion during fasting and hypoglycemia. The finding that mTORC1 activity is important for proper potentiation of glucagon secretion during fasting is

counterintuitive, as this complex is mostly inactive during starvation. However, it is possible that the physiological increase in circulating amino acids during fasting could provide stimulatory signals to induce mTORC1 in α -cells. To this end, we have observed that mTORC1 activity is increased in α -cells during hypoglycemia but is inactive in the fed state. Therefore, our observations are consistent with a model in which mTORC1 is active and essential for nutrient-induced glucagon secretion in α -cells in the fasting conditions. The similar glucagon secretory responses to KCl treatment in controls and α Raptor^{HET} islets suggested that the secretory defect occurred prior to cell depolarization (Shiota et al., 2005). In contrast, glucagon responses to arginine or tolbutamide were impaired in α Raptor^{HET}. While tolbutamide and arginine should also depolarize the α -cell, KCl likely provided a much stronger depolarization that supports the sustained activation of L-type Ca²⁺ channels, as opposed to the P/Q-type channels that appear to control glucagon secretion under more physiologic conditions (Rorsman et al., 2014; Zhang et al., 2013). Based on these findings, together with impaired responses to low glucose observed *in vivo*, we hypothesized that the mechanistic defect in the glucagon secretory pathways in α Raptor^{HET} lied at the level of the K_{ATP} channel. Therefore, we assessed glucagon secretion to pharmacologic agents that open or close K_{ATP} channels in a dose-response manner as described (MacDonald et al., 2007). The dose-response alterations to diazoxide and tolbutamide, K_{ATP} channel activity modulators, are consistent with reduced K_{ATP} channels and currents in α Raptor^{HET} α -cells. Titration of K_{ATP} channel activity can enhance action potential firing to the point at which voltage-gated Na⁺, Ca²⁺, and K⁺ channels undergo voltage-dependent inactivation (Gopel et al., 2000; Ramracheya et al., 2010; Spigelman et al., 2010) and thus suppress glucagon secretion (as seen with 100 mM tolbutamide in the controls). The lower density of K_{ATP} currents in the α Raptor^{HET} α -cells is therefore consistent with the suppressive effect of tolbutamide on glucagon secretion occurring at lower concentrations, and the lack of effect of diazoxide. The reduction in K_{ATP} channel activity results from reduction of *KIR6.2* and *SUR1* expression in α Raptor^{HET} mice, indicating that mTORC1 signaling controls gene expression of K_{ATP} channel components. These *ex vivo* data were complimented by studies showing that single α -cell expression analysis in α Raptor^{KO} and mTORC1 signaling inhibition by rapamycin in α TC-1 leads to

decreased mRNA and protein expression of K_{ATP} channel subunits, SUR1 and KIR6.2. In addition, expression of several genes involved in secretory machinery were reduced in α Raptor^{KO} mice, identifying novel targets that could be regulated by mTORC1 (*SNAP25*, *CHRM3*, *CACNA1S*) and suggesting that additional mechanisms could also be involved. Taken together, these results uncovered a previously unknown function of mTORC1 signaling on controlling fasting-induced glucagon secretion by modulating expression of K_{ATP} channel subunit expression and K_{ATP} channel activity.

Our data showed that inhibiting mTORC1 signaling in α Raptor^{KO} mice and by rapamycin administration *in vivo* leads to decreased glucagon content and glucagon secretion. Single-cell gene expression analysis further showed that the decreased glucagon content resulted from reduced glucagon (*Gcg*) gene expression in α Raptor^{KO} and key transcription factors important for α -cell development, maintenance and glucagon synthesis including *FoxA2*, *Neoreg3*, *Gata4*, *MafB*, *Pou3f4*, and *Nkx2.2* (Artner et al., 2006; Mastracci et al., 2011; Ritz-Laser et al., 2005; Wang et al., 2009). The changes on *FoxA2* were particularly interesting, as this transcription factor has been shown to play a major role in regulating *Gcg*, *SUR1* and *KIR6.2* expression (Heddad Masson et al., 2014; Lantz et al., 2004; Lee et al., 2005; Philippe et al., 1994; Wang et al., 2002). *FoxA2* protein levels and nuclear *FoxA2* levels were also significantly reduced in α -cells from young α Raptor^{KO} mice. These data describe a novel link between mTORC1 and *FoxA2* gene transcription and provide evidence for the mechanisms responsible for alteration in *Gcg*, *SUR1* and *KIR6.2* expression in α Raptor^{KO} mice. Decreased *Gcg*, *MafB*, *Pou3f4*, *Nkx2.2*, *SUR1* and *KIR6.2* also support the decrease in *FoxA2*-dependent transcription, as *FoxA2* directly promotes transcription of these genes (Heddad Masson et al., 2014). Overall, our data identified an mTORC1/*FoxA2*/ K_{ATP} axis as a critical component linking nutrient signaling to α -cell function and glucagon synthesis.

In summary, dysregulation of glucagon secretion plays a major pathogenic role in the development of hyperglycemia in T2D and failure to secrete glucagon in T1D or advanced T2D patients results in recurrent hypoglycemia. These studies provide novel

insights into the molecular mechanisms and signaling pathways regulating glucagon secretion and α -cell mass. Our findings identify mTORC1 as a major signaling pathway controlling glucagon secretion under states of low glucose and identify a novel mechanistic link between mTORC1/FoxA2 on transcriptional regulation of K_{ATP} channel subunits and glucagon. These alterations were recapitulated by treatment with the immunosuppressant rapamycin, a known mTORC1 inhibitor used in the clinic. The findings obtained by rapamycin treatment could have major clinical implications in responses to hypoglycemia in post-transplant diabetics and perhaps explain the defects in counterregulation to hypoglycemia in patients after islet transplantation under chronic immunosuppression by rapamycin analogs (Paty et al., 2002; Rickels et al., 2007).

CHAPTER 3

Deletion of Tuberous Sclerosis Complex 2 (TSC2) in alpha cells results in hyperglucagonemia and alpha cell hypertrophy in the absence of diabetes

Introduction

Type 2 Diabetes (T2D) is characterized by defective adaptation of β -cells to insulin resistance. Most of the research effort has focused on elucidating the physiological, molecular, and genetic components that regulate β -cell mass and insulin secretion, presenting diabetes as a unihormonal disorder. Contrary to this current approach, clinical data and animal experiments have shown that increased α -cell mass and glucagon secretion play a role in the pathogenesis of hyperglycemia in diabetes (Dinneen et al., 1995; Mezza et al., 2014; Orci et al., 1976; Rahier et al., 1983; Sherwin et al., 1976; Yoon et al., 2003).

Increase in glucagon levels in T1D and T2D patients can be explained in part by increase in α -cell mass (Orci et al., 1976; Rahier et al., 1983; Yoon et al., 2003). Although the mechanisms leading to the increase in α -cell mass and glucagon levels in diabetic patients are not fully understood, several hypotheses have been developed based on animal models. Mice fed with high protein diet or high fat diet develop α -cell hyperplasia and hypertrophy suggesting that nutrient environment and/or insulin resistance could regulate α -cell mass (Ellingsgaard et al., 2008; Morley et al., 1982). In addition to the changes in α -cell mass, prolonged hyperinsulinemia in early stages of T2D could also induce α -cell insulin-resistance with loss of suppression of glucagon release by insulin (Liu et al., 2011). Studies using liver-specific glucagon receptor knock

out mice suggest that a circulating hepatic factor(s) can increase α -cell proliferation independent of direct pancreatic input (Gromada et al., 2007; Longuet et al., 2013). The metabolomics profile in the glucagon receptor knock out mice showed significant increase of circulating amino acids that could be responsible for the increase in α -cell mass observed in this mouse model (Yang et al., 2011). These studies support the concept that changes in α -cell mass are regulated by extracellular signals including nutrients (amino acids, glucose) and growth factors (insulin) but the intrinsic molecular mechanisms are largely unclear.

Previous data from our lab showed that mTORC1 signaling maintains the α -cell mass and potentiates glucagon secretion during fasting in a K_{ATP} channel-dependent manner. We also showed that complete ablation of β -cells and insulin levels by Streptozotocin (STZ) results in significant increase in α -cell mass and glucagon levels in control mice. The increase in α -cell mass was associated with increased mTORC1/phospho S6 signaling in α -cells of control mice treated with STZ. In the present studies, we tested the hypothesis that a gain in mTORC1 activity potentiates α -cell mass expansion and glucagon secretion as observed in diabetic patients. To test this hypothesis, we increased mTORC1 activity in α -cells by conditional deletion of *TSC2*, a negative mTORC1 regulator, in α -cells (α TSC2^{KO}). Our findings showed that α TSC2^{KO} mice exhibited severe hyperglucagonemia as a result of increased α -cell mass. Despite hyperglucagonemia, these mice had normal fed blood glucose levels, but upon fasting their blood glucose was decreased in comparison to controls. Further, α TSC2^{KO} mice had improved glucose tolerance, attributed to decreased hepatic glucose production. Surprisingly, β -cell destruction after Streptozotocin (STZ) treatment showed that these mice exhibited further increase in glucagon levels, but had lower blood glucose levels compared to the hyperglycemic STZ-treated controls. These studies demonstrated that activation of mTORC1 signaling in α -cells is sufficient to induce α -cell mass expansion and hyperglucagonemia and presents a molecular mechanism for increased glucagon levels and α -cell mass in diabetic patients.

