

ENDOPLASMIC RETICULUM CALCIUM DYNAMICS AND INSULIN
SECRETION IN PANCREATIC β CELLS

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Under normal conditions, ER Ca^{2+} levels are estimated to be at least three orders of magnitude higher than intracellular Ca^{2+} . This steep Ca^{2+} concentration gradient is maintained by the balance of Ca^{2+} uptake into the ER via the sarco-endoplasmic reticulum Ca^{2+} ATPase (SERCA) pump and ER Ca^{2+} release through Ryanodine receptors (RyR) and Inositol 1,4,5-triphosphate (IP_3) receptors (IP_3R). Emerging data suggest that alterations in β cell ER Ca^{2+} levels lead to diminished insulin secretion and reduced β cell survival in both type 1 and type 2 diabetes. However, the mechanisms leading to β cell ER Ca^{2+} loss remain incompletely understood, and a specific role for either RyR or IP_3R dysfunction in diabetes has been largely untested. To this end, we applied intracellular and ER- Ca^{2+} imaging techniques in INS-1 β cells and isolated mouse and human islets to define whether RyR or IP_3R activity were altered under diabetogenic conditions. Results revealed preferential alterations in RyR function in response to ER stress, while pro-inflammatory cytokine stress primarily impacted IP_3R activity. Consistent with this, pharmacological inhibition of RyR and IP_3Rs prevented ER Ca^{2+} loss under ER and pro-inflammatory stress, respectively. However, RyR inhibition was unique in its ability to prevent β cell death, delayed initiation of the unfolded protein response (UPR), and dysfunctional glucose-induced Ca^{2+} oscillations in tunicamycin-treated INS-1 β cells and islets from Akita mice. Monitoring at the single cell level revealed that ER stress acutely increased intracellular Ca^{2+} transients and this was dependent on both ER Ca^{2+} leak from the RyR and plasma membrane depolarization, suggesting ER Ca^{2+} dynamics regulate cellular excitability. Collectively, our findings

suggest that ER-stress induced RyR dysfunction regulates β cell ER Ca^{2+} dynamics, propagation of the UPR, insulin secretion, and cell survival. These data indicate that RyR-mediated loss of ER Ca^{2+} and β cell hyperexcitability may be early pathogenic events in diabetes.

Carmella Evans-Molina, M.D., Ph.D, Chair

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LIST OF ABBREVIATIONS

ATF4	Activating transcription factor 4
ATF6	Activating transcription factor 6
ATP	Adenosine triphosphate
APCs	Antigen presenting cells
BABYDIAB	Baby Diabetes
Bim	Bcl-2-interacting mediator of cell death
Ca ²⁺	Calcium
CaMKII	Ca ²⁺ /calmodulin dependent protein kinase II
cAMP	Cyclic AMP
CICR	Ca ²⁺ induced Ca ²⁺ release
CPVT	Catecholaminergic polymorphic ventricular tachycardia
Cx36	Connexin 36
DIPP	Diabetes Prediction and Prevention Project
DPP4	Dipeptidyl peptidase-4
EC	Electrical – contraction
ER	Endoplasmic reticulum
ERAD	ER-associated degradation
GWAS	Genome-wide association studies
GAD	Glutamic acid decarboxylase
GICOs	Glucose-induced Ca ²⁺ oscillations
GIP	Glucose-dependent insulinotropic polypeptide
GLP-1	Glucagon-like peptide-1
Glut	Glucose transporters

GPDH	Glycerophosphate dehydrogenase
GPCR	G protein coupled-receptor
IA2	Islet antigen 2
IGF2	Insulin-like growth factor 2
IL-1 β + HG	Interleukin 1 β combined with high glucose
Ins	Islet proteins
IP ₃	Inositol 1,4,5-triphosphate
IP ₃ R	Inositol 1,4,5-triphosphate receptors
IRE1	Inositol-requiring enzyme 1
JNK	c-Jun N-terminal kinase
K _{ATP} channels	ATP-sensitive K ⁺ channels
LETM1	Leucine- zipper EF-hand-containing transmembrane protein 1
MCU	Mitochondrial Ca ²⁺ uniporter
NCLX	Na ⁺ /K ⁺ /Ca ²⁺ -exchange protein 6
NCX	Na ⁺ /Ca ²⁺ exchanger
Ngn3	Neurogenin-3
Pdx-1	Pancreatic and duodenal homeobox 1
PERK	PKR-like ER kinase
PKA	Protein kinase A
PKG	cGMP-dependent kinase
PMCA	Plasma membrane Ca ²⁺ ATPase
PPAR- γ	Peroxisome proliferator-activated receptor gamma
RyR	Ryanodine receptors
SERCA	Sarco-endoplasmic reticulum Ca ²⁺ ATPase
SNS	Sympathetic nervous system

SOICR	Store overload induced Ca^{2+} release
SR	Sarcoplasmic reticulum
SSTR2	Somatostatin receptor 2
T1DM	Type 1 diabetes mellitus
T2DM	Type 2 diabetes mellitus
TEDDY	the Environmental Determinants of Diabetes in the Young
T_{eff}	Effector T cell
TM	Tunicamycin
T_{reg}	Regulatory T cell
UPR	Unfolded protein response
VDCCs	Voltage-dependent Ca^{2+} channels
V_m	Membrane potential
XBP1	X-box binding protein 1
ZnT8	Zinc transporter 8

Chapter 1. Introduction

1.1 Diabetes Mellitus and Pancreatic β Cells

Diabetes Mellitus is an important public health concern that affects the health and prosperity of individuals throughout the world. According to data from the International Diabetes Federation, 415 million adults aged 20-79 were affected by diabetes in 2015, whereas another 318 million adults had impaired glucose tolerance with an associated increased risk of developing diabetes (1). Moreover, the number of adults with diabetes is expected to increase to approximately 642 million in 2040, accounting for nearly 1 in 10 individuals. Annually, diabetes is estimated to cause over 5 million deaths, and the financial burden of this disease is enormous. It is estimated that diabetes accounts for 5 – 20% of the total health care expenditures of an individual country. In the US, 29.3 million adults had diabetes in 2015, and diabetes-related expenditures were estimated at 320 millions US dollars. To reverse these trends, improvements are needed in the prevention, diagnosis, management, and treatment of diabetes. Given the close association between obesity and Type 2 diabetes, continued efforts focused on lifestyle and improvements in nutrition are required. To stem the tide of Type 1 diabetes, an improved understanding of disease triggers and the identification of agents that both prevent immune activation and improve the health of the β cell will be needed.

The research in this thesis will explore the mechanisms underlying failure of pancreatic β cells in diabetes with an emphasis on dysregulated calcium storage in the endoplasmic reticulum, an intracellular organelle that is crucial for insulin biosynthesis by the pancreatic β cell and normal control of blood glucose.

1.1.1 The main forms of Diabetes: Type 1 and Type 2 Diabetes Mellitus

The hallmark of diabetes mellitus is an elevated blood glucose level (hyperglycemia) that occurs secondary to either a complete or relative deficiency of insulin secretion and/or insulin action. Insulin is a hormone produced solely by the pancreatic β cells that activates glucose transport into cells via glucose transporters, where it is utilized as a source of energy. In the case of insulin deficiency or impaired insulin action, peripheral tissues cannot efficiently take up glucose. The resulting hyperglycemia damages a number of tissues, resulting in diabetic macrovascular complications (i.e heart disease and stroke) and several microvascular complications, including, kidney failure, retinopathy, and neuropathy.

Diabetes is a heterogenous disease, rarely caused by single gene mutations (2) and is typically caused by a diverse input of many modest influences dictated by environment, lifestyle, aging, and genetics. The two main subtypes of diabetes are phenotypically categorized as Type 1 and Type 2 diabetes mellitus (3,4). Type 1 diabetes (T1DM) is an autoimmune disease characterized by auto-immune mediated β cell destruction and a nearly complete absence of insulin production. T1DM accounts for 5 – 10% of all cases of diabetes. To regulate blood glucose and decrease diabetes-associated complications, persons with T1DM must administer multiple daily injections of exogenous insulin or wear an insulin pump that delivers continuous insulin infusions subcutaneously (5).

T1DM is characterized by β cell destruction that is mediated by islet infiltrating autoreactive immune cells (6). The mechanism of T1DM is not fully understood. However, it is generally accepted that insufficient T regulatory cells (Treg) suppression of effector T cells (Teff) that target the β cells is an early pathogenic event in T1DM (7). More recently it has been appreciated that β cell failure also contributes to T1DM pathogenesis (8). Clinically, T1DM is typically first detected by the onset of severe

hyperglycemia that may also be accompanied by ketoacidosis. A hallmark of T1DM is the presence of circulating autoantibodies against key autoantigens including insulin, islet antigen 2 (IA2), glutamic acid decarboxylase (GAD), and zinc transporter 8 (ZnT8). Individuals at risk of developing T1DM are identified by the presence of these autoantibodies at a time prior to the onset of clinically significant hyperglycemia (9).

What triggers the autoimmune attack against the β cells in T1DM remains unclear. However, T1DM is thought to arise in genetically susceptible individuals in response to an environmental or viral triggering event that initiates the autoimmune response. A family history of T1DM plays an important role in determining risk. For first-degree relatives, the risk of T1DM is estimated to be approximately 3 – 8%, depending on whether an individual's mother, father, or a sibling has T1DM (10,11). In addition, human leukocyte antigen serotype *HLA-DR3-DQ2* and *HLA-DR4-DQ8* class II haplotypes are known to be robustly associated with T1DM, and 90% of children with T1DM have one or both of these haplotypes (12,13). Other than the *HLA* Class II locus, other genetic variants have been associated with T1DM risk. These include differences in the variable number of tandem repeat regions in the insulin gene (14) and polymorphisms in the *CTLA-4* gene that negatively regulate immune responses (15), variants in protein tyrosine phosphatase, non-receptor type 22, *PTPN22*, encoding the lymphoid protein tyrosine phosphatase that negatively regulates the T-cell receptor (16), and *IL2RA* that forms the IL-2 receptor complex with CD25 expressed on activated T-cells and on regulatory T-cells (Tregs) (17).

The pathogenesis of T1DM begins with the interactions of the innate and adaptive immune system with β cells. Initially, islet resident antigen presenting cells (APCs) such as macrophages and dendritic cells receive and process islet antigens. As a consequence, APCs migrate to pancreatic lymph nodes (15). Within the lymph nodes, islet antigens are presented to and activate naïve circulating autoreactive T cells. This

causes T cell activation and initiates immune cell infiltration into the islet (18). Increased levels of pro-inflammatory and toxic cytokines and chemokines are released from resident APCs, infiltrating T cells, and the β cells themselves, causing additional immune cell recruitment into the islet (19). These cytokines indirectly cause β cell death, while further β cell death occurs through direct interactions between CD8⁺ T cells and the β cell (20,21).

Currently a number of prevention efforts are being tested in individuals who already have established autoimmunity and autoantibody positivity. Prevention efforts are also being tested in birth cohorts identified on the basis of genetic risk, who are then followed longitudinally to identify both environmental contributors as well as patterns of immune activation before and after antibody seroconversion (5). Studies include the Environmental Determinants of Diabetes in the Young (TEDDY) (22), Baby Diabetes (BABYDIAB) (23), Diabetes Prediction and Prevention Project (DIPP) (24), and the double-blind, placebo-controlled, dose-escalation, phase 1/2 clinical pilot study (Pre-POINT studies) (25).

A number of recent studies have also tested immunomodulatory therapies to either prevent T1DM. These include efforts focused on restoration of tolerance (26,27), T cell or B cell inhibition (28), T_{reg} induction (29), suppression of innate immunity and inflammation (4,30), immune system reset (31), and islet transplantation (32). Trials have tested antigen-specific therapies to induce immune tolerance (33), monoclonal antibodies (28,34,35) and fusion proteins (36,37) that target specific immune cells, and strategies to alter the effector T cell (T_{eff})/T_{reg} balance. Overall, each treatment has limited duration of effect, and no single therapy has stopped the autoimmune attack on β cells.

Given these disappointing outcomes, there has been a recent emphasis on testing a combination of therapies at T1D onset. (6). Additionally, there is an emphasis

on testing prevention efforts in individuals who already have established autoimmunity and autoantibody positivity, but lack clinical hyperglycemia. Prevention efforts are also being tested in birth cohorts identified on the basis of genetic risk, who are then followed longitudinally to identify both environmental contributors as well as patterns of immune activation before and after antibody seroconversion (5).

Type 2 diabetes (T2DM) is the most common form of diabetes and accounts for 90 – 95% of all diabetes cases. Similar to T1DM, the exact cause of this disease is still unknown but risk factors include obesity, poor nutrition, physical inactivity, smoking, (38) and a variety of genetic factors (3,38). Classically, T2DM begins with peripheral insulin resistance, in which glucose uptake and the metabolic effects of insulin are decreased in all tissues in body (39). In the setting of obesity, insulin resistance, and high fat diet lead to increased release of free fatty acids from the adipose tissue, which further exacerbate glucose uptake into muscle. A second key contributing factor is increased gluconeogenesis at the level of the liver that also worsens hyperglycemia (40).

Initially, β cells are able to overcome insulin resistance through increased insulin production and secretion. However, as T2DM progresses, β cell dysfunction ensues and insulin secretion from the β cells begins to diminish (41). In addition to gluco-lipotoxicity as a primary cause of β cell failure (42), emerging areas of research have focused on pathways leading to pro-inflammatory stress or ER stress (43), and oxidative stress in the β cells (44). Recently, dedifferentiation, which is defined as loss of expression of key β cell specific genes has been proposed as a cause of T2DM (45,46).

Genome-wide association studies (GWAS) have identified a number of risk variants associated with T2DM risk. Susceptibility loci identified to date have primarily been linked to the regulation of β cell function (38). For example, polymorphisms have been identified in the *KCNJ11* gene that encodes the potassium inwardly rectifying

channel subfamily J, member 11 (38,45-47). In addition, variants in *TCF7L2* have been identified. This gene encodes the ubiquitous transcription factor 7-like 2 (48), a mediator of Wnt signaling (49) and inhibitor of insulin secretion (50). Polymorphisms have also been identified in the *IRS1* gene that encodes insulin receptor substrate 1. *IRS1* plays a role in β cell health and function as well as peripheral insulin signaling (51). Islets from *IRS1* knock-out mice and *IRS1* deficient β cells exhibited decreased insulin content and reduced glucose stimulated insulin secretion (52). Variants in *MTNR1B* gene, which encodes the melatonin receptor 1B, is thought to increase the risk of T2DM by inducing impaired early insulin secretion (53).

Polymorphisms have also been identified in genes with more pleiotropic metabolic effects. The *PPARG2* gene encodes peroxisome proliferator-activated receptor gamma (PPAR- γ) 2, which is a member of the nuclear hormone receptor subfamily. PPAR- γ is thought to regulate insulin action, but has also been shown to be expressed in the β cell. Agonists of PPAR- γ improve insulin sensitivity and have been associated with improved β cell function. Our lab has previously shown that PPAR- γ regulates transcription of the ER Ca^{2+} transporter Sarco-endoplasmic reticulum Ca^{2+} ATPase (SERCA) 2 level in the β cell, leading to improved β cell Ca^{2+} signaling and ER Ca^{2+} storage (54), which will be discussed later. Additional risk variants have been identified in the *IGF2BP2* gene that encodes the insulin-like growth factor two binding protein 2 and regulates translation of the insulin-like growth factor 2 (IGF2), and the fat mass and obesity-associated gene, *FTO*, which is associated with obesity and weight gain (55).

1.1.2 Therapy for Type 1 and Type 2 Diabetes Mellitus

The treatment of T2DM is complicated and often requires multiple agents to achieve glycemic control. Treatment is typically initiated with an oral agent, and the first line agent for most newly diagnosed individuals with T2DM is the biguanide metformin

(56). The precise molecular mechanisms of metformin action are not fully understood. However, this drug is thought to primarily lower blood glucose levels by reducing hepatic glucose output through reduced gluconeogenesis. The use of metformin has also been associated with increased insulin induced glucose uptake and increased glycogenesis in skeletal muscle (57). Metformin has been shown to regulate the expression of genes related to hepatic gluconeogenesis through activation of AMP-activated protein kinase (AMPK) (58,59). Additionally, recent data have shown that metformin inhibits mitochondrial glycerophosphate dehydrogenase (GPDH) to alter the hepatocellular redox state, which result in reduced gluconeogenesis (60). Other advantages using metformin include reduced cardiovascular events, decreased mortality (61,62), and lower risk of hypoglycemia using this drug (63).

Other commonly utilized oral agents include sulfonylureas, which close the ATP-sensitive potassium channel of the pancreatic β cells to stimulate insulin secretion (64). However, the effect of sulfonylureas depends on the presence of enough functional β cells to increase insulin secretion, and diabetes progression is typically associated with failure to respond to sulfonylureas. Adverse effects of these medications include an increased risk of hypoglycemia (65) and weight gain. The risk of hypoglycemia is higher for older persons with impaired renal and hepatic function (66).

Incretins are a group of hormones that decrease blood glucose levels by promoting insulin secretion. Incretin-based therapies have been introduced in recent years. The incretin hormones include glucagon-like peptide-1 (GLP-1), primarily arise from the intestinal enteroendocrine L cells (67), and glucose-dependent insulinotropic polypeptide (GIP), which are released in response to a meal, leading to increased insulin secretion. Incretin secretion is dramatically diminished in T2DM (68,69). In T2DM, administration of supraphysiological amounts of GLP-1 can lead to enhanced glucose-stimulated insulin secretion, whereas administration of GIP does not induce insulin

secretion regardless of the concentration utilized (70). Therefore, GLP-1 is therapeutically more favored than GIP, and inhibitors of dipeptidyl peptidase-4 (DPP-4), the enzyme that degrades GLP-1, have been developed for clinical use (71,72).

Plasma levels of GLP-1 are relatively low compared to other hormones, and GLP-1 has a very short half-life due to DPP4 activity. GLP-1 is metabolized within 1 minute around the L cells (73,74), which generated considerable controversy as to the source of GLP-1 that acts on distant organs such as the pancreatic β cells. Recently, an updated model was proposed whereby GLP-1 derived from the L cells activates neurons to regulate insulin secretion, and GLP-1 derived from islet α cells serves as paracrine factor to induce insulin secretion in β cells (75).