Results

Mice with gain of mTORC1 signaling in α -cells have fasting hypoglycemia despite severe hyperglucagonemia

Alpha cell-specific deletion of *TSC2* was achieved by crossing Glucagon-Cre and *TSC2*^{flox/flox} mice (α TSC2^{KO}) (Hernandez et al., 2007; Shiota et al., 2013). Phospho-S6 (Serine240) staining showed that mTORC1 activity was lost in control glucagon-positive cells incubated in Krebs Buffer supplemented with 2 mM glucose for 2 hours. Unlike control cells, phospho-S6 (Serine240) was preserved in the glucagon-positive cells from 2 month-old α TSC2^{KO} mice, despite lack of complete media (Figure 15A). α TSC2^{KO} had decreased body weight from 1-month of age, which persisted until 3 months (Figure 15B). The decrease in body weight was attributed to increased locomotor activity and no changes in food intake of α TSC2^{KO} compared to control mice at 2 months of age (Figure 16A,B). In addition, *Cre*-recombination was detected in brainstem and hypothalamic regions (dorsomedial hypothalamic nucleus, DMH), which could contribute to changes in feeding and activity levels of these mice (Figure 2C). Although α TSC2^{KO} had a tendency of lower random blood glucose, they were hypoglycemic after a 12-hour fasting (Figure 15C,D). Fed and fasting glucagon measurements revealed that α TSC2^{KO} mice have severe hyperglucagonemia (Figure 15E,F). Insulin levels were slightly lower in α TSC2^{KO} mice compared to controls, reflecting potential compensatory decrease in insulin to the lower blood glucose levels of these mice (Figure 15G). Insulin levels after a 12-hour fast were undetectable in all groups. Fed and fasting active GLP-1 levels were not different between α TSC2^{KO} and control mice, suggesting that increased glucagon levels detected in α TSC2^{KO} are not due to aberrant proglucagon processing (Figure 15H,I).

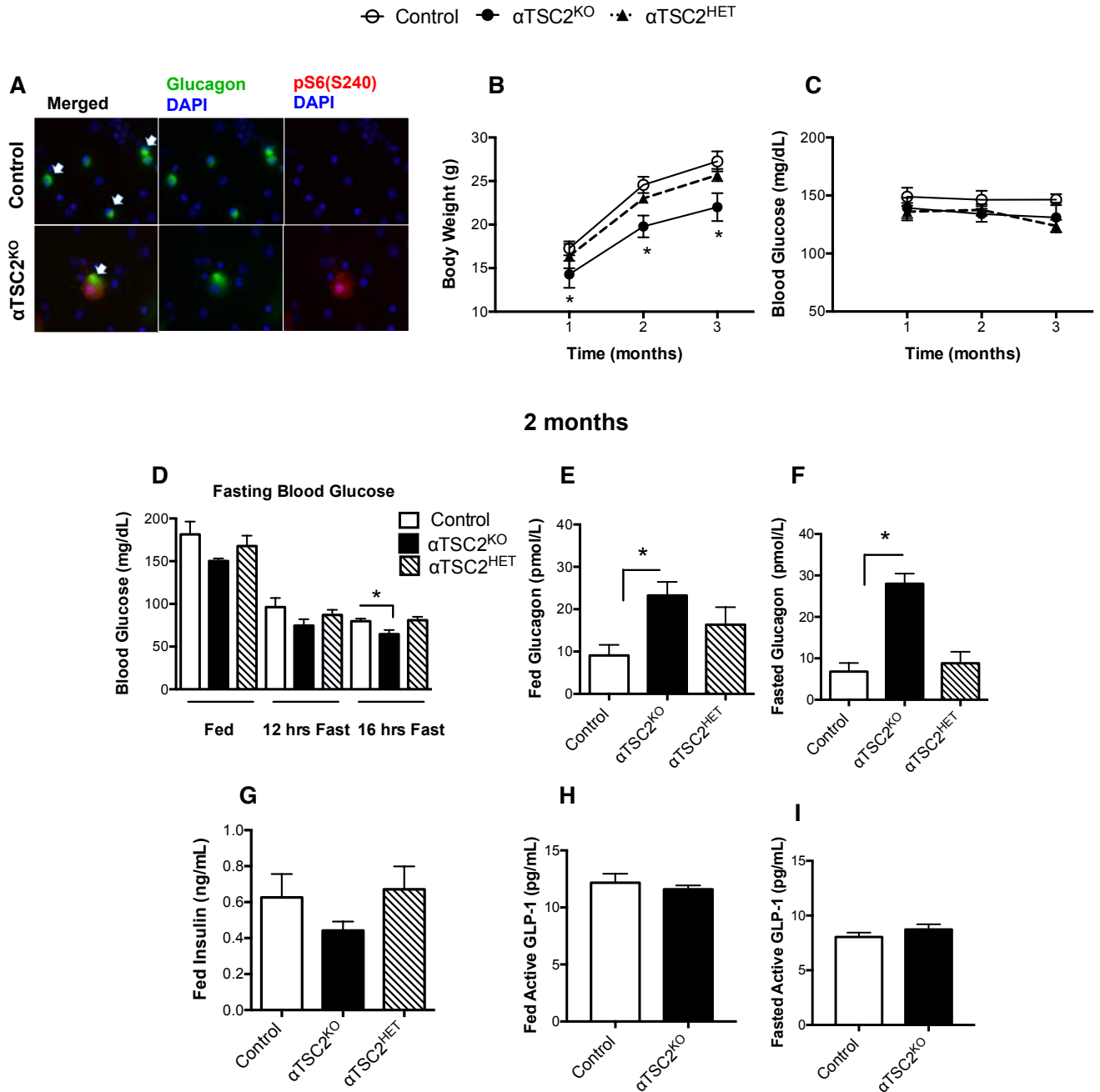
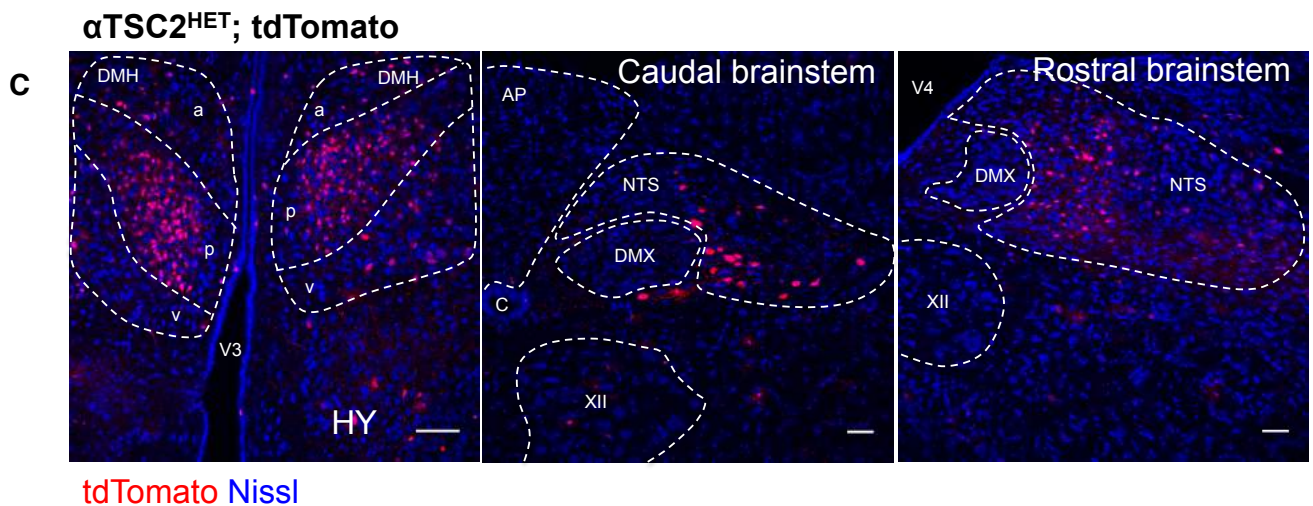
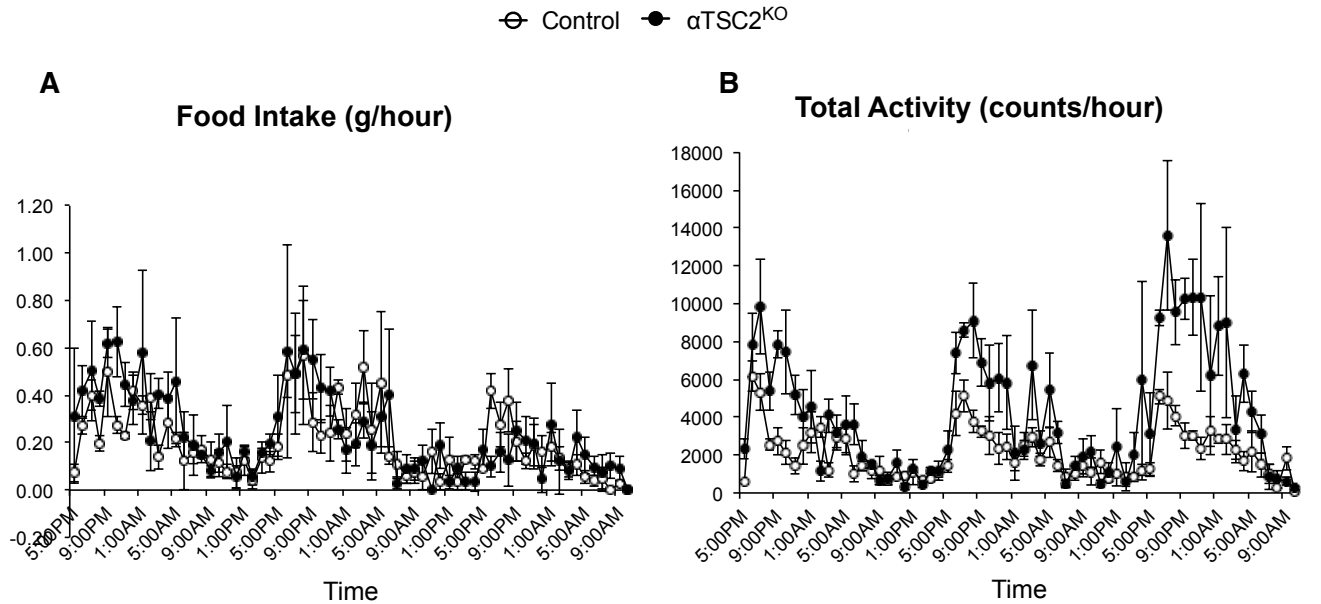