As described, GLP-1 has a short half-life due to DPP-4 activity, so the effects of GLP-1 by subcutaneous injections were very short-lasting (76). That led to the development of inhibitors of DPP-4, or stable DPP-4 resistant GLP-1 analogs (77). Exendin 4, isolated from *Heloderma suspectum*, is a peptide that has 50% sequence homology to GLP-1. This peptide was found to be resistant to DPP-4 activity and is eliminated only by glomerular filtration by the kidney (78), thereby increasing the plasma half-life of Exendin 4 to as long as 30 minutes (79).

Other orally active agents include α -glucosidase inhibitors, which inhibit breakdown and digestion of carbohydrates in the intestine, and thiazolidinediones (TZD), which activate PPARs, including PPAR gamma. These agents are less widely utilized and their clinical effects are summarized in Table 1. A large percentage of individuals with T2DM will eventually fail oral agents and incretin-based therapies and require insulin injections as β cell failure ensues (3).

A recent option to treat diabetes in morbidly obese patients is bariatric surgery, which either reduces the size of stomach to decrease food intake or re-routes the small intestine to cause malabsorption (80). Clinical studies show that blood glucose is often

normalized within a week of surgery, even prior to significant weight loss. At present, the exact mechanisms of improved glycemia in the short-term are not well understood but it is hypothesized that surgery leads to either increased release of GLP-1, alterations in gut microbiota, and the anticipated metabolic effects of acute and severe caloric restriction peri-operatively (3).

Table 1. Drug Treatment for Type 2 Diabetes

Class Name	Drug Name	Target	Action
α-glucosidase inhibitors (AGIs)	Acarbose	α-glucosidase	Carbohydrate absorption↓ No weight gain
	Miglitol		
	Voglibose		
Biguanides	Metformin	AMPK	Blood glucose↓ (60,61)
		GPDH	Insulin action↑
		(Still debated)	Hepatic output↓
			Cardiac risk↓
			Hypoglycemia Risk↓ No weight gain
GLP-1 Analog	Exenatide	GLP-1R	Insulin secretion↑ (81)
	Liraglutide		Glucagon secretion↓
			Satiety↑
			Hypoglycemia Risk↓ No weight gain
Sulfonylurea	Glyburide	K _{ATP} channels	Insulin secretion↑ (65) Weight ↑
	Glipizide		
	Gliclazide		
	Glimepiride		
Thiazolidinedione (TZDs)	Troglitazone	PPAR-γ	Insulin action↑ (82)
	Rosiglitazone		Hypoglycemia Risk↓
	Pioglitazone		Weight ↑ Glycemic control↑
Insulin	Lispro	Direct target	Blood glucose↓
	Aspart		Weight ↑
	Glulisine		

1.1.3 Pancreatic islet β cells, and other cell types

The endocrine pancreas consists of the islets of Langerhans that make up about ~5% of the total pancreatic mass. The endocrine islets were named for the German physician Paul Langerhans, who discovered the cells that secrete insulin. Islets consist of aggregates of ~1000 different cells. The insulin producing β cells make up ~75% of cells found in the islet. Additional cell types found in the islet include α cells, δ cells, PP cells and ϵ cells. The α cells consist of ~20% of total islet cells (83), and secrete glucagon. Glucagon is described as a counter-regulatory hormone to the effects of insulin and acts to raise blood glucose levels. Glucagon promotes gluconeogenesis in the liver and induces fatty acid oxidation and ketogenesis in the liver. The δ cells consist of less than 10% of islet cells (83), and these cells secrete somatostatin. Somatostatin receptors are expressed on both α and β cells, and the somatostatin receptor 2 (SSTR2) is the functionally dominant form of the receptor in humans and mice (84). The SSTR2 is a G_i -coupled G protein coupled-receptor (GPCR) that inhibits adenylyl cyclase activity and cyclic AMP (cAMP) generation. Activation of SSTR induces hyperpolarization of cells and thus suppression of glucagon and insulin secretion (84). In response to elevated blood glucose levels, insulin and somatostatin levels rise. Both insulin and somatostatin act on α cells to lower cAMP production and suppress glucagon secretion (85). Precisely how exactly these cells communicate *in vivo* remain to be completely understood.

Other endocrine cells in islet include the polypeptide-producing PP cells and ghrelin-producing ϵ cells, which consist of less than 5% and 1% of islet cells, respectively (83). The function of these cells is less understood in terms of regulation of β cell function. Ghrelin is known to inhibit insulin secretion (86) and also has activity as a “hunger hormone” by acting on hypothalamus (87).

The development and differentiation of the endocrine cell in the islet has been extensively studied using a variety of knockout mouse models. Neurogenin-3 (Ngn3) serves as the key marker for the endocrine pancreatic progenitor cell and is first expressed in the pancreatic buds around E9.5 in the mouse. Ngn3 expression is crucial for commitment to the endocrine cell lineage (88). Lineage-tracing studies have shown that Ngn3 positive cells serve as the precursor for all five endocrine cell subtypes (89). During this differentiation process, Ngn3 coordinates with the pancreatic and duodenal homeobox 1 (Pdx-1) transcription factor in a time specific manner (90). Additional research is needed to define the differentiation pathway to establish β cells from stem cells, elucidate transcriptional micro RNA and epigenetic factors that regulate β cell differentiation, establish signature of β cell “specific” gene expression, and delineate pathological changes in these areas that are causative or associated with diabetes.

1.1.4 Mechanisms of insulin secretion

A striking feature of the pancreatic β cell is its ability to monitor blood glucose on a minute to minute basis and to precisely match ambient glucose levels with regulated levels of insulin secretion to maintain euglycemia in the range of 3.9 – 5.5 mM. To accomplish this task, the β cell relies on several unique pathways to monitor blood glucose concentrations and regulate insulin release (Fig. 1) (91). Glucose transporters (Glut), mitochondrial ATP synthesis, closure of ATP-sensitive K^+ channels (K_{ATP} channels), Ca^{2+} influx from plasma membrane channels are all involved in this process and any disruption of any of these steps will lead to impaired insulin secretion.

β cells are electrically excitable, and they possess a variety of channels that modulate membrane potential (V_m) and Ca^{2+} influx. In response to an increase in plasma glucose, glucose first enters the β cell through Glut transporters. Glucose

metabolism in the mitochondria leads to an increase in the ATP/ADP ratio (92). The main regulators of β cell electrical activity are the K_{ATP} channels. Under low glucose conditions, K_{ATP} channels are open to induce a K^+ outward current to maintain plasma membrane hyperpolarization at $\sim -70\text{mV}$ (91). In β cells at rest, the constitutive hyperpolarizing K^+ efflux and the constitutive unknown background-depolarizing current are balanced to achieve the resting membrane potential. Under high glucose concentrations, an increase in the ATP/ADP ratio leads to K_{ATP} channel closure. The reduced hyperpolarizing current by the closure of K_{ATP} channels will be exceeded by background-depolarizing current to depolarize cells. The mechanism that induces this background-depolarizing current and whether that current is modulated by glucose per se are not well understood. It has been speculated that forward operation of the $\text{Na}^+/\text{Ca}^{2+}$ exchanger (93), Cl^- efflux, or Na^+ (94) or Ca^{2+} influx (95) through unknown channels are involved in this background-depolarizing current. This depolarization activates voltage-dependent Ca^{2+} channels (VDCCs), and the resulting Ca^{2+} influx triggers exocytosis of insulin vesicles and insulin secretion. Action potentials generated by this process are primarily result from Ca^{2+} influx in mice. However, a Na^+ current is also involved in human and rat β cells.

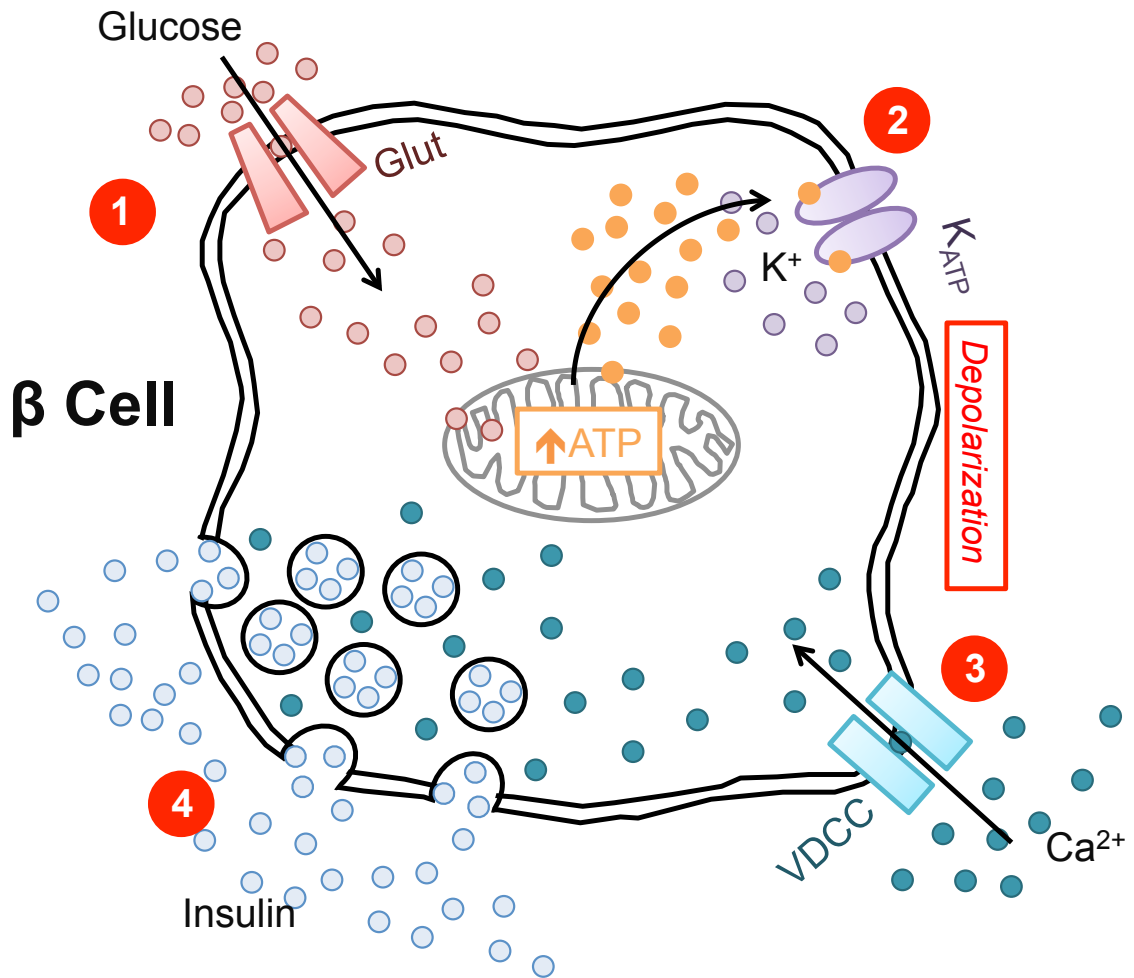


Figure 1. Molecular mechanisms of insulin secretion in the pancreatic β cells.

(1) Glucose uptake occurs through the Glut glucose transporters, and glucose is metabolized to produce adenosine triphosphate (ATP). (2) The increase in ATP will close ATP-sensitive K^+ channels (K_{ATP}) to trigger depolarization. (3) VDCCs open and Ca^{2+} influx occurs. (4) Ca^{2+} induces exocytosis of insulin vesicles. The colored circles indicate glucose (pink), ATP (orange), K^+ (purple), Ca^{2+} (green), and insulin (blue).

1.1.5 ER stress and various stresses are present in diabetes

During the evolution of both Type 1 and 2 diabetes, β cells are exposed to multiple stressors, including elevated levels of pro-inflammatory cytokines, glucose, and free fatty acids, hypoxia, and misfolded protein accumulation, leading to activation of a number cell intrinsic stress pathways such as oxidative and ER stress, and maladaptive changes in autophagy (96). These multiple stressors activate the stress pathways and contribute to β cell dysfunction and death and may contribute to β cell de-differentiation (97,98).

Pancreatic β cells possess a highly developed endoplasmic reticulum in order to meet the high demands of insulin protein synthesis and secretion. As a result, β cells are particularly susceptible to endoplasmic reticulum stress, which has been a focus of my thesis studies. Specifically, my studies have investigated novel pathways that lead to dysregulation of ER Ca^{2+} homeostasis and how loss of ER Ca^{2+} leads to ER stress.

The endoplasmic reticulum (ER) is an organelle found in all eukaryotic cells. The structure of ER is a continuous membranous network surrounding a series of sacs known as cisternae. The ER is divided into a ribosome-rich “rough” ER and a ribosome-free “smooth” ER (99). Rough ER is abundant in cells that secrete large amount of proteins including insulin-producing pancreatic β cells (100). The ER membrane constitutes more than half of the total cellular membrane structure and it functions as the site of (a) synthesis, folding, modification and transport of proteins; (b) quality control for newly synthesized proteins; and (c) Ca^{2+} storage that plays a role both in the maintenance of normal ER functions and as a source of released Ca^{2+} that serves a cellular second messenger to regulate a variety of signaling pathways (101). Under normal conditions, Ca^{2+} - dependent chaperone proteins assist in the folding of proteins. These folded proteins are transported to the Golgi apparatus for further maturation. Proteins that are improperly folded or “misfolded” are removed by a quality control

system called ER-associated degradation (ERAD) (102). ERAD involves protein ubiquitination that promotes retro-translocation from the ER to the cytosol, where misfolded proteins undergo proteasome-induced degradation. On the contrary to the effect favor to help the ER functions, once the demand of the protein synthesis surpasses the ER capacity of protein folding and quality control, misfolded proteins can accumulate within the ER lumen, leading to ER stress. Accumulation of misfolded proteins triggers an adaptive cascade aimed at restoring normal ER function, which is referred to as the unfolded-protein response (UPR) (103,104). This adaptive response induces downregulation of overall protein translation, while chaperone proteins and ERAD-associated proteins are preferentially translated (103,105). If the UPR's adaptive response cannot restore normal ER function, prolonged activation of UPR will eventually initiate cellular apoptosis (106). ER stress can impact a variety of different cell types and contributes to a number of disease pathologies, including cardiac and neurodegenerative diseases as well as diabetes.

The molecular mechanisms of the UPR have been well studied (Fig. 2). There are three main branches of this signaling pathway and the initiation of each branch is regulated by three different ER stress sensors located on ER membrane. These include the inositol-requiring enzyme 1 (IRE1), activating transcription factor 6 (ATF6), and PKR-like ER kinase (PERK). Upon binding of unfolded proteins to these three sensor proteins, the dissociation of Bip protein from the sensor proteins occurs. Although the exact mechanisms of how Bip protein attaches and dissociate from each sensor is unknown (107), this is thought to initiate the unfolded proteins response, UPR. In addition, the direct interaction of misfolded proteins with the luminal portion of IRE1 has also been shown to activate the UPR (108). Following Bip dissociation, IRE1 undergoes oligomerization and autophosphorylation, initiating this branch of the UPR. IRE1 has

dual functions as endoribonuclease and kinase. To reduce the overall protein load, IRE1 degrades a large number of mRNAs (109), while X-box binding protein 1 (XBP1) mRNA is spliced by IRE1, allowing translation of XBP1 protein. XBP1 is a transcription factor that increases the expression of genes related to both UPR and ERAD (110). Included in these targets are chaperone proteins, which play a central role in the folding of client proteins in the ER, ATF6 that is the second of these ER stress sensors with which activation of this branch is initiated by translocation of ATF6 to the Golgi apparatus under ER stress conditions. ATF6 is subsequently cleaved to give rise to a cytosolic fragment known as p50 that forms either a homodimer or heterodimer with XBP1 to promote transcription of additional UPR effectors including ATF6 itself (105,111). Finally, the PERK branch of the UPR is thought to be initiated BiP dissociation, followed by the oligomerization and autophosphorylation of PERK. Phosphorylated PERK phosphorylates eukaryotic initiation factor eIF2 α to inhibit activity of this translation factor. This results in a global translational block to prevent further accumulation of misfolded protein. However, selective translations of transcription factor, such as transcription factor 4 (ATF4), will be taken place. ATF4 expression is repressed in the unstressed state, but the phosphorylation of eIF2 under ER stress will initiate the translation of ATF4 (112).

In contrast to this adaptive effect, prolonged activation of the UPR results in apoptosis. Key transcriptional regulators in this pathway, ATF4, ATF6, and XBP1, also initiate transcription of genes encoding proapoptotic proteins, such as C/EBP homologous protein (CHOP). The function of CHOP is to decrease expression of the anti-apoptotic protein Bcl-2 and activate the pro-apoptotic factor Bcl-2-interacting mediator of cell death (Bim) (113,114). Similarly, phosphorylated IRE1 can activate the apoptotic pathway via activation of c-Jun N-terminal kinase (JNK), which leads to inactivation of

anti-apoptotic Bcl-2 and activation of pro-apoptotic Bim (115). As a consequence of Bcl-2 inhibition, the pro-apoptotic proteins Bax and Bak undergo oligomerization that permeabilizes the outer mitochondrial membrane, resulting in Ca^{2+} overload in the mitochondria. Cytochrome C is subsequently released from mitochondria, leading the initiation of caspase-mediated cell death pathways.

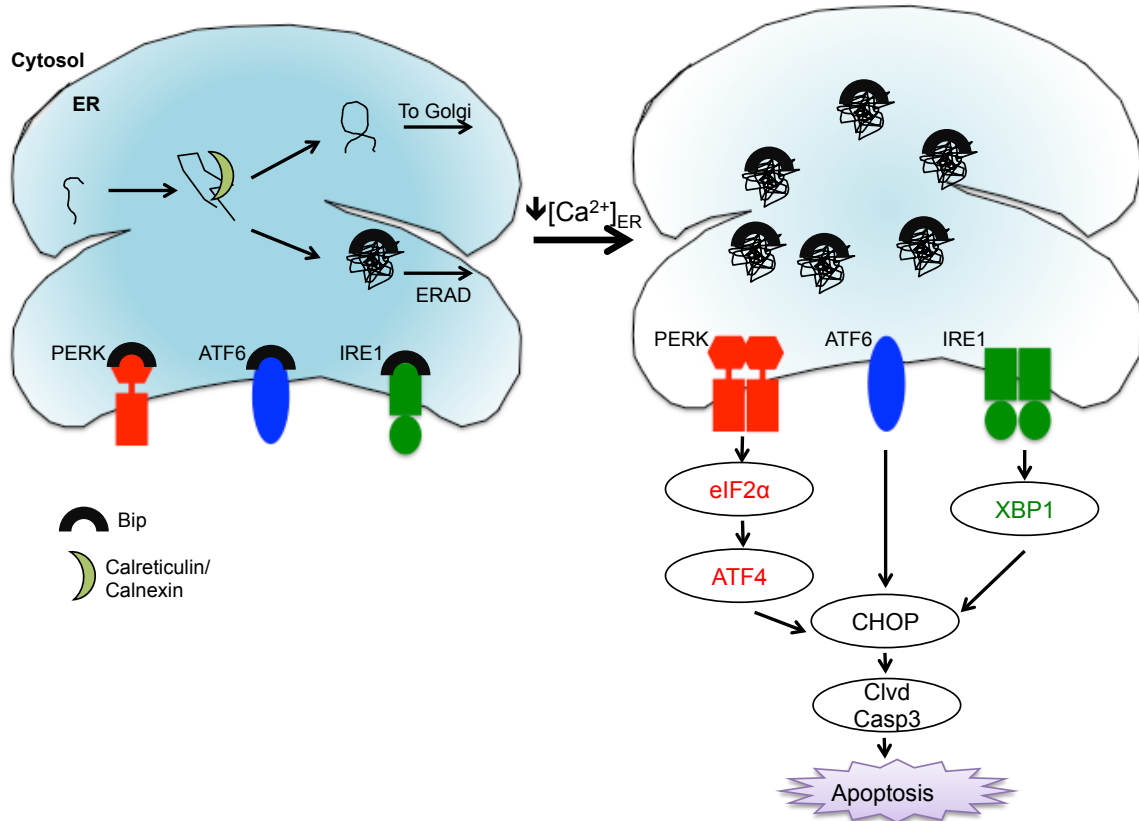


Figure 2. Unfolded protein response and ER Ca^{2+}

Under ER stress conditions, ER Ca^{2+} homeostasis is disrupted and Ca^{2+} -dependent chaperone proteins cannot meet the excess demand for protein folding leading to the accumulation of unfolded proteins. As a result, dissociation of chaperone protein Bip from the ER stress sensor proteins PERK, ATF6, and IRE1 occur. This triggers the activation of unfolded protein response (UPR). Prolonged activation of the UPR eventually causes apoptosis.

1.2 ER Ca²⁺ dynamics and diseases

A focus of my thesis work has been on the identification of pathways that maintain ER Ca²⁺ levels. Cells possess a variety of systems and safeguards to maintain distinct Ca²⁺ stores and concentration gradients that are crucial for cellular function and survival. Specifically, a distinct Ca²⁺ gradient exists between the membranes of the extracellular space, cytosol, and intracellular organelles. These gradients allow cells to maintain organelle function, while also contributing to spatiotemporal calcium signaling. Disruption of gradients can contribute to disease pathophysiology. In the pancreatic β cell, disruption of these gradients leads to impaired insulin production and secretion as well as apoptosis. Under resting conditions, intracellular Ca²⁺ is maintained at a level at least four orders of magnitude lower than extracellular Ca²⁺. In addition, free ER Ca²⁺ is maintained at approximately two orders of magnitude higher than the intracellular Ca²⁺ (116), while mitochondrial Ca²⁺ levels are comparable to that of intracellular Ca²⁺ (117,118). The rank order of Ca²⁺ concentration in each compartment at rest is summarized as: Extracellular Ca²⁺ (~2 mM) > ER Ca²⁺ (~100 μ M) > Mitochondria Ca²⁺ (~200 nM) \geq Intracellular Ca²⁺ (~100 nM).

Meticulous coordination of ion transporters including channels on the plasma and organelle membranes establish these Ca²⁺ gradients. On the β cell plasma membrane, the Na⁺/Ca²⁺ exchanger (NCX) and the plasma membrane Ca²⁺ ATPase (PMCA) transfer excess intracellular Ca²⁺ into the extracellular space to maintain low cytosolic calcium levels. Among the many cellular organelles, the ER is the largest Ca²⁺ store. As is the case for NCX and PMCA, the Sarco/endoplasmic reticulum Ca²⁺ ATPase (SERCA) also works to eliminate excess intracellular Ca²⁺ by pumping calcium into the ER. This process is regulated by SERCA, PMCA, and NCX and is called Ca²⁺ clearance. The process of calcium clearance is particularly important following a β cell secretory burst. Mathematical modeling based on the experiments performed in

dispersed mouse β cells suggests 50-64% of intracellular Ca^{2+} transients induced by KCl, which causes depolarization, are removed by the SERCA pump (119). After that, 21-30% of the excess Ca^{2+} will be cleared by NCX when intracellular Ca^{2+} is high $\sim >1$ μM , and 21-27% of Ca^{2+} will be removed by PMCA when intracellular Ca^{2+} is low at around ~ 0.5 μM (119). Other factors such as the mitochondrial calcium uniporter (MCU) and the gap junction channels, connexin 36 (Cx36), are anticipated to play a role, but have been less well studied (91).

Like the PMCA pump, the SERCA pump uses ATP to transport Ca^{2+} against the steep calcium concentration gradient between the cytosol and ER. In contrast to SERCA, inositol 1,4,5-trisphosphate and ryanodine receptors (IP_3R and RyR) are Ca^{2+} releasing channels that passively release Ca^{2+} from the ER lumen into the cytosol. Another important organelle for cellular Ca^{2+} homeostasis is the mitochondria, which has been less characterized in β cells, but may function as a transient Ca^{2+} buffer. The MCU and leucine- zipper EF-hand-containing transmembrane protein 1 (LETM1) are localized to the mitochondrial inner membrane and drive Ca^{2+} uptake into mitochondria (120). In contrast, $\text{Na}^+/\text{K}^+/\text{Ca}^{2+}$ -exchange protein 6 (NCLX) is the transporter that releases Ca^{2+} from mitochondria into the cytosol (96,121).

1.2.1 The role of the SERCA in health and disease

ER Ca^{2+} levels represent the balance of calcium uptake via the SERCA pump and calcium release via the RyR and the IP_3R . SERCA is an active transporter that senses and pumps excess intracellular Ca^{2+} into the ER. Since this process is also ATP dependent, SERCA functions as a metabolic sensor (122,123).

SERCA protein is encoded by three distinct genes: *ATP2A1*, *ATP2A2*, *ATP2A3* (SERCA1, SERCA2 and SERCA3 respectively). There is a high level of conservation among the different isoforms, with more than 75% structural homology observed

between the isoforms (124). Each gene encodes 2-6 alternatively spliced transcripts. SERCA1 is expressed exclusively in fast-twitch skeletal muscle. SERCA2 splice variants are expressed in a tissue-specific manner. SERCA2a is expressed mainly in cardiac and slow-twitch skeletal muscle, whereas SERCA2b is ubiquitously expressed. SERCA3 is expressed only in particular tissues including β cells and is usually co-expressed with SERCA2b (125).

Acquired SERCA deficiencies have been implicated in a variety of diseases. Darier-White disease is an inherited skin disease that arises as a result of SERCA2 haploinsufficiency and is characterized by the loss of keratinocyte adhesion, which is termed acantholysis, occurring as a result of disruption of ER Ca^{2+} levels in the keratinocytes (126,127). Persons with Darier-White disease also have higher rates of epilepsy and depression (126,128). Whether these individuals are more susceptible to metabolic disease has not been tested. SERCA2a expression and Ca^{2+} affinity are decreased in heart failure (129) and have been associated with cardiac myopathies (130). Moreover, cardiac function was improved by overexpression of SERCA2a in a rat model of heart failure (131,132). In addition, the Ca^{2+} affinity of SERCA2 was increased by suppression of the phosphorylated form of the membrane-localized inhibitory protein, phospholamban in a hamster model of heart failure (133). Also, ablation of phospholamban in cardiomyopathic mice (134) has been shown to improve contractility in heart failure (135). Therefore, improving SERCA function may represent a potential therapeutic strategy for a variety of diseases.

The dominant form of SERCA in the pancreatic β -cells is SERCA2b (54). The structural difference between SERCA2a and SERCA2b is limited to the COOH-terminal (C-terminal) of each protein. SERCA2b contains a unique 49-amino acid C-terminal extension that creates an 11th transmembrane α -helix in this protein with the C-terminus

tail projecting into the lumen of the ER. This structural difference grants this isoform the highest affinity to Ca^{2+} ($2b > 2a > 3$) and the lower ATPase turnover rate ($3 > 2a > 2b$) (136).

Accumulating evidence suggests that altered SERCA expression and activity contributes to the pathophysiology of diabetes, leading to both impaired insulin secretion and β cell death (137-139). The contribution of SERCA to Ca^{2+} clearance following glucose exposure has been experimentally assessed using dispersed mouse islet β cells. Chen et al. demonstrated that about two-thirds of the depolarization-induced Ca^{2+} influx was removed by SERCA (119). This suggests that SERCA can indirectly regulate insulin secretion by controlling intracellular Ca^{2+} . Moreover, SERCA may play a significant role in the amplitude and the downward phase of the glucose-induced Ca^{2+} oscillations (GICOs) that additionally regulate insulin secretion. Functional studies of SERCA have been enabled due by the SERCA inhibitor, thapsigargin (TG). Inhibition of SERCA leaves only Ca^{2+} releasing channels, RyR and IP_3R functional, which results in the depletion of ER Ca^{2+} across the concentration gradient. Prolonged TG treatment leads to ER stress and apoptosis (140), again emphasizing that ER Ca^{2+} is required for cell survival and function.

1.2.2 The role of the Ryanodine Receptor in health and disease

Whereas SERCA functions to pump Ca^{2+} into ER to maintain ER Ca^{2+} levels, ER Ca^{2+} releasing channels, IP_3R and RyR, are both expressed in the β -cell (141-143) and coordinately function to maintain ER Ca^{2+} homeostasis and ER function. For instance, excess ER Ca^{2+} is released by IP_3R and RyR to maintain Ca^{2+} balance and homeostasis. In addition, acute release from these channels also contributes to a variety of intracellular signaling pathways. Mammalian RyR has three different isoforms. RyR1 is mainly expressed in skeletal muscles and is localized in junctional terminals between the plasma membrane and sarcoplasmic reticulum (SR), while RyR2 is predominantly

expressed in cardiac muscles. RyR3 was found to be ubiquitously expressed (144-146). Functional RyRs consist of homotetramers (147). RyRs are also expressed in other nonmammalian vertebrates such as birds and fish with the isoforms RyRa and RyRb (148). Furthermore, RyR expression has been found in other metazoans, including *C. elegans* and *Drosophila melanogaster* (149,150).

RyRs are associated with many different human diseases, with the majority of diseases arising as a result of alterations in channel gating properties (147). Diseases caused by mutations in the RyR1 gene include malignant hyperthermia, leading to increased sensitivity to inhalation anesthetics that can lead to sustained muscle contraction (151). RyR1 mutations may also lead to exertional rhabdomyolysis, characterized by the breakdown of striated muscles in response to heat or exercise (152); central core disease, which is a mild congenital myopathy characterized by hypotonia and muscle weakness of the upper legs and hips (153); and multiminicore disease that is autosomal recessive myopathy with degeneration of muscle fibers causing weak limb muscles (154).

Diseases caused by mutations in the RyR2 include catecholaminergic polymorphic ventricular tachycardia (CPVT), which is characterized by stress- or exercise-induced ventricular tachycardia that can lead to sudden death (155). Calstabin1 and 2 (also called FKBP12 and FKBP12.6) are expressed in most tissues and function to bind and stabilize the RyR1 and RyR2 in the closed state (156-159). Mutation of the V2461 in RyR1 abolished calstabin1 binding (160). Inhibition or loss of calstabin1 binding greatly increased the open probability and open duration for the channel (161,162) Calstabin1 displacement in skeletal muscle alters EC coupling between RyR1 and Cav1.1 (163), whereas loss of calstabin1 in cardiac muscle results in cardiomyopathy as well as developmental congenital heart defects (164).

In vitro and animal studies have shown that the CPVT associated mutation in RyR2 results in Ca^{2+} leak through the receptor by lowering affinity for FKBP12.6, also known as calstabin2 (165) or by increasing sensitivity to β -adrenergic receptors to induce prolonged Ca^{2+} transients (166). In CPVT, protein kinase A (PKA) and Ca^{2+} /calmodulin dependent protein kinase II (CaMKII) phosphorylation of RyR2 has been also been documented to change RyR2 function (167,168). Thus, in persons with CPVT, β -adrenergic stress and exercise induced PKA phosphorylation along with a leaky RyR2 are thought to contribute to arrhythmias. Mutations in RyR2 are also responsible for arrhythmogenic right ventricular dysplasia type 2 (ARVD2), which is an autosomal dominant disease characterized by degeneration of myocardium, leading to ventricular arrhythmias and sudden death (169). The mutation associated with ARVD2 also leads to dysfunction in RyR2 via Ca^{2+} leak from myocardial SR (170). In contrast to RyR1 and RyR2, RyR3 is the isoform that has been least studied. One study suggested that upregulation of RyR3 in cortical neurons may play a protective role in Alzheimer's disease (171).

The RyRs exhibit approximately 65% sequence homology, but each RyR isoform has different modes of regulation. RyRs form a macromolecular complex with a variety of proteins including L-type voltage dependent channels, Cav1.1/Cav1.2, PKA, Calstabin1 and 2, CaM, CaMKII and calsequestrin. Therefore, receptor function can be modulated by proteins within these larger complexes. The regulation of these complexes have been extensively studied in electrical – contraction (EC) coupling, which is regulated by Ca^{2+} release from SR in skeletal and cardiac muscles. In skeletal muscle, multiple regions of Cav1.1 and RyR1 physically interact to regulate EC coupling (172-174). Due to this physical interaction rather than Ca^{2+} induced activation, EC coupling in skeletal muscle is prolonged even in the absence of extracellular Ca^{2+} (175,176). In contrast, RyR2 in cardiac muscle is activated by Ca^{2+} influx through Cav1.2, and this

mode of RyR2-mediated ER Ca^{2+} release is called Ca^{2+} induced Ca^{2+} release (CICR) (177). Ca^{2+} influx through Cav1.2 does not directly induce muscle contraction, but much larger Ca^{2+} release from RyR2 by CICR mediates muscle contraction (178).

Single channel studies have shown that RyRs exhibit biphasic activation by Ca^{2+} . Low intracellular Ca^{2+} concentrations (<0.01-20 μM) can activate RyRs, whereas higher intracellular Ca^{2+} concentration (~100 μM – 10 mM) can inhibit RyRs (179). In addition to the activation from the cytosolic side, single channel recordings have shown that Ca^{2+} can activate RyR from ER luminal side in response to increased ER Ca^{2+} (180,181). This is referred to as store overload induced Ca^{2+} release (SOICR). Structural studies indicate that highly electronegative luminal loop domains are responsible for RyR activation in SOICR (182). Spontaneous SOICR in cardiac cells are capable of inducing Ca^{2+} waves and delayed after depolarizations resulting in ventricular tachyarrhythmias (183). This is caused by the abnormal RyR2 activation due to RyR2 mutations associated with CPVT, which lowered the threshold of the SOICR (22 23).

Ca^{2+} may also regulate RyR function through calmodulin (CaM), which is a ubiquitously expressed Ca^{2+} binding protein. CaM contains four EF-hand Ca^{2+} binding sites. CaM is known to bind to each RyR monomer (184) and also plays a role in regulating Cav1.1 and Cav1.2 (185-187). Studies have shown that CaM is capable of suppressing RyR2 function by elevating the threshold of intracellular Ca^{2+} for RyR2 activation in cardiac muscle (188). Decreased CaM binding affinity for RyR2 was observed in the mouse model of CPVT that has a RyR2 R2474S mutation, resulting in lethal arrhythmias (189).

Post-translational modification of RyRs also regulate their activity. RyRs possess multiple phosphorylation sites in the cytoplasmic domains including sites for phosphorylation by PKA, CaMKII and cGMP-dependent kinase (PKG) (190-193). During the “fight or flight” stress response, the sympathetic nervous system (SNS) is activated

resulting in increased calcium transients and faster muscle contractions (194). This pathway involves β adrenergic receptor and PKA activation leading to RyR phosphorylation and altered gating properties (167,195). In addition hyperphosphorylation of RyR2 serine residues at the calstabin 2 binding site and concomitant dissociation of calstabin 2 and resulting RyR2-mediated Ca^{2+} leak are suggested to play a role in both heart failure and during severe stress (168). CaMKII dependent phosphorylation of RyR2 is also suggested to enhance SR Ca^{2+} leak and decrease of SR Ca^{2+} load in heart failure (196).

In addition, alterations in redox state of RyRs can both activate (197,198) or inhibit channels (199). Cysteines in RyR1 and RyR2 are covalently bound by NO (S-nitrosylation) (200), and high level of ROS/RNS can irreversibly modify RyR function (201). For example, S-nitrosylation of Cys3635 in RyR1 has been found to reverse the CaM mediated inhibition leading to channel activation (202), which can facilitate muscle contraction (203). S-nitrosylation of Cys3635 in RyR1 has also been observed in muscular dystrophy leading to elevated SR Ca^{2+} leak (204). On the contrary, RyR2 cannot be S-nitrosylated by NO, and RyR2 has to go through S-nitrosoglutathione, endogenous NO carriers and donors, to undergo S-nitrosylation (205). In addition to Ca^{2+} , Mg^{2+} and ATP also regulate RyRs. Mg^{2+} is suggested to reduce the open probability of RyR by competing with Ca^{2+} for the Ca^{2+} activation site (206,207). ATP may also activate RyRs in absence of Ca^{2+} , but will have a maximum effect in the presence of Ca^{2+} (206,208).