Figure 15. Mice with gain of mTORC1 signaling in α -cells have increased fed and fasting glucagon levels. **A.** Immunofluorescent staining showing lack of positive mTORC1 activity (shown by phospho-S6 S240) stain in the control and the sustained mTORC1 activity in glucagon positive-cells of the α TSC2^{KO} mice in dispersed islets incubated in 2 mM Glucose KRBB for 2 hours. **B.** Body weight and **C.** Random-fed blood glucose of control, α Raptor^{KO} and α Raptor^{HET} mice (n=4-8). **D.** Fasting blood glucose (n=3-7). **E.** Fed glucagon (n=5-7) and **F.** Fasted glucagon levels (n=3-6). **G.** Fed insulin levels (n=4-5). **H.** Fed active GLP-1 (n=4) and **I.** Fasted active GLP-1 levels (n=3-4). Data are shown as means \pm S.E.M. * $p \leq 0.05$; Nonparametric *U* test (Mann Whitney)



HY – Hypothalamus
DMH – Dorsomedial Nucleus of Hypothalamus (a-anterior, p-posterior, v-ventral)
V3 – Third Ventricle
AP – Area Postrema
NTS – Nucleus of the Solitary Tract
C – Central Canal
DMX – Dorsal Motor Nucleus of Vagus
XII – Hypoglossal Nucleus
V4 – Fourth Ventricle

Figure 16. α TSC2^{KO} mice have lower body weight associated with increase in activity levels. A. Food intake (grams/hour) for 3 days in 2-month old male control and α TSC2^{KO} mice (n=3). **B.** Locomotor activity levels (counts/hour) in for 3 days in 2-month old male control and α TSC2^{KO} mice (n=3). **C.** Immunofluorescent staining showing *Cre*-expressing neurons by positive tdTomato (*Cre*-expression) and Nissl (neuron) stain in α TSC2^{HET} mice (scale 50 μ m).

Gain in mTORC1 signaling in α -cells results in α -cell hypertrophy and hyperplasia

Morphometric analysis at postnatal day 1 demonstrated that α TSC2^{KO} mice were born with normal α -cell mass (Figure 17A), reflecting previous data from our lab that mTORC1 signaling is dispensable for α -cell development. Morphologic evaluation by electron microscopy in 1 month-old α TSC2^{KO} showed an increase in α -cell size that was confirmed by cell size measurements at 2 months of age (Figure 17B,F). In addition, the number of glucagon granules appeared to be largely increased and this was confirmed by the increase in total pancreatic glucagon content at 2 months (Figure 17E). α TSC2^{KO} mice also showed an increase in α -cell mass and proliferation, with no changes in apoptosis at 2 months (Figure 17D,G, H). In contrast, β -cell mass at 2 months was not altered in α TSC2^{KO} mice compared to controls (Figure 17I). The pancreas weight normalized to body weight was reduced in α TSC2^{KO} mice compared to controls (Figure 17J). Overall, our data show that gain of mTORC1 signaling in α -cells results in increased α -cell mass, size and proliferation contributing to increased pancreatic glucagon content and severe fed and fasting hyperglucagonemia.

Newborn

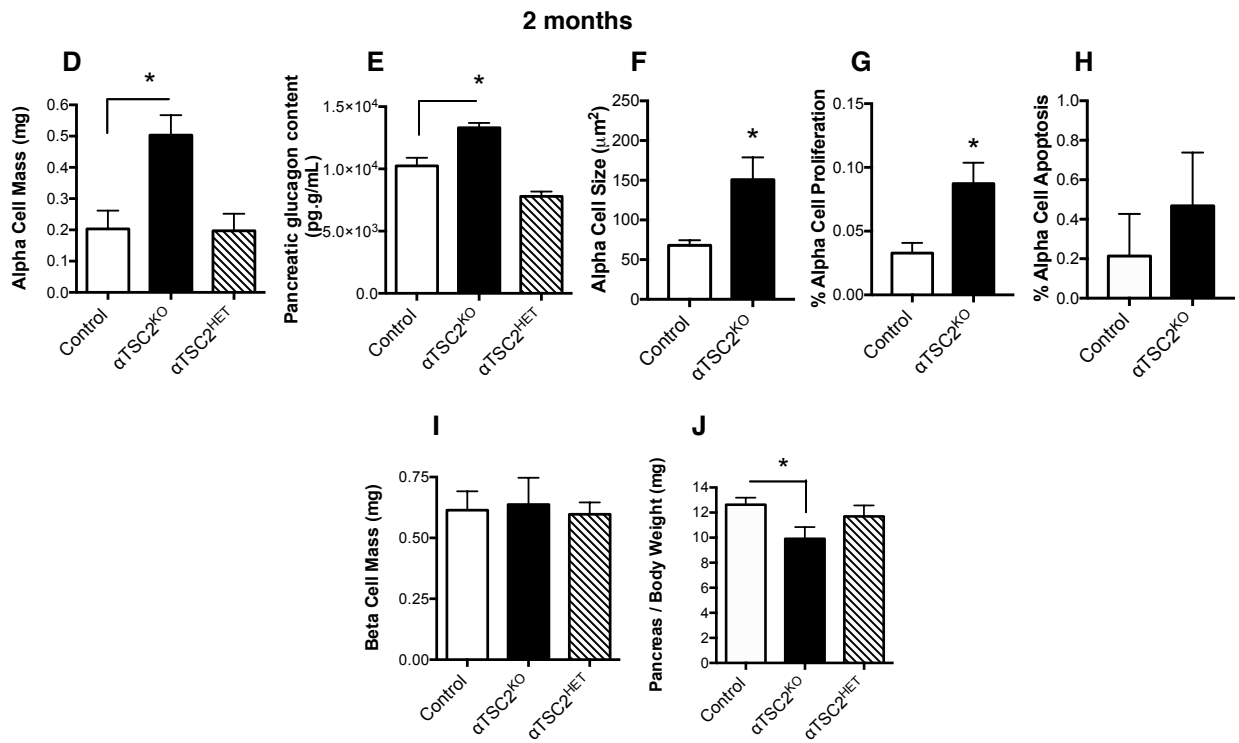
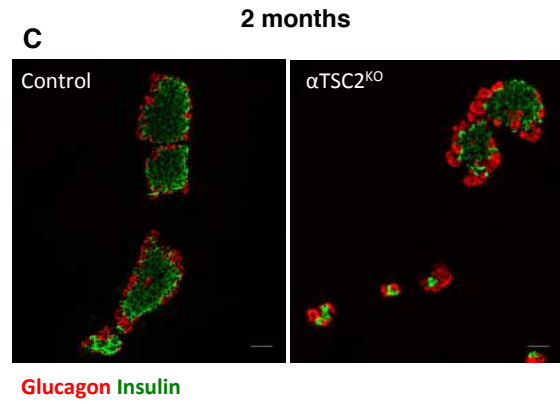
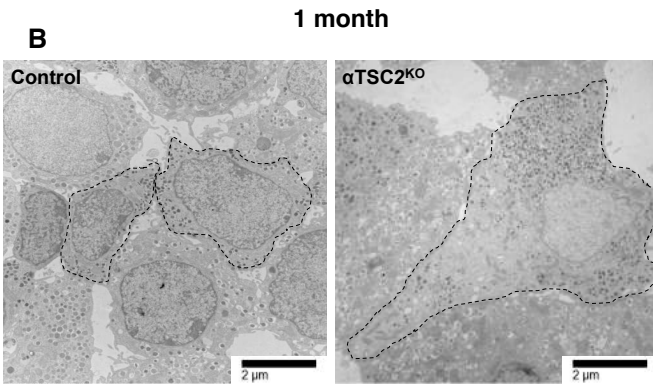
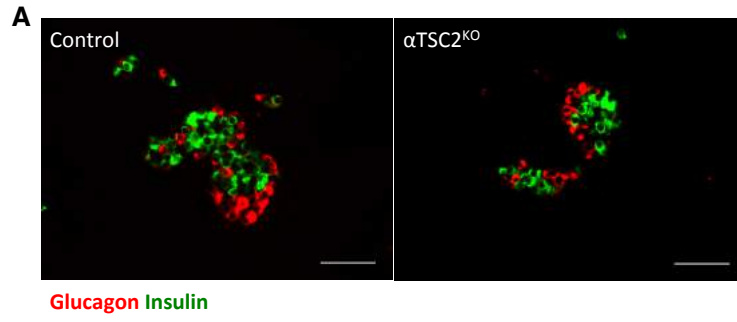


Figure 17. Gain in mTORC1 signaling in α -cells results in α -cell hypertrophy and hyperplasia. **A.** Immunofluorescent images of glucagon (red) and insulin (green) in pancreas at postnatal day 1 (scale 50 μ m). **B.** Electron microscopy images from 1 month-old control and α TSC2^{KO} mice. **C.** Immunofluorescent images of glucagon (red) and insulin (green) at 2 months (scale 50 μ m). **D.** Quantification of α -cell mass at 2 months (n=3-4). **E.** Pancreatic glucagon content at 2 months (n=4). **F.** Quantification of α -cell size (n=4) and **G.** Proliferation by positive ki67 and glucagon co-stain (n=3) and **H.** Apoptosis by positive TUNEL and glucagon co-stain (n=4) in 2 month-old mice. **I.** Quantification of β -cell mass in 2 month-old mice (n=3-4). **J.** Pancreas weight in 2 month-old mice (n=7-10). Data are shown as means \pm S.E.M. * $p \leq 0.05$; Nonparametric *U* test (Mann Whitney).

α TSC2^{KO} mice have reduced glycemic counterregulation to hypoglycemia despite hyperglucagonemia

To further investigate the role of gain in mTORC1 signaling on glucagon secretion, we subjected these mice to hypoglycemia by administration of insulin. Examination of the glycemic response by insulin-induced hypoglycemia in 2 month-old mice showed that hypoglycemia by exogenous insulin administration induced similar decreases in blood glucose in control and α TSC2^{KO} mice at 30 minutes (Figure 18A). However, α TSC2^{KO} mice had sustained low blood glucose at 120 minutes, suggesting that the compensatory counterregulation of blood glucose to hypoglycemia was compromised in these mice (Figure 18A). Glucagon secretion after insulin-induced hypoglycemia was increased in all mice; however α TSC2^{KO} mice maintained hyperglucagonemia before and after insulin-induced hypoglycemia (Figure 18B).

In vivo data showed that α TSC2^{KO} mice are severely hyperglucagonemic in the fed and fasting state. To uncover the mechanisms responsible, we examined the secretory responses of isolated islets to inhibitory and stimulatory secretagogues. Pancreatic α -cells are exposed to high levels of intra-islet insulin secreted from the β -cells and insulin is a potent inhibitor of glucagon secretion and glucagon gene transcription (Asplin et al., 1981; Maruyama et al., 1984; Philippe, 1989; Weir et al., 1976; Zhang et al., 2012). We measured the effect of exogenous insulin in suppressing glucagon secretion. Administration of insulin decreased glucagon secretion in control, but had no effect in suppressing glucagon in α TSC2^{KO} islets (Figure 18C). Next, we examined the glucagon

response to depolarization induced by a strongly depolarizing concentration of potassium chloride (KCl; 30 mM). Glucagon secretion was increased in α Raptor^{KO} compared to control islets in response to KCl (Figure 18C). Our data showed that the α -cells of α TSC2^{KO} are resistant to insulin-dependent regulation of glucagon secretion, and they are more sensitive to cell depolarization, culminating in increased glucagon levels.

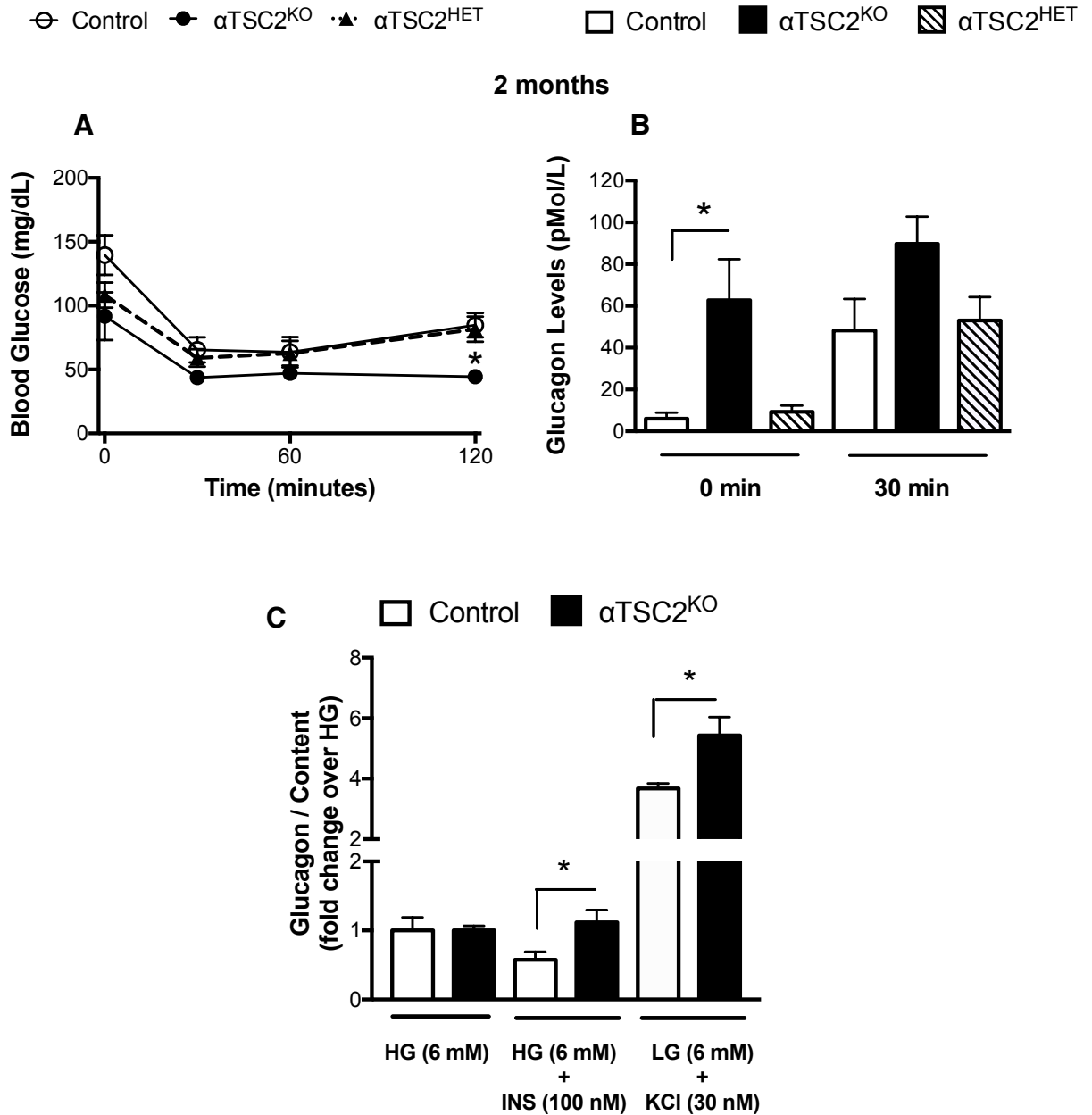


Figure 18. α TSC2^{KO} mice have reduced blood glucose counterregulation in response to hypoglycemia. A. Blood glucose response and **B.** Glucagon response to Insulin Tolerance Test, ITT (0.75 U/kg.bw) at 2 months (n=4-6). **C.** Glucagon response from isolated islets to exogenous insulin (100nM) and KCl (30nM) (HG=6 mM Glucose; LG=1 mM Glucose; n=3-8 mice). Data are shown as means \pm S.E.M. * $p \leq 0.05$; Nonparametric *U* test (Mann Whitney).

α TSC2^{KO} mice have improved glucose tolerance and decreased gluconeogenesis

Intraperitoneal glucose-tolerance test revealed that α TSC2^{KO} mice have improved glucose clearance at 2 months (Figure 19A). This was accompanied by decreased pyruvate tolerance and hepatic glucose production. These data suggested that α TSC2^{KO} mice have improved glycemic tolerance associated with decreased gluconeogenesis (Figure 19B).

Fed liver glycogen content was not different between α TSC2^{KO} and control mice (Figure 19C). RNA expression of the glucagon receptor (*GCGR*), phosphoenolpyruvate carboxykinase (*PEPCK*) and glucokinase (*Gck*) were decreased in fed liver of α TSC2^{KO} mice compared to controls (Figure 19D,E,G). No changes were observed in the RNA expression of glucose 6-phosphatase (*G6Pase*) and fatty acid synthase (*FAS*) in fed liver (Figure 19F,H). The fasting-induced increase in non-esterified free fatty acids (NEFA) was observed in α TSC2^{KO}, α TSC2^{HET} and control mice; however, α TSC2^{KO} mice had lower fed and slightly lower fasting levels of free fatty acids compared to the controls (Figure 19I). We measured the insulin sensitivity of the liver by administration of insulin *in vivo* (1 Unit/kg). Control and α TSC2^{KO} mice responded similarly to exogenous insulin by a robust increase in AKT (phosphor-Ser473) activation, suggesting that hepatic insulin sensitivity was not increased in α TSC2^{KO} (Figure 19 J).