While the association of abnormal RyR function has been well-described in heart disease, how RyRs function and dysfunction affects the pancreatic β cell and the development of diabetes is not well understood. Since only Cav1.2 and Cav1.3 are detected in rodent and human β cells (209), depolarization induced RyR activation mediated by Cav1.1 does not exist in β cells. Rather, CICR mediated by Cav1.2 and

RyR2 is thought to be the major form of RyR regulation in the β cell. Santulli et al. reported the metabolic phenotype of mice with RyR2 mutation in R2474S and N2386I and, humans with CPVT mutation in RyR2. Collectively, these mutations induced dysregulated ER Ca^{2+} release through RyRs and led to impaired insulin secretion (210). This group found that these mutations caused dissociation of calstabin2 from RyR2, and thus pharmacologically stabilizing interactions between calstabin2 and RyR2 by S107. S107 functioned to enhance binding of calstabin2 to RyR2, and therefore partially rescued the ER Ca^{2+} release through RyR and abnormal insulin secretion (210). Furthermore, it was found that Dantrolene, which is an inhibitor of RyR1 and RyR3, reduced cell death under TG-induced ER stress in Min6 β cells (211). Similarly, Lu et al. reported that treating with Dantrolene protected from apoptosis induced by TG using INS-1 cells where the WFS1 gene was knocked down (212). However, these studies were performed by inducing ER Ca^{2+} loss through SERCA inhibition, and they provide limited insight into how physiological stressors may change RyR function and ER Ca dynamics. Thus, a goal of my project has been to study β cell RyR function in the context of pro-inflammatory stress and ER stress.

1.2.3 The role of the IP₃R in health and disease

Inositol 1,4,5-triphosphate receptors (IP₃R) are expressed in most eukaryotes and play an important role in regulating ER calcium release. In contrast to RyRs, functional IP₃Rs consist of tetramers assembled by either identical subunits or by mixture of the three subtypes IP₃R1, IP₃R2 and IP₃R3 and each subtype has many splice variants (213-215). IP₃R are activated by IP₃, which is produced by the G α_q G-protein coupled receptor (GPCR) pathway and acts to stimulate Ca^{2+} release from the major IP₃-sensitive Ca^{2+} stores, including the nucleus, ER (216), Golgi, and likely the secretory vesicles. (217-219). In response to various endogenous ligands, G α_q subunit

activates phospholipase C (PLC) to catalyze hydrolysis of phosphatidylinositol 4,5-bisphosphate (PIP₂) to produce IP₃ and diacyl glycerol (220). IP₃ interacts with α - and β -domains of IP₃R, pulling the two domains closer (221). IP₃Rs play a central role in the propagation of Ca²⁺ waves, which is regenerative increased intracellular Ca²⁺. The increased intracellular Ca²⁺ is sensed by RyR or IP₃R to induce ER Ca²⁺ release called Ca²⁺-induced Ca²⁺ release (CICR) (222). The Ca²⁺ wave can propagate throughout the entire cell or even between cells to induce various biological effects. This was first observed during fertilization, which was found to occur through an IP₃R dependent process (223). IP₃ can hierarchically induce different forms of IP₃R activation, ranging from activation of a single IP₃R, to activation of a cluster of several IP₃Rs, and finally to activation of all cellular IP₃R to induce a Ca²⁺ wave (224,225). Activation of IP₃Rs requires both IP₃R and intracellular Ca²⁺ (226,227). However, whether each subunit of IP₃R tetramer requires the occupancy of an IP₃ molecule is still not known. In parallel to RyRs, the effects of Ca²⁺ are biphasic. Modest increases in intracellular Ca²⁺ (~ μ M) enhance IP₃ responses, whereas higher intracellular Ca²⁺ (μ M-mM) can inhibit the IP₃R response (226,228). Experiments performed using purified IP₃Rs reconstructed in a lipid bilayer have confirmed the activation of IP₃R by Ca²⁺, but not its inhibition (229,230). These results suggest that proteins might be responsible for inhibition mediated by high Ca²⁺ levels, rather than direct Ca²⁺ binding to the IP₃R (231). CaM has been suggested to be such a protein responsible for this effect based on the presence of CaM binding domains in the IP₃R. However, this as yet to be proven (232). Other IP₃R regulators include intracellular ATP (233) and cyclic AMP (cAMP), which is an intermediate product of G α_s -GPCR pathway. Cyclic AMP can regulate IP₃R through multiple mechanisms. First, cAMP induces production of IP₃ through EPAC-mediated activation of PLC and IP₃ production (232,234). In addition, all three IP₃R subtypes are phosphorylated by PKA, which is in turn activated by cAMP. Thus, cAMP-mediated phosphorylation potentiates

IP₃-induced Ca²⁺ release by IP₃R1 and IP₃R2 (235). Finally, high cAMP concentrations induce a direct interaction between cAMP and IP₃Rs to sensitize their activities (236).

Structurally speaking, very little is known about how Ca²⁺ regulates IP₃R. Unlike the RyR, there are no EF Ca²⁺-binding motifs within IP₃R. However, there are clusters of negatively charged residues that could serve as Ca²⁺ binding sites (237). A study that mutates the Glu2100 residue to a aspartic acid or glutamine reduced the Ca²⁺ sensitivity of the IP₃R by 5 – 10 fold, suggesting might serve as the site of IP₃R regulation by Ca²⁺ (238,239). Two studies have suggested that an increased ER Ca²⁺ load increased the sensitivity of IP₃R to IP₃ (240,241). Thus, regulation of the IP₃R by luminal ER Ca²⁺ regulation is possible, but has yet to be definitively proven. A high-affinity Ca²⁺-binding site exists within the luminal loop of the transmembrane domain 5 and 6 contains conserved acidic residues that could mediate luminal Ca²⁺ regulation (242).

While altered IP₃R function has been suggested in a variety of diseases, including cardiac and neurodegenerative diseases, overall this topic has been less studied than RyR dysfunction. The expression level of IP₃Rs have been shown to be increased in cardiac hypertrophy, atrial fibrillation and hypertension (243-245). Among the three subtypes, IP₃R1 is the dominant form in brain (214), and impaired IP₃R1 function has been associated with Huntington's disease (246) and Alzheimer's disease (247). Mutations in the gene encoding IP₃R1 leads to spinocerebellar ataxia, a disorder characterized by progressive loss of muscle coordination (248,249). Compared to studies investigating RyR dysfunction, even fewer number of studies have linked IP₃R dysfunction to diabetes pathophysiology. So far, it has been shown that TG induced cell death was partially protected by inhibiting IP₃Rs in the Min6 β cell line (211). Further investigation will be necessary to fully define a role for the IP₃R in diabetes pathophysiology.

1.2.4. ER Ca²⁺ dynamics and cellular excitability

As with other secretory cells, pancreatic β cells are electrically excitable and capable of firing action potentials. Action potentials exist in both metazoan and plant cells, and they serve as a means to facilitate rapid communication between cells or tissues. In this regard, action potentials are used in β cells within islets to achieve rapid and synchronous insulin secretion, thus minimizing the time gap between glucose sensing and integrated insulin secretion at a whole-islet level (250).

Action potentials in β cells are generated mostly via Ca²⁺ influx through the activation of voltage-gated Ca²⁺ channels (47). Unlike mouse β cells, Na⁺ current also contributes to action potentials in human β cells (47,251). The pattern of action potential firing can increase the toxic Hyperexcitation is described as a state of excess action potential generation and has been shown to contribute to neurological disorders such as Alzheimer's disease (252,253), Parkinson's disease (254), epilepsy (255), and neuropathic pain (256). Hyperexcitation is also known to be toxic to cells and is referred to by the term "excitotoxicity". In neurons, cells undergo excitotoxicity due to overstimulation by excitatory amino acids, such as glutamate, resulting in excessive depolarization and action potential generation leading to cell death (257). In this process, glutamate receptors and Ca²⁺ channels induce Ca²⁺ overload, which triggers mitochondrial production of reactive oxygen species and induction of apoptosis (257,258). Another mechanism that induce neural excitotoxicity is hypoglycemia, because glucose is required for cells to take up a glutamate in the brain (259). In addition to neuronal diseases, hyperexcitability of cells may also contribute to cardiac arrhythmias (260,261).

Limited studies have been performed to investigate the relationship between β cell hyperexcitability and diabetes. In this regard, studies have investigated the relationship between sulfonylureas, which block K_{ATP} channels to induce β depolarization

and hyperexcitability. Clinical studies have suggested that sulfonylureas may hasten β cell failure (262), but the mechanisms underlying loss of insulin secretion by sulfonylureas remains poorly understood and is controversial. However, a leading hypothesis is that chronic hyperexcitation of β cells (263) eventually causes excitotoxic response, leading to loss of β cell function (264-266) and eventual cell death (267) and. Chronic glucotoxicity has been similarly implicated. In fact, in the presence of high glucose for extended periods, glucose-stimulated insulin secretion was impaired and islet insulin content was depleted in rat and human islets (268-270). This was prevented by co-treatment with the K_{ATP} channel opener diazoxide, as opening of K_{ATP} channel resulted in hyperpolarization, which inhibits Ca^{2+} influx from Cav (271-273). Furthermore, gain-of-function mutation of K_{ATP} channels, which increases excitability of β cells, caused high insulin secretion independent of blood glucose level and caused congenital hyperinsulinism of infancy (274). The loss-of-function mutation of K_{ATP} channels, which decreases excitability of β cells, caused neonatal diabetes mellitus (275). Therefore, K_{ATP} channels plays a critical roles of the excitability of β cells in health and disease. The exact molecular mechanisms for excitotoxicity, including the channels responsible for this phenomenon are yet to be found.

1.2.5. Ca^{2+} oscillation and ER Ca^{2+} dynamics

In response to elevated blood glucose levels, β -cells begin to oscillate intracellular Ca^{2+} levels synchronously in waves that propagate throughout the entire islet, with a frequency ranging from one per second to minutes (250). This phenomenon is referred to as glucose-induced Ca^{2+} oscillations (GICOs) and result from synchronous oscillation of V_m leading to Ca^{2+} influx through voltage-gated Ca^{2+} channels (250,276). The synchrony of oscillations among all islet β -cells are due to gap junction channels, which are composed of connexin 36 (Cx36) and mediate diffusion of ions and

small molecules between neighboring β cells (277). Cx36 has high affinity for K^+ , and K^+ influx from K_{ATP} channels is uniformly diffused throughout β cells establishing a uniform V_m that is a key basis for synchronous Ca^{2+} oscillation (278). Ca^{2+} triggers insulin exocytosis, GICOs are coupled with the rhythms of pulsatile insulin secretion. Therefore, studying the mechanisms of Ca^{2+} oscillation in health and in diabetes has clinical significance. The pulsatile insulin secretion in humans is crucial for maintaining normal glycemic control (279). Loss of oscillations are observed in diabetes, and disruptions in the normal patterns of oscillatory insulin secretion is thought to contribute to insulin secretion secondary to desensitization of receptors in peripheral tissues (280,281). Despite this background knowledge, the exact mechanisms of how GICOs occur and how loss of GICOs occurs under diabetic stress have not been fully established. Since it is known that ER Ca^{2+} dynamics modulates V_m and action potential firing, dysfunction of ER Ca^{2+} dynamics may contribute to impaired GICOs and altered insulin secretion in diabetes.

2.1 ER stress and pro-inflammatory cytokine stress caused ER Ca²⁺ loss and disruption of glucose-induced Ca²⁺ oscillations.

The pathophysiology of type 1 and type 2 diabetes involves both β cell ER stress and pro-inflammatory cytokine-induced β cell dysfunction. To define how these stress paradigms influenced the ER Ca²⁺ store, we treated with compounds and factors that induce ER stress and pro-inflammatory cytokine stress. INS-1 β cells were treated with 300 nM Tunicamycin (TM) or 5 ng/ml Interleukin 1 β combined with 25 mM high glucose (IL-1 β + HG) in time-course experiments, and Ca²⁺ imaging was performed according to the schematic shown in Figure 3A. Results revealed a time-dependent loss of ER Ca²⁺ with TM (Fig. 3B-C) and IL-1 β + HG (Fig. 3D-E), where significant reductions in ER Ca²⁺ were observed within 6 hrs and further reductions were observed throughout the 24 hr exposure period. We next studied the effect of TM and IL-1 β + HG on glucose-induced Ca²⁺ oscillations (GICOs) in islets from 8 wk old C57BL6/J mice. Under control conditions, regular intracellular Ca²⁺ oscillations were observed in response to glucose stimulation (Fig. 3F). In contrast, both chemically induced ER stress and pro-inflammatory cytokine stress abolished normal patterns of GICOs in mouse islets (Fig. 3G). To compare these findings in analogous mouse models, islets were isolated from 6-8-wk old Akita mice, which harbor a spontaneous mutation in one allele of the *INS2* gene, resulting in impaired proinsulin folding and severe ER stress (282,283). To recapitulate pro-inflammatory cytokine stress, islets were isolated from 9-12-wk old hyperglycemic db/db mice. The strain has a mutated form of the leptin receptor resulting in hyperglycemia, obesity, and elevated systemic levels of pro-inflammatory cytokines (283,284). Similar to results observed with *ex vivo* TM and IL-1 β +HG treatment, GICOs were significantly impaired in islets isolated from Akita and db/db mice (Fig. 3H). Taken together, these data indicate that ER and pro-inflammatory stress are sufficient to disrupt

ER Ca^{2+} storage as well as GICOs in pancreatic β cells.

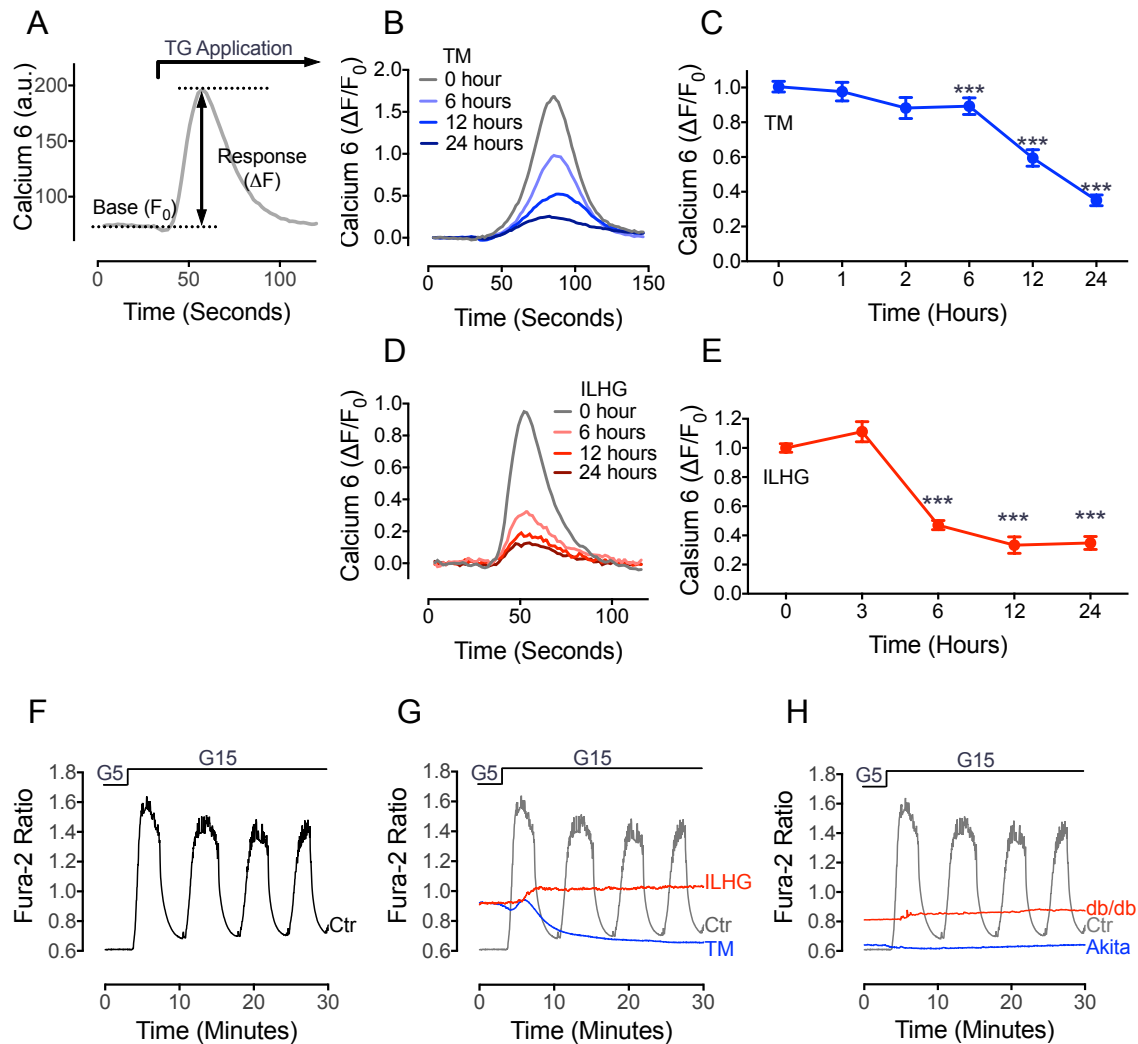


Figure 3. ER stress and pro-inflammatory cytokine-induced stress led to ER Ca^{2+} loss and disruption of glucose-induced Ca^{2+} oscillations

Experiments were conducted using INS-1 cells (A-E) and mouse islets (F-G). (A) To estimate ER calcium storage, Calcium 6 was used to measure intracellular Ca^{2+} levels before and after application of 10 μM thapsigargin (TG), a potent inhibitor of SERCA pump activity. (B) Representative traces for TG-induced Ca^{2+} release following treatment with 300 μM TM for indicated times. (C) TM-treatment led to a time-dependent reduction in ER Ca^{2+} levels; $n =$ at least 7 replicates for each timepoint. (D) Representative traces for TG-induced Ca^{2+} release following treatment with 300 μM IL-

1 β + 25 mM glucose (ILHG) for indicated times. (E) ILHG-treatment led to a time-dependent reduction in ER Ca²⁺ levels; n = at least 3 replicates for each time point. (F) Representative trace of changes in Fura2 intensity in islets from 8-12 week old wild-type C57BL6/J mice. Islets were incubated in 5 mM glucose (G5) and then stimulated with G15 to induce GICOs; n = 3 biological replicates. (G) Representative traces of GICOs in C57BL6/J islets under control conditions (Ctr) or following treatment with either 5 ng/ml IL-1 β +25mM glucose for 24 hours (ILHG) or 10 μ M TM for 48 hrs (TM); n = at least three biological replicates for each condition. (H) Representative GICO traces in islets from 9-12 week old db/db mice or 6-7 wk old Akita mice overlaid with GICOs of islets from C57BL6/J (Ctr) mice; n = at least three biological replicates for each genotype. For (C) and (E); ***p \leq 0.001 compared to Time 0.

2.2 RyR and IP₃R function are differentially altered in response to ER and cytokine-induced stress

Whereas previous studies have implicated β cell SERCA2 dysfunction in diabetes, a role for either RyR and IP₃R dysfunction remains incompletely characterized (285). To define whether RyR and IP₃R activity were altered in models of ER stress and pro-inflammatory stress, TM and IL-1 β +HG-treated INS-1 β cells were loaded with the low-affinity Ca²⁺ indicator Mag-Fluo-4 AM, followed by membrane permeabilization with saponin. As shown in Figure 2A, Mag-Fluo-4 AM was efficiently cleared from the cytosol, but remained sequestered within the ER, as indicated by overlap with RFP-calnexin (Fig. 2A). Next, ATP was added to achieve steady state ER Ca²⁺ levels via SERCA activation. Caffeine and IP₃ were added to activate RyRs and IP₃Rs, respectively, and dose-response curves were generated (Fig. 4B). Interestingly, this analysis revealed that TM-induced ER stress primarily altered RyR responses (Fig. 4C), while IP₃R function was minimally impacted by TM treatment (Fig 4D). In the short-term, TM increased the maximal RyR response, while reductions in RyR activity were observed with chronic TM treatment (Fig. 4C). In contrast to TM treatment, RyR activity remained largely unaffected by IL-1 β + HG (Fig. 5A). Longer-term IL-1 β + HG treatment reduced the EC₅₀ of the IP₃R response to agonist (Fig. 5B). Together, these results suggest that ER stress preferentially impacted RyR function, while chronic pro-inflammatory stress preferentially impaired the IP₃R response to agonist.

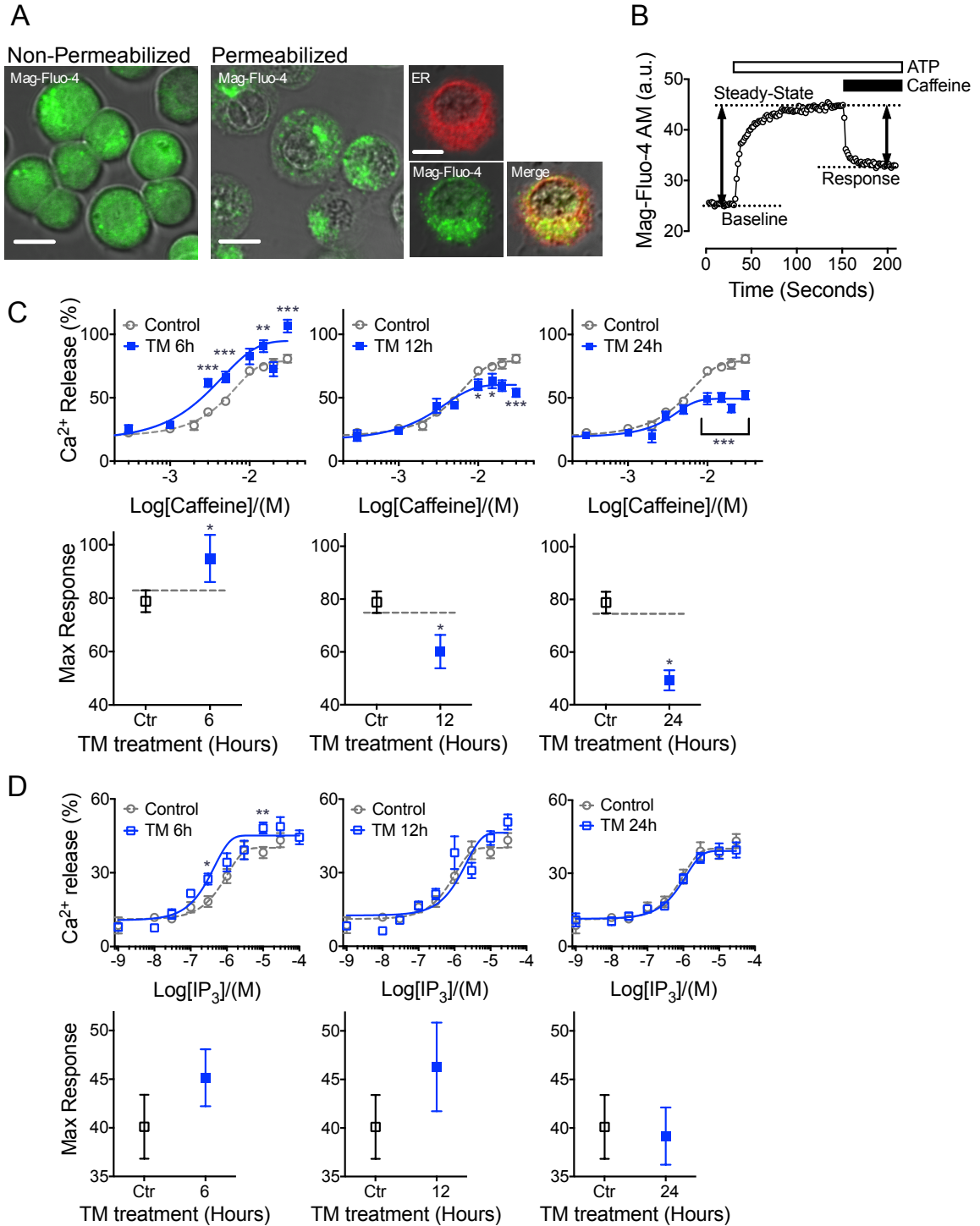


Figure 4. RyR function was preferentially altered by TM-induced ER stress

(A) INS-1 cells were loaded with the low affinity Ca²⁺ indicator Mag-Fluo-4 AM (Green). Following plasma membrane permeabilization, Mag-Fluo-4 AM was retained in the ER as demonstrated by co-localization with calnexin (Red). To estimate RyR and IP₃R

activity, calcium imaging was performed according to the schematic shown in Panel (B). First, 1.5 mM Mg-ATP was added to establish steady-state ER Ca²⁺ levels. Caffeine is an agonist for RyR, while IP₃ is an agonist for IP₃R. Caffeine or IP₃ was applied in the indicated concentrations to generate-dose response curves of RyR and IP₃R activation, respectively. Decreases in Mag-Fluo-4 AM intensity were used to calculate relative ER Ca²⁺ release, and GraphPad Prism Software was used to fit data from IP₃R and RyR functional assays to sigmoidal dose-response curves, which were analyzed by two-way ANOVA with Tukey-Kramer post-test. (C) Upper panels show the dose-response curves for RyR activation by caffeine in INS-1 cells pre-treated with 300 nM TM or DMSO for 6, 12, and 24 hrs. Lower panels show the maximal response and 95% confidence intervals for each timepoint; n = at least 3 replicates for each timepoint in different caffeine concentration. (D) Upper panels show the dose-response curves for IP₃R activation by IP₃ in INS-1 cells pre-treated with 300nM TM for 6, 12, and 24 hrs. Lower panels show the maximal response and 95% confidence intervals; n = at least 3 replicates for each timepoint and IP₃ concentration. *p ≤ 0.05; **p ≤ 0.01; ***p ≤ 0.001 compared to control conditions.

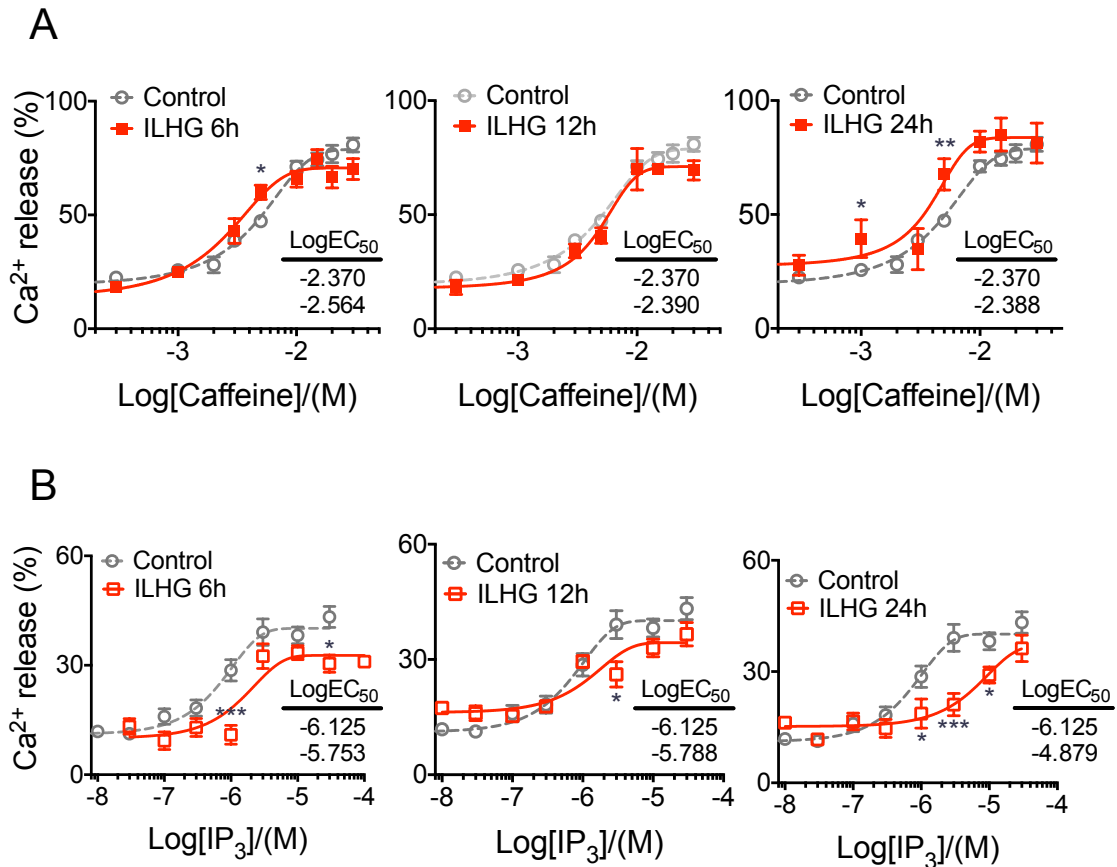


Figure 5. Pro-inflammatory cytokine stress impaired IP₃R function

(A) Dose-response curves for RyR activation by caffeine in INS-1 cells pre-treated with 5 ng/mg IL + 25 mM glucose (ILHG) for 6, 12, and 24 hrs; n = at least 3 replicates for each timepoint and caffeine concentration. (B) Dose-response curves for IP₃R activation in INS-1 cells pre-treated with pretreated with ILHG for 6, 12, and 24 hrs. *p ≤ 0.05; **p ≤ 0.01; ***p ≤ 0.001 compared to control conditions. Values shown are the LogEC₅₀ for INS-1 cells analyzed under control conditions (top) and following ILHG-treatment (bottom).

2.3 Stress-mediated ER Ca²⁺ loss was reduced by RyR and IP₃R inhibition

To test whether RyR or IP₃R inhibition was sufficient to prevent ER Ca²⁺ loss under diabetogenic stress conditions, we tested the effects of RyR antagonists, dantrolene and ryanodine (Ry), and the IP₃R antagonist, xestospongine C (XeC) using INS-1 cells. Since Ry can activate RyR at low concentration (~ 1 nM) Ry 100 μM was used to inhibit RyR. Following tunicamycin treatment, there was a trend towards improved ER Ca²⁺ levels with dantrolene (Fig. 6A), while inhibition of RyR with Ry (Fig. 6B) significantly prevented ER Ca²⁺ loss compared to TM alone. Consistent with results from the functional assays, Ry was unable to block ER Ca²⁺ loss in response to IL-1β+HG (Fig. 6D), whereas inhibition of IP₃R with XeC partially rescued ER Ca²⁺ levels following IL-1β+HG treatment (Fig. 6C).

ER stress and cytokines are known to induce β cell death (286), so we next tested whether modulation of ER Ca²⁺ loss via RyR or IP₃R inhibition were sufficient to protect against β cell death. TM-treatment resulted in a time-dependent increase in caspase 3- and 7 activity (Fig. 7A) and led to increased expression of cleaved-caspase 3 protein (Fig. 7B). Interestingly, cell death was partially abrogated by Ry co-treatment (Fig. 7A-B), suggesting that cell survival was improved through prevention of RyR-mediated ER Ca²⁺ leak in response to TM-induced ER stress. In contrast, despite an observed effect to partially restore ER Ca²⁺ levels (Fig. 5C), XeC was unable to reduce caspase activity in response to IL-1β+HG (Fig. 7C).

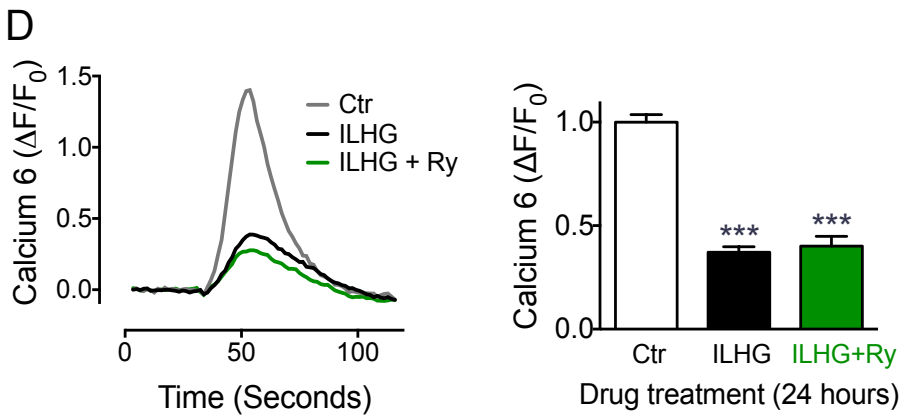
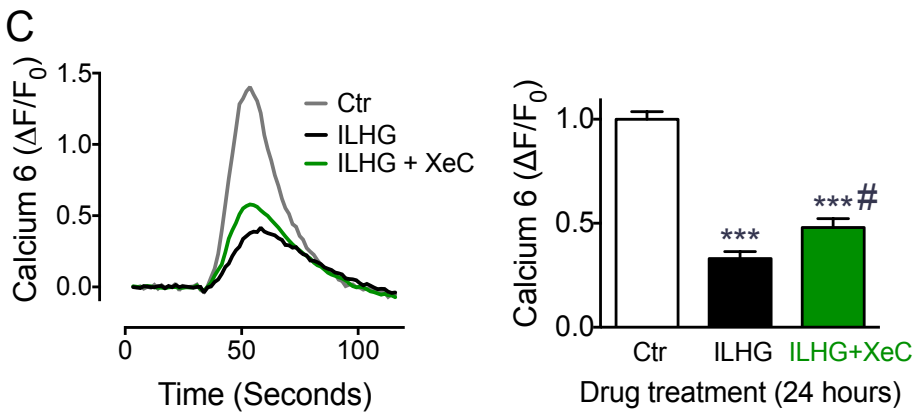
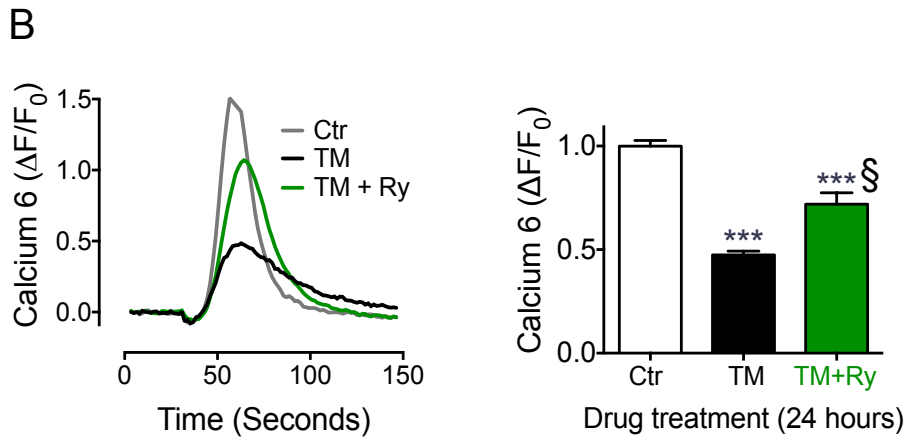
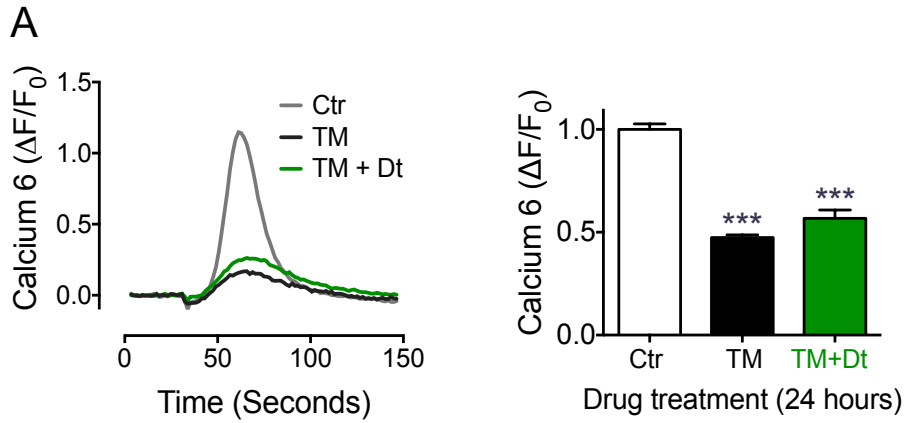


Figure 6. ER Ca²⁺ loss was prevented by blocking RyR under ER stress conditions and by IP₃R blockade under pro-inflammatory cytokine stress conditions

INS-1 cells were treated with 300nM TM for 24 hours with or without 1 μM Dantrolene (Dt) (A) or 100 μM Ryanodine (Ry) (B). (A-B) Representative traces for TG-induced Ca²⁺ release (left), and quantified results (right); n = at least 11 replicates per condition. (C-D) INS-1 cells were treated with 5 ng/ml IL1β+25 mM glucose (ILHG) for 24 hrs with or without 5 μM XeC (C) or 100 μM Ry (D). (C-D) Representative traces for the TG-induced Ca²⁺ release (left), and quantified results (right); n = at least 15 readings per condition; *p ≤ 0.05; **p≤ 0.01; ***p≤ 0.001 compared to control conditions. §p ≤ 0.001 for comparison between TM and TM + Ry. #p ≤ 0.05 for comparison between ILHG and ILHG + XeC.