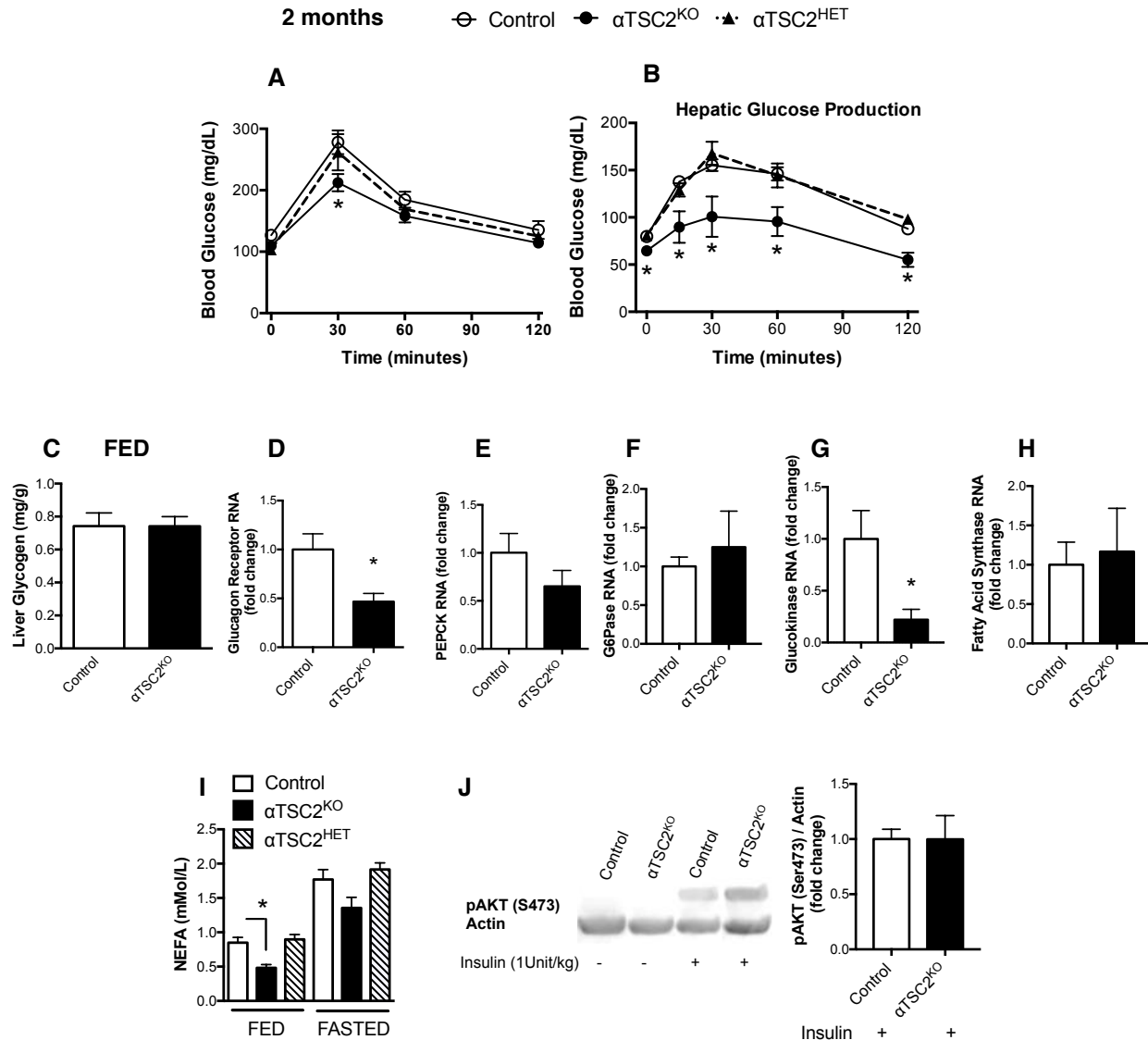


Figure 19. α TSC2^{KO} mice have improved glucose tolerance and decreased gluconeogenesis. A. Glucose tolerance test (2g/kg.bw) in 2-month old mice (n=5-8). **B.** Pyruvate tolerance test (2 g/kg) in 2-months old mice (n=3-6). **C.** Fed liver glycogen content (n=6-8). Fed liver mRNA levels of **D.** Glucagon Receptor, **E.** PEPCK, **F.** G6Pase, **G.** Glucokinase, **H.** Fatty acid synthase (n=5-8). **I.** Fed and fasting NEFA levels at 2 months (n=3-6). **J.** Western blot and quantification showing hepatic insulin sensitivity measured by phospho-AKT (S473) after insulin administration *in vivo* (1 Unit/kg). Data are shown as means \pm S.E.M. * $p \leq 0.05$; Nonparametric *U* test (Mann Whitney).

Hyperglycemia after STZ-induced diabetes is reduced in α TSC2^{KO} mice

Previous findings have shown that mTORC1 signaling is enhanced in α -cells from control mice treated with Streptozotocin (STZ) (Figure 11A) and therefore we wanted to evaluate if gain in mTORC1 will recapitulate the effect of STZ in α -cell mass expansion and increased glucagon levels. Fed insulin levels were not detectable after a week of a single, high-dose STZ injection (150 mg/kg) and β -cell mass was nearly ablated (Figure 20E). All mice had a rapid increase in fed blood glucose levels, but α TSC2^{KO} mice maintained slightly lower blood glucose compared to controls (Figure 20A). Examination of glucagon levels after STZ showed an increase in glucagon levels of control mice (Figure 20B). α TSC2^{KO} mice remained hyperglucagonemic before and after STZ, although they presented a tendency of increased glucagon levels post-STZ (Figure 20B). Consistent with these findings, α TSC2^{KO} mice maintained higher α -cell mass, size and proliferation compared to controls (Figure 20D,F,G). Liver glycogen content was not different between control and α TSC2^{KO} mice and liver glycogen levels of control and α TSC2^{KO} mice were similarly decreased in response to STZ (Figures 19E and 20I). Hepatic mRNA expression of glucagon receptor (*GCGR*), *PEPCK*, *G6Pase*, glucokinase (*Gck*) and fatty acid synthase (*FAS*) showed a trend of increased expression in α TSC2^{KO} mice compared to controls after STZ (Figure 20 J-N).

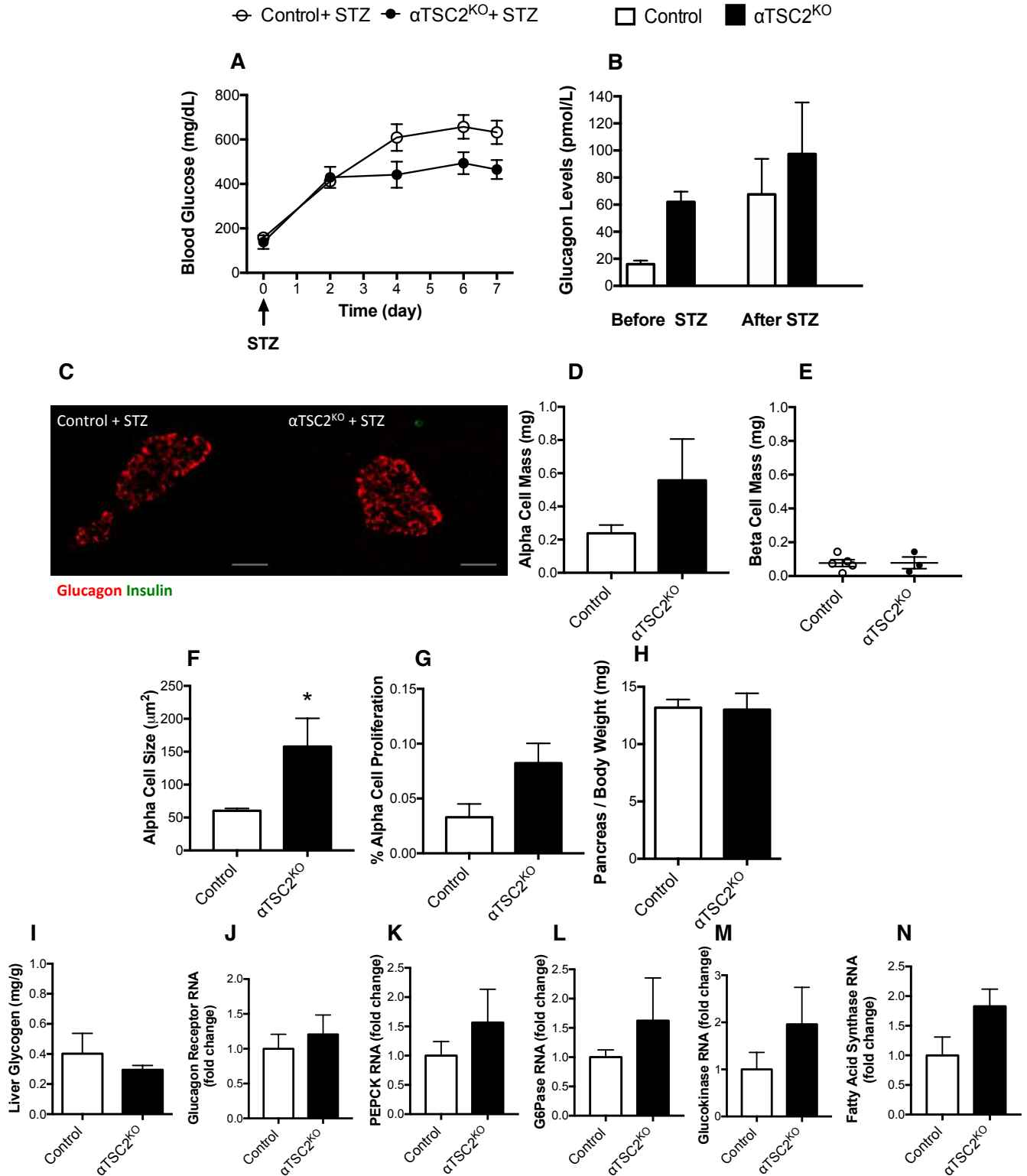


Figure 20. Hyperglycemia after STZ-induced diabetes is reduced in α TSC2^{KO} mice. **A.** Fed blood glucose from day 0 to day 7 after single IP dose of 150 mg/kg STZ (n=3-5). **B.** Circulating glucagon levels before and 7 after STZ (n=3-5). **C.** Immunofluorescent images representing insulin (green) and glucagon (red) in pancreas

sections from control and α TSC2^{KO} mice treated with STZ (scale 50 μ m). **D.** α -cell and **E.** β -mass of mice after STZ (n=3-5). **F.** α -cell size and **G.** Proliferation after STZ (n=3-5). **H.** Pancreas weight of control and α TSC2^{KO} mice treated with STZ (n=3-5). **I.** Liver glycogen content (n=3-5). RNA levels of **J.** Glucagon receptor, **K.** PEPCK, **L.** G6Pase, **M.** Glucokinase, **N.** Fatty acid synthase (n=3-4). Data are shown as means \pm S.E.M. * $p \leq 0.05$; Nonparametric *U* test (Mann Whitney).