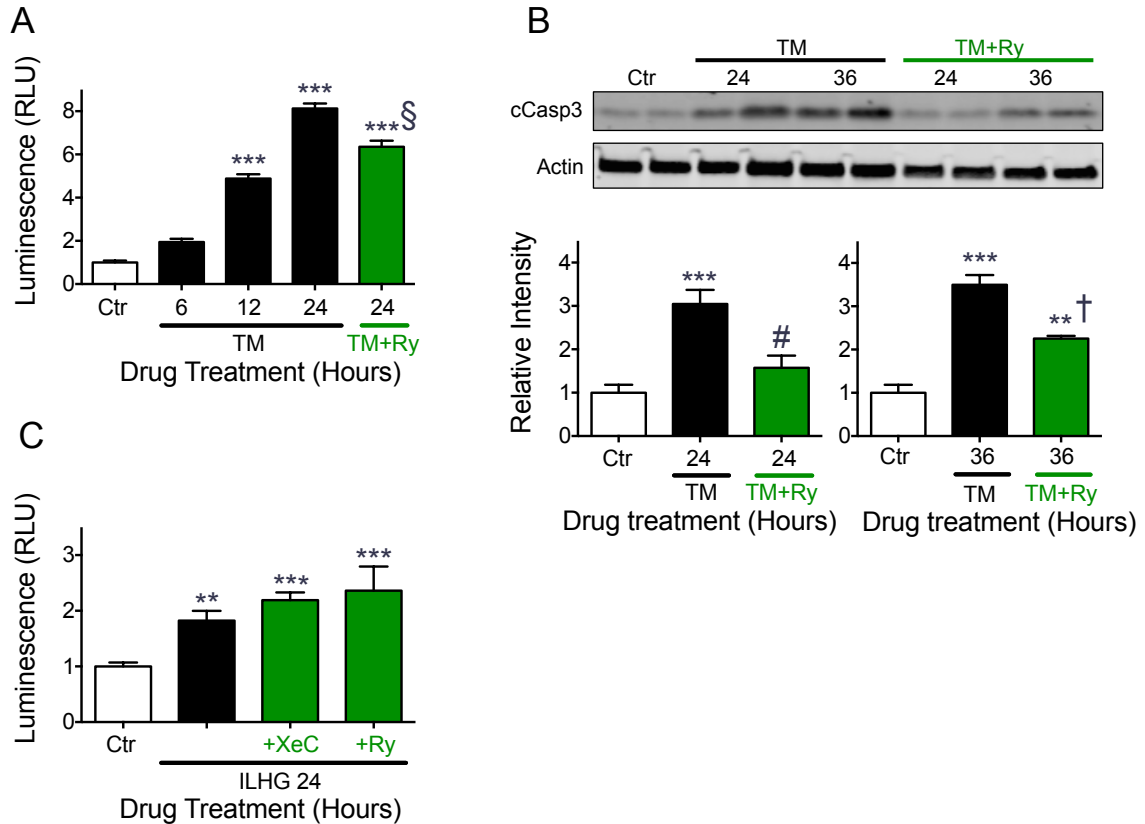


Figure 7. Ryanodine treatment prevented TM-induced cell death

(A) Caspase 3/7 activity was measured in INS-1 cells treated with 300 nM TM with or without 100 μ M uM Ryanodine for indicated times; n = 4 replicates for each timepoint and condition. (B) Immunoblot analysis was performed in INS-1 cells treated with 300 nM TM with or without 100 μ M Ryanodine for indicated times using antibodies against cleaved caspase-3, and Actin. Quantitative protein levels from three independent experiments are shown graphically. (C) Caspase 3/7 activity was measured in INS-1 cells treated with 5 ng/ml IL1 β + 25 mM glucose (ILHG) for 24 hours; n = 4 replicates for each condition. **p \leq 0.01 and ***p \leq 0.001 compared to control conditions. In (A), \S p \leq 0.001 for the comparison between TM for 24 hrs and TM+Ry for 24 hrs. In (B), #p \leq 0.05 and †p \leq 0.01 for the comparisons between TM and TM + Ry for 24 and 36 hrs, respectively.

2.4 Reduction of ER Ca²⁺ leak via the RyR suppressed TM-induced Ca²⁺ transients and activation of the UPR

Results thus far suggested a dominant role for RyR dysfunction under ER stress conditions, but primarily focused on bulk analysis of Ca²⁺ dynamics in large cell populations. To define patterns of ER Ca²⁺ leak through the RyR in real-time at the single-cell level, spontaneous Ca²⁺ transients were measured in response to graded Ca²⁺ loading. Ca²⁺ serves as the primary ligand of the RyR. Spontaneous Ca²⁺ transients are observed in excitable cells, such as neurons and cardiac myocytes and have been shown to be coupled with ER Ca²⁺ leak through the RyR (287). To date, this process has not been studied in the pancreatic β cell, either under normal or stress conditions. By increasing extracellular Ca²⁺ concentration up to 2 mM, oscillating and spontaneous Ca²⁺ transients were induced in 10.40 % \pm 1.54 % (S.E.M) of β cells under control conditions. In response to TM-induced ER stress, the percentage of responding cells increased significantly, to a maximum of 55.74 % \pm 6.67 % of cells after 12 hrs of treatment (Fig. 8A, C). Ryanodine co-treatment was found to significantly decrease TM-induced Ca²⁺ transients (Fig. 8A, D), suggesting the ER Ca²⁺ leak was mediated through the RyR. Notably, the response to caffeine, a pharmacological agonist of the RyR, was inhibited in the presence of 100 μ M Ry (Fig. 8B), confirming that Ry was indeed acting through inhibition of RyR-mediated Ca²⁺ transients and cellular hyperexcitability.

To define whether β cell depolarization contributed to these ER-stress induced Ca²⁺ transients, cells were hyperpolarized by diazoxide (Dz) to inhibit activation of voltage-dependent Ca²⁺ channels (VDCCs). In this context, spontaneous Ca²⁺ transients induced by tunicamycin were similarly reduced (Fig. 8E), suggesting that ER-stress induced Ca²⁺ transients originate from ER Ca²⁺ leak from the RyR as well as through secondary signals generated by Ca²⁺ influx through VDCCs.

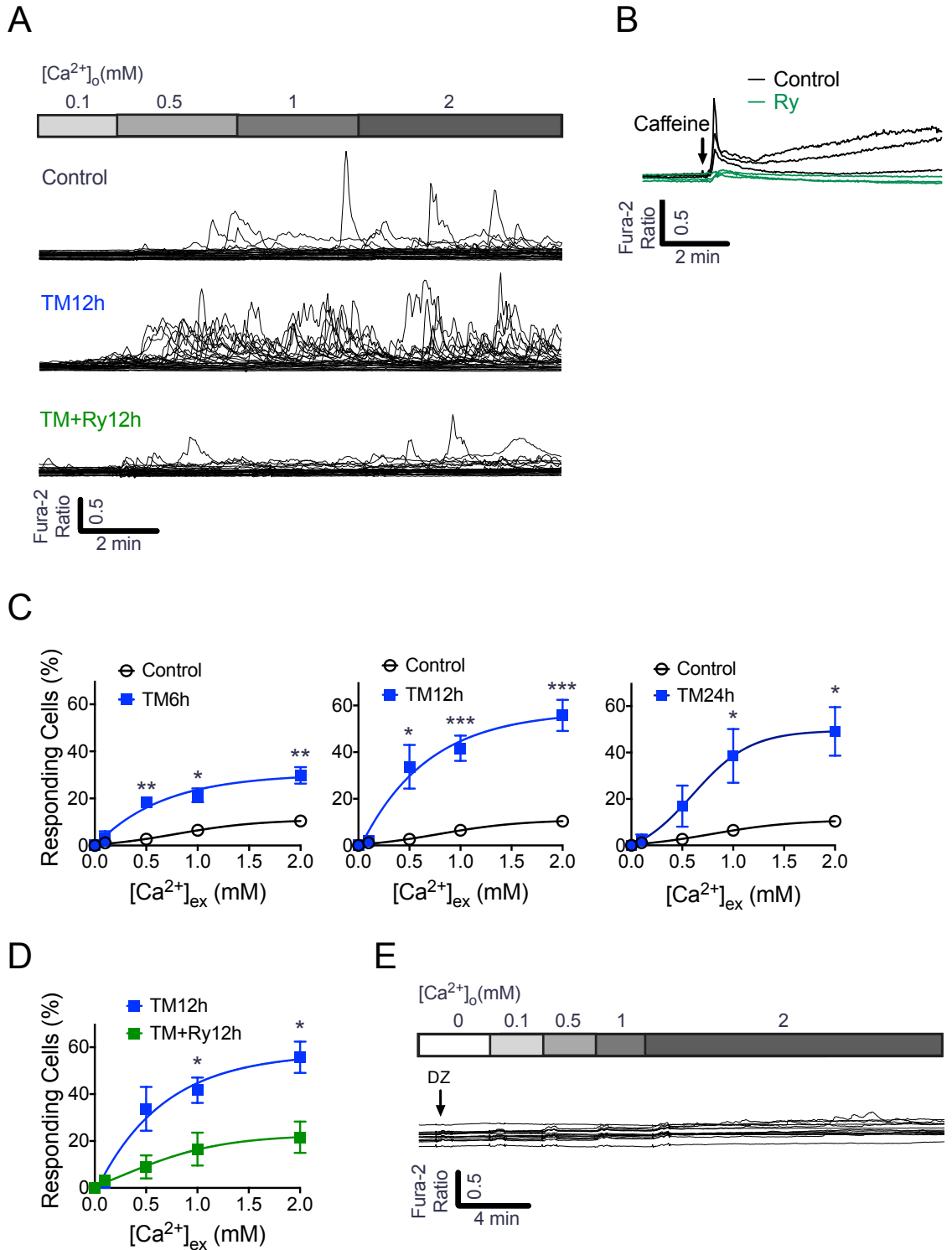


Figure 8. ER Ca²⁺ dynamics regulated electrical activity of β cells

(A) Intracellular Ca²⁺ transients were measured in response to graded Ca²⁺ loading in INS-1 cells treated under control conditions (top), following treatment with TM for 12 hrs

(middle), or following co-treatment with TM + Ry for 12 hrs (both). Data shown are representative of 30 single cell recordings from at least three independent experiments. (B) Traces show intracellular Ca^{2+} levels in INS-1 cells in response to caffeine treatment under control conditions and with ryanodine pre-treatment. (C) Percentages (%) of responding cells in INS-1 cells treated with TM for 6 hrs (n= 2 replicates); 12 hrs (n = 5 replicates); and 24 hrs (n = 4 replicates). (C) The % of responding cells was significantly reduced by Ry co-treatment (n = 3 replicates per conditions). (D) Representative trace indicates that spontaneous TM-induced Ca^{2+} transients were reduced by diazoxide (Dz). Data shown are representative of 15 single cell recordings. * $p \leq 0.05$; ** $p \leq 0.01$; *** $p \leq 0.001$ for indicated comparisons.

During ER stress, cells activate an adaptive response known as the UPR in order to both clear unfolded proteins and increase the folding capacity of the ER (288). However, prolonged UPR activation eventually leads to apoptosis if cellular homeostasis is not restored (289,290). While UPR activation has been linked with ER Ca^{2+} loss (138), the temporal relationships and causal effects between UPR activation and ER Ca^{2+} loss remain poorly understood. To address, we first measured *XBP1* mRNA splicing to validate this marker as an early upstream indicator of UPR activation. An increase in the spliced to total *XBP1* ratio was observed within 2 hrs of TM treatment and occurred prior to induction of both AFT4 and CHOP expression, which both increased around 6 hrs (Fig. 9A). Next, time-course experiments were performed to define how suppression of ER Ca^{2+} leak from the RyR impacted UPR activation. Our results revealed that ryanodine was able to significantly delay TM-induced UPR activation (Fig. 9B). To study this further, single-cell Ca^{2+} transients were measured at these early timepoints. Intracellular Ca^{2+} transients were found to increase within 3 hrs of TM treatment. Similar to results obtained with chronic TM treatment, co-treatment with Ry was sufficient to suppress these Ca^{2+} transients (Fig. 9C-D), indicating that ER Ca^{2+} leak is an early response to misfolded protein accumulation that occurs prior to full expression of the ER stress signaling cascade. Moreover, our results indicated that suppression of RyR-mediated Ca^{2+} leak was sufficient to reduce propagation of the UPR.

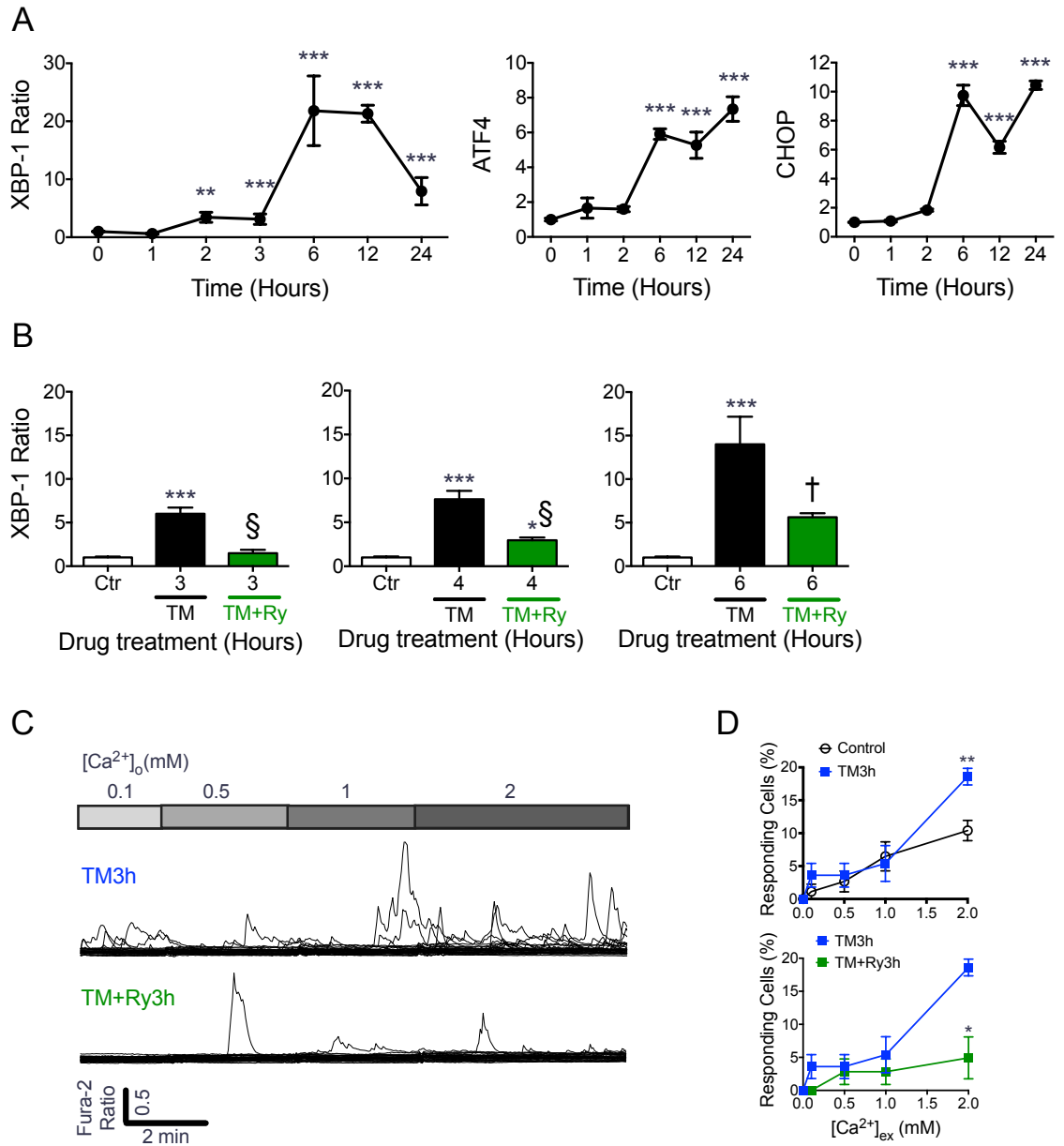


Figure 9. Inhibition of RyR-mediated ER Ca²⁺ leak attenuated activation of the unfolded protein response

(A) INS-1 cells were treated with 300 nM TM for indicated times, and mRNA levels of the spliced/unsliced XBP-1 ratio, ATF4, and CHOP were measured by RT-PCR. (B) The spliced/unsliced XBP-1 ratio was measured by RT-PCR in INS-1 cells treated with TM or TM+Ry for 3 hrs (left panel), 4 hrs (center), and 6 hrs (right panel). ** $p \leq 0.01$; *** $p \leq 0.001$ compared to time 0 or control conditions; † $p \leq 0.01$ and § $p \leq 0.001$ for

comparisons between TM and TM + Ry groups. (C) Intracellular Ca^{2+} transients were measured in response to graded Ca^{2+} loading in INS-1 cells treated with TM for 3 hrs (top) or following co-treatment with TM+Ry for 3 hrs (bottom). Data shown are representative of 30 single cell recordings with n=at least 3 replicates for each condition. (D) Quantification of the % of responding cells in INS-1 cells treated under controls conditions, with TM or with TM + Ry for 3 hrs; n = at least 3 replicates for each condition. * $p \leq 0.05$; ** $p \leq 0.01$ for comparison between indicated groups.

2.5 Pharmacological inhibition of the RyR improved intracellular Ca²⁺ dynamics in TM-treated human islets and islets isolated from Akita mice

To test whether these findings could be recapitulated in a human model system, dispersed cadaveric human islets were treated with tunicamycin and intracellular Ca²⁺ transients were measured. Similar to results observed in INS-1 β cells, spontaneous Ca²⁺ transients were induced under ER stress evoked by TM, and ryanodine co-treatment decreased TM-induced Ca²⁺ transients (Fig. 10A-B),

Finally, we tested whether RyR inhibition would show similar result in an islet model of misfolded protein accumulation and ER stress (283,284). To this end, islets were isolated from 6-week old Akita mice and incubated with ryanodine or DMSO for 24 hours. Fura-2 AM imaging was performed to measure glucose-induced Ca²⁺ oscillations (GICOs). GICOs were markedly diminished in Akita islets under control conditions, while treatment with ryanodine improved the oscillation frequency and area under the curve of the glucose-induced Ca²⁺ responses (Fig. 10C-E). Moreover, Ry treatment significantly decreased the area of dead cells in islets from Akita mice (Fig. 10F-G). Finally, glucose stimulated insulin secretion (GSIS) was measured, the fold-increase of insulin secretion was the same between DMSO and Ry treated Akita islets.