Discussion

Glucagon plays a major role in maintaining glucose homeostasis by promoting glucose production *via* hepatic glycogenolysis and gluconeogenesis. Clinical data has shown that α -cell mass and glucagon levels are elevated in insulin-resistant/non-diabetic, T1D, and T2D patients, leading to enhanced hepatic glucose output and thereby exacerbating the diabetic hyperglycemic state (Dinneen et al., 1995; Mezza et al., 2014; Orci et al., 1976; Rahier et al., 1983; Sherwin et al., 1976; Yoon et al., 2003). The current studies provide new insights into the signaling mechanisms that play a role in potentiating the increase in glucagon secretion and α -cell mass observed in diabetic patients. Our studies were designed to test the hypothesis that gain in mTORC1 activity plays a role in α -cell mass expansion and glucagon secretion as observed in diabetic patients. To test this hypothesis, we increased mTORC1 activity in α -cells by conditional deletion of *TSC2*, a negative mTORC1 regulator (α TSC2^{KO}). Our findings showed that gain in mTORC1 signaling in α -cells of α TSC2^{KO} increased postnatal α -cell mass (hypertrophy and hyperplasia) and pancreatic glucagon content. Fed and fasting glucagon levels were greatly increased in α TSC2^{KO} mice compared to controls. Fed insulin levels were slightly lower in α TSC2^{KO} mice, which could be attributed to compensation in response to the lower blood glucose levels of these mice.

Body weight was significantly reduced in young α TSC2^{KO} mice and persisted through the lifespan of these mice. Recent studies have shown that glucagon increases energy expenditure in humans, similarly to that of cold-activation, but independent of brown adipose fat (Salem et al., 2016). Food intake and locomotor activity measurements revealed that α TSC2^{KO} mice had increased activity compared to controls. However, no changes were detected in food intake. The central nervous system integrates nutrient

signals to the regulation of energy balance by the mediobasal hypothalamus. Studies have shown that mTORC1 activation in the caudomedial nucleus of solitary tract (NTS) in the brainstem decreases food intake and body weight (Blouet et al., 2009; Blouet et al., 2008; Blouet and Schwartz, 2012). Assessment of *Cre*-recombination in CNS revealed that *Cre*-expressing neurons are present in the brainstem and dorsomedial hypothalamic nucleus (DMH), which could contribute to changes in feeding and activity levels. However, increased plasma levels of glucagon could be directly acting in the CNS to decrease body weight in α TSC2^{KO} mice. Importantly, recent study has shown that chronic glucagon receptor signaling agonism is coupled with increased locomotor activity, in agreement with our data showing increased activity levels of α TSC2^{KO} mice (Habegger et al., 2013).

Increased glucagon levels increase gluconeogenesis and glycogenolysis in control mice; however, α TSC2^{KO} mice were hyperglucagonemic, but had reduced fasting blood glucose levels. These data were puzzling and therefore, we examined whether the increased glucagon levels detected in α TSC2^{KO} mice were result of abnormal proglucagon processing. Glucagon is processed from proglucagon in pancreatic α -cells by prohormone convertase (PC2). Mice lacking expression of *PC2* have reduced fasting blood glucose, α -cell hyperplasia and hypertrophy and increased glucose tolerance, all of which we observed in α TSC2^{KO} mice (Blouet and Schwartz, 2012). As a result of abnormal proglucagon processing, GLP-1 levels were also increased in *PC2* knock out mice (Blouet and Schwartz, 2012). However, we did not detect any changes in fed or fasting active GLP-1 levels between α TSC2^{KO} and control mice, suggesting lack of abnormal proglucagon processing. Further analysis of *PC2* mRNA and protein expression in α -cells from α TSC2^{KO} and control mice is needed to fully exclude the role of abnormal proglucagon processing as result of increased mTORC1 signaling in α -cells.

Despite hyperglucagonemia, α TSC2^{KO} mice had normal fed blood glucose levels, but upon fasting their blood glucose was decreased in comparison to controls. These mice also lacked counter-regulatory increase in blood glucose levels after severe

hypoglycemia. Further, α TSC2^{KO} mice had improved glucose tolerance, attributed to decreased gluconeogenesis and hepatic glucose production. Ample evidence has shown that inhibiting glucagon signaling results in hypoglycemia. Administration of glucagon-neutralizing antibodies and the genetic ablation of the glucagon receptor *in vivo* result in mild hypoglycemia (Blouet et al., 2009; Blouet et al., 2008; LaPierre et al., 2015). Although fed liver glycogen content was not different, the expression analysis of genes involved in gluconeogenesis, glycolysis and fatty acid synthesis revealed that α TSC2^{KO} have reduced hepatic gluconeogenesis. RNA expression of the glucagon receptor in fed liver was reduced in α TSC2^{KO} compared to controls. Phosphoenolpyruvate carboxykinase (*PEPCK*) catalyzes a rate-limiting step in early gluconeogenesis and its mRNA expression is increased in response to glucagon signaling during fasting. Expression of *PEPCK* mRNA was slightly lower in the fed liver of α TSC2^{KO}. Glucokinase is suppressed by glucagon (as part of glucagon's inhibitory role in glycolysis) to decrease glucose entry into glycolysis. Glucokinase mRNA expression was reduced in α TSC2^{KO} mice in cohort with hyperglucagonemia in these mice and proper glucagon inhibition of glucokinase. In addition, lack of changes in *G6Pase* and fatty acid synthase expression suggests that hyperglucagonemia in α TSC2^{KO} mice does not impact glycogenolysis and fatty acid synthesis (Longuet et al., 2008). This is in cohort with data showing that glucagon signaling plays an essential role in fatty acid oxidation, but does not regulate the expression of genes involved in fatty acid synthesis. Free fatty acids rise during fasting as result from hydrolysis of triglycerides within the adipocyte (Karpe et al., 2011) and exogenous administration of glucagon decreases the plasma levels of triglycerides and free fatty acids (Longuet et al., 2008). Fed free fatty acid levels were lower in α TSC2^{KO}, and although they increased with fasting, they remained slightly lower in comparison with controls. In addition, our data suggest that the role of glucagon in inhibiting glucokinase and suppressing glycogenolysis and glucagon's suppression of plasma free fatty acid levels is preserved and consistent with increased levels of fed glucagon in α TSC2^{KO} mice. Hepatic insulin sensitivity was not increased in α TSC2^{KO} and therefore does not contribute to the observed improvement in glucose tolerance. Based on our data, we suggest that chronic hyperglucagonemia in α TSC2^{KO} mice leads to decrease in hepatic

glucagon signaling and gluconeogenesis, contributing to decreased fasting blood glucose and improved glucose tolerance.

Previous data from our lab showed that complete ablation of β -cells and insulin levels by Streptozotocin (STZ) administration results in significant increase in α -cell mass and glucagon levels and the development of severe hyperglycemia in control mice. The increase in α -cell mass was associated with increased mTORC1/phospho-S6 signaling in α -cells of control mice treated with STZ. Surprisingly, β -cell ablation after Streptozotocin (STZ) treatment of α TSC2^{KO} showed that these mice exhibited further increase in glucagon levels, but had lower blood glucose levels compared to the hyperglycemic STZ-treated controls. The mRNA expression levels of glucagon receptor and gene targets involved in gluconeogenesis (*GCGR*, *PEPCK*, *G6Pase*), glycolysis (glucokinase) and fatty acid synthesis (fatty acid synthase) had a trend of increased hepatic expression in α TSC2^{KO} mice compared to controls after STZ.

In summary, our findings showed that gain of mTORC1 signaling in α -cells results in increased α -cell mass (hyperplasia and hypertrophy) and hyperglucagonemia in α TSC2^{KO} mice. Despite hyperglucagonemia, these mice had normal fed blood glucose levels and reduced fasting blood glucose, improved glucose tolerance and decreased hepatic glucose production. Surprisingly, β -cell destruction after Streptozotocin (STZ) treatment showed that these mice exhibited further increase in glucagon levels, but have decreased blood glucose compared to the hyperglycemic STZ-treated controls. These studies demonstrated that activation of mTORC1 signaling in α -cells is sufficient to induce α -cell mass expansion and hyperglucagonemia. However, it remains unclear what downstream molecular mechanisms are responsible for the mTORC1-dependent increase in α -cell size and proliferation and increased glucagon content.

CHAPTER 4

Conclusions and Future Directions

The presented studies revealed a novel role of mTOR complex 1 (mTORC1) as a major regulator of α -cell mass and glucagon secretion. By ablating mTORC1 activity by generating mice deficient of *raptor* exclusively in the α -cell, we revealed that mTORC1 potentiates glucagon secretion in the fasting state by modulation of K_{ATP} channels and glucagon expression. A novel mTORC1/FoxA2 axis provided a link between mTORC1 and transcriptional regulation of key genes responsible for α -cell function (Figure 21). Furthermore, we also found that mTORC1 signaling promotes the maintenance of islet α -cells by an autophagy-mediated process (Figure 21). Streptozotocin-ablation of β -cells ablation revealed that α -cell mass expansion is associated with an increase in mTORC1 activity. In following studies we showed that increased mTORC1 activity in α -cells by deletion of *TSC2*, a negative mTORC1 regulator, resulted in severe hyperglucagonemia as a result of increased α -cell mass. Despite hyperglucagonemia, these mice had fasting hypoglycemia, improved glucose tolerance and decreased gluconeogenesis. However, the molecular mechanisms responsible for mTORC1-dependent increase in α -cell size and proliferation and increased glucagon content remain unclear.