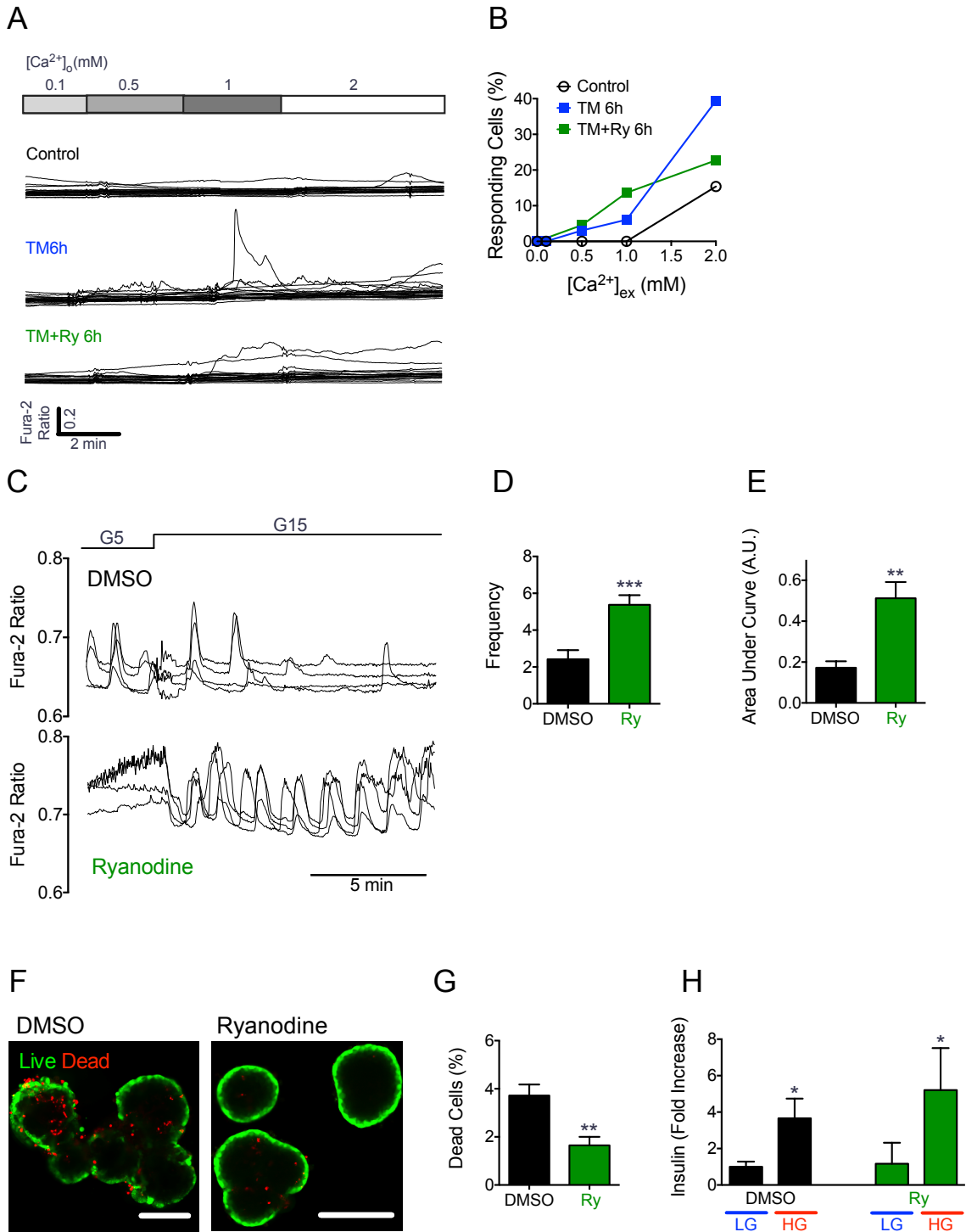


Figure 10. Ca²⁺ signaling and cell death were rescued by ryanodine treatment in tunicamycin-treated human islets and islets from Akita mice

(A) Representative data from 20 single cell calcium recordings performed in dispersed cadaveric human islets from a single biological donor analyzed under control conditions (top), following treatment with TM for 6 hrs (middle), and following co-treatment with TM + Ry for 6 hrs (bottom). (B) The % of responding cells was quantified for each condition. (C) Glucose-stimulated calcium oscillations were measured in islets isolated from Akita mice treated with DMSO or Ryanodine for 24 hrs. Shown are representative recordings from 4 individual islets. (D) The frequency of oscillations and area under curve for calcium responses (E) were quantified from 3 biological replicates per conditions. (F) Representative pictures of Live (green) and Dead (red) staining performed in Akita islets treated with DMSO or Ryanodine for 48 hrs. (G) Quantification of the % of dead cells from n=3 replicates per condition. (H) Using Akita islets GSIS was measured after treating DMSO or 100 μ M Ry for 48 hrs. LG indicates low-glucose treated group and HG indicates high-glucose treated group with n=3 replicates; *p \leq 0.05; **p \leq 0.01; ***p \leq 0.001 for comparisons between indicated groups.

3.1 Summary and significance

The Ca^{2+} concentration within the lumen of the β cell ER is estimated to be three orders of magnitude higher than intracellular Ca^{2+} levels. Ca^{2+} within this cellular compartment serves as an essential cofactor for protein chaperones and foldases required for insulin processing, while Ca^{2+} release from the ER regulates glucose-stimulated Ca^{2+} oscillations and phasic insulin secretion. Loss of ER Ca^{2+} has been shown to lead to impaired insulin secretion as well as activation of cell-intrinsic stress pathways including ER and oxidative stress and reduced β cell survival. Whereas a prominent role for reduced β cell SERCA pump activity has been identified in diabetes, the question remains if alterations in RyR or IP_3 function, which regulate ER Ca^{2+} release, similarly contribute to these processes.

To test this, we applied intracellular and ER- Ca^{2+} imaging techniques to measure ryanodine receptor (RyR) and inositol 1,4,5-triphosphate receptor (IP_3R) activity in response to two distinct stress paradigms known to contribute to the pathogenesis of both type 1 and type 2 diabetes. The stress paradigms tested were ER stress, which was induced chemically using tunicamycin in INS-1 β cells and in cadaveric human islets. Aspects of our model were also evaluated in islets from Akita mice, a strain harboring a spontaneous mutation in one allele of the *INS2* gene, resulting in impaired proinsulin folding and severe ER stress (283,284). To recapitulate pro-inflammatory cytokine induced dysfunction, INS-1 cells were treated with high glucose (25 mM glucose) in combination with $\text{IL-1}\beta$, a cytokine known to be systemically elevated in diabetes. In aggregate, our results revealed a preferential sensitivity of the RyR to ER stress, while pro-inflammatory cytokine stress was found to primarily impact IP_3R activity. Pharmacological inhibition of the RyR with ryanodine and inhibition of the IP_3R

with xestospongins C were both able to prevent ER Ca^{2+} loss under these respective stress conditions. However, inhibition of RyR-mediated Ca^{2+} loss was distinct in its ability to prevent β cell death. Additional analysis showed that RyR inhibition also delayed the initiation of the UPR and an improvement of glucose-induced Ca^{2+} oscillations and insulin secretion.

The RyR is a large macromolecular complex that is primarily localized to the ER or sarcoplasmic reticulum membranes. The RyR remains closed at low intracellular Ca^{2+} concentrations. However, as intracellular Ca^{2+} levels increase in the range of 0.01-20 μM , Ca^{2+} binds the receptor, leading to channel opening and ER Ca^{2+} release (179). In addition to ligand binding, channel activity is modulated by a number of interacting proteins contained within this macromolecular complex (156-159). RyR was found to be expressed on the surface of β cell dense core secretory vesicles (291), and two independent groups have demonstrated secretory vesicle Ca^{2+} release in response to RyR activation, (291) indicating the RyR may also regulate localized Ca^{2+} signals responsible for granule exocytosis.

RyR dysfunction has been well-documented in a number of other disease states including cancer-associated muscle weakness (153), Alzheimer's disease (171), and cardiomyopathy (164). In contrast, only a handful of studies have investigated whether β cell RyR dysfunction contributes to the diabetes pathophysiology. Luciani and colleagues found that both RyR and IP_3R inhibition were able to attenuate thapsigargin-induced ER stress in MIN6 β cells (211). This approach caused ER stress by inducing ER Ca^{2+} loss, therefore this does not likely show how ER stress affects ER Ca^{2+} dynamics and cell death. To address this, we have induced ER stress directly by using TM, and our analysis was uniquely able to distinguish the impact of two different stress paradigms on RyR and IP_3R activity and function, a topic unaddressed in previous studies. Our results indicate that RyR dysfunction is uniquely induced by misfolded

protein accumulation, while pro-inflammatory cytokine stress had little impact on RyR function. In support of our findings, the RyR antagonist, dantrolene, was previously shown to reduce cell death in INS-1 β cells lacking WSF1 protein, another model of severe ER stress (212).

To document the mode of RyR dysfunction in response to ER stress, we measured spontaneous intracellular Ca^{2+} transients at the single cell level in response to graded increase in extracellular Ca^{2+} . Our results indicate that ER-stress lowers the threshold and frequency of RyR-mediated ER Ca^{2+} release in both INS-1 cells and cadaveric human islets. We also found these ER-stress induced Ca^{2+} transients were composed of both ER Ca^{2+} release and Ca^{2+} influx through VDCCs, thus contributing to an overall state of β cell hyperexcitability. These results are consistent with findings in other excitable cells and pathologic states. For example, prion as well as amyloid-beta protein accumulation in cortical neurons has been shown to lead to ER stress, ER Ca^{2+} release from the RyR, and increased neuronal excitability (292).

A handful of molecular pathways have been implicated as potential contributors to β cell RyR dysfunction. Mice with a mutated form of the RyR2 leading to constitutive CaMKII-mediated phosphorylation and chronic RyR2 gain of function exhibited impaired glucose-induced insulin and Ca^{2+} responses as well as glucose intolerance (293). Similarly, RyR mutations that lead to dissociation of calstabin2 have been shown to lead to RyR gain of function, resulting in a condition known as catecholaminergic polymorphic ventricular tachycardia (CPVT) in humans. Mice expressing two mutated forms of the RyR2 associated with CPVT were shown to be glucose intolerant. Isolated islets exhibited decreased glucose-stimulated insulin secretion and impaired mitochondrial metabolism. Intriguingly, humans with CPVT were found to have higher glucose levels and lower insulin levels during an oral glucose tolerance test compared to age and BMI-matched controls (210). Oxidative stress has been shown to contribute to both calstabin

dissociation from the RyR as well CaMKII-mediated RyR phosphorylation. Indeed, alterations in calstabin and RyR association have been demonstrated in islets from donors with Type 2 diabetes (210). Recently, loss of sorcin, a Ca^{2+} sensor protein that inhibits RyR activity, was similarly shown to lead to glucose intolerance, while sorcin overexpression improved GSIS and ER Ca^{2+} storage. Palmitate-induced lipotoxicity decreased sorcin expression in human and mouse islets (294). Interestingly, in a model of Parkinson's disease, ER stress itself led to aberrant accumulation of RyR, resulting in increased ER Ca^{2+} release (295). Thus, whether RyR dysfunction occurs secondary to loss of stabilizing or inhibitory protein, through impaired receptor degradation, or through yet another distinct mechanism in the pancreatic β cell will be explored in future studies. Notwithstanding this unknown, our data suggests that targeting the RyR receptor has the potential to improve β cell survival through attenuation of ER stress as well and β cell function through restoration of glucose-induced Ca^{2+} oscillations and improved insulin secretion (Fig. 11). Drug discovery efforts are actively done aimed at identifying small molecular RyR-stabilizers (296). In aggregate, our data suggest such compounds may have utility in improving the health of the diabetic β cell.

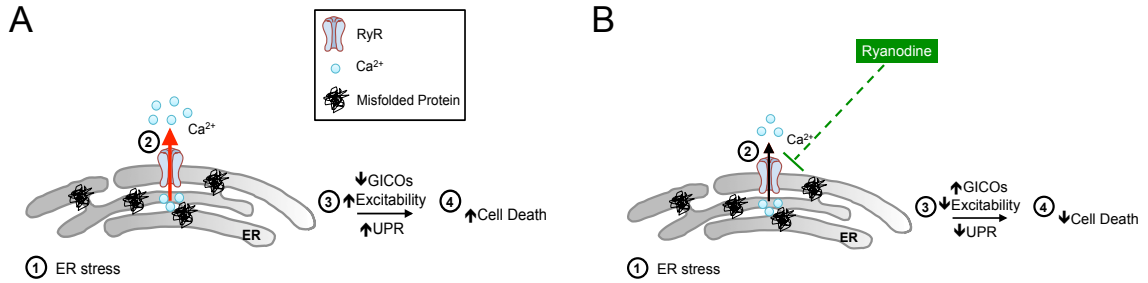


Figure 11. Model for protecting ER Ca²⁺ dynamics by RyR inhibition under ER stress

ER stress leads to RyR-mediated ER Ca²⁺ leak, while inhibition of RyR-mediated ER calcium loss restores ER Ca²⁺ dynamics, glucose-stimulated calcium oscillations and attenuates UPR activation and cell death. (A) Our data indicate that under ER stress conditions, RyR function is disrupted, leading to decreased ER Ca²⁺ storage and altered ER Ca²⁺ dynamics. As a consequence, cellular excitability and GICOs are disrupted and activation of the UPR is increased, eventually leading to cell death. (B) Inhibition of RyR-mediated loss of ER Ca²⁺ leads to a partial rescue of ER Ca²⁺ dynamics under ER stress conditions. This leads to improved cellular excitability, improved GICOs, delayed initiation of the UPR, and improved cellular survival.

3.2 Limitations and Future Study

3.2.1 Techniques to measure ER Ca²⁺ dynamics

In the current research, we have estimated free ER Ca²⁺ concentration in populations of β cells under stress conditions by measuring the increase in intracellular Ca²⁺ following pharmacological inhibition of SERCA in Ca²⁺ free extracellular solutions using the calcium indicator, Calcium 6. SERCA inhibition results in passive ER Ca²⁺ release from RyR and IP₃R until ER Ca²⁺ is depleted (Fig. 3). The kinetics of ER Ca²⁺ release induced by TG is slow process due to the passive release from RyR and IP₃R and reaches a peak fluorescent intensity in tens of seconds to minutes. The kinetics of this process is also affected by the function of plasma membrane ion transporters such as PMCA and NCX whose function may also have been altered by the stress conditions (297). While this technique is widely accepted, inhibition of plasma membrane and organellar Ca²⁺ transporters would have given better estimation especially when it comes to the small change induced by weaker stress.

Furthermore, TG induced minimal elevations in intracellular Ca²⁺ in intact islets, so estimation of ER Ca²⁺ levels in islets was not successfully using this approach. Within the islets, β cells are known to be physically connected through gap junction channels (278) and the increase in intracellular Ca²⁺ is likely buffered by neighboring cells. In addition, TG simply may not penetrate cells inside the islet. Therefore, techniques to directly measure ER Ca²⁺ concentration more reliably should be considered.

We also measured directly ER Ca²⁺ release by using low affinity Ca²⁺ indicator, Mag-fluor 4 AM (Fig. 4 and 5). This was a technique that enabled a high-throughput format and was beneficial in making dose-response curves with agonists. Although this directly measured Ca²⁺ in ER, imaging was done after permeabilization of plasma membrane and by studying population of cells.

The approaches taken above can capture only one aspect of ER Ca^{2+} such as ER Ca^{2+} concentration or ER Ca^{2+} release. These approaches do not capture ER Ca^{2+} dynamics, which are more relevant to physiological activities. Our approach to measure spontaneous intracellular Ca^{2+} transients provides some insight into ER Ca^{2+} dynamics, and showed that bursts of ER Ca^{2+} release increased under ER stress conditions (Fig. 8). Nevertheless, the techniques that can reliably detect ER Ca^{2+} dynamics by directly measuring ER Ca^{2+} will be beneficial, which will be discussed in the future direction.

3.2.2 Basis of RyR and IP₃R dysfunction

Our results from functional assays showed that RyR function was altered under ER stress, while IP₃R function was preferentially altered under pro-inflammatory stress conditions (Fig. 4 and 5). This data was supported by results showing that ER Ca^{2+} loss induced by these respective stress conditions were rescued by inhibiting RyR under ER stress conditions and IP₃R in response to pro-inflammatory stress (Fig. 6 and 7). This approach enabled us to document receptors dysfunction. However, the basis of the dysfunction was not addressed in the current study. This information will be crucial in order to identify more specific drug target.

Possible molecular mechanisms that may cause changes in overall receptor function include changes in expression levels and post-translational modifications. The known regulation of RyR and IP₃R by post-translational modification was summarized in detail in the Introduction section. For instance, RyR undergoes phosphorylation and oxidation, and nitrosylation that can cause dissociation of RyR stabilizing protein calstabin resulting in Ca^{2+} leak from ER (298-300). It is likely that ER stress may have induced one of these modifications, leading to ER Ca^{2+} release and increased intracellular Ca^{2+} transients that exacerbate UPR activation and lead to cell death.

Inhibition of RyR by Ry under ER stress conditions may have mitigated the deleterious effects of these post-translational modifications. Our result showed that S107, which stabilizes the RyR and calstabin interaction did not restore the ER Ca^{2+} under ER stress (Fig. 12). This indicates either ER stress was robust enough to nullify the effects of S107 or that other post-translational modifications were involved in this process. These possibilities could be tested in future studies.

Likewise, IP_3R can be regulated by phosphorylation or by the binding of associated proteins to its regulatory domain. For instance, PKA activation leads to an opening of IP_3R (301,302). Therefore, a more thorough understanding of the effects of post-translational modifications will be necessary. In addition, these results may need to be studied within the context of ER Ca^{2+} dynamics, because efforts to stabilize the calstabin interaction or prevent oxidative stress, for example, may impact spontaneous ER Ca^{2+} release without being able to restore ER Ca^{2+} .