The findings that decrease in mTORC1, as shown by α Raptor^{KO} mice, is important to promote glucagon secretion and plays a role in α -cells during fasting is counterintuitive, as this complex is mostly inactive during starvation. However, it is possible that the physiological increase in circulating amino acids during fasting could provide stimulatory signals to increase mTORC1 in α -cells and consequently, to increase glucagon

secretion. The amino acids glutamine, lysine, leucine, tyrosine and cysteine plasma concentrations increase in fasting and some of these amino acids, particularly glutamine, are potent stimulants for glucagon secretion (Daniel et al., 1977; Marroqui et al., 2014). To this end, we have observed that mTORC1 activity is increased in α -cells during hypoglycemia, but not mTORC1 activity is blunted in α -cells in the fed state. Future studies will evaluate the role of glutamine in mTORC1-dependent activation in α -cells during fasting conditions. Our conclusions are consistent with a model in which mTORC1 is active and essential for nutrient-induced glucagon secretion in α -cells during fasting. Therefore, mice with lack of mTORC1 signaling represent α -cells “stuck” in the fed state and therefore their response to fasting is blunted. Increasing mTORC1 signaling, as in α TSC2^{KO} mice, presents a model of α -cells “stuck” in the fasting state that have a consistent signal to increase glucagon secretion. We also hypothesize that the increase in α -cell mass in α TSC2^{KO} mice is secondary and in response to the increased demand of glucagon secretion due to a constitutively active mTORC1.

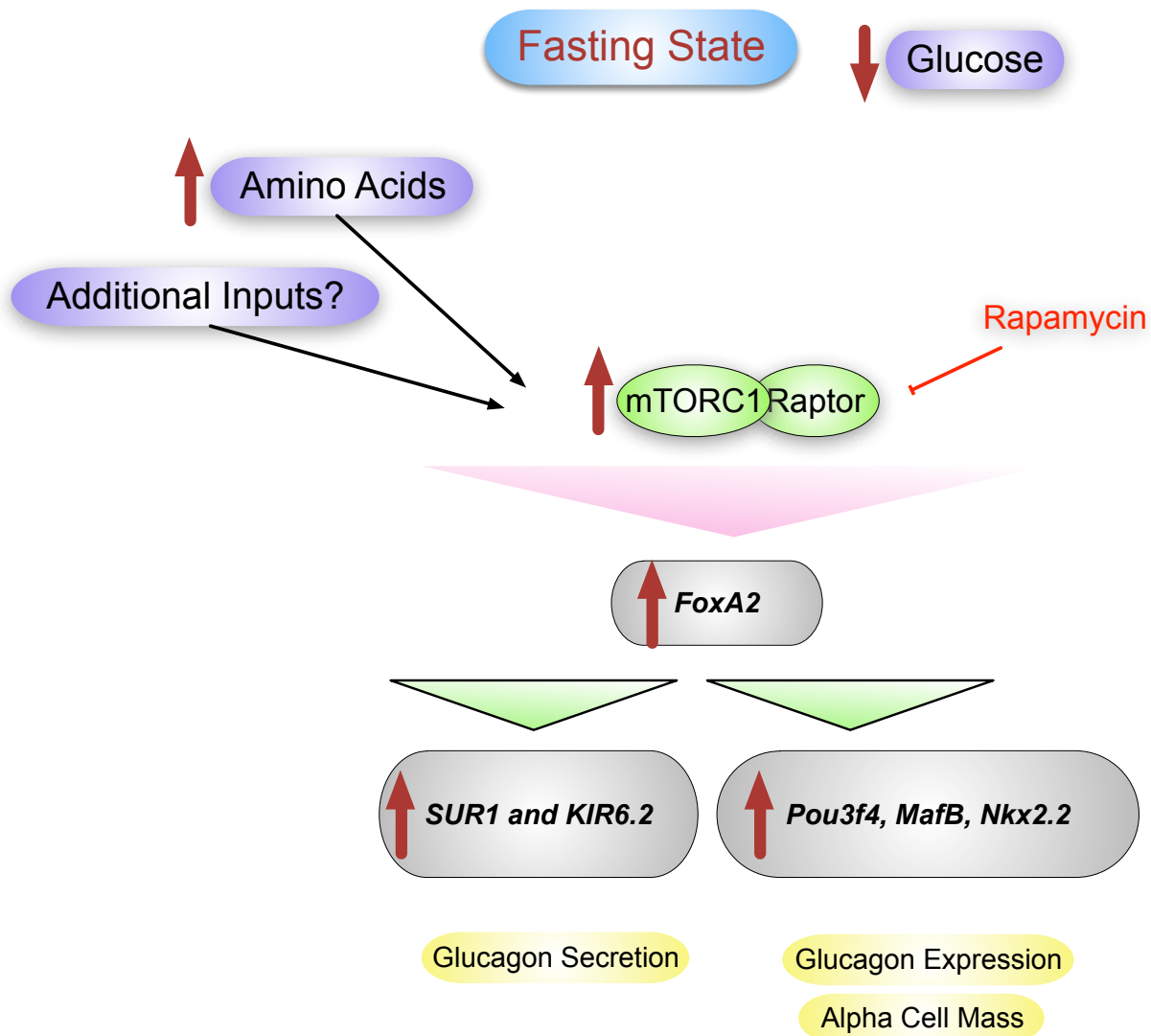


Figure 21. mTOR complex 1 (mTORC1) is a major regulator of α -cell mass and glucagon secretion. Using mice deficient of *raptor* exclusively in α -cells, we revealed that mTORC1 potentiates glucagon secretion in the fasting state by promoting K_{ATP} channels and glucagon expression. A novel mTORC1/FoxA2 axis provided a link between mTORC1 and transcriptional regulation of key genes responsible for α -cell function. Furthermore, we also found that mTORC1 signaling modulates the maintenance of islet α -cells by an autophagy-mediated process.

Chapter 2: Nutrient signaling maintains alpha cell mass and promotes K_{ATP} channel-dependent regulation of glucagon secretion

Despite very low circulating levels of glucagon and low α -cell mass, the α Raptor^{KO} mice had an increased circulating fed active GLP-1 levels. The β -cell mass of these animals were comparable to the controls at 2 months of age; however, by 8 months the β -cell mass was much higher in the α Raptor^{KO} compared to controls. In addition, the pancreas weight (particularly the exocrine pancreas weight) was increased in α Raptor^{KO} mice at 2 months of age. Studies have shown that GLP-1 increases β -cell mass and pancreas weight (Brubaker and Drucker, 2004; Kim et al., 2003; Rolin et al., 2002; Stoffers et al., 2000; Wang et al., 2004). Therefore, the increase in active GLP-1 levels could contribute to the increased pancreas weight at 2 months and increased β -cell mass in older α Raptor^{KO} mice. The presence of intra-islet GLP-1 has been proposed by recent studies (summarized in (Fava et al., 2016)). The total pancreatic active GLP-1 content at 2 and 8 months was lower in α Raptor^{KO}, ruling out the possibility that the increased circulating active GLP-1 was of pancreatic origin and a result of abnormal proglucagon processing within the α -cell. However, this data supports that the majority of intra-islet GLP-1 comes from α -cells. We measured active GLP-1 levels in intestinal extracts from 2-month old mice, and our data showed that α Raptor^{KO} mice have increased active GLP-1 levels. Therefore, we concluded that the increase in circulating active GLP-1 levels α Raptor^{KO} mice is of intestinal origin. However, it still remains unknown as to why active GLP-1 levels were increased in an animal model of low α -cell mass and glucagon levels. Future studies will examine the response of plasma, pancreatic and gut active GLP-1 levels using toxin receptor-mediated α -cell knockout model by crossing Glucagon-Cre mice to mice expressing diphtheria toxin (DT) receptor. In addition to increased plasma active GLP-1 levels, increased plasma amino acids could also contribute to the increase in pancreas weight and β -cell mass in α Raptor^{KO} mice. Decreased glucagon availability and decreased hepatic glucagon signaling in α Raptor^{KO} mice could result in increased plasma amino acids which act as potent anabolic agents that could expand pancreas weight and β -cell mass. Future studies will evaluate the plasma amino acid levels in control and α Raptor^{KO} mice.

Contrary to the regulation of glucagon release in high glucose conditions, it has been shown that extrinsic paracrine signals (insulin/GABA, somatostatin) do not play a role in regulating glucagon secretion in low glucose concentration (1-6 mM) (Walker et al., 2011). Mice with genetic ablation of the insulin receptor in α -cells (α IRKO) have increased glucagon levels in the fed state, with no differences detected during fasting. However, data from α IRKO mice also show that inhibiting insulin signaling in the pancreatic α -cells does not prevent an increase in glucagon levels after Streptozotocin (STZ)-induced hypoinsulimic-hyperglycemia. This suggests that insulin is necessary for inhibiting glucagon secretion in hyperglycemia; however, other signaling mechanisms likely contribute to an increase in glucagon levels in STZ-model of diabetes (Kawamori and Kulkarni, 2009). Further, mild hyperglycemia in α IRKO mice can be reversed with phloridzin without restoration of glucagon levels, showing that glucopenia does not contribute to rise in glucagon levels (Kawamori and Kulkarni, 2009). In order to further evaluate whether the role of mTORC1 signaling in α -cells is insulin-dependent, we induced hypoinsulimic-hyperglycemia in α Raptor^{KO} and α Raptor^{HET} mice using STZ. STZ-induced diabetes has been a well-characterized model for the study of α -cell mass expansion and increase in circulating glucagon levels (Plesner et al., 2014; Zhang et al., 2012). Particularly interesting, we found that mTORC1 signaling is enhanced in α -cells from control mice treated with a single, high dose of STZ. Our findings showed that hypoinsulimic-hyperglycemia did not promote an increase in mass and glucagon levels from the remaining α -cells of α Raptor^{KO} mice. Although, this was partly expected because α Raptor^{KO} mice have a substantial loss of α -cell mass, a study had shown that two percent of remaining α -cells (after an extreme loss of α -cell mass) is sufficient to produce enough glucagon and maintain normal glucagonemia (Thorel et al., 2011). The partial inhibition of mTORC1 signaling in α Raptor^{HET} mice was not sufficient to fully rescue the increased cell mass and glucagon levels following STZ. These data show that partial ablation of mTORC1 signaling in α Raptor^{HET} mice inhibits glucagon response during hypoglycemia and neuroglycopenia, but is not sufficient to prevent the rise in glucagon levels in a model of STZ-diabetes. Taken together, further studies utilizing an inducible model of complete mTORC1 inhibition in adult mice, are needed to sufficiently show whether α -cell mass expansion and glucagon increase following STZ treatment

are mTORC1-dependent. Further, future studies will examine the distinct or culminating roles of insulin receptor and mTORC1 signaling in promoting α -cell mass expansion and glucagon increase in the STZ model.

Chapter 3: Deletion of Tuberous Sclerosis Complex 2 (TSC2) in alpha cells results in hyperglucagonemia and alpha cell hypertrophy in the absence of diabetes

Recent studies have shown that glucagon increased energy expenditure in humans, similarly to that of cold-activation but independent of brown adipose fat (Salem et al., 2016). Body weight was significantly reduced in young α TSC2^{KO} mice and persisted through the lifespan of these mice. Food intake and activity measurements revealed that α TSC2^{KO} mice had increased activity compared to controls and no changes were detected in food intake. The central nervous system integrates nutrient signals to the regulation of energy balance by the mediobasal hypothalamus. Studies have shown that mTORC1 activation in the caudomedial nucleus of solitary tract (NTS) in the brainstem decreases food intake and body weight (Blouet et al., 2009; Blouet et al., 2008; Blouet and Schwartz, 2012). Assessment of *Cre*-recombination in CNS revealed that *Cre*-expressing neurons are present in the brainstem and dorsomedial hypothalamic nucleus (DMH), which could contribute to changes in feeding and activity levels. The central nervous system integrates nutrient signals to the regulation of energy balance by the mediobasal hypothalamus. Studies have shown that mTORC1 activation in the caudomedial nucleus of solitary tract (NTS) in the brainstem decreases food intake and body weight (Blouet et al., 2009; Blouet et al., 2008; Blouet and Schwartz, 2012). Based on these data, increased mTORC1 in in the DMH and brainstem could drive the decrease we see in body weight and increased activity levels of α TSC2^{KO} mice. However, increased plasma levels of glucagon could be directly acting in the CNS to decrease body weight in α TSC2^{KO} mice. Importantly, recent study has shown that chronic glucagon receptor signaling agonism is coupled with increased locomotor activity, in agreement with our data showing increased activity levels of α TSC2^{KO} mice (Habegger et al., 2013). Additional studies will dissect the role of 1) *Cre*-expression in brain and 2) the increase in plasma glucagon levels in regulating the decrease in body

weight of α TSC2^{KO} mice. In addition, further measure the respiration quotient and energy expenditure of α TSC2^{KO} and control mice.

Increased glucagon levels increase gluconeogenesis and glycogenolysis in control mice; however α TSC2^{KO} mice were hyperglucagonemic, but had reduced fasting glycemia. These data were puzzling and therefore we examined if the increased glucagon levels detected in α TSC2^{KO} mice were result of abnormal proglucagon processing. We did not detect any changes in fed or fasting active GLP-1 levels between α TSC2^{KO} and control mice, suggesting lack of abnormal proglucagon processing. Further analysis of PC2 mRNA and protein expression in α -cells from α TSC2^{KO} and control mice is needed to fully exclude the role of abnormal proglucagon processing as result of increased mTORC1 signaling in α -cells. Based on our data, we suggest that chronic hyperglucagonemia in α TSC2^{KO} mice may lead to decrease in hepatic glucagon signaling and gluconeogenesis, contributing to decreased fasting blood glucose levels and improved glucose tolerance. In addition, our data suggest that the role of glucagon in inhibiting glucokinase and suppressing glycogenolysis and glucagon's suppression of plasma free fatty acid levels is preserved and consistent with increased levels of fed glucagon in α TSC2^{KO} mice. Hepatic insulin sensitivity was not increased in α TSC2^{KO} and therefore does not contribute to the improvement in glucose tolerance. Additional studies will determine the adaptation of fasting on hepatic glycogen content and the expression of these genes in α TSC2^{KO} and controls. We will further measure glucagon signaling by exogenous administration of glucagon in controls and α TSC2^{KO} and analyze glucagon-signaling activation in the liver. In addition, we will evaluate the role of hyperglucagonemia on β -cell function to test whether alterations in insulin secretion are contributing to the improved glycemia in this mouse model.

The present data suggest that chronic hyperglucagonemia in α TSC2^{KO} mice leads to decreased hepatic glucagon signaling and gluconeogenesis contributing to decreased fasting blood glucose levels and improved glucose tolerance; however, the mechanism responsible for these effects is unknown. Recent study has shown that elevated plasma glucagon levels as a result of high-protein feeding lower blood glucose levels and

hepatic glucose production *via* the CNS (LaPierre et al., 2015). These data show that elevated circulating glucagon levels act in the brain to lower plasma glucose levels and the same mechanisms could be play a role in the decreased hepatic production of α TSC2^{KO} mice. The actions of glucagon to reduce body weight through decreased adipose tissue expansion and increase energy expenditure requires FGF-21 in mice. Activation of the glucagon receptor leads to increased plasma FGF-21 levels and hepatic *FGF-21* RNA (Habegger et al., 2013). Interestingly, a recent study has shown that pancreatic β and α -cells produce and secrete FGF21 (Omar et al., 2014). Inhibition of the glucagon receptor in the global glucagon receptor knock out mice results in α -cell hyperplasia and hyperglucagonemia and increased plasma FGF21 levels, which improved glucose tolerance in these mice in an insulin-independent manner. It is possible that the improvement in glucose homeostasis in the α TSC2^{KO} mice could be mediated by increase in FGF21 levels. Future studies will be designed to determine if the effects on body weight, improved glucose tolerance and decreased hepatic production of α TSC2^{KO} mice are dependent on glucagon signaling and the regulation of plasma, α -cell and hepatic expression levels of FGF21.

Previous data showed that complete ablation of β -cells and insulin levels by Streptozotocin (STZ) administration results in significant increase in α -cell mass and glucagon levels and the development of severe hyperglycemia in control mice (Chapter 2, Figure 11). The increase in α -cell mass was associated with increased mTORC1/phospho-S6 signaling in α -cells of control mice treated with STZ. Surprisingly, β -cell ablation after Streptozotocin (STZ) treatment of α TSC2^{KO} lead to an increase in glucagon levels but lower blood glucose levels compared to the hyperglycemic STZ-treated controls. The mRNA expression levels of glucagon receptor and gene targets involved in gluconeogenesis (*GCGR*, *PEPCK*, *G6Pase*), glycolysis (glucokinase) and fatty acid synthesis (fatty acid synthase) had a trend of increased expression in α TSC2^{KO} mice compared to controls after STZ. Ultimately, the number of animals in this experiment will need to be increased for complete analysis of the role of hyperglycemia-hyperinsulinemia in the glycemic response of this model of hyperglucagonemia.

CHAPTER 5

Clinical Implications

Rapalogs (rapamycin analogs) are FDA-approved drugs that suppress mTORC1 activity and are routinely used as immunosuppressants in transplantation surgeries and for the treatment of several malignancies. The findings presented in these studies show that rapamycin treatment decreases islet glucagon content and glucagon secretion in response to hypoglycemia. These data could have major clinical implications in responses to hypoglycemia in post-transplant diabetics. Further, these data could perhaps explain the defects in counterregulation of blood glucose in response to hypoglycemia in patients after islet transplantation surgeries that are under chronic immunosuppression therapy with rapamycin analogs (Paty et al., 2002; Rickels et al., 2007).

Rapalogs have also been linked to the development of new-onset diabetes by clinical and animal studies (Bussiere et al., 2006; Gyurus et al., 2011; Kulke et al., 2009; Larsen et al., 2006). Based on our data, we rapalogs do not cause hyperglycemia and new-onset diabetes by increasing glucagon levels. However, it is important to highlight that inhibiting mTORC1 in α -cells leads to decreased glucagon content and glucagon secretion in hypoglycemia, because that proposes a major challenge in employing insulin therapy and maintenance proper glucose control of these patients.

Despite the increasing number of oral medications becoming available, Sulfonylurea derivatives have been a mainstay approach for enhancing insulin secretion in diabetic patients. Sulfonylureas increase insulin secretion by blocking ATP-sensitive K^+ (K_{ATP}) channels *via* binding to SUR subunit of the channels. Sulfonylurea therapy has also been linked to increased episodes of hypoglycemia, which has been attributed to the increased insulin levels. However, clinical and animal studies have shown that acute administration of Sulfonylurea derivatives blunts the glucagon response to hypoglycemia (Efendic et al., 1979; Ostenson et al., 1986; ter Braak et al., 2002). Therefore, it should be noted that further consideration should be taken into the treatment approach of new-onset diabetes in patients who are undergoing immunosuppressive treatment by rapalogs, as these may create a dangerous predisposition to hypoglycemic episodes.

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