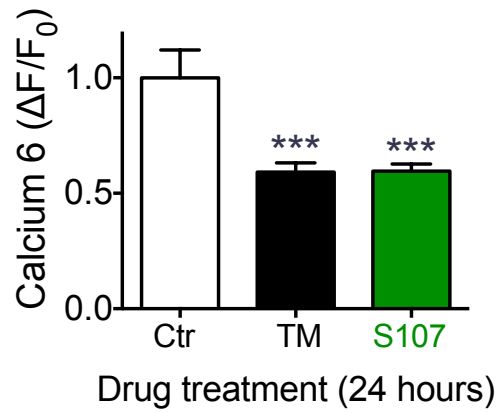


Figure 12. ER Ca²⁺ loss was not prevented by the RyR stabilizer S107 under ER stress conditions

INS-1 cells were treated with 300nM TM for 24 hours with or without 10 μM S107; n = at least 3 replicates per condition; ***p≤ 0.001 compared to control conditions.

3.2.3 Limitations arising from the use of rodent models

The current study was performed using cell lines and through *ex vivo* analysis of islets from rodent models. These models may not necessarily recapitulate *in vivo* findings. Therefore, key aspects of our model need to be confirmed using *in vivo* models and in human islets and humans. There are considerable difference even in islets between mouse and humans. In a mouse islet, α cells reside mostly on the surface of an islet, while β cells tend to be more in the center of the islet (303). In contrast, α cells and β cells are equally distributed throughout the human islet (303). In addition to localization within islets, channels regulating to Ca^{2+} dynamics and action potentials in β cells are different between mice and human. For instance, human and mouse β cells both express Na^+ channels. Na^+ channels in human β cells amplify action potentials (47), but the Na^+ channels in mouse β cells has minimal effects (251). P/Q-type Ca^{2+} channels and L-type Ca^{2+} channels (Cav 1.2 and 1.3) elicit about 40% of Ca^{2+} current each in human β cells (47), but L-type Ca^{2+} channels elicits more than 60% of total Ca^{2+} current in mouse β cells and P/Q-type Ca^{2+} channels have minimal effects (251).

In addition, *in vivo* plasma glucose levels are continuously fluctuating, and β cells will be exposed to a countless number of molecules such as hormones, lipids or cytokines that can regulate channel activities and as well as cellular activities. To make matters more complicated, there are neuronal innervations to islets and β cells. These include efferent neurons coming from brain as well as inter and intra-islet neuronal networks (304). Therefore, studying β cell function *in vivo* is crucial.

Finally, our apoptosis or cell death assay was difficult to apply to islets. This may be because islets the expression levels of proteins related to apoptosis are low, or macrophages clear dead cells fairly quickly (305). Therefore studying *in vivo* with all these things could tell you more about the relevance of human diseases.

3.2.4 Future directions

Studying ER Ca^{2+} dynamics in islets or β cells is challenging due to the limitations with currently available techniques mentioned above. The genetically-encoded Ca^{2+} indicator D4ER maybe able to resolve the problem, however islet cells exhibits autofluorescence when excited at blue or green light (~430-490 nm) (306), which will cross contaminate and mask the fluorescence of D4ER (Ex. 435 nm, Em. 540 and 475 nm), which is the fluorescent Förster resonance energy transfer (FRET)- based ER Ca^{2+} indicator widely used. To solve the issue with autofluorescence, a Ca^{2+} indicator with other wavelenghtes such as mCherry CEPIA (307), or bioluminescence resonance energy transfer (BRET)- based Ca^{2+} indicator (308) would be worthwhile options. BRET is advantageous because it does not require any excitation light, and does not undergo photobleaching because of illumination.

To overcome the limitations with *in vitro* studies, it will be beneficial to perform experiments *in vivo*. To conduct Ca^{2+} imaging *in vivo*, our lab has recently generated an insulin Cre-induced GCaMP6s mouse line. Using this line, we can express GCaMP6s, which are genetically encoded high affinity Ca^{2+} indicator, in β cells. Our approach could be to apply intravital microscopic techniques to image the mouse pancreas (309,310). With this approach, pancreata will be surgically exposed outside the body and the pancreas can be imaged using two-photon microscopy. With this technique, Ca^{2+} oscillation *in vivo* could be studied and this will greatly advance the field to study hormonal, neuronal, and pharmacological regulation of Ca^{2+} in β cells. To follow up the current study, mouse with inducible RyR knockout model under stress conditions could be used to replicate what we found in β cell line and mouse pancreatic islets.

This intravital microscopy will be beneficial not only for the Ca^{2+} imaging, but can also be applied to visualize many other biological assays. For instance, the apoptosis and cell death assay could be tested *in vivo*, and the interactions of immune cells could

be clarified by also visualizing macrophages. Furthermore, UPR marker such as Xbp1 or Chop could be visualized *in vivo* as well.

Chapter 4. Materials and Methods

4.1 Materials

4.1.1. Animals, islet isolation and human islet preparation

a. Mice

C57BL/6J (WT) mice, Akita mice, and db/db mice were obtained from Jackson Laboratories (Bar Harbor, ME) at 5 - 10 weeks of age, and maintained under protocols approved by the Indiana University Institutional Animal Care and Use Committee, the U.S. Department of Agriculture's Animal Welfare Act (9 CFR Parts 1, 2, and 3), and the Guide for the Care and Use of Laboratory Animals

b. Human islets

Human cadaveric islets isolated from non-diabetic donors were obtained from the Integrated Islet Distribution Program or the National Disease Research Interchange. Upon receipt, human islets were hand-picked and allowed to recover overnight in Dulbecco's modified essential medium (DMEM) medium containing 5.5mM glucose, 10% fetal bovine serum (FBS), 100U/ml penicillin, and 100µg/ml streptomycin.

4.1.2 Cell culture and islet isolation

INS-1 832/13 rat insulinoma cells were cultured in regular 11mM glucose Roswell Park Memorial Institute medium (RPMI) 1640 supplemented with 10mM 4-(2-hydroxyethyl)-1-piperazineethanesulfonic acid (HEPES) buffer, 1mM sodium pyruvate, 50µM β-macapt ethanol and, 10% FBS, penicillin and streptomycin.

Mice islets were isolated by collagenase digestion as described previously (311). The islets were hand-picked, and allowed to recover overnight in regular RPMI supplemented with 10% FBS, 100U/ml penicillin, and 100µg/ml streptomycin.

4.1.3. Primers, antibodies and reagents

Standard polymerase chain reaction (PCR) reactions for quantitative PCR (qPCR) for gene expressions were performed using oligonucleotides synthesized by Invitrogen (**Table 3**).

Antibodies used in western blotting, immunofluorescent and immunohistochemistry staining are listed in **Table 2**. Chemicals and reagents used in the research are listed in **Table 4**.

Table 2. Antibodies for Western Blotting and Immuno-staining

Targeted protein	Host Species	Manufacturer	Dilution
Total caspase 3	Rabbit	Cell Signaling	1:1000
Mouse IgG (IRDye 800CW)	Donkey	Li-cor	1:10000

Table 3. Quantitative RT-PCR Primers

Gene	Species	Forward (5'-3') Reverse (5'-3')
<i>Total Xbp-1</i>	<i>Rattus rattus</i>	AGCACTCAGACTACGTGCGCCTC CCAGAATGCCCAAAGGATATCAG
<i>Spliced Xbp-1</i>	<i>Rattus rattus</i>	CTGAGTCCGCAGCAGGT TGTCAGAGTCCATGGGAAGA
<i>ATF4</i>	<i>Rattus rattus</i>	GTTGGTCAGTGCCTCAGACA CATTGAAACAGAGCATCGA
<i>CHOP</i>	<i>Rattus rattus</i>	CCAGCAGAGGTCACAAGCAC CGCACTACCACTCTGTTTC

Table 4. Chemicals and Reagents

Name	Manufacturer
Caffeine	Santa Cruz
D-Glucose	Sigma-Aldrich
Hanks' Balanced Salt Solution (HBSS)	Lonza
D-myo-Inositol-1,4,5-triphosphate hexapotassium salt (IP ₃)	Santa Cruz
Xestospongine C	Santa Cruz
Tunicamycin	Cayman Chemicals
Thapsigargin	Cayman Chemicals
Fura-2-acetoxymethylester (Fura-2 AM)	Thermo Fisher
Mag-Fluo-4 AM	Thermo Fisher
Mouse IL-1 beta Recombinant Protein (IL-1 β)	Thermo Fisher
Diazoxide	Sigma-Aldrich
Dantrolene	Sigma-Aldrich
Adenosine 5'-triphosphate magnesium salt (ATP)	Sigma-Aldrich
Ryanodine	Tocris
Carbonyl cyanide-4-(trifluoromethoxy)phenylhydrazone (FCCP)	Tocris
Calcium 6	Molecular Devices

Table 5. Ca²⁺ indicators and Wavelengths

Name	Excitation and Emission Wavelength	Manufacturer
Calcium 6	Ex. 490 nm, Em. 525 nm	Molecular Devices
Fura 2AM	Ex. 340 and 380 nm, Em. 510 nm	Thermo Fisher
Mag-fluor 4AM	Ex. 490 nm, Em. 525 nm	Thermo Fisher

4.2 Methods

4.2.1 Animal studies and cell culture

Male C57BL/6J, heterozygous $Ins2^{Akita}$ (Akita), and C57BLKS-homozygous Lep^{db} (db/db) mice were obtained from Jackson Laboratories (Bar Harbor, ME) and maintained under protocols approved by the Indiana University Institutional Animal Care and Use Committee. Mice were kept in a standard light-dark cycle with *ad libitum* access to food and water. Pancreatic islets were isolated by collagenase digestion, hand-picked, and allowed to recover overnight as described previously (311). INS-1 832/13 rat insulinoma cells were maintained according to previously published protocols (312,313).

4.2.2 Immunoblot and quantitative PCR

Immunoblot experiments were performed as described (314). In brief, cells were lysed in 1% IGEPAL reagent supplemented with 10% glycerol, 16 mM NaCl, 25 mM HEPES, Sigma-Aldrich, St. Louis, MO), 60 mM n-octylglucoside (Research Products International Corp.), phosphatase inhibitor cocktails (PhosSTOP tablets, Roche) and phosphatase inhibitor cocktails (EDTA-free cOmplete tablets, Roche). Protein concentration was measured using the Bio-Rad DC protein assay (Bio-Rad, Hercules, CA) and a SpectraMax M5 multiwell plate reader (Molecular Devices, Sunnyvale, CA). Equal concentrations of proteins were suspended in 10% SDS solution. Protein lysates were electrophoresed and transferred to methanol-activated PVDF membrane (Immobilon-FL Transfer Membrane from Millipore). Membranes were then blocked with Odyssey blocking buffer (LI-COR, Lincoln, NE) prior to incubation with primary antibodies listed in **Table 2**. Subsequently, membranes were incubated with IRDye 800 or 680 fluorophore-labeled secondary antibodies from LI-COR. The total protein levels

were normalized to actin protein levels. Images were analyzed using LI-COR Image Studio and Image-J software (National Institutes of Health, Bethesda, MD, USA).

For qPCR, Cultured cells or isolated islets were processed for total RNA using the Qiagen RNeasy Mini Plus kit (Valencia, CA, USA). For reverse transcription-PCR experiments, total RNA was processed using Moloney murine leukemia virus (MMLV) reverse transcriptase (Invitrogen, Grand Island, NY). Subsequently, qPCR was performed using JumpStart™ Taq DNA Polymerase (Sigma-Aldrich, St. Louis, MO), and using SYBR Green I dye and previously published methods (312). Primers used for qPCR is listed in **Table 3**.

4.2.3 Stress simulation

To mimic the pro-inflammatory stress milieu of diabetes, cells and mouse islets were treated in RPMI media containing 5 ng/mL of mouse IL-1 β for indicated times. To mimic the ER stress in diabetic milieu, INS-1 cells or mouse islets were cultured in RPMI containing 300 nM TM with indicated times.

4.2.4 Intracellular calcium (Ca²⁺) imaging

Intracellular Ca²⁺ was measured using the FLIPR Calcium 6 Assay Kit and the Molecular Devices FlexStation 3 system (Sunnyvale, CA, USA) or using the ratiometric Ca²⁺ indicator Fura-2 AM as previously outlined (315). In brief, INS-1 832/13 cells were plated in black wall/clear bottom 96-multiwell plates from Costar (Tewksbury, MA, USA) and cultured for 2 days. Following drug or stress treatment, cells were transferred to Ca²⁺ free Hanks' balanced salt solution from Lonza (Basel, Switzerland) supplemented with 0.2% BSA and EGTA. Calcium 6 reagent was added directly to cells, and cells were incubated for an additional 2 hours at 37 °C and 5% CO₂. ER Ca²⁺ was estimated by

measuring the increase of intracellular Ca^{2+} upon application of 10 μM thapsigargin (TG). Data acquisition on the FlexStation 3 system was performed at 37°C using a 1.52-s reading interval with an excitation wavelength of 485 nm and emission wavelength of 525 nm. For data analysis, values derived from the TG response (ΔF) were divided by resting intracellular calcium $[\text{Ca}^{2+}]_i$ (F_0), using the formula $\Delta F / F_0$. Fura-2 AM fluorescence intensity was measured using an excitation wavelength of 340 nm and 380 nm and an emission wavelength of 510 nm. Images were captured using a Zeiss Z1 microscope with a 10x or 20x objective. Spontaneous intracellular Ca^{2+} transients were measured using the method described by Tang et al (287). Briefly, INS-1 cells or dispersed mouse islets were imaged under Ca^{2+} free conditions using Fura-2AM. Extracellular Ca^{2+} was increased in a step-wise fashion to evoke Ca^{2+} transients until a physiological extracellular Ca^{2+} concentration of 2mM was reached. Data were analyzed using Zeiss Zen Blue software (Oberkochen, Germany). The wavelength used for this experiment is summarized in **Table 5**.

4.2.5 IP₃R and RyR functional assays

IP₃R and RyR activation were evaluated in response to IP₃ and caffeine, respectively using modifications to the protocol described by Tovey and Taylor (285). INS-1 cells were loaded with the low-affinity Ca^{2+} indicator, Mag-Fluo-4 AM followed by permeabilization of the plasma membrane with 10 $\mu\text{g}/\text{ml}$ saponin, leaving Mag-Fluo-4 AM in the lumen of cellular organelles. Data acquisition on the FlexStation 3 system was performed at 37°C using a 1.52-s reading interval, with an excitation wavelength of 490 nm and an emission wavelength at 525 nm. To establish steady-state ER Ca^{2+} levels, 1.5mM Mg-ATP was added; then IP₃ or caffeine were applied at the indicated concentrations to activate IP₃R and RyR respectively.

4.2.6 Cell death assays and insulin secretion

To measure Caspase 3/7 activity, INS-1 cells were cultured in black wall/clear bottom 96-multiwell plates for 2 days. Following drug or stress treatment, Caspase-Glo reagent (Promega, Madison, WI) was added directly to cells, and cells were incubated for an additional 30 minutes at room temperature. The luminescence of each sample was measured by using a SpectraMax M5 microplate reader (Molecular Devices). Cell viability in mouse islets was quantitated using the Live/Dead Cell Viability Assay from Thermo Fisher (Waltham, MA), according to the manufacturer's instructions. Images were acquired using a Zeiss LSM 510 confocal microscope, and the area of dead cells was calculated by the ratio of ethidium homodimer-1 positive red area (Dead) and calcein-AM positive green area (Live). Glucose-stimulated insulin secretion was measured in isolated mouse islets as previously described. Insulin secretion into the supernatant was normalized to DNA concentration, and insulin was measured using a mouse insulin ELISA from Mercodia (Uppsala, Sweden) (54,316).

4.2.7 Statistical analysis

Results are displayed as the means \pm S.E.M. GraphPad Prism Software (La Jolla, CA, USA) was used to fit data from IP₃R and RyR functional assays to sigmoidal dose-response curves. Differences between groups were analyzed for significance using GraphPad Prism Software and an unpaired Student's t-Test or one-way ANOVA with Tukey-Kramer post-test. A p value < 0.05 was used to indicate a significant difference between groups.

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CURRICULUM VITAE

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- Using Ca^{2+} imaging and biochemical assays, studying roles of ER Ca^{2+} releasing channels during the progression to diabetes.
- Establishing techniques to do *in vivo* Ca^{2+} imaging on mouse pancreatic β cell.

Indiana University Bloomington, Kyung-Tai Min lab / Department of Biology

Sept 2007 – June 2009, Junior Technician

- Supported the projects to study (1) synaptic dysfunction in Down syndrome using *Drosophila*, (2) mitochondrial dynamics in neurons.
- Maintained over 500 transgenic *Drosophila* lines.

LANGUAGES

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PUBLICATIONS

- Yamamoto, WR., Bone, RN., and Evans-Molina, C. ER Calcium Transporters Are the Key Determinants for the Loss of Calcium Oscillation in Pancreatic β -Cell under Diabetic Stress. In preparation
- Tong, X., Kono, T., Anderson-Baucum, EK., Yamamoto, W., Gilon, P., Lebeche, D., Day, RN., Shull, GE., and Evans-Molina, C. (2016) SERCA2 Deficiency Impairs Pancreatic β -Cell Function in Response to Diet-Induced Obesity. *Diabetes* **65**, 3039-3052
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REPRESENTATIVE CONFERENCE PRESENTATIONS

- Yamamoto, W., Kono, T., Tong, X., and Evans-Molina, C. Stress Induced β cell-ER Calcium Depletion is Mediated Via Calcium Leak From the Ryanodine Receptor. *The Midwest Islet Club*, Indianapolis, IN. May 18, 2016
- Yamamoto, W., Kono, T., Tong, X., and Evans-Molina, C. ER Stress Induced Ryanodine Receptor Dysfunction in the Pancreatic Beta Cell. *The Advances & Breakthroughs in Calcium Signaling*, Honolulu, HI. April 8, 2016
- Yamamoto, W., Kono, T., Johnson, J., Tong, X., Day, R., and Evans-Molina, C. SERCA2b Overexpression Improves Beta Cell Survival Under Inflammatory and ER Stress Conditions. *The Midwest Islet Club*, Birmingham, AL. May 22, 2014

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